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Evolution of the northern Australian flora: role of the Sunda-Sahul Floristic Exchange

Thesis submitted by

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General abstract

The convergence of the Sunda continental shelf (Peninsular Malaysia and parts of Indonesia and the Philippines), the Sahul continental shelf (Australia and New Guinea) and Wallacea (Timor, parts of Indonesia and the Philippines) from c. 25 Mya was a significant event in global biogeography. The collision of the shelves facilitated exchange between the Sundanian and Sahulian floras that had evolved in isolation from each other in a phenomenon known as the 'Sunda–Sahul Floristic Exchange' (SSFE). The SSFE is considered to have had an important role in shaping the flora of the region, and has long been the subject of research, most notably by Alfred R. Wallace in the 19th century. However, critical gaps in knowledge about the SSFE patterns and processes remain. As such, in this body of research I employ floristic, phenetic, phylogeographic and cutting-edge phylogenomic methods across multiple lineages and scales to investigate various aspects of the effect and drivers of the SSFE.

In Chapter 1, I examine and synthesise the current state of knowledge on the SSFE and outline the key gaps in knowledge on the topic. A major finding was that a lack of a regional checklist of the flora has been a substantial obstacle to advancing our understanding of the SSFE. As such, in Chapter 2 I employ a floristic approach and systematic analytical pipeline to compile the first preliminary checklist of vascular plants for the Sunda-Sahul Convergence Zone ('SSCZ'; Sunda, Sahul and Wallacea). The list was compiled from 24 Flora volumes, online databases and unpublished plot data with updated taxonomic nomenclature, and regional biogeographic coding. I found that there are 60,415 species in 5,135 genera and 363 families of vascular plants in the SSCZ, confirming that the species richness of the SSCZ is comparable to that of the Neotropics. Moreover, the list provides a critical resource for understanding the phytogeography of the region and how it may have been impacted by the SSFE.

In Chapter 3, I conduct a phenetic, multivariate analysis using the checklist of SSCZ vascular plants generated in Chapter 2 to quantify the extent of floristic exchange, characterise phytogeographical patterns and investigate the abiotic drivers. I found that Lydekker's and Wallace's Lines are not reflected in floristic composition at any taxonomic level, and that environment (particularly annual rainfall and seasonality) is significantly correlated with floristic composition. Mainland Asia, Borneo, the Philippines, New Guinea and Australia were major sources of exchange throughout the Cenozoic, possibly because these areas have been persistent landmasses throughout the period of shelf convergence. I conclude that the SSFE has substantially influenced the assembly of the regional flora, with 46% of genera in the region shared across biogeographic lines, and that modern phytogeographical patterns have been influenced more by environmental variables and available landmass than by putative barriers to movement such as Wallace's and Lydekker's Lines.

Although Chapter 3 added to the growing body of evidence suggesting that the SSFE had a substantial impact on the composition of the SSCZ flora, the pathways of exchange between Australia and Southeast Asia remained poorly understood. To address this, in Chapter 4 I conduct a molecular phylogeographic case-study on the widespread tropical monsoonal tree species *Aglaia elaeagnoidea* (Meliaceae). I implemented DArTseq analysis of 141 herbarium and silica-dried samples sourced from across the range of *A. elaeagnoidea*. 176, 331 single nucleotide polymorphisms (SNPs) across 90, 456 loci were retrieved and analysed using multivariate, admixture, genetic differentiation and coalescent methods to characterise phylogeographic and phylogenetic patterns. An environmental niche model for the last glacial maximum was also generated. Two floristic exchange tracks were identified: one from New Guinea to Cape York Peninsula in north-east Australia, and a second from Timor to the Kimberley Plateau of north-west Australia. The Cape York Peninsula track is contemporary, characterised by ongoing genetic exchange, whereas the Kimberley Plateau track is historic, facilitated by multiple past exposures of the Arafura Shelf during the Pleistocene. Overall, I suggest that phylogeographic patterns of *A. elaeagnoidea* have resulted from a combination of repeated range expansion and contraction cycles concurrent with Quaternary climate fluctuations and stochastic dispersal events. This chapter provides the first phylogeographic evidence for two floristic exchange tracks between northern Australia and Southeast Asia. It also highlights the influence of Quaternary climate fluctuations on the complex biogeography of the region, and supports the idea that the Kimberley Plateau and Cape York Peninsula in northern Australia have separate biogeographic histories, in part due to independent SSFE tracks.

In Chapter 5, I investigate the effect of ancient evolutionary history on the dynamics of the SSFE throughout the Miocene with a cutting-edge phylogenetic approach. I used

Angiosperms353 target capture sequence data to generate the most densely sampled phylogenetic tree of the angiosperm order Sapindales to date, with 81% of the genera represented. The relationships of sapindalean families are robustly resolved for the first time: Nitrariaceae, Biebersteiniaceae and Sapindaceae form a basal grade, and the relationship between Meliaceae, Simaroubaceae and Rutaceae is shown to be incongruent with current understanding. Bayesian dating indicates that most sapindalean families arose in the Cretaceous. I then developed a methodological pipeline to integrate the target capture data with legacy Sanger data to produce a species-level phylogenetic tree of Anacardiaceae representing 90% of the generic and 47% of the species diversity. This tree broadly supports the subfamily classification of Anacardiaceae while indicating that the tribal classification is in need of review. Biogeographic analysis of the dated, species-level tree of Anacardiaceae supports a Sundanian origin for the family, confirms the eastward bias in exchange from Sunda to Sahul, and highlights the importance of the emergence of Wallacea in facilitating the exchange. Most interestingly, the results also indicate that extinction of lineages on Sahul coincident with Miocene aridification likely contributed to the observed eastward directionality bias in the SSFE. This study has shed new light on sapindalean evolution and the SSFE, and emphasises the importance of considering ancient evolutionary history when attempting to understand recent and current biogeographic processes such as the SSFE.

In Chapter 6, I synthesise the findings of this research and discuss it in the context of the wider literature.

This work emphasises the scale and importance of the collision Sunda and Sahul shelves in shaping the region’s flora and the dynamic, complex nature of the exchange through space and time. Overall, I find that the Sunda-Sahul collision contributed to the accumulation of diversity in the region, not only through the admixture of previously separated floras, but also through diversification stimulated by geological and climatic changes and reticulate migration patterns of plant lineages as they move between shelves. It is clear that the presence of suitable establishment conditions has played a major role in the spatio-temporal of the exchange, and on the interaction of plant functional traits and dispersal ecology on exchange dynamics. My phylogeographic study shows that movement across the SSCZ by plant lineages is likely to be reticulated rather than unidirectional due to the availability of suitable establishment conditions, and possibly encourages diversification in the region. It also highlighted the presence of multiple exchange tracks between Southeast Asia and Australia that are likely to have had a role in the independent evolutionary histories of the Kimberley, Top End and Cape York Peninsula regions of northern Australia. Finally, recent advancements in sequencing technology and computational power herald an exciting time for improving our understanding of the SSFE within a phylogenetic framework. The development of a bioinformatic pipeline for integrating target capture data with legacy Sanger data to produce phylogenetic estimates with unprecedented sampling density and resolution enables the investigation of questions previously unanswerable. In particular, this work has indicated that ancient extinction on Sahul is likely to be a major explainer of bias in the directionality of the SSFE. Finally, I highlight questions for future research.

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Publications produced during my candidature

Journal articles from this thesis

Chapter 2

Joyce EM, Thiele KR, Slik FJW, Crayn DM (2020) Checklist of the vascular flora of the Sunda-Sahul Convergence Zone. *Biodiversity Data Journal* **8**, e51094. doi:10.3897/BDJ.8.e51094.

Chapter 3

Joyce EM, Thiele KR, Slik JWF, Crayn DM (2021) Plants will cross the lines: climate and available land mass are the major determinants of phytogeographical patterns in the Sunda–Sahul Convergence Zone. *Biological Journal of the Linnean Society* 132, 374–387. doi:https://doi.org/10.1093/biolinnean/blaa194.

Chapter 4

Joyce EM, Pannell CM, Rossetto M, Yap J-YS, Thiele KR, Wilson PD, Crayn DM (2021) Molecular phylogeography reveals two geographically and temporally separated floristic exchange tracks between Southeast Asia and northern Australia. *Journal of Biogeography*. doi:https://doi.org/10.1111/jbi.14072.

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Nauheimer L, Weigner N, **Joyce EM**, Crayn DM, Clarke C, Nargar K (In press) HybPhaser: a workflow for the detection and phasing of hybrids in target capture datasets. *Applications in Plant Sciences*.

McLay TG, Birch JL, Gunn BF, Ning W, Tate JA, Nauheimer L, **Joyce EM**, Simpson L, Weigner N, Schmidt-Lebuhn AN (In press) New targets acquired: improving locus recovery from the Angiosperms353 probe set. *Applications in Plant Sciences*.

Kooyman RM, Morley RJ, Crayn DM, **Joyce EM**, Rossetto M, Slik JWF, Strijk JS, Su T, Yap J-YS, Wilf P (2019) Origins and Assembly of Malesian Rainforests. *Annual Review of Ecology, Evolution, and Systematics* 50, 119–143. doi:https://doi.org/10.1146/annurev-ecolsys-110218-024737.

Mitchell JD, Pell SK, Bachelier J, **Joyce EM**, Canadel LC, da Silva CL, Warschefsky E, (In prep.) A treatment of Neotropical Anacardiaceae. *Brazilian Journal of Botany*.

Conference presentations and invited seminars

Joyce, EM (2021) Untangling the effects of the Sunda-Sahul Floristic Exchange on the evolution of the Southeast Asian and northern Australian flora. *Royal Botanic Gardens Sydney Science Seminar Series*, Sydney, Australia.

Joyce, EM (2020) The Sunda-Sahul floristic exchange through time and space: new insights into a classical biogeographic hotspot. *University of Leipzig Department of Molecular Evolution and Plant Systematics Seminar Series*, Leipzig, Germany.

Joyce, EM (2020) Two floristic exchange tracks between Asia and northern Australia: Insights from molecular phylogeography of *Aglaia elaeagnoidea*. *James Cook University College of Science and Engineering Postgraduate Seminar,* Cairns, Australia.

Joyce, EM & Crayn, DM (2020) The Sunda-Sahul floristic exchange through time and space. *International Biogeography Society International Humboldt Day*, Online.

Joyce, EM (2020) Solastalgia, writing and the origins of the northern Australian flora. *Museum of Art, Architecture and Technology*, Lisbon, Portugal.

Joyce, EM, Thiele, KR & Crayn, DM (2019) The lines don't matter for plants! Insights into the Sunda-Sahul Floristic Exchange from floristic patterns. *James Cook University College of Science and Engineering Postgraduate Seminar,* Cairns, Australia.

Joyce, EM, Thiele, KR & Crayn, DM (2019) Exchange insights from floristic composition across the Sunda-Sahul Convergence Zone. *Australian National University Centre for Biodiversity Analysis Crossing Lines Synthesis Group Meeting,* Canberra, Australia.

Joyce, EM & Crayn, DM (2018) New Guinea as a major generator of Malesian and Australasian plant diversity: evidence from multi-lineage analysis of diversification through time. *Association for Tropical Biology and Conservation Conference,* Kuching, Malaysia. **Winner: Alwyn Gentry Prize for best student presentation.**

Joyce, EM, Nauheimer, L, Nargar, K, Thiele, KR, Holtum, J & Crayn, DM (2018) Evolution of *Geosiris* (Iridaceae): historical biogeography and plastid-genome evolution in a genus of non-photosynthetic tropical rainforest herbs disjunct across the Indian Ocean. *James Cook University College of Science and Engineering Postgraduate Seminar,* Cairns, Australia.

Joyce, EM, & Crayn, DM (2018) A SAD model for an uplifting story: how the Sunda-Sahul collision boosted the megadiversity of the Malesian flora. *Centre for Tropical Environmental and Sustainability Science Annual Conference*, Cairns, Australia. **Winner: best student presentation award.**

Joyce, EM, Nauheimer, L., Nargar, K., Thiele, KR, Holtum, J. & Crayn, DM (2018) Evolution of *Geosiris* (Iridaceae): historical biogeography and plastid-genome evolution in a genus of non-photosynthetic tropical rainforest herbs disjunct across the Indian Ocean. *Australasian Systematic Botany Society Conference,* Brisbane, Australia.

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Joyce, EM & Crayn, DM (2017) Origins of the northern Australian flora: Role of the Sunda-Sahul floristic exchange, *Centre for Tropical Environmental Sustainability Science Conference*, Cairns, Australia. **Winner: best student presentation award.**

Joyce, EM, Nauheimer, L, Schulte, K, Thiele, KR, Holtum, J & Crayn, DM (2017) Origins of the northern Australian flora: Role of the Sunda-Sahul floristic exchange, *Southeast Asian Gateway Evolution Meeting*, 28-31 August 2017, Bogor, Indonesia.

Chapter 1

General introduction

The convergence of the Sunda continental shelf (Peninsular Malaysia and parts of Indonesia and the Philippines; Figure 1.1) and the Sahul continental shelf (Australia and New Guinea; Figure 1.1) from c. 25 Mya was a significant event in global biogeography. The collision of the shelves caused widespread geological change in the region, including the trapping of Wallacea between the shelves, orogenesis in Wallacea and New Guinea, and the torsion of Sunda (Zahirovic *et al.* 2016; Hall 2017; Figures 1.1 & 1.2). The convergence also facilitated exchange between the Sundanian and Sahulian floras that had evolved in isolation from each other. This floristic exchange has fascinated scientists since Alfred R. Wallace (1860, 1869), whose observations of disjunct Sundanian and Sahulian biota in the region gave rise to the field of biogeography itself.

Due to the longstanding biogeographic interest in the region, a plethora of terms for the areas within the region and the floristic exchange have accumulated. Parts of the region of focus have been variously referred to as the 'Indo-Australian archipelago' (Lohman *et al.* 2011), the 'Southeast Asian-Australian region' (Metcalfe 2001; Morley 2002), the 'Malay archipelago' (Wallace 1860; Hall 2017), 'Malesia' (Steenis 1979; Brummitt *et al.* 2001; Van Welzen *et al.* 2005), 'Papuasia' (Brummitt *et al.* 2001) and 'Australasia' (Heads 2014). However, these areas were demarcated based on floristic or political boundaries, and do not encompass all of the Sunda shelf, Sahul shelf and Wallacea. To adequately describe the geology of the area of focus, I herein introduce the term 'The Sunda-Sahul Convergence Zone'. This zone comprises the entire Sahul shelf (Australia and New Guinea), Wallacea (the Moluccas, Sulawesi, the Philippines and the Lesser Sunda Islands), and the Sunda shelf (Borneo, Sumatra, Java, and mainland Asia to Myanmar) (Figure 1.1). Similarly, two names have been used in the literature to describe the floristic exchange: the 'Malesian Floristic Interchange' (Richardson *et al*. 2012) and the 'Sunda-Sahul Floristic Exchange' (Crayn *et al*. 2015). Here I here adopt the term 'Sunda-Sahul Floristic Exchange' (Crayn *et al*. 2015), as it most accurately describes the exchange of flora upon the convergence of the two continental shelves.

Despite the long history of research on the topic, much remains to be understood about the effects and drivers of the Sunda-Sahul Floristic Exchange (SSFE). Investigating these is critical for understanding why the flora of the Sunda-Sahul Convergence Zone (SSCZ) is the way it is today, and can provide insight into how to conserve it into the future. In this chapter, I summarise current understanding of the SSFE and highlight key gaps in knowledge that I address in the chapters that follow.

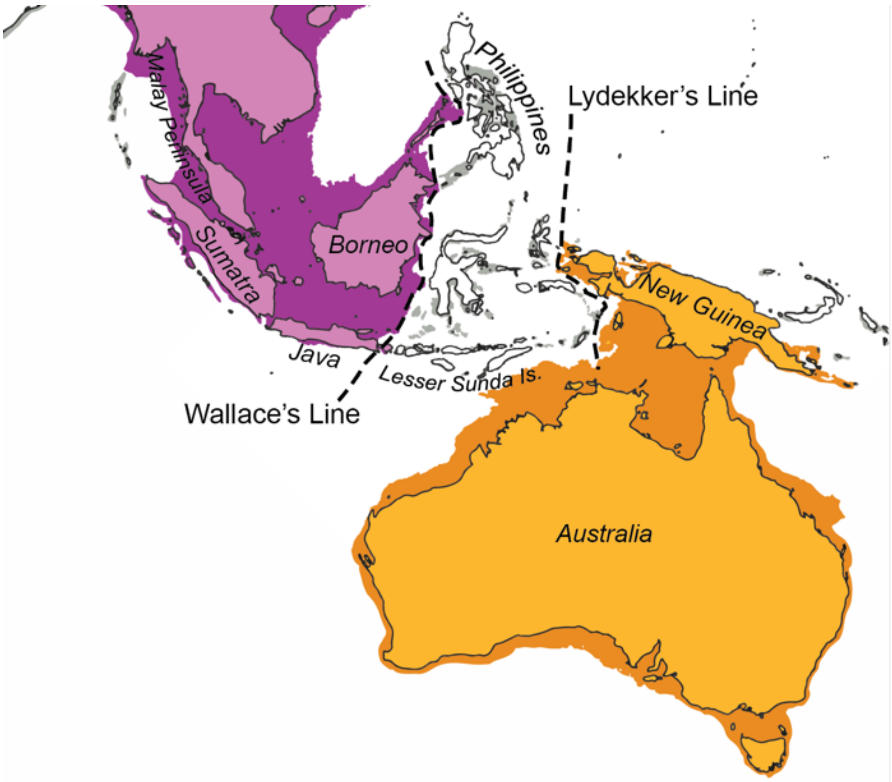

Figure 1.1 Map of the Sunda-Sahul Convergence Zone (SSCZ) showing the Sunda shelf (pink), Sahul shelf (orange), and Wallacean islands between (white). Wallace's Line and Lydekker's Line follow the edges of the Sunda and Sahul continental shelves respectively, and bound Wallacea. Wallace's Line as shown is the modified version from Merrill (1924) and Dickerson *et al*. (1928), also referred to as the 'Merrill-Dickerson Line' or 'Huxley's Line' (Ali and Heaney 2021). The Sunda and Sahul shelves are bounded by the 135 m below sea level contour.

Geological and climatic history of the Sunda-Sahul Convergence Zone

The SSCZ has an extremely complex geological and climatic history, much of which remains to be understood. In the early Cenozoic (c. 66–45 Mya), the Sunda shelf was a continental promontory at the southern end of Eurasia, just crossing the equator (Hall 2012). At that time, the Sahul shelf was connected to Antarctica at around latitude 30° south, only rifting from Antarctica and starting its northwards drift c. 45 Mya (Zahirovic *et al.* 2016; Figure 1.2a, b). This northward drift into warmer latitudes counteracted the influence of a cooling global climate, and Sahul avoided the widespread glaciation that occurred elsewhere in the world (Metcalfe 2002; Byrne *et al.* 2008). The rifting of Sahul from Antarctica also led to the establishment of the Antarctic circumpolar current, and this initiated the aridification of Sahul (Byrne *et al.* 2008; Christensen *et al.* 2017). Thus, the climate of Sahul during its northward drift was characterised by aridification interspersed by warm-wet periods (Greenwood and Christophel 2005). Meanwhile, the Sunda shelf maintained a warm and moist climate that was relatively stable even through the terminal Eocene cooling event, and may have acted as a global refugium for biota from higher latitudes (Lohman *et al.* 2011; Buerki *et al.* 2013).

From approximately 25 Mya, the northern-most promontory of the Sahul shelf – the Sula Spur – began collisional accretion with island arcs to the north (Hill and Hall 2003; Baldwin *et al.* 2012; Figure 1.2d). This collision trapped a complex conglomerate of continental fragments and arcs of various origins in the area between the two shelves, an area now referred to as Wallacea (Hall 2012a). The collision also resulted in rapid orogenesis in New Guinea, and by the middle Miocene (15 Mya) (Figure 1.2f ; see Cloos *et al.* 2005; Baldwin *et al.* 2012) isolated islands had emerged to the north of Australia ('the proto-Papuan Archipelago' of Jonsson *et al.* 2011). By c. 12 Mya a 500 km long fold-and-thrust belt had formed in western New Guinea (Cloos *et al.* 2005), with uplift of its eastern section starting c. 10 Mya (Abers and McCaffrey 1988; Hill and Hall 2003; Figure 1.2g). Papua New Guinea is now the largest and highest island in Malesia, with the Central Ranges extending for 1300 km along its spine and reaching a maximum elevation of 4,884 m (Dewey and Bird 1970). Significant orogenesis also occurred in the Wallacean islands of Maluku and Nusa Tengarra, both rising to 3000 m after 3 Mya (Hall 2009), while Sulawesi reached over 3000 m in the mid-Pliocene (Nugraha and Hall 2018). The collision with Sahul also resulted in the torsion of the Sunda shelf, with evidence of counter-clockwise rotation of Borneo between 25-10 Mya (Hall 1996; Fuller *et al.* 1999).

At the commencement of the convergence of the Sunda and Sahul shelves in the Early

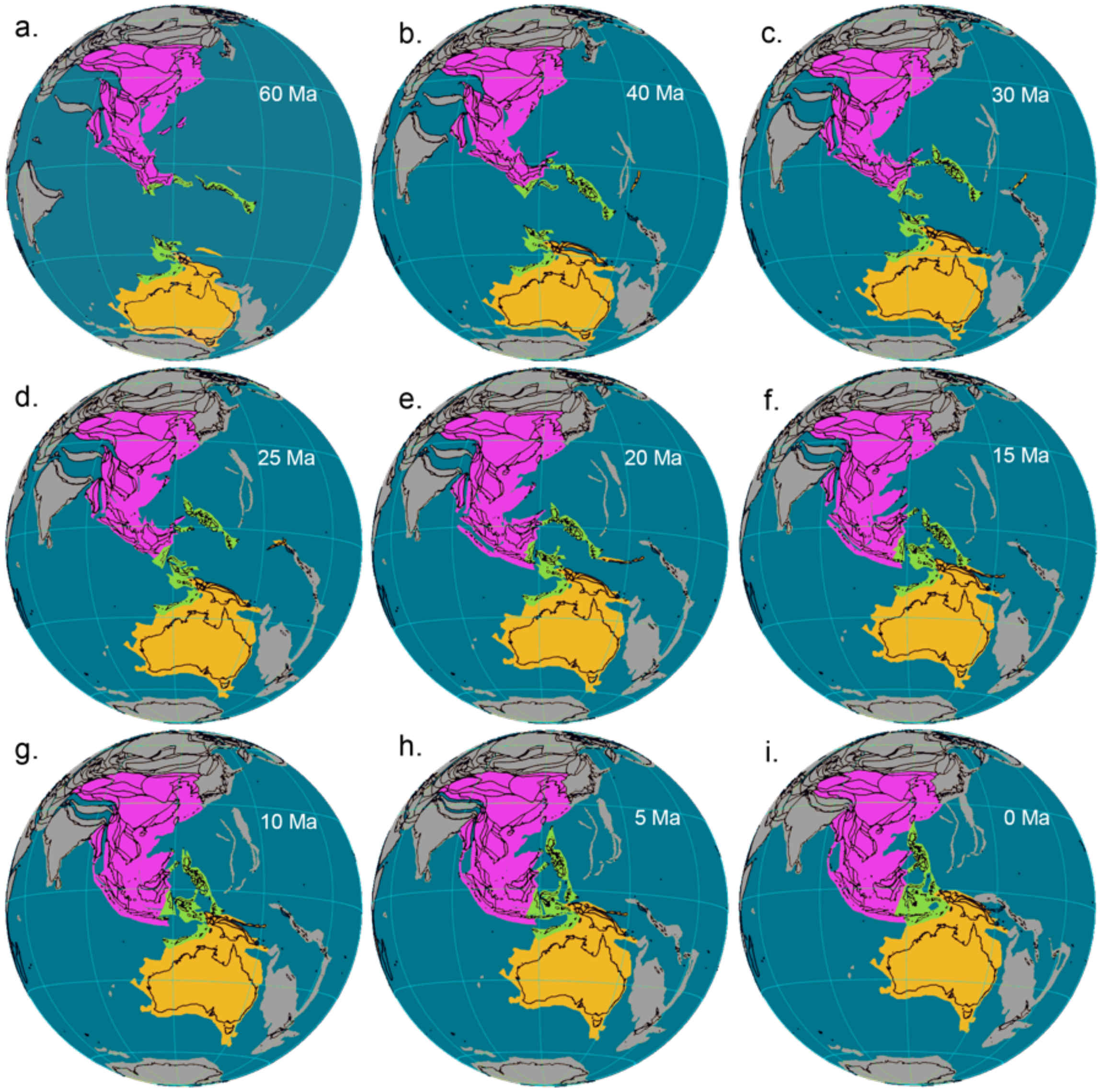

Figure 1.2 Inferred tectonic movements of the Sunda and Sahul shelves through the Cenozoic, following the geological model of (Zahirovic *et al.* 2016). The plates that make up the Sunda shelf are shaded pink, plates that form the Sahul shelf are orange, and plates forming modern-day Wallacea are shaded green. Plates outside of the SSCZ are shaded grey. Black lines indicate modern coastline on each plate.

Miocene, temperatures increased on the Sunda shelf to a level that was maintained throughout most of the Miocene and Early Pliocene (Lohman *et al.* 2011). Most of the Sunda shelf is thought to be subaerial until 400 kya, when areas between Borneo, Java, Sumatra and the Malay Peninsula were inundated during interglacial sea level high stands (Husson *et al.* 2020). In Sahul, aridification intensified in the mid-Miocene (Byrne *et al.* 2008). Global cooling during the Late Pliocene and Quaternary resulted in a drier, more seasonal climate throughout the Sunda shelf and Wallacea (Morley 2002), while Sahul experienced relatively warm and wet conditions, followed by major climatic oscillations from the Pleistocene (Byrne *et al.* 2008).

Effect of the Sunda-Sahul Floristic Exchange on contemporary phytogeography

Wallace's Line and other biogeographic lines

The convergence of the Sunda and Sahul shelves and resultant biotic exchange provided a natural evolutionary experiment that scientists have investigated for over 150 years. In 1845, the German naturalist Salomon Müller was the first to comment on an abrupt change in the biota in the SSCZ across the arid corridor between Mindanao and the Lesser Sunda Islands (Müller 1846). Most famously, Alfred R.Wallace spent over nine years in Southeast Asia and, like Müller, observed an abrupt disjunction in the avian and mammalian faunas across the Makassar Strait (Wallace 1860). Wallace's work was remarkable in that he was able to infer underlying processes from observed patterns; Wallace interpreted the biotic disjunction in the context of geology, deducing that the faunas on either side of the Makassar Strait had separate origins ('Oriental' and 'Australian') and were unable to disperse across the strait (Darwin 1859; Wallace 1878). This revelationary insight contributed to the birth of the field of biogeography, and the Makassar Strait disjunction became part of the most famous biogeographic boundary in the world – the eponymous Wallace's Line (Wallace 1860; Wallace and Costa 2013; but see Ali and Heaney 2021 for a review of past and current circumscriptions of Wallace's Line). Moreover, Wallace's work in Southeast Asia and Wallacea contributed to the development and publication of the theory of natural selection (Darwin and Wallace 1858; Darwin 1859), giving insight not only into the assembly of the SSCZ biota but all life on Earth.

Wallace suggested that the line that now bears his name may not represent a biogeographic barrier for all groups of life, observing that patterns of diversity were harder to decipher for insects and plants and hypothesising that this may be due to differences in generation time and dispersal abilities (Wallace 1878). Later biogeographic studies proposed many alternative zoogeographical lines, mostly reflecting distributional limits in lineages of interest to the author, such as gallinaceous birds [Huxley's Line (Huxley *et al.* 1868)], mammals [Lydekker's Line (Lydekker 1896); Murray's Line (Murray 1866); Sclater's Line (Sclater and Sclater 1899)], and freshwater fish [Weber's Line (Pelseneer 1904; Pieter and de Visser 1993)]. The plethora of regions and lines across the SSCZ have been reviewed in detail by Simpson (1977), and more recently by Ali and Heaney (2021).

A Wallace's Line for plants?

The phytogeography of the region was first considered in detail by Elmer D. Merrill, who observed the abrupt distributional limit of dipterocarp-dominated forests at Wallace's Line (Merrill 1923). Merrill suggested that there was a degree of congruence between floristic and faunal distributional patterns; however, no single line could adequately delimit phytogeographic boundaries in the region. Instead, Merrill suggested that the area between Wallace's Line and Weber's Line represented a zone where Sundanian and Sahulian floras 'mingle'; he went on to suggest that this pattern was caused by the geological 'instability' of Wallacean islands acting as a barrier to plant dispersal (Merrill 1923, 1924). Merrill modified the northern limits of Wallace's Line to run along the west of the Philippines (now often known as the Merrill-Dickerson Line; although Ali and Heaney (2021) note it is also identical to Huxley's Line), and it was suggested that it represented the western-most distributional limit of Australian biota, while Weber's Line represented the eastern-most distributional limit of Asian biota. Merrill was the first to dub the area between these lines as 'Wallacea', and it was regarded as a biogeographic transition zone, 'botanically and zoologically… fundamentally Asian, with Papuan and Australian overtones' (Merrill 1924; Dickerson *et al.* 1928).

Subsequent researchers disputed the recognition of Wallacea as a transition zone and argued that Wallace's Line represented an abrupt phytogeographic barrier for plants as well as animals. From his analysis of plant generic distributions, van Steenis determined that the major biogeographic barrier in the region occurred across the Torres Strait, separating 'Malaysia' (Peninsular Malaysia, Indonesia, Philippines, and New Guinea) from Australia (van Steenis 1950). Van Steenis further divided Malaysia into the biogeographic provinces 'West Malaysia', 'East Malaysia' and 'South Malaysia'; West and East Malaysia were separated by the original Wallace's Line, and South Malaysia comprised Java, the lesser Sunda Islands and Timor. He suggested that 'the Australian [and] Pacific floras play, measured by figures, a very unimportant role in the general picture [of the] …Asiatic-Malaysian flora'. This biogeographic regionalisation was later supported by a phenetic study of the Pacific flora (van Balgooy 1971). Like van Steenis, van Balgooy recognised biogeographic units delineated by the Torres Strait which he referred to as “Malesia”; however, van Balgooy recognised only two subregions within his Malesian region – ‘West Malesia’ and ‘East Malesia’. These subregions were separated by Wallace’s Line, incorporating van Steenis’ ‘South Malaysia’ province into West Malesia. These studies not only suggested that Wallace’s Line held for plants, but that the Australian flora was completely distinct from the Asian flora.

More recent phenetic analyses of floristic composition have restored support for the idea of recognising Wallacea as a transitional phytogeographic zone (van Welzen *et al.* 2005, 2011; van Welzen and Slik 2009). These studies indicate that the Sunda Shelf (minus Java) and the Sahul Shelf (as delimited by the Merrill-Dickerson Line and Lydekker’s Line) are floristically distinct, and that Wallacea (including Java) is intermediate in its floristic composition. Although Wallacea showed the lowest degree of endemism and coherence, 35% of the flora was still found to be endemic, suggesting that Wallacea may in fact warrant recognition as a distinct phytogeographic zone.

More than 150 years of biogeographical study has not led to a consensus on the definition and importance of phytogeographical lines or regions in the SSCZ (Ali and Heaney 2021); however, identifying phytogeographical patterns in detail is critical to understanding the dynamics of SSFE that might have contributed to them.

A major obstruction to characterising the phytogeography of the region is the lack of a census of the flora of the SSCZ. The availability of open access biodiversity data repositories such as the Global Biodiversity Information Facility and the Atlas of Living Australia now facilitates the compilation of a list of the flora of the SSCZ and analysis of phytogeographic patterns at a floristic scale. In concert with publicly available environmental and climate databases, these online resources also provide new opportunities to explore the relationship between environment and phytogeography. For the first time, it is possible to assess the relative importance of biogeographical lines such as Wallace’s Line and environment as determinants of SSFE and phytogeographic patterns.

The contribution of the SSFE to the northern Australian flora

The extent of the impact of the SSFE on Australia's northern flora has been debated since European colonisation of Australia. The proportion of Australia's flora that is shared with Asia has not yet been rigorously quantified; all estimates to date have been based on a subset of taxa, and the origins of lineages were assigned to the area of greatest species richness for that lineage. Joseph Hooker was the first to consider the affinities of the Australian flora, suggesting that while the Australian flora was predominantly ancient and autochthonous, it also included lineages from Indo-Malaysia, New Zealand, Pacific Islands, Antarctica, Europe and South Africa (Hooker 1859). He proposed that while the perhumid tropical 'Malayan Flora' did not make a significant contribution to the northern Australian flora, the more seasonal tropical flora "of the plains and lower hills of India" did, being distributed from India throughout Malesia and then continuing "with great force over the whole of tropical Australia". The view that Sundanian taxa are an important component of the tropical Australian flora was promulgated in subsequent studies of Australian phytogeography by Burbidge (1960) and Specht (1981).

The idea that flora of Sundanian origin comprised a substantial component of the tropical Australian flora was questioned following the advance of tectonic theory and vicariance biogeography in the late 20th century (Croizat *et al.* 1974; Wiley 1980). Vicariance became the major explanation for phytogeography, and the influence of long-distance dispersal between Australia and Asia was considered to be negligible. It was argued that many Australian rainforest fruits were too large, and their seed viability too short, for long-distance dispersal to be a tenable factor in their distributions (Webb *et al.* 1984). It was also contended that fossil evidence indicated rainforest lineages were present in Australia prior to the collision of the Sunda and Sahul shelves (Werren and Sluiter 1991). The idea that northern Australia experienced a substantial influx of flora from Asia was therefore rejected, and Australian rainforests were considered to be predominantly Gondwanan in origin. The antiquity of the Australian Wet Tropics flora, rather than its recent arrival from Asia, was a core value contributing to its recognition on the UNESCO World Heritage List in 1988 (Frawley 1991).

The past 50 years has seen the establishment of a more nuanced view on the origins of the tropical Australian flora (e.g. Thorne 1986; Barlow and Hyland 1988). It is now clear that the tropical Australian flora comprises a combination of autochthonous Gondwanan lineages and Asian immigrants, but their relative contributions remain uncertain. Phylogenetic and paleobotanical studies across multiple lineages have shown unequivocally that many tropical Australian plants have their origins in Asia (e.g. Sniderman and Jordan 2011; Grudinski *et al.* 2014; Murphy *et al.* 2020; see section 'Temporal and directional patterns in the SSFE' later this chapter for further discussion). However, the question remains as to what extent the SSFE has influenced the composition of Australia's flora as a whole. Without a checklist of flora of the whole SSCZ region, it remains impossible to determine how much of Australia's flora is shared with Asia, or the origins of those lineages. Generation of a comprehensive account of the flora of the entire SSCZ region, and further phylogenetic and paleobotanical studies, are needed to empirically ascertain the influence of the SSFE on the Australian flora.

Exchange tracks between northern Australia and Asia

Central to understanding the influence of the SSFE on the northern Australian flora is the question of where the exchange tracks between Australia and Southeast Asia (the Sunda shelf, Wallacea and New Guinea) lay. It is generally assumed that the major floristic exchange track between Australia and Southeast Asia is between New Guinea and Cape York Peninsula. In part, this is because Australia and most of New Guinea are both part of the Sahul shelf, and the seaway between New Guinea and Cape York – the Torres Strait – represents the smallest gap between the two regions (c. 150 km, with many intervening islands) that repeatedly formed a land bridge during Pleistocene glacial maxima. This track, with New Guinea linking the east coast of Ausralia to Wallacea and Sunda, is thought to have been particularly important for the exchange of tropical montane and rainforest lineages (van Steenis 1934; Burbidge 1960; Specht 1981; Sniderman and Jordan 2011).

However, anecdotally, many species native to Southeast Asian islands (on the Sahul shelf [New Guinea], Sunda shelf and Wallacea) are also found in the Australian monsoon regions of the Northern Territory and the Kimberley in north-westen Australia (R. Barrett pers. comm.; B. Maslin pers. comm.). The tracks of exchange between these monsoonal regions and Southeast Asia remain unclear: Do they exchange tropical lineages with Sahulian tropical regions (such as the Australian Wet Tropics, Cape York Peninsula and New Guinea), or do they have independent exchange tracks with Southeast Asian islands in

Wallacea and Sunda? Phytogeographic studies of Australia indicate that the Australian Wet Tropics is floristically more similar to the east and south coast of Australia rather than to the northern monsoon tropical regions of Cape York Peninsula, the Northern Territory, and the Kimberley (Crisp *et al.* 1995; González-Orozco *et al.* 2014). In support of this, Edwards *et al.* (2017) identified 13 phytogeographic barriers across northern Australia and established that while most barriers are impermeable, the two in the Australian Wet tropics are permeable to biotic interchange with regions along the east coast. More recently, this has been supported by genetic data across multiple lineages, which indicates that Sundanian species have migrated rapidly down the east coast of Australia in expansion/contraction cycles throughout the Quaternary (Yap *et al.* 2020). These lines of evidence indicate that plant lineages exchanged between Cape York Peninsula and Southeast Asia moved southwards down the east coast of Australia, but that east-west dispersal of tropical lineages across northern Australia and into the monsoon tropics is limited.

Direct evidence for how Southeast Asian taxa entered the Australian monsoon tropical regions of Arnhem Land and the Kimberley remains scant. Van Steenis (1979) was the first to suggest that monsoonal plants in Arnhem Land and the Kimberley Plateau may have independent exchange tracks with Asia rather than via Cape York Peninsula. The presence of these alternative monsoon exchange tracks between Arnhem Land and New Guinea and the Kimberley Plateau and New Guinea has only been formally investigated since by Crisp *et al.* (1995), in a cladistic biogeographic analysis of 11 plant clades. This study found support for an exchange track between Arnhem Land and New Guinea. However, the presence of exchange tracks between Asia and the Kimberley Plateau or Arnhem Land are yet to be tested with genetic data.

Modern genetic methods offer opportunities to explore how exchange tracks into Australia relate to phylogeographic patterns across Southeast Asia. Little is known about phylogeographic patterns in Southeast Asia, with the few studies conducted mostly focusing on fauna and covering a restricted geographic range (Cannon 2001; Liao *et al.* 2007; Ueda *et al.* 2010; Tnah *et al.* 2012; Pedersen *et al.* 2018; Jusoh *et al.* 2019; Grismer *et al.* 2019; Husson *et al.* 2020; Lim *et al.* 2020). In Australia, phylogeographic studies of rainforest plants have revealed varied expansion-contraction responses to the climatic fluctuations of the Quaternary (Rossetto *et al.* 2004; Mellick *et al.* 2012, 2013; Fahey *et al.* 2019). Elucidation of Southeast Asian phylogeographic patterns and identification of exchange tracks with northern Australia is critical for understanding past evolutionary processes and present biogeographic patterns, knowledge which is in turn necessary for effective conservation of the region's biota.

Temporal and directional patterns in the SSFE

Before key drivers of the SSFE can be identified, a sound understanding of the timing and directionality of floristic exchange throughout the Cenozoic is required. Hooker (1859) was the first to suggest that there was a bias in the exchange of taxa between tropical Asia and Australia, suggesting that while what he referred to as 'Indian' lineages were common in Australia, very few 'Australian' lineages were present in India (Hooker 1859). Building on this idea, subsequent researchers took a species-counting approach to determine the directionality of the SSFE. In such studies, subsets of species for regions across the SSCZ are listed and the origin of each genus is assigned to its centre of diversity ('Age-Area Theory'; Willis 1922), thus giving an estimate of SSFE directionality (i.e. any Sahulian species without congeners endemic to Sahul but with congeners in Sunda is considered to be an immigrant from Sunda, and vice versa). Kalkman (1955) was the first to use this approach, and found that the number of Sundanian taxa gradually decreased in an eastwards direction. However, he noted the disproportionate representation of putatively Sundanian taxa in the Lesser Sunda Islands, considering their proximity to Australia, and suggested that there was 'no substantial admixture' of Sahulian flora in the Lesser Sunda Islands and an eastward bias in exchange (Kalkman 1955, p. 206). Similarly, Richardson *et al.* (2012) reported that while the number of Sundanian species decreased in an eastward direction, a relatively high proportion of Sundanian species were present in the Australian wet tropical rainforests (47.2%) compared to the proportion of Sahulian species in Sundanian Kalimantan (1.8%). The flora of New Guinea was also estimated to comprise predominantly Sundanian taxa despite its proximity and recent land connections to Australia, with an estimated 63.2-64.9% of species determined to have a Sundanian origin. From this they also inferred a strong eastward bias in the SSFE.

Although these species-counting studies may give a general indication of SSFE directionality, they are problematic for two main reasons. Firstly, without a comprehensive species checklist, these studies rely on subsets of taxa that may not be representative of the flora as a whole, and assessment of endemism and diversity will be inaccurate. Secondly, Age-Area Theory has now been largely discredited as a reliable method for determining the area of origin for a lineage, and is especially dubious in the SSCZ (Webb *et al.* 1984), with the complex geological history of the region likely to lead to unique patterns of diversification and endemism that do not satisfy the assumptions of the Age-Area Theory. Biota on continental island systems with a history of intermittent dry land connections can have low diversification rates relative to discrete island systems, often leading to high species richness and endemism in archipelagos (Heaney 2007). Islands in Wallacea may thus have a higher species richness than expected relative to Sunda and Sahul, even though lineages may not have originated there. Additionally, there is evidence of Gondwanan lineages immigrating to Sunda from India in the Paleogene, prior to the Sunda-Sahul floristic exchange (Morley 2002; Kooyman *et al.* 2019), and from Gondwanan fragments (now modern-day Myanmar) in the Middle Eocene (Hall 2012b; Poinar and Chambers 2017). This means that lineages may have multiple source areas depending on scale of time. Other methods are therefore necessary to gain a more accurate and nuanced understanding of SSFE directionality dynamics.

Paleobotanical evidence has shed light on the directionality of the SSFE, and suggests that exchange directionality may have changed through time and space. Palynological studies have confirmed that the early Tertiary floras of Sunda and Sahul were markedly different prior to collision (Greenwood and Christophel 2005; Morley 2002). The Early Eocene pollen record shows that West Papua was characterised by assemblages of Australian lineages, including Casuarinaceae, Proteaceae, Myrtaceae, *Dissiliaria* (or *Austrobuxus*), *Nothofagus* and *Nypa* (Morley 2002). Palms were a relatively late arrival to Australia, only comprising a significant component of the Australian rainforest palynological record from the Early Paleocene, despite being well-represented in the fossil floras in other parts of the world before then (Greenwood and Christophel 2005). Morley (2002) documented other floristic exchange events from the Early Miocene as signified by the sudden appearance of pollen of the Australasian taxa *Phormium* (Phormiaceae), *Casuarina* (Casuarinaceae) and *Dacrydium* (Podocarpaceae) in the palynological record of Java at 21 Mya, Myrtaceae at 17 Mya, *Camptostemon* (Bombacaceae) at 14 Mya, the fern *Stenochlaena milnei* (Blechnaceae) at 9 Mya, and *Dacrycarpus imbricatus* in Indochina and *Phyllocladus* (Podocarpaceae) in Borneo at 3.5 Mya. Morley (2002) concluded that all dispersal events observed in the palynological record occurred in a westward direction, in contrast to the overall eastward bias in directionality reported by species-counting studies. However, in a study of the macrofossil record of Australia, Sniderman and Jordan (2011) reported a nine-fold eastward bias in exchange, suggesting that the majority of immigration of Sundanian flora occurred during the late Neogene and Quaternary. Although providing invaluable insight into the historical changes in the Australian flora, the palynological and macrofossil records of northern Australia and southeast Asia west of Wallacea are depauperate. Reliable data are scanty and fossil sites are biased in their distribution, limiting the number of comparable sites with which to infer patterns of floristic exchange.

More recently, advances in molecular phylogenetic analysis methods and the accumulation of relevant data have enabled empirical determination of lineage origin, as well as estimation of the timing of biogeographic exchange events across the SSCZ (e.g. Su and Saunders 2009; Thomas *et al.* 2012; Bacon *et al.* 2012; Grudinski *et al.* 2014). An understanding of broader patterns of exchange can be gained by comparing the timing and direction of exchange events estimated from phylogenies of multiple lineages. De Bruyn *et al.* (2014) were the first to undertake a comparative phylogenetic analysis of the biota of the SSCZ, including six plant clades distributed across Southeast Asia in addition to clades of vertebrate and invertebrate fauna. The authors compared the ages of nodes in each clade that represented a biogeographic transition between Sunda and Sahul, and found a bias in the directionality of floristic exchange across Wallacea, with eastward dispersal outweighing westward dispersal by a factor of 1.5. Crayn *et al.* (2015) conducted a larger comparative phylogenetic study of 21 published dated molecular phylogenies across 49 plant clades. As in previous studies (including De Bruyn *et al*. (2014), all species-counting studies and most paleobotanical studies), Crayn *et al*. (2015) reported an eastward bias in exchange, in this case by a factor of 2.4. They also characterised the temporal dynamics of the SSFE, finding that the earliest phylogenetic evidence of an exchange event occurred 33 Mya. Exchange events in any direction occurred at a rate of 0.41 Myr^{-1} until 12 Mya, after which the rate increased substantially to 3.33 Myr^{-1}.

The meta-analysis undertaken by Crayn *et al*. (2015) provides the most comprehensive overview of the temporal and directional patterns in the SSFE to date; however, the conclusions of this study could be confounded by methodological limitations. The studies included in the meta-analysis differed in their choice of approaches to phylogenetic analysis, molecular clock dating and ancestral area analysis. This methodological inconsistency makes deriving general patterns of exchange and underlying explanations problematic, as differences in the ages of biogeographic transitions across studies are difficult to the interpret. Furthermore, dating methods used in some studies, such as Penalised Likelihood, rely on rate smoothing to model rate variation across the tree. Such models can be inappropriate in old lineages or lineages with many missing or extinct taxa, and hence the ages of nodes estimated with these methods may be inaccurate (Linder *et al*. 2005). This combination of methodological limitations may have resulted in inaccurate assignment of origin to lineages, affecting the interpretation of the directionality of the biogeographic transition. Additionally, 47% of clades included in Crayn *et al*. (2015) were in phylogenies that sampled <50% of species for their respective genera. Low sampling densities can dramatically influence the topology and estimates of node ages on trees (Linder *et al.* 2005). Further comparative phylogenetic work using a consistent methodological pipeline and increased sampling is needed to clarify temporal patterns in the SSFE. The advance of large-scale, phylogenomic analysis provides an excellent opportunity for investigating spatio-temporal dynamics of exchange between Sunda and Sahul in a rigorous, consistent phylogenetic framework.

Drivers of SSFE patterns

Biome conservatism and connectivity

Historically, biologists have intuitively categorised the SSCZ flora into biomes, noting differences in composition and dynamics of montane, savannah and lowland rainforest floras. Van Steenis (1934) split the flora of the SSCZ into three major biomes and suggested that each had its own exchange track. Firstly, he suggested that the montane flora followed three sub-tracks through Wallacea: the Papuan track through Australia, New Guinea and Borneo; the Sumatran track through Sumatra and the Lesser Sunda Islands; and the Luzon track through east Asia, the Philippines and Sulawesi (intersecting the Papuan track). Secondly, he suggested that wet tropical rainforest lineages were exchanged through Borneo, New Guinea and Cape York Peninsula. Finally, he posited that dry-adapted savannah taxa were exchanged through the Lesser Sunda Islands. These exchange tracks have been sparingly discussed in the literature, and studies of floristic composition generally provide support for them (e.g. Gupta 1972; Raven 1973; Smith 1982; Laumonier 1997; Brandon-Jones 2001; Richardson *et al.* 2012). In a more recent empirical study, Brambach *et al*. (2020) found that throughout the SSCZ there are more Australian tree species and individuals, relative to those of Asian origin, at higher elevations and in areas on ultramafic soils and in areas closer to Australia (i.e. in environments more similar to Australia). This led the authors to suggest that lineages retain their biome of origin – that is, are conservative – when transitioning between Sunda and Sahul. As phylogenetic niche conservatism is likely to be a strong constraint on spatio-temporal dynamics in the SSFE, it is reasonable to infer that the dynamics of the SSFE may differ between biomes and that changes in connectivity of biomes resulting from climatic and sea level changes may have influenced spatio-temporal patterns in the SSFE.

The idea that flora of different biomes within the SSCZ may have separate histories is also supported by paleobotanical evidence. Morley's (2002) study documented the sudden appearance of dry-adapted, presumably Sahulian, taxa in the pollen record of Java from the Early Miocene, and noted that there was a westward bias in exchange directionality in that flora. As discussed earlier, this contrasts to other lines of evidence that suggest an eastward bias in exchange directionality for the SSFE generally. A similar discrepancy in exchange directionality inferred from paleobotanical and phylogenetic data was observed in studies of the Great American Biotic Interchange (GABI; the exchange of biota that occurred between South and North America with the emergence of the Isthmus of Panama). Bacon *et al.* (2015) suggested that this was due to a biome sampling bias in each data type, with the fossil record having a greater representation of temperate taxa and phylogenetic studies of contemporary lineages having a greater representation of tropical taxa, resulting in a difference in the detected dynamics of exchange. Similarly, the fossil record in the SSCZ has a biased representation of savannah biome taxa (e.g. *Casuarina*, *Camptostemon*, *Dacrycarpus*), while most phylogenetic studies in the region to date have focused on species from the wet tropics (e.g. c. 82% of clades included in the study by Crayn *et al.* (2015) were rainforest taxa). Sniderman and Jordan (2011) reported differences in the extent and timing of SSFE in different Australian rainforest biomes (following the bioclimatic classification of Nix (1991)). They concluded that the microthermal forest fossil record contains few Sundanian immigrant lineages, that the mesothermal (upland) forest fossil record comprises a combination of Gondwanan and Sundanian immigrant lineages, and that the lowland tropical, dry rainforest and coastal/mangrove forest fossil records are dominated by Sundanian immigrants. A difference in the timing of exchange in these rainforest biomes was also noted, suggesting that immigration of lowland tropical, coastal and mangrove lineages was episodic but occurred primarily in the Quaternary. Costion *et al.* (2015) showed that lowland rainforests in northeastern Australia have higher phylogenetic diversity than upland rainforests, which they attributed to a higher proportion of Sundanian immigrants in lowland rainforests, suggesting in turn that different vegetation communities within the rainforest biome may have different exchange dynamics.

Despite evidence of complex separate spatio-temporal dynamics between biomes (and communities within biomes) from floristic, ecological and paleobotanical studies, to date no studies have specifically investigated this in a phylogenetic framework. Most phylogenetic studies on SSCZ groups have focused on lineages restricted to single biomes (usually rainforest), have sample sizes too small to detect differences in SSFE dynamics between biomes, and do not reconstruct ancestral biomes (Crayn *et al.* 2015). With advances in phylogenomic methods, integration of information about biomes into a phylogenetic framework presents an exciting opportunity to directly compare spatio-temporal dynamics of exchange across biomes in the SSCZ. It also provides an opportunity to formally test for phylogenetic niche conservatism in the flora of the region, and investigate how this in turn may affect the evolution of the region's plant lineages.

Source-sink area effects

Directionality of exchange in the SSFE may be affected by differences in land area between Sunda and Sahul. Lowland tropical rainforest is much more extensive on Sunda than on Sahul, which may generate higher propagule pressure in an easterly direction (Sniderman and Jordan 2011; Richardson *et al.* 2012). In ecological theory and conservation biology, smaller communities are thought to be more susceptible to invasion (e.g. Marvier *et al.* 2004). However, it may be incompatible with island biogeography theory, which suggests that immigration and establishment will in general be higher in larger areas (MacArthur and Wilson 2001). Other evidence suggests that fragmented or disconnected areas experience less frequent invasion events than more highly connected areas (Hoffmeister *et al.* 2005). In future studies, areas need to be categorised by biome rather than total land mass, and modelling approaches are needed to determine the roles of different source and sink areas in SSFE dynamics.

Available land mass

The SSCZ has an extremely complex and poorly understood geological history, characterised by dynamic landscapes influenced by moving terranes, rapid orogenesis and subsidence, and fluctuating sea levels. An emerging view is that the dynamism of the physical landscape has played an important role in affecting exchange dynamics of faunal lineages. Oliver *et al*. (2018) detected signals of ancient island arc origins in *Lepidodactylus* lizards, with diversification reconstructed to geological fragments of previously more-continuous island arcs. This suggests that modern spatial patterns may not be adequate to investigate lineage origins and thus SSFE dynamics. Similarly, timing of orogenesis is likely to have affected movement and triggered diversification across the SSCZ in the diversification of *Exocelina* arthropods during the past 10 Ma (Toussaint *et al.* 2014). More recently, Shee *et al.* (2020) showed that the colonisation of New Guinea by the woody angiosperm genus *Schefflera* was dictated by available land mass as different parts of the island became subaerial. These studies indicate that the changing connectivity and emergence of land mass is likely to have affected the spatio-temporal dynamics of the SSFE, and that incorporation of geologically plausible time-sliced models into phylogenetic ancestral area reconstructions, and careful consideration of biogeographic coding, are necessary to understand them.

Relative community stability

Paleoclimatic and geological data suggest that there was a difference in climatic stability between Sunda and Sahul throughout the Cenozoic, and this is thought to affect the spatio-temporal dynamics of the SSFE. While Sunda remained relatively climatically stable, Sahul experienced an overall trend of aridification throughout the Cenozoic, with glacial cycles throughout the Quaternary. The shifting climate of Sahul and Quaternary glacial cycles led to repeated expansions and contractions of the remaining tropical rainforests (Rossetto *et al.* 2007, 2012; Mellick *et al.* 2012; Yap *et al.* 2020), presumably rendering these areas ecologically unstable. These periods of rainforest instability are thought to be optimal times for invasion by Sundanian lineages. Indeed, fossil and genetic evidence indicates that the Australian lowland flora experienced a high influx of Sundanian lineages during this time (Sniderman and Jordan 2011; Yap *et al.* 2020). This could help explain the overall eastward bias in the direction of the SSFE; however, how the Quaternary glacial cycles, and particularly changing sea levels, affected exchange dynamics and the phylogeography of Sunda and Wallacea is yet to be investigated.

Invasive functional traits

Since Hooker documented the 'Indian' element in the Australian flora, the Sundanian flora has been anthropomorphised as 'invasive', 'intrusive', 'aggressive' and having 'great force' (Hooker 1859; Burbidge 1960; Morley 2002). Such descriptions imply that Sundanian lineages possess traits that render them better than Sahulian lineages at invading new areas, which could help explain the overall eastward bias in the directionality of the SSFE. There is some empirical support for this idea. In eastern Australian rainforests, woody plants of Sundanian origin possess traits consistent with higher invasiveness (e.g. more efficient dispersal and faster growth) than plants of Sahulian origin (Yap *et al*. 2018). While ancestry is correlated with differences in functional traits in Australian rainforests, the lack of a comprehensive checklist of the flora of the SSCZ has precluded a similar analysis of Sahulian lineages that migrated into Sunda, or lineages that never successfully crossed Wallacea. Comprehensive pairwise comparisons of functional traits between invasive and sedentary Sahulian and Sundanian lineages could shed more light on whether Sundanian lineages are generally superior at invading new territory than Sahulian ones. Whether traits are advantageous for invasion is highly dependent on time scale, spatial scale, ecological stability of the new area, and biotic interactions in the new area (Kempel *et al.* 2013; Leffler *et al.* 2014; Maron *et al.* 2014; Funk *et al.* 2017). Therefore, further in-depth ecological studies are required to assess the impact of invasive functional traits on the dynamics of the SSFE.

Dispersal vectors

Wind and ocean currents

The prevailing equatorial and eastern Australian ocean currents are westward, as are the prevailing winds (Richardson *et al*. 2012; Christensen *et al.* 2017), both thus being counter to the eastward bias in the SSFE. Richardson *et al.* (2012) therefore dismissed wind and ocean currents as drivers of the SSFE. However, on a finer scale wind and ocean currents are more complex and may play an important role in localised patterns of connectivity, which then feed into broader patterns of exchange between the continental shelves. As such, integration of information about wind and ocean currents with phylogeographic information could provide more nuanced insights into the role of wind and ocean dispersal in the SSFE, especially for coastal species.

Fauna

Animal dispersal is thought to have played an important role in the patterns observed in the SSFE. In Australian rainforests, animal dispersal is known to be an important driver of plant distributions (Rossetto and Kooyman 2005; Rossetto *et al.* 2008, 2015). On a global scale, more than 40% of invasive tree species and more than 60% of invasive shrubs are dispersed by birds (Richardson and Rejmánek 2011), and plants with zoochorous propagules are known to rapidly establish relationships with birds in new areas (Gosper *et al.* 2005). Crayn *et al.* (2015) found that 90% of taxa that were exchanged between Sunda and Sahul had zoochorous (mostly bird-dispersed) propagules. Further, a recent study has shown that vagility of fauna has dramatically influenced the zoogeography of the SSCZ and that this has changed over time; whether the biogeography of plants matches those of their dispersers through space and time remains to be understood (White *et al.* 2021). Finally, it is unclear how turnover in disperser composition across the SSCZ has affected the evolution of plant lineages. Plants may fail to migrate further once they reach new territory without adequate dispersers, or evolve new dispersal syndromes. Some evidence suggests that new disperser-plant relationships evolved in the Australasian genus *Aglaia* as it crossed Wallace's Line, and this may have driven morphological diversification in the genus (Pannell and White 1988). Ancestral trait reconstruction of dispersal syndromes in large phylogenies, and comparison of animal and plant phylogenetic histories, show strong promise for understanding the relationships between animal dispersers and plant evolution in the SSCZ.

Conclusion and rationale for this thesis

Despite a long history of research on the origins of the Australian flora and the biogeography of the SSCZ, much remains to be understood about spatio-temporal patterns in the SSFE and their underlying driving processes. Advances in technologies such as publicly available biodiversity information systems, high-throughput sequencing, high performance computing, phylogenomics, herbariomics (sequencing of herbarium specimens) and reduced-representation phylogeographic techniques present exciting opportunities to gain a deeper and more nuanced understanding of the SSFE and its influence on the floras in and bordering Wallacea. In the following chapters, I use these technologies to:

- compile the first comprehensive, digitised checklist of the vascular flora of the SSCZ region (**Chapter 2**);
- characterise full-flora phytogeographic patterns and their main drivers in the SSCZ, and quantify the extent of floristic exchange between Sunda and Sahul (**Chapter 3**);
- identify colonisation tracks between Asia and northern Australia, and investigate phylogeographic patterns across the SSCZ (**Chapter 4**), and
- infer spatio-temporal patterns of floristic exchange and the primary drivers of these patterns in the angiosperm order Sapindales (**Chapter 5**).

I conclude by synthesising the outcomes of this research, and what it means for our understanding of this important biogeographic region and the evolution of Australia's northern flora (**Chapter 6**).

Chapter 2

Checklist of the vascular flora of the Sunda-Sahul Convergence Zone

Preface

To begin to understand the effect that the exchange of flora between Sunda and Sahul had on the northern Australian flora, we must first know what plants are in the region, and where. In Chapter 2, I present the first checklist of vascular plants recorded in the Sunda-Sahul Convergence Zone, and document the major islands on which they are found. The results of the compilation and analysis of the checklist follow, whereas the checklist itself is not presented here due to its size – instead it is available from the Research Data JCU repository (DOI: http://dx.doi.org/10.25903/5ea0dd85f8ea9).

This chapter has been published in Biodiversity Data Journal:

Joyce EM, Thiele KT, Slik FJW, Crayn DM (2020) Checklist of the vascular flora of the Sunda-Sahul Convergence Zone. *Biodiversity Data Journal* **8**, e51094. doi:10.3897/BDJ.8.e51094.

EMJ conceived the idea for this research, conducted all work and data analysis, and wrote the manuscript. DMC, KRT and FJWS provided comment on the work and assisted with manuscript writing.

Abstract

The Sunda-Sahul Convergence Zone, defined here as the area comprising Australia, New Guinea, and Southeast Asia (Indonesia to Myanmar), straddles the Sunda and Sahul continental shelves and is one of the most biogeographically famous and important regions in the world. Floristically, it is thought to harbour a large amount of the world's diversity. Despite the importance of the area, a checklist of the flora has never before been published. Here I present the first working checklist of vascular plants for the Sunda-Sahul Convergence Zone. This is the first species-level checklist of the region and presents an updated census of the region's floristic biodiversity. The list was compiled from 24 flora volumes, online databases and unpublished plot data. Taxonomic nomenclature was updated, and each species was coded into nested biogeographic regions. The list includes 60,415 species in 5,135 genera and 363 families of vascular plants. The checklist confirms that species richness of the SSCZ is comparable to that of the Neotropics, and highlights areas in need of further documentation and taxonomic work. This checklist provides a novel dataset for studying floristic ecology and evolution in this biogeographically important region of very high global biodiversity.

Introduction

The Sahul continental shelf comprises Australia and the island of New Guinea, while the Sunda continental shelf comprises mainland Southeast Asia (Myanmar, Cambodia, Vietnam, Laos, Thailand, Peninsular Malaysia) and Indonesia west of Wallace's Line. Between the Sunda and Sahul shelves lies Wallacea, a biogeographic region composed of a complex conglomerate of continental fragments and island arcs of varied origins (Hall 2012b). Wallacea encompasses the Philippines, Timor, and parts of Indonesia (Figure 2.1).

The Sunda and Sahul shelves converged approximately 25 Mya, following the rifting of Sahul from Antarctica approximately 45 Mya, its northward drift, and its contact with Wallacea and Sunda at the Oligocene-Miocene boundary (Hall 2002; Zahirovic *et al.* 2016). This collision facilitated the exchange of biota that had been evolving in isolation for at least 20 My (Sniderman and Jordan 2011; Crayn *et al.* 2015; Kooyman *et al.* 2019). The Sunda-Sahul biotic exchange provides a natural experiment to study evolution and biogeography, and has fascinated scientists since the time of Alfred Wallace (Wallace 1860). However, despite considerable interest, study and speculation on the biogeography of the region, much remains to be understood regarding which taxa were exchanged, when they were exchanged and the processes by which this occurred.

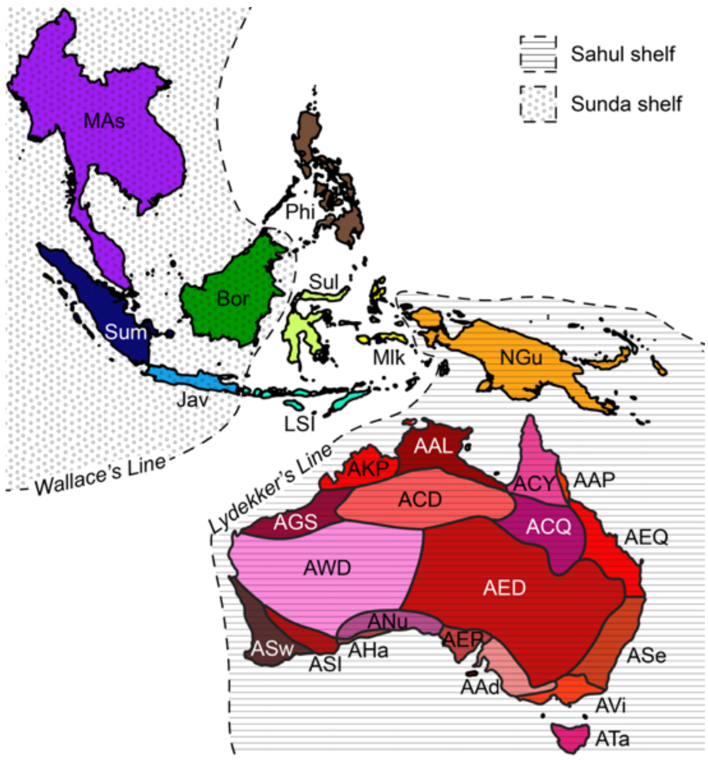

Figure 2.1 Map showing the continental shelf, island group and Australian phytogeographic subregions (Ebach *et al.* 2015) that species were coded to in the SSCZ vascular plant checklist. Islands forming part of the same island group are indicated by colour. MAS, Mainland Asia; Sum, Sumatra; Bor, Borneo; Jav, Java; Phi, Philippines; Sul, Sulawesi; LSI, Lesser Sunda Islands; Mlk, Maluku Islands; NGu, New Guinea; AKP, Kimberley Plateau; AAL, Arnhem Land; ACY, Cape York Peninsula; AAP, Atherton Plateau; AGS, Great Sandy Desert Interzone; ACD, Central Desert; ACQ, Central Queensland; AEQ, Eastern Queensland; AWD, Western Desert; AED, Eastern Desert; ASe, Southeastern; ASw, Southwestern; ASI, Southwest Interzone; AHa, Hampton; ANu, Nullarbor; AEP, Eyre Peninsula; AAd, Adelaide; AVi, Victoria; ATa, Tasmania.

A plethora of terms for areas and the floristic exchange that occurred between them has accumulated due to the longstanding biogeographic interest in the region. Parts of the area of focus have been variously referred to as the 'Indo-Australian archipelago' (Lohman *et al.* 2011), the 'Southeast Asian-Australian region' (Metcalfe 2001; Morley 2002), the 'Malay archipelago' (Wallace 1860; Hall 2017), 'Malesia' (Steenis 1979; Brummitt *et al.* 2001; Van Welzen *et al.* 2005), 'Papuasia' (Brummitt *et al.* 2001) and 'Australasia' (Heads

2014), based on floristic or political boundaries. Richardson *et al*. (2012) referred to the floristic exchange as the 'Malesian Floristic Interchange', while Crayn *et al*. (2015) named it the 'Sunda-Sahul Floristic Exchange'. To adequately describe the geological history of the area and the area likely to be affected by the exchange of flora between the Sunda and Sahul shelves, I herein introduce the term 'The Sunda-Sahul Convergence Zone' (SSCZ) to describe the area of focus. This area comprises the entire Sahul shelf (Australia and New Guinea), Wallacea (the Moluccas, Sulawesi, the Philippines and the Lesser Sunda Islands), and the Sunda shelf (Borneo, Sumatra, Java, and mainland Asia to Myanmar) (Figure 2.1). Furthermore, I here adopt the term 'the Sunda-Sahul floristic exchange' (Crayn *et al*. 2015), as it most accurately describes the exchange of flora upon the convergence of the two continental shelves.

The SSCZ is thought to harbour a significant proportion of the world's biodiversity, yet much of this biodiversity remains to be documented. Four of the world's 'biodiversity hotspots' occur in the SSCZ - the Philippines, Sundaland, Wallacea and Southwest Australia (Myers *et al.* 2000). The SSCZ also contains the 'major wilderness area' of New Guinea—an area thought to have a high degree of endemism and diversity but that is not currently considered to be under threat (Mittermeier *et al.* 1998). However, despite the clear importance of the region and its biodiversity, its flora has never been documented as a whole.

Checklists for some parts of the SSCZ exist, but their completeness, currency and availability differ. Some are in hard-copy form in books or journals (e.g. Soepadmo and Wong 1995; Kessler *et al.* 2002), some are online (e.g. Pelser *et al.* 2011), and some are unpublished (e.g. Slik 2018). Many are not publicly available or are out of print. The hard-copy formats are static and not up-to-date with new taxonomic discoveries or revised taxonomic concepts. The taxonomies used in these lists also often differ, mostly due to their differing publication dates, making comparison of taxa between regions difficult.

The flora of the SSCZ must be documented for it to be studied, analysed and conserved. Documentation is also necessary to appreciate the significance of the SSCZ flora on a global scale, and to further our understanding of its ecology and evolution. Therefore, I provide here for the first time a digital, comprehensive, updateable and publicly available dataset of vascular plants for the SSCZ.

Materials and methods

A checklist of the vascular flora of the SSCZ was compiled from 26 sources including flora volumes, published checklists and databases, and unpublished plot data and checklists (Table 2.1). For areas where these data were inadequate or lacking, they were supplemented with herbarium specimen-based occurrence records from GBIF.

For floras and checklists in hard-copy, scanned copies were converted into plain text with Optical Character Recognition (OCR). Scientific binomial names were extracted from the plain text documents using the Global Names Recognition and Discovery Service v.0.8.5 (Marine Biological Laboratory 2016; http://gnrd.globalnames.org/name_finder). All names were manually checked for accuracy against the original source and corrected as necessary. Species noted to be non-native in floras and checklists were removed.

The taxonomic status of names from each source was checked using the Taxonomic Name Resolution Service v.4.0 (iPlant Collaborative (2019), Boyle *et al.* 2013; http://tnrs.iplantcollaborative.org/TNRSapp.html). Names were processed in the "Perform Name Resolution" mode allowing partial matches with a minimum threshold of 0.05. Sources selected to check names were Tropicos.org (Missouri Botanical Garden 2019), the Global Compositae Checklist (Flann 2009), the International Legume Database and Information Service (ILDIS 2018), The Plant List (The Plant List 2013) and The PLANTS Database (USDA, NRCS 2019). Tropicos.org was selected as the family classification source as the nomenclature is known to be actively updated and current. All matches were manually inspected for anomalies and corrected where necessary. For synonymised names, the currently accepted name according to the Taxonomic Name Resolution Service v.4.0 was included in the checklist. Names returning the taxonomic status of 'No Opinion' were also included; these names are awaiting assessment by name-checking sources, but for the purposes of this study were assumed to be accepted to ensure they were not prematurely excluded from the final list. Phrase names, manuscript names, hybrids and infraspecific taxa were omitted to increase the likelihood that the species included are recognised internationally. All species names were then classified to a major group: Angiosperms, Fern and fern allies and Gymnosperms.

Table 2.1 Sources of species names for the Sunda-Sahul Convergence Zone vascular plant checklist.

Island area	Country	Shelf	Source
Australia	Australia	Sahul	Centre for Australian National Biodiversity Research and Council of Heads of Australasian Herbaria 2017
Australia	Australia	Sahul	Royal Botanic Gardens, Kew 2018
Borneo	Brunei, Malaysia and Indonesia	Sunda	GBIF 2017
Borneo	Indonesia	Sunda	Slik 2018 XMalesia 2019
Borneo	Brunei	Sunda	Slik 2018 Slik 2019
Borneo	Malaysia	Sunda	Soepadmo and Wong 1995 Soepadmo *et al.* 1996, 2002, 2004, 2007 Soepadmo and Saw 2000
Java	Indonesia	Sunda	GBIF 2017b Slik 2018
Lesser Sunda Islands	Indonesia, Timor	Wallacea	Monk *et al.* 1997 GBIF 2017b XMalesia 2019
Lesser Sunda Islands	Indonesia	Wallacea	XMalesia 2019
Mainland Asia	Malaysia	Sunda	Forest Research Institute Malaysia 2017 Slik 2018 BGCI 2019
Mainland Asia	Cambodia	Sunda	GBIF 2017d Slik 2018 Botanic Gardens Conservation International 2019
Mainland Asia	Laos	Sunda	Newman *et al.* 2007 GBIF 2017e Slik 2018 Botanic Gardens Conservation International 2019
Mainland Asia	Myanmar	Sunda	Kress *et al.* 2003 GBIF 2017f

Mainland Asia	Thailand	Sunda	Chayamarit *et al.* 2014 GBIF 2017a Slik 2018 Botanic Gardens Conservation International 2019
Mainland Asia	Vietnam	Sunda	GBIF 2017h Slik 2018 Botanic Gardens Conservation International 2019
Mainland Asia	Singapore	Sunda	Chong *et al.* 2009 Slik 2018
Maluku Islands	Indonesia	Wallacea	Monk *et al.* 1997 GBIF 2017i XMalesia 2019
New Guinea	Papua New Guinea, Indonesia	Sahul	Atrium Biodiversity Information System 2017 James 2017 GBIF 2017j
New Guinea	Papua New Guinea	Sahul	Womersley 1978 Henty 1981 Conn 1995 Slik 2018
New Guinea	Indonesia	Sahul	Slik 2018 XMalesia 2019
Philippines	Philippines	Wallacea	Pelser *et al.* 2011 GBIF 2017j Slik 2018
Sulawesi	Indonesia	Wallacea	Kessler *et al.* 2002 GBIF 2017k Slik 2018
Sumatra	Indonesia	Sunda	GBIF 2017d Slik 2018

Species from each source were coded according to their country, island group and continental shelf (Figure 2.1). Australian species from the Australian Plant Census (APC; Centre for Australian National Biodiversity Research and Council of Heads of Australasian Herbaria 2017) were further coded by their occurrence in the Australian Bioregionalisation Atlas phytogeographic subregions (Ebach *et al.* 2015). This was done by downloading occurrence data for every species on the APC from GBIF using the rgbif v.1.3.0 package in R (Chamberlain *et al.* 2019). Occurrence data were cleaned to include only herbarium records from after 1960 with a geospatial coordinate uncertainty of less than 25 km. Geospatial coordinates for each species were then coded into phytogeographic subregion polygons using the speciesgeocodeR package in R (Töpel *et al.* 2017). Phytogeographic subregion polygons were modified from the study of González-Orozco *et al*. (2014) and Ebach *et al*. (2015) to incorporate the administrative boundary of Australia so that offshore islands (e.g. the Torres Strait Islands) were included. Species occurrences in the Australian external territories of Norfolk Island, Australian Antarctic Territory, Heard and McDonald Islands, Coral Sea Islands, Christmas Island, Ashmore and Cartier Islands were excluded. This process was repeated for the Australian Orchidaceae list from Christenhusz and Byng (2016) and WCSP (2019).

Source lists were then merged and duplicates removed. Consistency in family classification was checked.

Checklist of the vascular flora of the SSCZ

The checklist of the vascular flora of the SSCZ (Appendix A) has been stored in the Research Data JCU (formerly, the 'Tropical Data Hub') repository (doi: http://dx.doi.org/10.25903/5ea0dd85f8ea9). Updated versions of the checklist can be accessed via www.ath.org.au/australian-tropical-herbarium/datasets.

Analysis

A total of 60,415 species in 5,135 genera and 363 families of vascular plants are recorded in the Sunda-Sahul Convergence Zone. The number of taxa in each island group and continental shelf is summarised in Table 2.2.

Discussion

Here I present the first comprehensive species checklist of native vascular plants for the Sunda-Sahul Convergence Zone, comprising 60,415 species. An estimated 374,000 vascular plant species are known globally (Christenhusz and Byng 2016); thus, this checklist indicates that the SSCZ harbours at least 16.2% of all known vascular plant species. Considering the land area of the SSCZ (c. 12,215,000 km^2, c. 8% of the global land

Table 2.2 Summary of number of species, genera and families in each island group and continental shelf

Shelf	Island group	No. species	No. genera	No. families
Sahul	Australia	20430	2188	258
	New Guinea	15765	2231	275
	Sahul total	34229	3252	310
Wallacea	Lesser Sunda Islands	1488	793	169
	Maluku Islands	2590	1116	208
	Philippines	10212	2023	263
	Sulawesi	3094	1188	212
	Wallacea total	12802	2308	272
Sunda	Borneo	8458	1641	235
	Java	1676	837	180
	Mainland Asia	17861	3189	302
	Sumatra	2941	1035	202
	Sunda total	23331	3499	309
SSCZ	SSCZ total	60526	5135	363

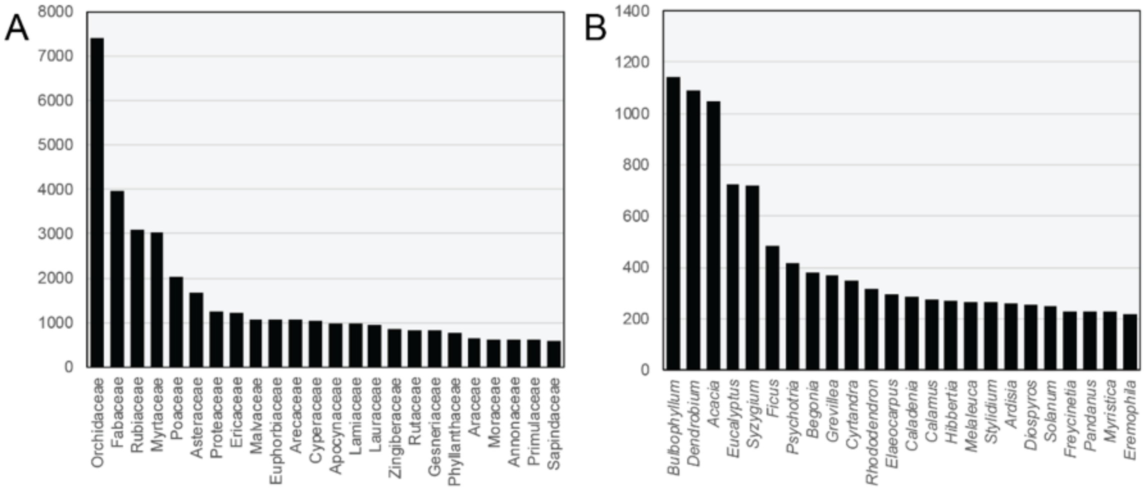

Figure 2.2 Histogram showing the number of species (x-axis) for the 25 most species-rich families (A) and genera (B) in the SSCZ.

area), the estimated diversity for the region is substantially higher than the global average number of species per unit area.

It has long been assumed that the Neotropics are more species-rich than the Southeast Asian tropics. However, the findings of the present study suggest that floristic richness in the SSCZ is comparable to that of the Neotropical ecozone (*sensu* Schultz 2005) which extends from central Mexico to southern Brazil, a latitudinal range similar to that of the SSCZ. Approximately 90,000–110,000 seed plant species are estimated to occur in the Neotropical ecozone (Antonelli and Sanmartín 2011), an average of 0.0062 seed plant species per km^2. By comparison, the SSCZ has an average of 0.0047 seed plant species per km^2. The average for the whole SSCZ is lowered by the inclusion of Australia, which mostly comprises savannah and arid biomes known to have relatively low floristic richness. Excluding Australia, the SSCZ has 0.0088 vascular plant species per km^2, which is slightly higher than the richness of seed plants in the Neotropical ecozone. Similar species richness between the Southeast Asian tropics and Neotropics was also recently reported for tropical tree species by Slik *et al*. (2015).

The five most species-rich families in the region, in order, are Orchidaceae, Fabaceae, Rubiaceae, Myrtaceae and Poaceae (Figure 2.2). The most species-rich genera are *Bulbophyllum* and *Dendrobium* (Orchidaceae), *Acacia* (Fabaceae), and *Eucalyptus* and *Syzygium* (Myrtaceae). Orchidaceae, Fabaceae and Poaceae are some of the most species-rich plant families on Earth, and thus their predominance in the region is expected. The pattern of the most diverse families in the SSCZ is similar to that of the Amazon; however, the Amazon includes a high number of Melastomataceae species, fewer species of Proteaceae and Ericaceae, and the SSCZ has ten times the number of orchid species than the Amazon (Cardoso *et al.* 2017). Only one genus – *Psychotria* (Rubiaceae) – exhibits a similarly high diversity in the Amazon and the SSCZ, reflecting the independent evolutionary histories of these tropical floras.

It must be emphasised that this is a working checklist of vascular plants; the aim was to compile current knowledge of floristic distribution across the region in an objective and systematic way, and to publish it in a digital, updateable format. Some inevitable errors in taxonomy and distribution will be present in the dataset, reflective of errors in the taxonomic backbones used to standardise nomenclature across sources. These will be corrected over time through consultation with group experts and other regional flora projects, and updated versions of the checklists will be released. The number of errors is likely to be small and unlikely to invalidate results of analyses based on this checklist, given the size of the dataset and the diversity and reliability of source lists. The dataset also almost certainly under-represents actual floristic diversity in the region. Many areas within the SSCZ are underexplored, and therefore have a biodiversity that is not accurately documented. This is particularly the case in many parts of Indonesia, New Guinea, Cambodia and Vietnam. Additional taxonomic work is urgently needed to fully understand and refine species boundaries in poorly known groups. This is challenging in an area so geographically and politically diverse, and is particularly important given current and emerging threats to the biodiversity of the region (Myers *et al.* 2000). Given the digital format of this checklist, the checklist is able to be updated as new discoveries are made and taxonomies are revised. It provides a baseline overview of current knowledge of the regional flora for biodiversity research, which can be built on and refined over time.

The checklist is provided as a resource for scientists studying the biodiversity, evolution, biogeography and ecology of this region. Questions generated from this list include the following:

- Which taxa have been exchanged between the Sunda and Sahul shelves?
- Is there a difference between functional traits of plants between different islands, and what could be driving this?
- Where are the most diverse areas that should be considered for conservation priority?
- What are the environmental correlates of variation in floristic composition across the region?

The list of vascular flora of the SSCZ also offers opportunities to build a regional database of plant traits for ecological and evolutionary research. Ultimately, I hope that this checklist will provide a resource to enable researchers to generate and test biogeographic, ecological and evolutionary hypotheses in this globally megadiverse and biogeographically important region.

Chapter 3

Plants will cross the lines: climate and available land mass are the major determinants of phytogeographical patterns in the Sunda–Sahul Convergence Zone

Preface

In Chapter 2, I compiled and presented the first checklist of vascular flora in the Sunda-Sahul Convergence Zone. In Chapter 3, I analyse the distributional information from this checklist to characterise the phytogeography of the region and investigate how it has been influenced by the Sunda-Sahul Floristic Exchange.

This chapter has been published in the Biological Journal of the Linnean Society:

Joyce EM, Thiele KR, Slik JWF, Crayn DM (2021) Plants will cross the lines: climate and available land mass are the major determinants of phytogeographical patterns in the Sunda–Sahul Convergence Zone. *Biological Journal of the Linnean Society* **132**(2), 374-387. doi:10.1093/biolinnean/blaa194.

EMJ conceived the idea for this research, conducted all work and data analysis, and wrote the manuscript. DMC, KRT and FJWS provided comment on the work and assisted with manuscript writing.

Abstract

The Miocene convergence of the Sunda shelf, Sahul shelf and Wallacea facilitated the exchange of previously isolated floras across the Sunda–Sahul Convergence Zone (SSCZ). The SSCZ is a hotspot of biogeographical research; however, phytogeographical patterns across the region remain poorly understood. I conducted multivariate analysis on a comprehensive species checklist of SSCZ vascular plants to quantify the extent of exchange, characterize phytogeographical patterns and investigate their abiotic drivers. Lydekker's and Wallace's Lines are not reflected in floristic composition at any taxonomic level, with 46% of genera distributed across these biogeographical lines. In contrast, environment is significantly correlated with floristic composition, with annual rainfall and seasonality being the strongest correlates. Mainland Asia, Borneo, the Philippines, New Guinea and Australia were major routes of exchange throughout the Cenozoic, possibly because these areas have been persistent landmasses throughout the entire period of convergence. I conclude that Sunda–Sahul floristic exchange has substantially influenced the assembly of the regional flora and that modern phytogeographical patterns have been influenced more by environmental variables and available landmass (i.e. establishment conditions) than by putative barriers to movement such as Wallace's and Lydekker's Lines (i.e. vagility).

Introduction

Southeast Asia, Australia and the landmasses between them are home to some of the most unique, diverse and threatened floras in the world. This region – a hotspot for biogeographical research since Wallace (1860, 1869) – is characterized by the convergence of two continental shelves: the Sunda continental shelf (including Southeast Asia) and the Sahul continental shelf (including Australia). Herein, I use the term 'Sunda–Sahul Convergence Zone (SSCZ)' for the entire complex of landmasses (Joyce *et al.* 2020); Figure 2.1). Approximately 45 Mya the Sahul shelf rifted from Antarctica at high southern latitudes and drifted northwards, colliding with the Sunda shelf from approximately 25 Mya (Lohman *et al.* 2011). The collision resulted in widespread geological change, including the trapping of a complex conglomerate of terranes – now referred to as Wallacea – between the shelves, orogenesis in Wallacea and New Guinea, and the torsion of the Sunda plate (Zahirovic *et al.* 2016; Hall 2017). It also facilitated the exchange of biotas that had evolved in isolation. Undoubtedly, the exchange of flora (the

'Sunda–Sahul Floristic Exchange' (SSFE)) had an impact on the evolution and composition of the flora in the region and beyond (Kooyman *et al.* 2019), yet much remains to be understood about the patterns of this exchange and the processes underlying them.

Most early studies on the biogeography of the region focused on drawing lines to represent inferred barriers to exchange between the Sunda and Sahul shelf. Over time, this has resulted in a plethora of biogeographical lines, mostly reflecting the distributional limits of different taxa (reviewed by Simpson (1977)). The most famous of these are Wallace's Line and Lydekker's Line, which run along the deep-sea barriers separating Wallacea from Sunda and Sahul (Lydekker 1896; Dickerson *et al.* 1928). Later phenetic studies compared similarities and differences of floristic communities to examine phytogeographical patterns in the region (van Steenis 1950; van Welzen *et al.* 2005, 2011). These studies concluded that Wallacea was a floristic transition zone between Sunda and Sahul, creating barriers to exchange due to the presence of sea channels, submersion of islands and differences in climate (van Welzen *et al*. 2005).

Although valuable, these studies were restricted to subsets of taxa which probably underestimate the complexity of phytogeographical patterns, and excluded Australia, which is the largest landmass on the Sahul shelf and has been intermittently connected by dry-land corridors to New Guinea. As a consequence, the full scale of the SSFE (including the number and identity of taxa that have moved between Sunda and Sahul) and the role of Sahul has not been adequately investigated. Furthermore, environmental and geological data have never been integrated with a floristic study of the region, meaning that key assumptions, such as that the deep-sea barrier of Wallace's Line or Wallacea's presumed drier climate provide barriers to exchange, remain untested. This is especially relevant given that recent ecological studies have suggested that plants of different geographical origins (Sunda vs. Sahul) often show a difference in their preferred niche and suite of functional traits (Yap *et al.* 2018; Brambach *et al.* 2020). Given the complex geological history of the region, a more comprehensive account of phytogeographical patterns integrated with environmental data is essential to generate more nuanced, and therefore more useful, testable hypotheses regarding the evolution of the region's biota.

Joyce *et al*. (2020) compiled a checklist of the flora of the SSCZ, making possible a comprehensive analysis of phytogeographical patterns in the region. The checklist comprises 60,415 species in 5,135 genera and 363 families, coded by island groups, countries and continental shelves. The increased availability of environmental data now enables analysis of correlations between floristic composition and environmental variation across the region. Using the checklist of (Joyce *et al.* 2020) and environmental layers from WorldClim (Fick and Hijmans 2017), I aimed to characterize phytogeographical patterns across the SSCZ and identify their drivers. I first determined the number of taxa shared across Sunda, Sahul and Wallacea to quantify the scale of the SSFE, then used the results to identify drivers of phytogeography in the region through investigation of phytogeographical patterns in relation to Wallace's and Lydekker's Lines, environmental correlates of floristic composition, and floristic exchange tracks.

Material and methods

Quantification of shared taxa

Species, genera and families shared across each biogeographical region (Figure 2.1) were extracted from the checklist in Joyce *et al*. (2020). Percentages of taxa shared across regions and of endemic taxa were calculated. In this study I use the term endemic in the local not global sense, i.e. to refer to taxa occurring on only one of the three regions within the SSCZ, regardless of whether they also occur outside the zone.

Although Joyce *et al*. (2020) is the only available working checklist of vascular plants for the SSCZ, two caveats apply to its use for analysis of patterns and drivers of the Sunda–Sahul floristic exchange. First, taxonomic richness may be inaccurately estimated. For New Guinea, Joyce *et al*. (2020) overestimated species richness by 13.6% compared with an expert-verified approach (Cámara-Leret *et al.* 2020). If overestimation is a general feature of the dataset then an increased signal of sharedness and similarity across some islands may result. Second, all taxa are assumed to be monophyletic. Many taxa in the study have not yet been rigorously tested for monophyly, and some may be both non-monophyletic and shared across biogeographical units of analysis. However, it is not expected that non-monophyly is either common or biased with respect to taxonomic, ecological, functional or geographical groups in the dataset. Therefore, while the analysis may over-estimate sharedness slightly, I do not expect that future taxonomic rearrangements will significantly affect the result.

Multivariate analysis

Non-metric multi-dimensional scaling (nMDS) was conducted in R using the vegan package (Oksanen *et al.* 2019) to analyse floristic dissimilarity between island groups and Australian phytogeographical regions as coded by Joyce *et al*. (2020) (Figure 2.1). Jaccard distance matrices were generated based on presence-absence of taxa in each island group at the species, genus and family levels. For comparison, a Bray–Curtis similarity matrix was also generated at the genus and family levels, using the number of species in each family and genus per island group. In this application, Bray–Curtis similarity takes into account genus and family richness rather than abundance as in ecological applications; this enables exploration of whether patterns of similarity change when genus and family diversity in each area are considered. Dendrograms of floristic composition at the species, genus and family levels were generated using the hierarchical agglomerative clustering function in the R package cluster (Maechler *et al.* 2019). Ward's minimum variance method was used to determine clustering as it had the strongest agglomerative coefficient compared to complete, minimum and average linkage clustering.

Data for 19 bioclimatic variables were obtained from the WorldClim global climate data v.2 dataset (Fick & Hijmans, 2017; http://worldclim.org/version2) at 2.5-minute spatial resolution. The mean value for each variable in each region or island group polygon was calculated with the Zonal Statistics plugin in QGIS 3.4 (http://qgis.osgeo.org). Mean elevations were calculated from the USGS GMTED2010 dataset at 30-arcsec spatial resolution (U.S. Geological Survey (2019); https://earthexplorer.usgs.gov) using the Zonal Statistics plugin in QGIS 3.4. Latitude and longitude coordinates were estimated from the centroid of each region or island group polygon as estimated in QGIS 3.4. Values for environmental variables are given in Appendix A1.

The 22 environmental variables were visually inspected for correlation using draftsman plots (Appendix A2). Variables with high and significant correlation coefficients ($R > 0.7$) were removed, with the exception of mean annual temperature, temperature seasonality and annual precipitation, as these have been predicted to be important in shaping biogeographical patterns in the region (van Welzen *et al.* 2005). Ultimately, five environmental variables were selected as independent variables to include in the study:

mean annual temperature (BIO1), temperature seasonality (BIO4), annual precipitation (BIO12), precipitation seasonality (BIO15) and mean elevation.

The significance of the correlation between each environmental variable and floristic composition was tested in the R package vegan. Vectors were plotted to visually inspect the direction in which each environmental variable explained the patterns of floristic composition. Each environmental variable was plotted on the MDS plot as contours using the ordisurf function to further explore the directions of correlations. A modified version of the bioenv analysis (Clarke and Ainsworth 1993) as described in Taylor (2017) was conducted using Jaccard similarity to identify the best combination of environmental variables to describe compositional variance.

Connectivity analysis

I conducted a connectivity analysis to determine the minimum number of connection events between islands or island groups needed to explain the current distribution of taxa, based on an Mk model of discrete character evolution for trait data (Pagel 1994). Within this analysis, connection events refer to a shared distribution of a taxon between islands or island groups established by dispersal or vicariance, and are used as a general indication of routes of movement of lineages throughout the region. Each island or island group was scored as a state, giving a total of ten states for the analysis: Australia, Borneo, Java, Lesser Sunda Islands, Mainland Asia, Sumatra, Sulawesi, Maluku Islands, New Guinea and the Philippines. Australian phytogeographical subregions were merged to investigate connectivity between Asian islands and the island of Australia.

At the species level, single-state species (species found in one region or island group) were ignored as they have not been shared between regions or island groups within the time that these species have evolved. All multi-state species were coded for the minimum number of exchange events needed to achieve their current distribution using the formula:

$$p_{ij}(t) = \frac{1}{k}$$

where $p_{ij}(t)$ is the probability of a connection event occurring between area i and area j within the time that the taxon has evolved, and k is the number of area states observed for that taxon. Probabilities for each taxon were then summarized in an area transition matrix.

For example, for a species found in two areas *i* and *j* ($k = 2$), at least one connection event must have occurred between i and j since the time that species evolved for it to realize its current distribution. However, the ancestral range of the species is unknown, so the probability of the transition being from *i* to *j* is assumed to be equal to the probability of the transition having occurred from *j* to *i*, both being 0.5 (Figure 3.1). Therefore, in the area matrix the minimum number of transitions between i and j for that species is one. The probabilities of connection events for every taxon between each area are summarized in the connectivity matrix and visualized in a network where line thickness is proportional to the inferred number of connection events between each pair of areas.

Connectivity analyses were conducted at the species, genus and family levels. To ensure that patterns in connectivity at higher taxonomic levels were not confounded by more recent exchange events, multi-state lower taxa were removed. For example, at the genus level, multi-state species were removed from the analysis, and at the family level, multi-state genera were removed before calculating connectivity. This ensured that the connectivity analysis reflected exchange events at progressively earlier times. The super-tree analysis of Hedges *et al*. (2015) estimated the modal ages (with 95% confidence interval) of plant species to be 0.75 (0.58–0.98) Mya, of genera to be 14.13 (12.25–16.20) Mya, and of families to be 74.94 (69.06–80.06) Mya. As such, the species-level connectivity analysis can be regarded as representing connectivity between islands within the last 1 Myr, the generic exchange analysis represents connectivity between c. 1 and 16 Mya, and the family exchange analysis represents connectivity between c. 16 and 80 Mya. Although taxonomic rank is an imperfect proxy for time, the advantage of this analysis is that it includes every species in the region, and it is reasonable to expect that temporal changes in general spatial patterns of exchange are detectable across such a large and complete dataset.

In this formula, dispersal and vicariance are assumed to be equally likely between all islands. I also did not weight the number of connections by geographical distance; I only estimated the minimum number of connections that were necessary for the taxon to reach its current distribution. This provides a simplified overview of movement of taxa throughout the region, which is appropriate for two reasons. First, the geological history of the region is highly complex, and parameterizing distance or even presence of certain regions (islands may have emerged at different times) into the model of connectivity is likely to introduce errors and unwarranted assumptions. Second, only relative connectivities are compared, rather than raw numbers of connection events. This gives an indication of how common exchange was between certain islands or island groups compared to others without the need to incorporate geographical distance. The analysis also does not take into account extinction, so will not detect exchanges that have since been obscured by extinction in one or both areas. By estimating the minimum number of exchange events in a connection, I probably underestimate the number of actual exchanges. However, if I assume extinctions are random, the results should accurately reflect the relative importance of exchange routes through time. The main limitation of this analysis is that because taxonomic rank is an imperfect proxy for time, only general trends about how exchange routes have changed through time can be inferred with confidence. A recent study of a large group in Asteraceae has shown that biogeographical exchange routes estimated through phylogenetic analysis are similar to those estimated with phenetic distribution data, if the phenetic dataset is large enough (McDonald-Spicer *et al.* 2019). I believe the general patterns detected by this analysis are likely to reasonably approximate historical connectivity. An ideal analysis would use rigorously dated phylogenies encompassing all taxa in the SSCZ; in the absence of such a dataset, I believe this analysis provides valuable insights and a testable model to guide further work.

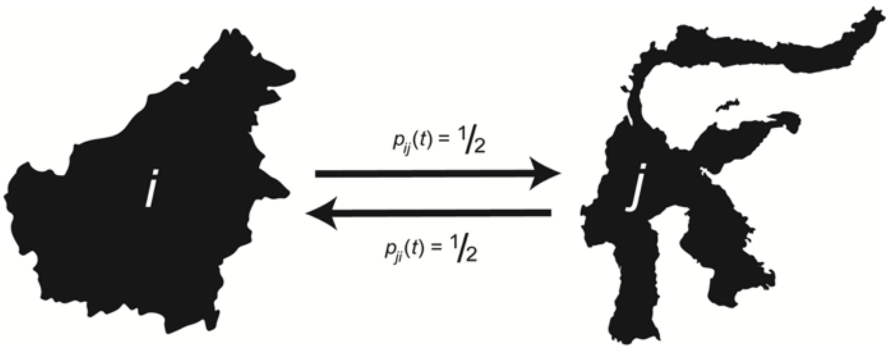

Figure 3.1 Schematic showing the calculation of the minimum number of exchange events needed for a taxon to be distributed across two island groups ($k = 2$): Borneo (i) and Sulawesi (j).

Results

Identification of shared taxa

Within the region, 48.6% of species are endemic to the Sahul shelf, 28.8% to the Sunda shelf and 10.7% to Wallacea (Figure 3.2A). Genera are more evenly distributed across areas, with 25.7% endemic to Sunda, 24.8% to Sahul and 3.4% to Wallacea (Figure 3.2B).

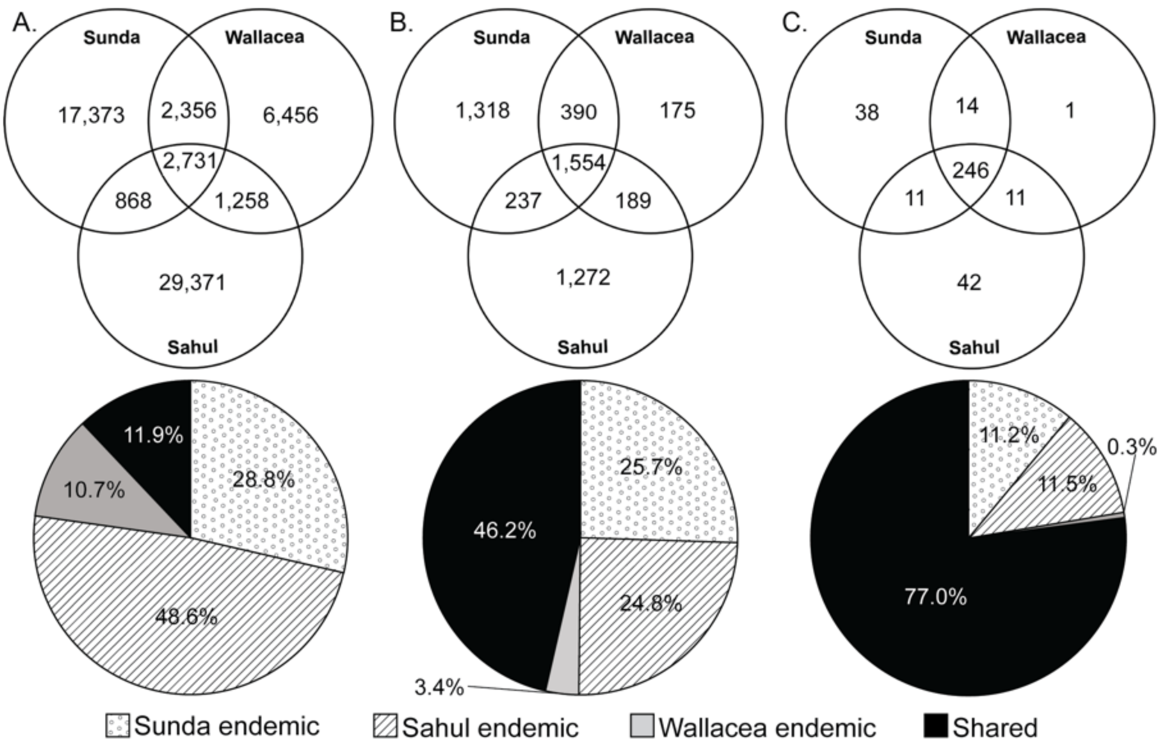

Figure 3.2 Venn diagrams showing raw numbers of (A) species, (B) genera and (C) families distributed in Sunda, Sahul and Wallacea and shared between biogeographical regions. Corresponding pie charts illustrate the proportion of taxa endemic to each region and taxa that are shared across two or more biogeographical regions.

Of the families, 11.5% are endemic to Sahul, 11.2% are endemic to Sunda and only one (the monogeneric fern family Rhachidosoraceae) is endemic to Wallacea (Figure 3.2B). Overall, most shared taxa occur between adjacent areas, with relatively few taxa present in Sunda and Sahul but not in Wallacea (Figure 3.2). In total, 11.9% of species, 46.2% of genera and 77% of families have crossed either or both Wallace's Line and Lydekker's Line. At all levels, Sunda shares more taxa with Wallacea than with Sahul.

Multivariate analysis

Overall patterns of floristic similarity were consistent across taxon rank, irrespective of the metric used to calculate the similarity matrix (i.e. Jaccard or Bray–Curtis; Figure 3.3). Stress values for MDS plots of floristic composition with two axes at the species, genus and family levels were low (0.07, 0.05 and 0.05, respectively).

At all taxonomic levels, Australian phytogeographical regions clustered separately from New Guinea despite being part of the same continental shelf. Despite geographical distance, the results suggest that New Guinea is floristically most similar to Mainland Asia at the species level (Figure 3.3A). At the genus level, New Guinea clustered with the Philippines separately from Mainland Asia, and at the family level it clustered with Mainland Asia and the Philippines (Figure 3.3B). The Maluku Islands, Lesser Sunda Islands, Sumatra, Sulawesi and Java clustered together at all taxonomic ranks, and with Borneo at the genus and family levels (Figure 3.3A–C). At the species level, Borneo was most similar to the Philippines (Figure 3.3A).

Floristic composition in Australia shows geographical signal, with geographically proximal phytogeographical regions having higher floristic similarity. However, geographical signal was not apparent in the floristic composition of Asia. At all taxonomic levels, New Guinea was as similar to south-eastern Australia and eastern Queensland as to the Atherton Plateau and Cape York Peninsula, despite being more distant from the first two areas. Likewise, despite their geographical proximity, New Guinea was floristically dissimilar to the Lesser Sunda and Maluku Islands, these having a higher similarity to Arnhem Land and the Kimberley Plateau in Australia than to New Guinea.

Correlation of floristic composition to environment

Temperature seasonality, mean annual temperature, precipitation seasonality, annual precipitation and mean elevation were all significantly correlated with species composition (Table 3.1; Figure 3.4). Annual precipitation was most strongly correlated with species composition (R^2 = 0.85) but mean annual temperature and temperature seasonality also showed a strong correlation (R^2 = 0.78 and 0.70, respectively). Precipitation seasonality and mean elevation were weakly but significantly correlated with floristic composition, both with R^2 = 0.26. The bioenv analysis corroborated these results, suggesting that annual precipitation alone best explained floristic composition, accounting for 23% of the variation in composition (Table 3.2).

Table 3.1 Results of permutation testing of environmental variable covariance with species composition

Environmental variable	**NMDS1**	**NMDS2**	**R^2**	**p**
Mean annual precipitation	0.46	-0.89	0.78	1×10^{-5}
Temperature seasonality	-0.98	-0.21	0.705	1×10^{-5}
Annual precipitation	0.84	0.54	0.85	1×10^{-5}
Precipitation seasonality	0.11	-0.99	0.26	0.023
Mean elevation	0.52	0.85	0.26	0.024

Table 3.2 Results of bioenv analysis showing the five best combinations of environmental variables that explain species composition as ranked by Spearman's correlation coefficient (ρ).

Combination of environmental variables	***ρ***
Mean annual precipitation	0.23
Temperature seasonality + mean annual temperature + mean annual precipitation	0.14
Temperature seasonality + mean annual precipitation	0.13
Mean annual precipitation + precipitation seasonality	0.12
Temperature seasonality	0.12

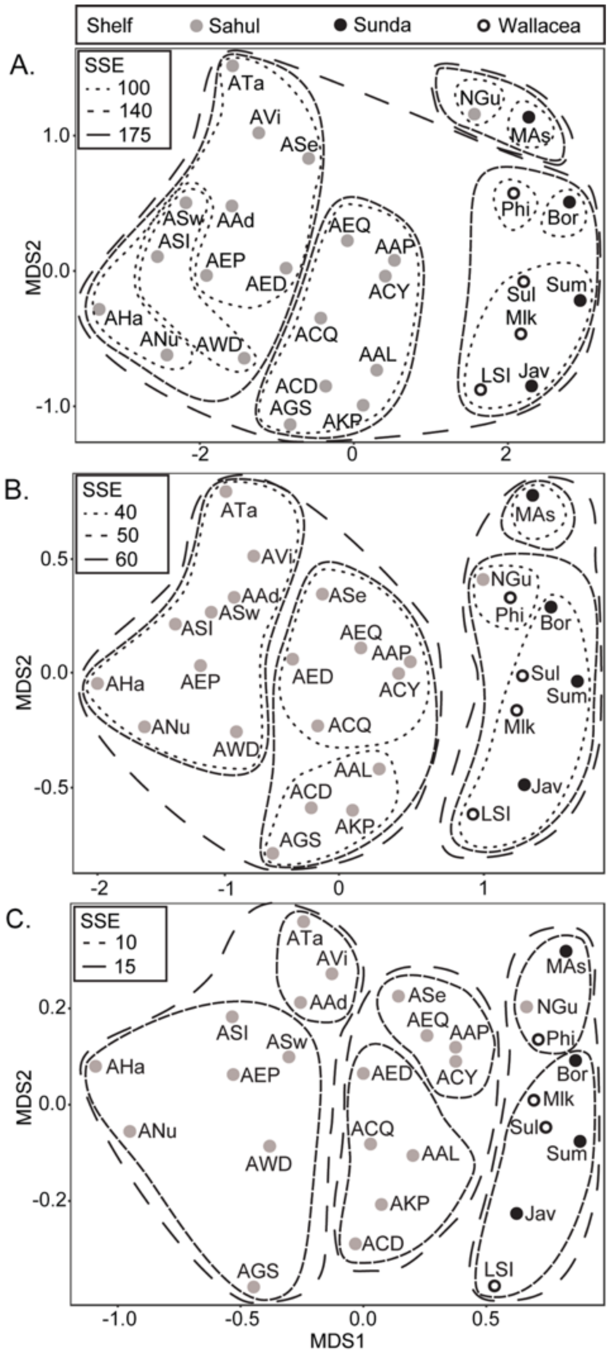

Figure 3.3 nMDS plots for: (A) species floristic community composition generated with presence-absence data for each island group under a Jaccard distance matrix; (B) genus floristic community composition generated with diversity data for each island group under a Bray–Curtis distance matrix; and (C) family floristic community composition generated with diversity data for each island group under a Bray–Curtis distance matrix. Different colours of symbols represent the shelf of that island group or Australian phytogeographical subregion. Clustering as represented by lines is supported by hierarchical agglomerative analysis. The abbreviations of island groups and phytogeographical regions follow Figure 2.1.

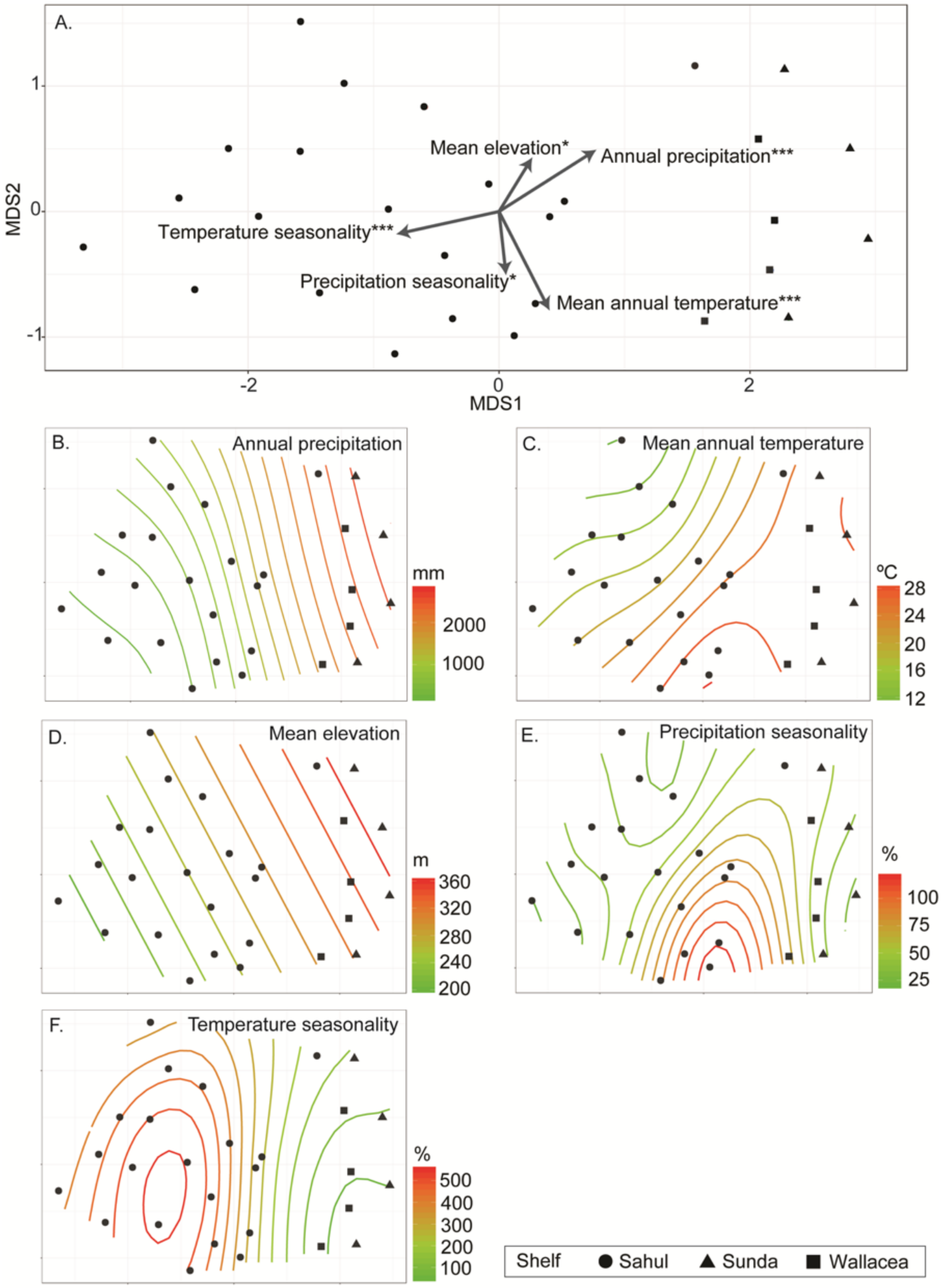

Figure 3.4 nMDS plots of species floristic composition showing correlation with environmental variables. Each point represents an island group as per Figure 2.1, with the symbol indicating the shelf for each island group. (A) envfit analysis plot with a vector for each environmental variable showing the direction of correlation with species composition.

The length of each vector corresponds to the strength of correlation with species composition (R^2), and asterisks indicate the significance of the correlation: *<0.05; **<0.01; ***~0.0. (B–F) ordisurf plots showing contours of each environmental variable fitted to the species composition ordination.

Connectivity analysis

Patterns of connectivity across the region change across taxonomic levels. At the species level, some connectivity exists between every pair of islands or island groups, independent of geographical proximity. Species have been most commonly exchanged between Borneo and Mainland Asia, with a minimum of 2137 connection events needed to explain the current distributions of species. However, this represents only 9% of the total number of connection events, with movement between other island groups almost as frequent (Figure 3.5A). The fewest connection events detected occurred between Sumatra and Australia; a minimum of 80 exchange events have occurred at the species level between these regions, representing 0.3% of all exchange events.

At the genus level, connectivity is not as homogeneous between island pairs as at the species level (Figure 3.5B). Little connectivity has occurred between Java, the Lesser Sunda Islands, Sulawesi and the Maluku Islands, these collectively being the source or sink

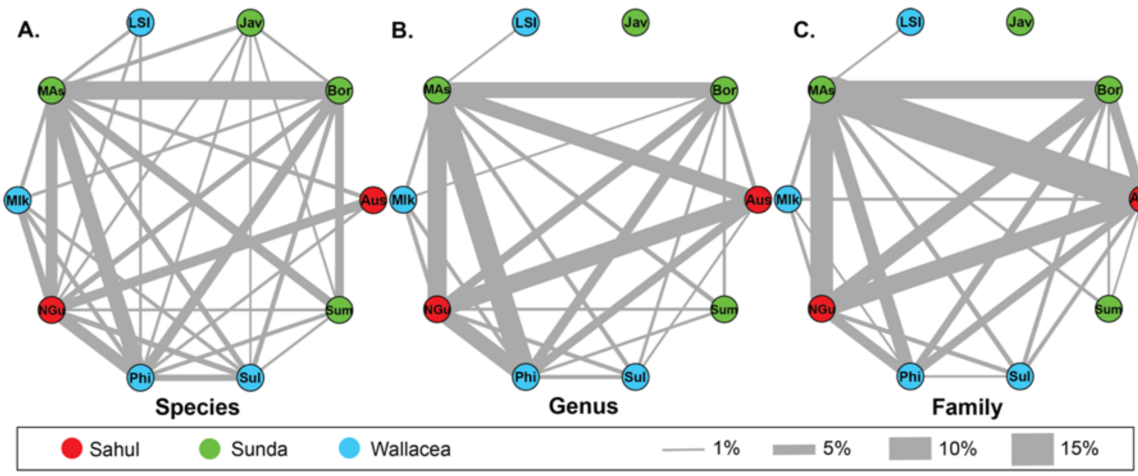

Figure 3.5 The minimum percentage of connection events of vascular flora occurring between island groups at (A) the species level, (B) the genus level and (C) the family level. Connectivity between islands representing less than 1% of all connection events at each level was omitted.

of 27% of connection events. By contrast, 98% of exchange events had Mainland Asia, Borneo, New Guinea, Australia, the Philippines and Sumatra as either the source or the sink. The highest genus-level exchange occurred between the Philippines and Mainland Asia, with a minimum of 345 connection events (11%) between these landmasses.

At the family level, connectivity between regions or island groups is highly heterogeneous (Figure 3.5C). Connectivity between Mainland Asia, Borneo, Australia, New Guinea and the Philippines accounted for 75% of all connection events of family-level exchanges. Overall, these island groups were the sink or source of 99% of connection events. Of particular note is the increase in the proportion of connection events between Australia and Mainland Asia, rising to 17% at the family level. Few family connection events are evident to or from Java, the Lesser Sunda Islands, Sumatra, Sulawesi and the Maluku Islands.

Discussion

Phytogeographical patterns in the SSCZ

For the first time, I have quantified the proportion of the SSCZ's flora that has been exchanged across Lydekker's and Wallace's Lines. At the species level, exchange has been limited – only 11.9% of species are distributed across two or more biogeographical regions, with most species endemic to either Sunda, Sahul or Wallacea. Exchange at the genus and family levels has been higher – almost half of the genera (46.2%) and 77.5% of the families in the region have crossed either or both Lydekker's and Wallace's Line (or, at the family level, were already distributed on both shelves prior to collision c. 25 Mya). I posit that the percentage of shared genera is the most accurate reflection of the scale of the SSFE, as most genera diverged in the mid-Miocene (12.25–16.20 Mya; Hedges *et al.*, 2015), which is when the collision of Sahul with Sunda commenced; considering species distributions would only capture Pleistocene and Holocene divergences (0–0.98 Mya; (Hedges *et al.* 2015)). Therefore, a substantial proportion of lineages have been exchanged between Sunda and Sahul; this indicates that the SSFE has strongly influenced the assembly of the region's floristic diversity, and that deep seas are not as effective biogeographical barriers for plants as previously assumed.

Regional endemism is heterogeneous across the SSCZ; Sahul has a much larger number and proportion of endemic species than Sunda, but a similar proportion of endemic genera and families. This difference in endemism at the species and genus levels may have several explanations. First, Sundanian species may be more likely to disperse and establish across Wallace's Line (i.e. cease to be endemic) than species in Sahul may in crossing Lydekker's Line. There is some support for this idea from phylogenetic and fossil evidence, which suggests a bias in exchange from Sunda to Sahul (Sniderman and Jordan 2011; Crayn *et al.* 2015). Furthermore, Sundanian immigrants in Australia often possess functional traits that are advantageous in novel and unstable environments compared to Sahulian natives (Yap *et al.* 2018). Second, *in situ* diversification on Sahul may be greater than on Sunda. Van Welzen (2005) found a higher degree of species endemism in New Guinea relative to Sundanian islands, and attributed this to the persistence of more ancient lineages on New Guinea. However, the higher ratio of species endemism to generic and familial endemism in Sahul relative to Sunda observed in the present study is best explained by recent speciation rather than the persistence of old lineages. Recent, rapid diversification coincident with the uplift of the New Guinea Central Ranges has been inferred in both animal and plant lineages (Thomas *et al.* 2012; Toussaint *et al.* 2014; Tallowin *et al.* 2018). In addition to rapid orogeny in New Guinea promoting speciation, there may have been less opportunity for diversification in Sunda given the stable geomorphology and climate of the region relative to Sahul (Morley and Morley 2011; Hall 2017). Finally, this pattern could in part be an artefact of disparity in survey effort and taxonomic concepts between and within Sunda and Sahul. Australia comprises the most extensive landmass of Sahul, and the flora of Australia is likely to be better known than some areas of Sunda and Wallacea. Taxonomic concepts may be narrower in Australia, leading to a higher number of recognized species endemic to Sahul (although I am not aware of direct evidence for this). Further studies are needed to elucidate the relative importance of these drivers in influencing endemism heterogeneity across the SSCZ.

Climate as a determinant of SSCZ phytogeography

Our multivariate analysis suggests that geographical proximity is not the main driver of phytogeographical patterning in the SSCZ. Although there is geographical structuring in Australia, the phytogeographical regions of Australia always cluster separately from New Guinea despite Australia and New Guinea occupying the same continental shelf and having a history of intermittent dry-land connection. The New Guinean flora is more similar to Mainland Asian, Philippine and Bornean floras despite being geographically closer to the

Maluku and Lesser Sunda Islands, Australia and Sulawesi. At the genus and family levels, Sumatra, Java and Borneo cluster with Sulawesi and the Maluku and Lesser Sunda Islands although they are part of the Sunda shelf. The question of whether it is appropriate to consider Java as part of Wallacea has been discussed before (van Welzen *et al.* 2011), but not Sumatra or Borneo. Overall, the results do not retrieve a signal for Lydekker's and Wallace's Lines, suggesting that overwater dispersal is not strongly limiting for plants in the region, and that other factors are more important determinants of floristic composition.

Environmental conditions, particularly annual precipitation and seasonality, are highly important in structuring phytogeography in the SSCZ. A recent ecological study has shown that the proportion of Sundanian and Sahulian species changes along environmental gradients (Brambach *et al.* 2020); the results support this finding at a regional and floristic scale. All environmental variables included in this analysis were significantly correlated with floristic composition, with annual precipitation being the strongest correlate. The analyses indicate that the greatest disparity in annual precipitation is between Australia and Asia, and is therefore likely to be the main determinant of exchange between Australia and New Guinea, in line with previous hypotheses (van Steenis 1950; van Welzen *et al.* 2005). Within Asia, the ordisurf analysis suggests that seasonality in precipitation and temperature are the major variables separating New Guinea, Mainland Asia, the Philippines and Borneo from Sulawesi, Java, the Maluku Islands and Lesser Sunda Islands. Given time, plants can traverse large distances, but their realized distribution is principally governed by their capacity to establish and persist.

The fact that the SSCZ is structured strongly by precipitation and seasonality suggests that phylogenetic niche conservatism has a major influence on the evolution of the region's flora (Crisp *et al.* 2009; Donoghue and Edwards 2014). This has implications for the way we should proceed in studying evolution in the area. First, it indicates that for plants, environmental units such as biomes should be the areas coded in phylogenetic ancestral area analyses rather than continental shelves. Second, these findings indicate that further research into plant traits will be vital in understanding drivers of the exchange: which traits are associated with which biomes, and which traits have enabled some lineages to expand into suboptimal environmental conditions while most are restricted to their ancestral niches? What implications does this have for conservation of lineages in certain biomes with climate change? Further studies are also needed on the effect of soil type and substrate because they are also likely to play an important role in determining floristic composition (Slik *et al.* 2011; Kooyman *et al.* 2019).

Available landmass as a determinant of SSCZ phytogeography

As well as environment, changing landmass availability over time has influenced modern phytogeography across the SSCZ. The connectivity analysis shows that phytogeographical connectivity tracks have changed through time. At the species level, relatively even connectivity was inferred between most pairs of islands or island groups. However, at the genus and family levels, the relative connectivity between Mainland Asia, Borneo, Australia, New Guinea and the Philippines increases dramatically, while very little connectivity is inferred between the Lesser Sunda Islands, Maluku Islands, Sulawesi and Sumatra.

The most likely explanation for this change in connectivity tracks through time is the changing availability of landmass across the SSCZ over time. Mainland Asia, Borneo, Australia and the Philippines have all maintained substantial emergent landmass available to support vegetation since the Eocene (de Bruyn *et al.* 2014). Although much uncertainty surrounds the geology of New Guinea, current research suggests some parts of New Guinea were also emergent from the Late Jurassic (Hill and Hall 2003; Cloos *et al.* 2005; Jonsson *et al.* 2011; Harrington *et al.* 2017). Furthermore, modern Mainland Asia, Borneo, the Philippines and parts of New Guinea have an ancient history of close geographical proximity; recent tectonic models suggest that from 43 Mya, the Philippine Arc, Melanesian Arc and proto-Caroline Arc formed a continuous island arc (Zahirovic *et al.* 2016). The long-term persistence of these emergent landmasses and historical connectivity is likely to explain the signature of exchange between these landmasses at higher taxonomic levels. The long-term persistence of lineages on these landmasses has previously been reported by Oliver *et al*. (2018), who found early-diverging lizard lineages distributed across modern landmasses of this ‘lost arc’. In contrast, Sumatra and Java on the Sunda shelf were mostly submerged during the mid-Miocene (de Bruyn *et al.* 2014), and most of Sulawesi, the Lesser Sunda Islands and the Maluku Islands did not emerge above sea level until the Pliocene (Nugraha and Hall 2018) – this explains why signatures of plant connectivity between these islands are mainly detectable at the species level. Depending on the amount of gene flow between island groups, connectivity may lead to speciation or range expansion and increased homogenization of the flora across the SSCZ.

This study contributes to a growing body of evidence suggesting that Mainland Asia, Borneo, Australia, New Guinea and the Philippines have a long history of emergence and are important regional refugia. It also emphasizes the temporal complexity of understanding biogeography in the region, and that introducing time-slicing to biogeographical phylogenetic studies could be a fruitful area of future research.

Conclusion

The SSFE has had a substantial impact on floristic assembly in the region. The results of this study suggest that Lydekker's Line and Wallace's Line do not mark strong biogeographical barriers for plants, and that plant distributions are mainly determined by annual rainfall, seasonality and available landmass. That is, establishment and persistence, rather than dispersal, are strongly limiting. These findings highlight the spatial and temporal complexity of exchange and suggest that further insight can be gained by researching functional traits, and incorporating ecological units (biomes) and geologically relevant time slices into analyses of evolutionary patterns and processes.

Chapter 4

Molecular phylogeography reveals two geographically and temporally separated floristic exchange tracks between Southeast Asia and northern Australia

Preface

In Chapters 2 and 3, I characterised the phytogeography of the Sunda-Sahul Convergence Zone, and investigated how the Sunda-Sahul Floristic Exchange affected the floristic composition of the region. In Chapter 4, I take a finer-scale approach, using a phylogeographic case-study to understand where floristic exchange occurs between Asia and Australia, and how this may influence northern Australian phytogeography.

This chapter has been published in Journal of Biogeography:

Joyce EM, Pannell CM, Rossetto M, Yap J-YS, Thiele KR, Wilson PD, Crayn DM (2021) Molecular phylogeography reveals two geographically and temporally separated floristic exchange tracks between Southeast Asia and northern Australia. *Journal of Biogeography* **48**, 1213–1227. doi:https://doi.org/10.1111/jbi.14072.

EMJ conceived the idea for this research, designed the study and conducted the field work, sampling, laboratory work and analysis and wrote the manuscript. DMC and KRT assisted EMJ in developing the design for the study. CMP conducted sampling with EMJ and contributed expertise on the biology of the target species. KRT conducted field work with EMJ. MR, J-YSY and PDW assisted EMJ with analysis and interpretation of results and MR funded the sequencing. CMP, KRT, MR, J-YSY, PDW and DMC all assisted with writing the manuscript.

Abstract

Aim

Exchanges of plant lineages between Australia and Southeast Asia have had a substantial impact on the evolution of Australia's northern, tropical flora, with important ramifications for its conservation and biosecurity. Despite this, floristic exchange tracks between northern Australia and Southeast Asia remain poorly understood. To address this, I conducted a molecular phylogeographic case study to identify exchange tracks between Australia and Southeast Asia.

Location

India, Southeast Asia, Australia and Pacific islands.

Taxon

The widespread tropical monsoonal tree species *Aglaia elaeagnoidea* (Meliaceae).

Methods

I conducted a phylogeographic study using DArTseq analysis of 141 herbarium and silica-dried samples sourced from across the range of *A. elaeagnoidea*. I identified 176,331 single nucleotide polymorphisms (SNPs) across 90,456 loci that I analysed using multivariate, admixture, genetic differentiation and coalescent methods to characterise phylogeographic and phylogenetic patterns. An environmental niche model for the last glacial maximum was also generated.

Results

Two exchange tracks were identified: one from New Guinea to Cape York Peninsula in north-east Australia, and a second from Timor to the Kimberley Plateau of north-west Australia. The Cape York Peninsula track is contemporary, characterised by ongoing genetic exchange, whereas the Kimberley Plateau track is historic, facilitated by multiple past exposures of the Arafura Shelf during the Pleistocene. Overall, I suggest that phylogeographic patterns of *A. elaeagnoidea* have likely resulted from a combination of repeated range expansion and contraction cycles concurrent with Quaternary climate fluctuations, and stochastic dispersal events.

Main conclusions

This study provides the first phylogeographic evidence for two floristic exchange tracks between northern Australia and Southeast Asia. It also highlights the influence of Quaternary climate fluctuations on the complex biogeography of the region, and supports the idea that the Kimberley Plateau and Cape York Peninsula in northern Australia have separate biogeographic histories.

Introduction

The fact that plant lineages were exchanged between Australia and Southeast Asia is well established; however, how the exchange has impacted phylogeography across the region is not understood. Joseph Hooker was the first to note affinities between the northern Australian and Asian floras, stating that Indian and Malesian flora "continued […] with great force over the whole of tropical Australia" (Hooker 1859). More recently, palaeobotanical and phylogenetic work indicates that floristic exchange between Australia and Southeast Asia commenced c. 30 Mya between Australia and Southeast Asia (Sniderman and Jordan 2011; Crayn *et al.* 2015; Murphy and Crayn 2017; Yap *et al.* 2018, 2020). This coincided with the increased connectivity of Australia and Southeast Asia as the continental shelf on which Australia is situated (the Sahul Shelf) began to collide with the Southeast Asian Sunda Shelf (McLoughlin 2001; Hall 2011, 2017). A recent checklist of the vascular flora of the region indicates that more than 2300 species of vascular plants are shared between Australia and Southeast Asia (Joyce *et al.* 2020). Of these, 635 are found in the northern Australian phytogeographic subregions of Kimberley Plateau, Arnhem Land, Cape York Peninsula and Atherton (*sensu* Ebach *et al.* 2015; Figure 4.1), representing approximately 10% of the plant species in northern Australia (Joyce *et al.* 2020). The biogeographic link between northern Australia and Asia is obvious, but the location of past and present exchange tracks, and the effects of the exchange on Southeast Asian and northern Australian phylogeography, are unclear.

It is generally assumed that the major floristic exchange track between Australia and Southeast Asia lies between New Guinea and Cape York Peninsula. In part, this is because the seaway between them – the Torres Strait – is the smallest gap between the two regions (c. 150 km, with many intervening islands) and repeatedly formed a land bridge during Pleistocene glacial maxima. Van Steenis (1934) postulated that tropical montane floristic elements were exchanged through a 'Papuan track' via Borneo, New Guinea and Cape York Peninsula. Similarly, rainforest lineages have been postulated to exchange between New Guinea and Cape York Peninsula, and along the east coast of Australia (Burbidge 1960; Specht 1981; Sniderman and Jordan 2011). In a study of floristic distributions, van Steenis (1979) was the first to suggest that plants adapted to the seasonally-dry monsoon may have exchange tracks in Arnhem Land and the Kimberley Plateau rather than via Cape York Peninsula. This was supported by a recent floristic study of all known species of vascular plants in the region, which showed that the floristic composition of the Australian monsoonal tropics has a high similarity to that of the Lesser Sunda Islands and Timor (Joyce *et al*. 2021a). The presence of these alternative monsoon exchange tracks between Arnhem Land and New Guinea and the Kimberley Plateau and New Guinea was first tested by a cladistic biogeographic analysis of 11 plant clades (Crisp *et al.* 1995). However, the presence of exchange tracks between the Kimberley Plateau or Arnhem Land are yet to be tested with genetic data.

More broadly, little is known about phylogeographic patterns in Southeast Asia, with the few studies conducted mostly focusing on fauna or covering a restricted geographic range (Cannon 2001; Liao *et al.* 2007; Ueda *et al.* 2010; Tnah *et al.* 2012; Pedersen *et al.* 2018; Jusoh *et al.* 2019; Grismer *et al.* 2019; Husson *et al.* 2020; Lim *et al.* 2020). In Australia, phylogeographic studies of rainforest plants have revealed varied expansion-contraction responses to the climatic fluctuations of the Quaternary (Rossetto *et al.* 2004; Mellick *et al.* 2012, 2013; Fahey *et al.* 2019); however, responses of the Southeast Asian flora are yet to be studied in detail. Elucidation of Southeast Asian phylogeographic patterns and identification of exchange tracks with northern Australia are critical for understanding past evolutionary processes and present biogeographic patterns, knowledge which is in turn necessary for effective conservation of the region's biota.

To investigate Southeast Asian phylogeography and exchange tracks between northern Australia and Southeast Asia, I conducted a case study using *Aglaia elaeagnoidea* (A.Juss.) Benth. *Aglaia* Lour. is one of the most widespread and species-rich genera in Meliaceae, comprising c. 120 species widely distributed in India, China, Southeast Asia, Australia and the Pacific islands (Pannell 1992, 2018; Grudinski *et al.* 2014). *Aglaia elaeagnoidea* is a small, dioecious tree usually found in monsoon secondary and beach forest (Pannell 1992). It has small, indehiscent fruits and seeds with a fleshy aril that are thought to be dispersed by primates and birds, particularly fruit pigeons. *Aglaia elaeagnoidea* was chosen for this study for three reasons. Firstly, to my knowledge, *Aglaia* is the only genus in the Southeast Asian region for which a complete morphological monograph (Pannell 1992) has been published. An understanding of morphological variation and distributional limits is essential in phylogeographic work, and Pannell's monograph enables this for *Aglaia elaeagnoidea*. Secondly, previous phylogenetic work provides a framework for the sampling of *A. elaeagnoidea* and its related taxa and establishes that Sunda is the ancestral area for *Aglaia*, allowing us to infer directionality of the phylogeographic patterns in *A. elaeagnoidea* (Grudinski *et al.* 2014). Finally, *A. elaeagnoidea* has an appropriate distribution for the questions in this study; its range extends from India in the west, throughout much of Southeast Asia, and to the Pacific islands of Wallis and Futuna at its eastern-most limit (Pannell 1992). Within Australia, *A. elaeagnoidea* has a discontinuous distribution, with populations in the Kimberley Plateau and Cape York Peninsula and no records between (Pannell 2008; Pannell pers. comm. 2020; Figure 4.1). This disjunct distribution (Asia-Kimberley Plateau-Cape York Peninsula) has also been observed in approximately 35 other plant species, but the reason for it is unclear (R. Barrett, pers. comm.; B. Maslin, pers. comm.; Joyce *et al.* 2020). Thus *A. elaeagnoidea* is an ideal taxon for investigating exchange tracks between northern Australia and Southeast Asia and Southeast Asian phylogeography.

Here I report the results of a study which used genome-wide DArTseq SNP data to characterise the phylogeography of *A. elaeagnoidea* throughout Southeast Asia, Australia and the Pacific islands. I aimed to characterise phylogeographic patterns to evaluate four historical biogeographical scenarios that can explain the current Australian distribution of *A. elaeagnoidea*: 1) one exchange track between Australia and Asia, with *A. elaeagnoidea* once widespread across northern Australia and subsequently vicariant into two widely disparate populations; 2) one exchange track between Australia and Asia with a second disjunct population established within Australia via long-distance intra-continental dispersal; 3) two exchange tracks between Australia and Asia, with both Australian populations established from the same source area in Asia, and 4) two exchange tracks between Australia and Asia, with different source areas in Asia. The first three scenarios predict that all Australian populations form a single genetic group, while the fourth scenario predicts that each Australian population would be more similar to different Asian populations that to each other.

Materials and methods

Sampling

Samples for this study were obtained predominantly from herbarium specimens, augmented by field-collected silica-dried material. The most recent phylogenetic study of *Aglaia* suggested (albeit with weak support) that *A. elaeagnoidea* is not monophyletic (Grudinski *et al.* 2014). To account for this, samples were taken from all species currently thought to be closely related to *A. elaeagnoidea*, i.e. *A. elliptica* Blume, *A. chittagonga* Miq., *A. simplicifolia* (Bedd.) Harms, *A. malabarica* Sasidh., *A. apiocarpa* (Thwaites) Hiern, *A. leucophylla* King and *A. korthalsii* Miq. (Grudinski *et al.* 2014). In addition, samples were taken from species morphologically similar to *A. elaeagnoidea* but thought to be more distantly related, including *A. smithii* Koord., *A. edulis* (Roxb.) Wall., *A. odoratissima* Blume and *A. scortechinii* King. *Aglaia lawii* (Wight) C.J. Saldanha ex Ramamoorthy and *A. spectabilis* (Miq.) S.S. Jain & Bennet were chosen as outgroup species due to their clear morphological and genetic distinction from *A. elaeagnoidea*. To further account for the potential non-monophyly of *A. elaeagnoidea*, extensive sampling was conducted to encompass the full suite of morphological variation in the taxon. In total, 254 *A. elaeagnoidea* and outgroup samples were obtained, 247 of these from herbarium specimens and seven (all Australian) from silica-dried material. Details of all samples used are provided in Appendix B1.

Dried leaf tissue was sampled from herbarium specimens from 14 herbaria (see Appendix B2 for list) following institutional destructive sampling guidelines. Species identity and *A. elaeagnoidea* morphotype of all sheets was confirmed by CMP (monographer of *Aglaia*) or EMJ. Notes on morphology and locality were made and a photograph taken of every sheet. A field trip to the Kimberley region, Western Australia was undertaken in April-May 2018 where silica-dried tissue was obtained from one population of *A. elaeagnoidea*. Vouchers for these samples are accessioned at PERTH. Silica-dried tissue for CNS accessions was obtained from Dr Wendy Cooper.

DNA extraction

For each sample, 15 mg of leaf material was ground with a TissueLyser (Qiagen; Hilden, Germany). DNA was extracted with a DNeasy Plant Mini Kit (Qiagen; Hilden, Germany) using a modified protocol as follows. At step two, where Buffer AP1 is added, 30 μl of βmercaptoethanol and 6 µl of 20 mg/ml Proteinase K were added to denature proteins and remove tannins and polyphenols. RNase A was not added as recommended in the manufacturer's protocol at this step as yield was slightly improved without it, likely due to the prevention of RNase A-DNA complex formation (Donà and Houseley 2014). Samples were incubated for 2 hours at 65°C instead of the recommended 10 minutes, and eluted in a total volume of 120 µl. DNA quantity and quality were ascertained with a Qubit fluorometer (Thermo Fisher Scientific, Invitrogen; Waltham, MA, USA) and Nanodrop spectrophotometer (Thermo Fisher Scientific; Waltham, MA, USA). For samples with low DNA concentrations, extractions were replicated and the products combined and concentrated.

Of 254 specimens sampled, 131 yielded > 2 ng/ul DNA, while 22 samples yielded < 1ng/ul DNA, of good quality. Samples with successful extractions were from *A. elaeagnoidea*, *A. korthalsii*, *A. chittagonga*, *A. edulis*, *A. elliptica*, *A. lawii*, *A. leucophylla*, *A. spectabilis* and *A. scortechinii*. Following optimisation, all successful samples were sent for sequencing.

Sequencing

Samples were sent to Diversity Arrays Technology Pty Ltd (DArT; www.diversityarrays.com/) for library preparation and DArTseq sequencing. DArTseq is a high throughput, restriction-based, reduced representation genome sequencing method. In plants, DArTseq retrieves thousands of single or low copy markers and SNPs within or close to genes from across the genome (Garavito *et al.* 2016; Rossetto *et al.* 2019). The proprietary DArT library preparation method is similar to that described by Kilian *et al.* (2012) and Cruz *et al.* (2013), whereby genomic DNA is reduced to a representative sample by restriction enzyme digestion, fluorescently labelled, and hybridised to arrays containing probes with reference DNA. The fluorescence of the arrays is then measured to estimate relative hybridisation intensity; sites that display significant differences in hybridisation intensity are scored by DArT proprietary software as polymorphic (Kilian *et al.* 2012). DArT proprietary analysis pipelines were used to remove poor-quality sequences, correct low-quality bases, call SNPs, BLAST search sequences to eliminate matches with microbial contaminants, and generate genotype data.

Resultant genotypes were initially processed in R using a pipeline described in Rossetto *et al*., (2019). Descriptive statistics for the genotype data were generated and SNP loci of poor quality filtered out to retain loci with a minimum reproducibility of 0.96 and with <20% of genotypes missing. Data were filtered to retain one randomly selected SNP per locus. Poor quality samples of *A. elaeagnoidea* (>20% missing loci) were identified and removed if they presented as outliers in subsequent analyses. Outgroup samples with more than 20% missing loci were retained, as the relatively high degree of missing loci could be due to differences in restriction enzyme site locations in taxa more distantly related to *A. elaeagnoidea*. Ploidy is poorly characterised in *Aglaia*, and the ploidy level of *A. elaeagnoidea* is unknown; it was assumed that *A. elaeagnoidea* is diploid in all analyses.

Identification of genetic structure in the A. elaeagnoidea complex

Phylogeographic studies address questions that bridge microevolutionary (e.g. population genetics) and macroevolutionary (e.g. phylogenetics) disciplines. In microevolutionary disciplines, a population is the unit of study and can be defined as a group of individuals from the same species that have a high probability of interacting with each other (e.g. Hastings 2013), while in macroevolutionary disciplines single representatives of independently evolving lineages (such as separate species) are often used as the unit of study. Deciding on an appropriate unit to conduct a phylogeographic study is difficult, and must be weighed against the logistics of sampling. I argue that at the spatial and temporal scale of this study, it is sensible to assume that interactions between individuals occupying the same island have been more frequent than those between islands. As such, for the purposes of this study, a ‘population’ refers to individuals from the same island, or in the case of Australia, on either side of the continent, although I acknowledge this is not the traditional definition of population. By using this definition of population as my unit of study, analyses based in phylogenetic theory (such as SVDquartets) are appropriate; however, care must be taken when interpreting analyses designed for conventional population genetic studies as the assumptions of some of these analyses may not be met (see, for example, Holsinger and Weir 2009). This is especially the case for islands where genetic material of only a single representative was able to be retrieved, as one individual is unlikely to accurately represent the genetic makeup of the island as a whole.

Similarities between *A. elaeagnoidea* and outgroup species were initially explored using Principal Components Analysis (PCA) of SNP data using the R package ‘adegenet’ v 2.1.0 (Jombart *et al.* 2020). NeighbourNet analysis (Bryant and Moulton 2004) was conducted in SplitsTree4 v.4.15.1 (Huson and Bryant 2006) to visualise a distance-based phylogenetic network. Phylogenetic relationships under a coalescence model were estimated using the SVDquartets (Chifman and Kubatko 2014) method as implemented in PAUP* v4.0a (Swofford 2003), with individuals assigned to island group populations as identified from PCA clusters. 100,000 quartets were sampled at random and assembled using the QFM quartet assembly method. Confidence in resultant bipartitions was assessed with 100 bootstrap replicates.

Phylogeographic analysis of eastern A. elaeagnoidea populations

Because *A. elaeagnoidea* samples were clearly differentiated into groups from the eastern and western parts of the species’ geographical range (see results), further analyses were conducted on the subset of eastern *A. elaeagnoidea* samples (n = 99) in order to focus on identifying exchange tracks with Australia.

Pairwise Fst statistics were calculated for each population with four or more samples using the R package ‘SNPrelate’ (Zheng *et al.* 2012).

TreeMix (Pickrell and Pritchard 2012) was used to characterise patterns of population splitting and mixing from allele frequencies among eastern *A. elaeagnoidea* populations. A Maximum Likelihood tree was generated, with Taiwan designated as the root population and SNPs partitioned into blocks of 1000 to account for linkage disequilibrium. Taiwan was chosen as the root because the SVDquartets analysis suggested that Taiwan is the earliest-diverging population among sampled eastern *A. elaeagnoidea*. Trees were generated incorporating zero to ten migration events with five iterations under each model. The optimum number of migration events to model population splitting and mixing was determined by calculating the second-order rate of change in likelihood for each iteration of each tree under zero to ten migration events, weighted by the standard deviation (Evanno method; Evanno *et al.* 2005), implemented in ‘OptM’ (Fitak in press) in R. This process was repeated with adjacent populations merged, to assess whether differences in tree topology occurred when the number of individuals per population was more even.

Admixture analysis of populations was conducted using sparse non-negative matrix factorisation (snmf) as implemented in the snmf function in the R package 'LEA' (Frichot and François 2015). The number of ancestral populations (K) was determined using the entropy criterion (Alexander and Lange 2011; Frichot and François 2015). Ancestry coefficients were visualised by plotting the Q-values of each individual in a bar plot and average Q-values for each population on a map.

Environmental niche modelling

Records for *Aglaia elaeagnoidea* were downloaded from GBIF (https://www.gbif.org) and filtered to only include those from the east of the distribution to specifically investigate exchange tracks between Australia and Southeast Asia and to avoid conflation of the multiple taxa in the *A. elaeagnoidea* complex as identified in this study. Records were further filtered to only include herbarium records collected after 1960 with coordinates without geospatial issues. Records were manually checked and those with obvious errors in coordinates (e.g. records in the ocean) removed. Eastern samples included for sequencing in this study were added to the dataset; many of these have not been digitised or the localities were manually determined from locality information provided on the specimen. Duplicate records were removed. This resulted in 344 occurrence records for eastern *A. elaeagnoidea* (Appendix B3).

Environmental variables used for modelling the distribution of *A. elaeagnoidea* were selected from 19 standard bioclimatic variables (Booth *et al.* 2014). I used the global downscaled climate dataset (Karger *et al.* 2017, 2018), an interpolated dataset that has been subject to rigorous quality assessment and that performs well across the Southeast Asian tropics. Nevertheless, there may still be some inaccuracies inherent in this dataset due to the uneven distribution of weather stations across the region (Hijmans *et al.* 2005; Karger *et al.* 2017, 2018). An initial model was run in MaxEnt using all environmental variables to ascertain the relative importance of each variable in determining the presence of *A. elaeagnoidea*. Autocorrelation between environmental variables was assessed using the corr function in R, and variables with a high degree of correlation (R >0.7; Appendix B4) removed (with the least-explanatory variable eliminated first). The resultant set of variables was then evaluated for biological significance and to ensure that variables thought to be important for determining the distribution of *A. elaeagnoidea*, such as seasonality, were included. A final set of eight environmental variables was included in the model: Bio03 (isothermality), Bio07 (annual temperature range), Bio08 (mean temperature of wettest quarter), Bio11 (mean temperature of coldest quarter), Bio13 (precipitation of wettest quarter), Bio15 (precipitation seasonality), Bio18 (precipitation of warmest quarter) and Bio19 (precipitation of coldest quarter).

The species distribution model was trained in MaxEnt v.3.4.0 (Phillips *et al.* 2006) allowing only linear, quadratic and product features, to minimise the risk of overfitting. A maximum of 100,000 background points was modelled and restricted to a 100km radius of presences. Ten cross-validation replicates were run.

The model was projected onto paleoclimatic data for the Last Glacial Maximum (LGM; approximately 21,000 years ago). The LGM was chosen to model distribution differences under the most extreme climatic conditions within the time that a species may have evolved. To account for climate model variation, I calculated mean climate rasters for each bioclimatic variable from nine available paleoclimatic datasets within the CHELSA dataset (Karger *et al.* 2017, 2018).

I considered ensemble methods for generating the ENM; however, there is much evidence that well-fitted and thoughtfully interpreted MaxEnt models perform well. Furthermore, a recent paper by Hao *et al*. (2019) supports the view that ensemble modelling can be helpful but has many of the same short-comings, constraints, trade-offs and subjective choices of any approach to modelling. Here, I have carefully considered and chosen the parameters to generate a model that makes good biological and statistical sense, and have interpreted the results conservatively.

Results

SNP data

This study is one of the first to use DArTseq on herbarium material for a phylogeographic study, recovering 176,331 SNPs from 90,456 loci in 141 of 153 samples (Besnard *et al.* 2018). Notable successes include genotype data from a nearly 200 year old specimen from NY (*Wight 140*, DNA no. G08438), and specimens treated with mercury (e.g. some US

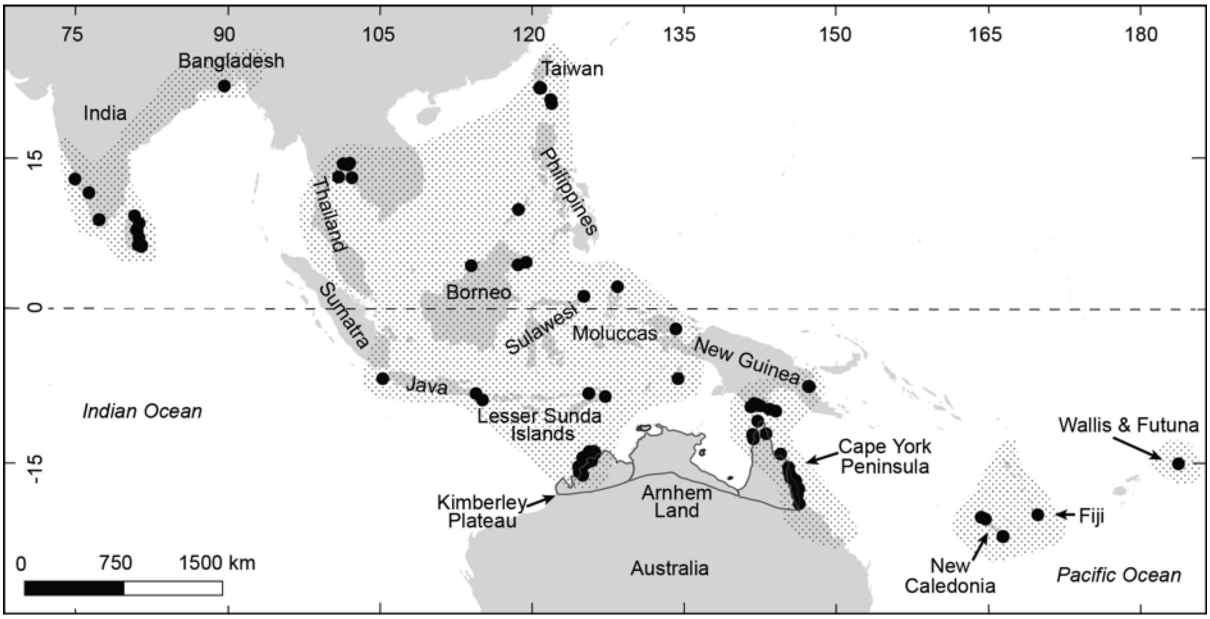

Figure 4.1 Map of the 129 *Aglaia elaeagnoidea* specimens sampled for this study. The shaded area represents the known distribution of *A. elaeagnoidea* according to Pannell (1992). The three northern Australian phytogeographic subregions referred to in this study (Kimberley Plateau, Arnhem Land and Cape York Peninsula *sensu* Ebach *et al.* 2015) are outlined.

specimens) and gamma irradiation (e.g. DNA no. G08724). Yield of extracted DNA was the main factor limiting successful sequencing; most samples that yielded >2 ng/µl of high-quality DNA were successfully sequenced. No specimens sampled from SING or BO were successful; observations made when sampling suggested that specimens kept in tropical conditions were generally browner in colour and presented greater difficulties in achieving adequate DNA yield (see also Brewer *et al.* 2019).

The final dataset, after removal of SNPs from poor quality loci or samples, comprised 22,834 loci with one SNP per locus for 136 samples (Appendix B1). Of these, 129 samples were *A. elaeagnoidea* from across its distribution (Figure 4.1) and the remaining seven samples were from the outgroup species *A. edulis* (two samples), *A. spectabilis* (two samples), *A. korthalsii*, *A. leucophylla* and *A. chittagonga*.

Lineage divergence in the A. elaeagnoidea complex

PCA (Figure 4.2a) and NeighbourNet analysis (Figure 4.2b) both showed substantial genetic structure in the *A. elaeagnoidea* complex, with a clear east-west divide. Individuals

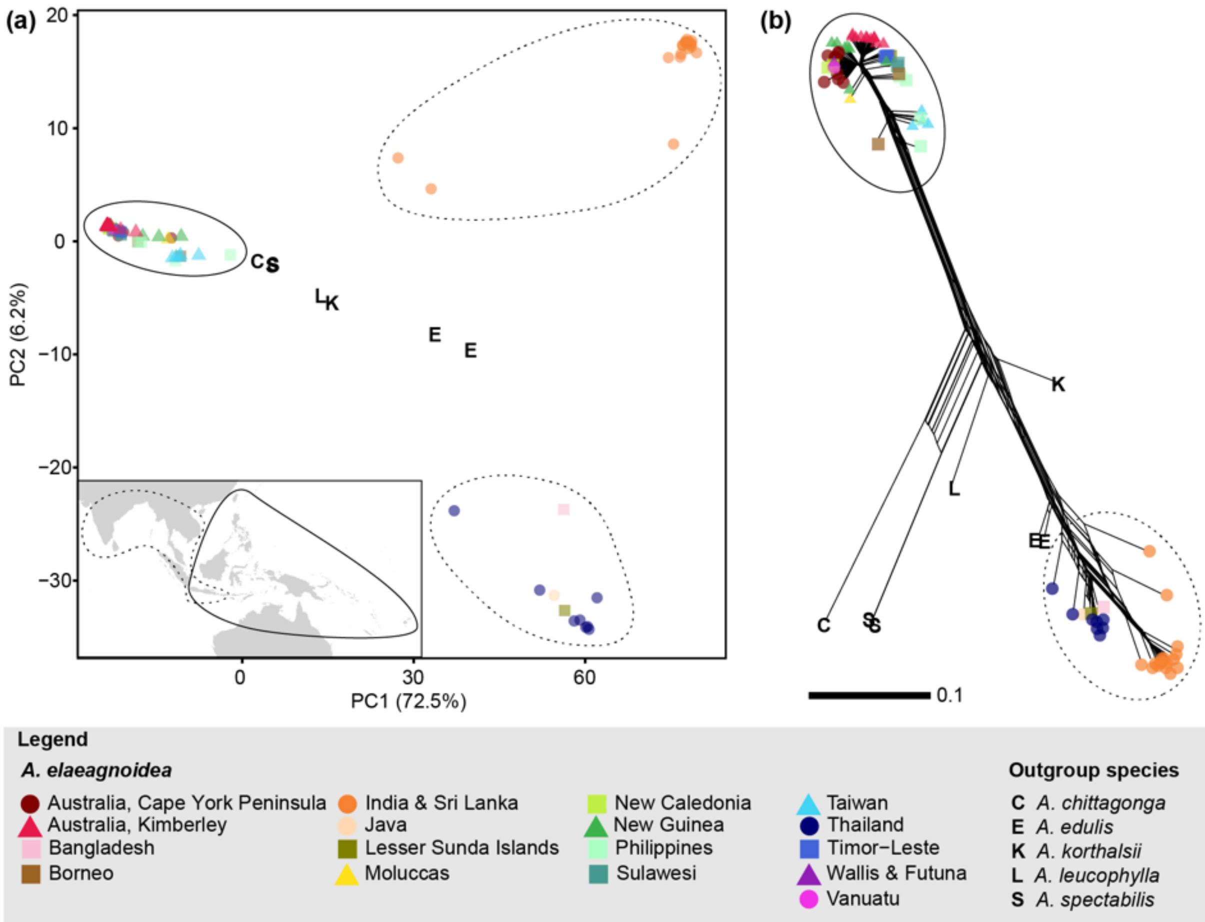

Figure 4.2 a) Principal Component Analysis (PCA) and b) NeighbourNet network of 22,834 loci with one SNP per locus for all *Aglaia* samples (*A. elaeagnoidea* and outgroup species *A. chittagonga, A. edulis, A. korthalsii, A. leucophylla* and *A. spectabilis*). Letter symbols represent outgroup samples, while coloured shapes represent *A. elaeagnoidea* samples from different populations. Points circled in dashed line represent samples from the west of the distribution of *A. elaeagnoidea* (India, Sri Lanka, Bangladesh, Thailand, Lesser Sunda Islands and Java), while samples circled in solid line are *A. elaeagnoidea* samples from the eastern end of the distribution (Australia, New Guinea, Pacific islands, Moluccas, Lesser Sunda Islands, Timor, Java, Sulawesi, Borneo, Philippines and Taiwan), as shown in inset map.

from the eastern part of the species' distribution (Borneo, Sulawesi, Philippines, Taiwan, the Moluccas, New Guinea, Australia, Timor, Pacific islands and some individuals from Java and the Lesser Sunda Islands) clustered together, while specimens from the western part (India, Sri Lanka, Bangladesh, Thailand and some individuals from Java and the Lesser

Sunda Islands), clustered separately. Within the western group, Indian (including Sri Lankan) individuals appear to be genetically distinct from individuals from Bangladesh, Thailand, Java and the Lesser Sunda Islands. Outgroup species clustered separately from *A. elaeagnoidea*, but the NeighbourNet analysis suggests that *A. edulis* is most closely related to the western *A. elaeagnoidea* groups.

The SVDquartets analysis sampled 17.84% of the total number of distinct quartets, 90.9% of which were compatible in quartet assembly. The resultant 50% majority rule consensus tree recovered eastern and western populations of *A. elaeagnoidea* in separate clades (Figure 4.3). Western *A. elaeagnoidea* populations were recovered with maximum (100%) support in a clade including *A. edulis*. Eastern populations of *A. elaeagnoidea* were recovered in a clade with maximum (100%) support, which included *A. korthalsii* with weak (54%) support.

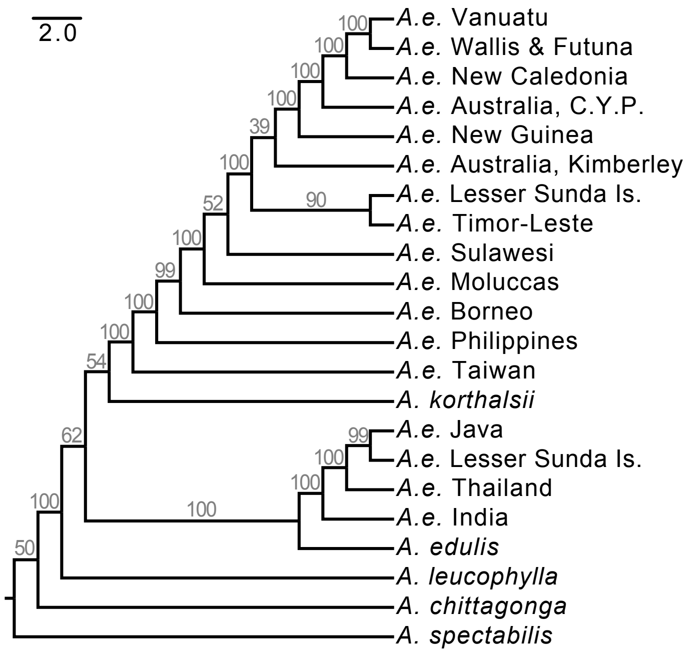

Figure 4.3 SVDquartets 50% majority rule consensus tree of 22,834 SNPs for all *Aglaia elaeagnoidea* (‘*A.e.*’) populations and sampled outgroup species (*A. chittagonga, A. edulis, A. spectabilis, A. leucophylla* and *A. korthalsii*) under a coalescence model with 100,000 quartets assembled using the QFM quartet assembly method. 7.84% of the total number of distinct quartets were sampled, 90.9% of which were compatible in quartet assembly. Figures on branches indicate bipartition bootstrap values from 100 bootstrap replicates. ‘C.Y.P.’ refers to Cape York Peninsula.

The genetic distinctiveness of eastern and western *A. elaeagnoidea* groups is consistent with morphological differences (including in indumentum, leaf shape, and fruit colour and shape) which, taken together, suggests that they represent separate species. The taxonomic implications of this finding are outside the scope of this study, however, and will be dealt with in a subsequent paper. Given the clear distinction between eastern and western *A. elaeagnoidea*, all further analyses were conducted on the eastern *A. elaeagnoidea* group, to investigate exchange tracks between Australia and Southeast Asia, and to avoid confounding patterns across multiple putative species.

Analysis of eastern A. elaeagnoidea phylogeography

Principal Components Analysis (PCA) showed substantial genetic structure in eastern *A. elaeagnoidea* (Figure 4.4a). Individuals from Taiwan, Philippines, Borneo and Sulawesi had a high degree of variation that was mostly captured by PC1 (31.2%), while PC2 (18.1%) largely represented variation among individuals from the Pacific islands, Australia

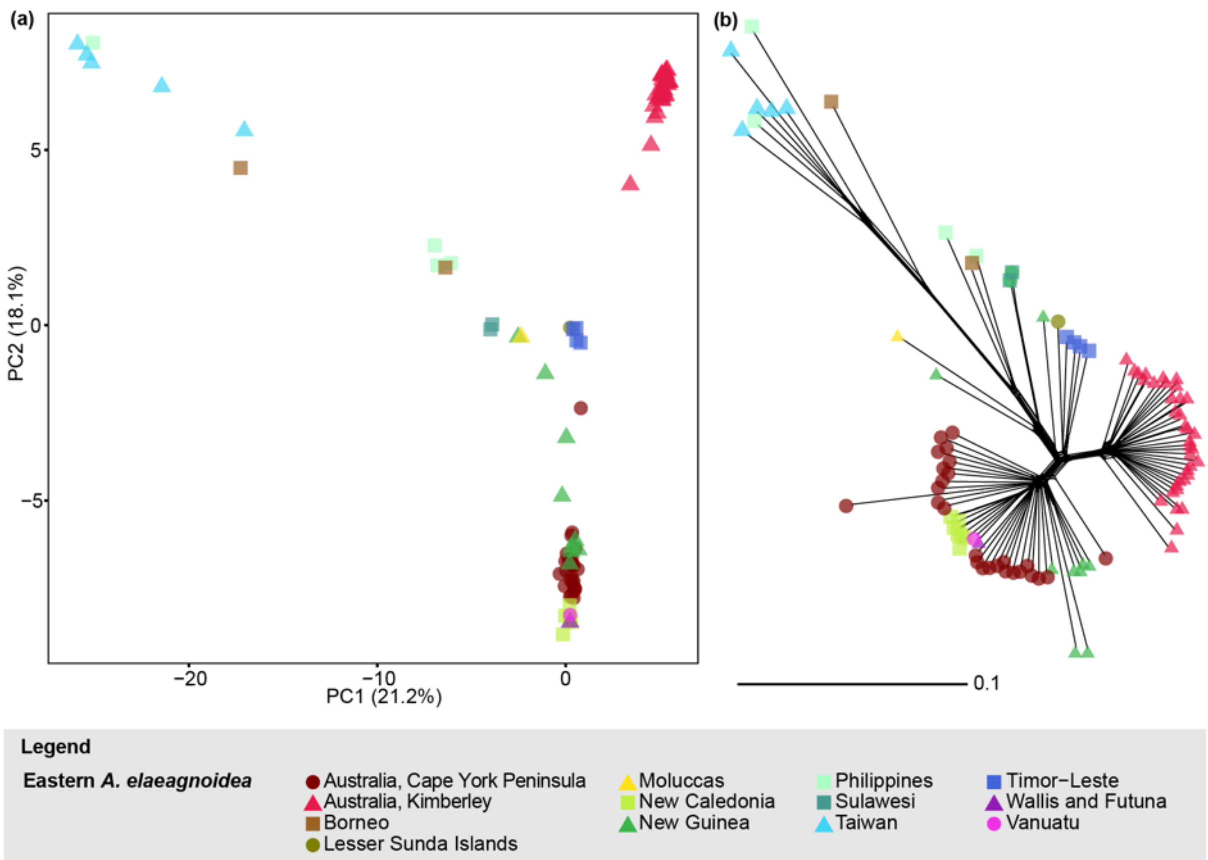

Figure 4.4 a) PCA and b) NeighbourNet network of 22,834 SNPs of the eastern *A. elaeagnoidea* group (see solid line in Figure 4.2 for distribution). Symbols represent each population in the eastern *A. elaeagnoidea* group.

and New Guinea. Individuals from the Kimberley clustered separately from Cape York Peninsula individuals, which clustered with individuals from New Guinea and the Pacific islands. These patterns, including the strong differentiation of the Australian populations, were also found in the NeighbourNet analysis (Figure 4.4b).

A high degree of genetic differentiation was observed between the eastern *A. elaeagnoidea* populations analysed, with the exception of Cape York Peninsula compared to New Guinea (Fst = 0.09). The Kimberley Plateau population is highly genetically divergent from all other populations analysed, but is most strongly differentiated from the Cape York Peninsula population (Fst = 0.50) and most similar to the Timor population (Fst = 0.29; Table 4.1).

Table 4.1 Pairwise Fst of eastern *A. elaeagnoidea* populations with n ≥ 4.

	Cape York Peninsula	**Kimberley Plateau**	**New Caledonia**	**New Guinea**	**Philippines**	**Taiwan**
Kimberley Plateau	0.50					
New Caledonia	0.20	0.49				
New Guinea	0.09	0.39	0.32			
Philippines	0.35	0.36	0.66	0.48		
Taiwan	0.56	0.48	0.84	0.79	0.35	
Timor	0.29	0.29	0.51	0.31	0.45	0.78

The topology of the TreeMix maximum likelihood tree suggests that the Philippines population is sister to the Taiwan population, with a high drift parameter (Figure 4.5; Appendix B5). Sulawesi, the Moluccas and Borneo form a clade, and Lesser Sunda Islands is sister to a clade including Australian, Pacific island, and New Guinea populations (Figure 4.5). Within this clade, the best model retrieved the Kimberley population as sister to the Timor population, and the Pacific island populations as sister to the Cape York Peninsula populations, which are sister to New Guinea (Figure 4.5). The OptM analysis indicated that allowing for four migration events yielded the most likely tree, increasing the likelihood from 458 with no migration events to 535. The migration event with the strongest migration

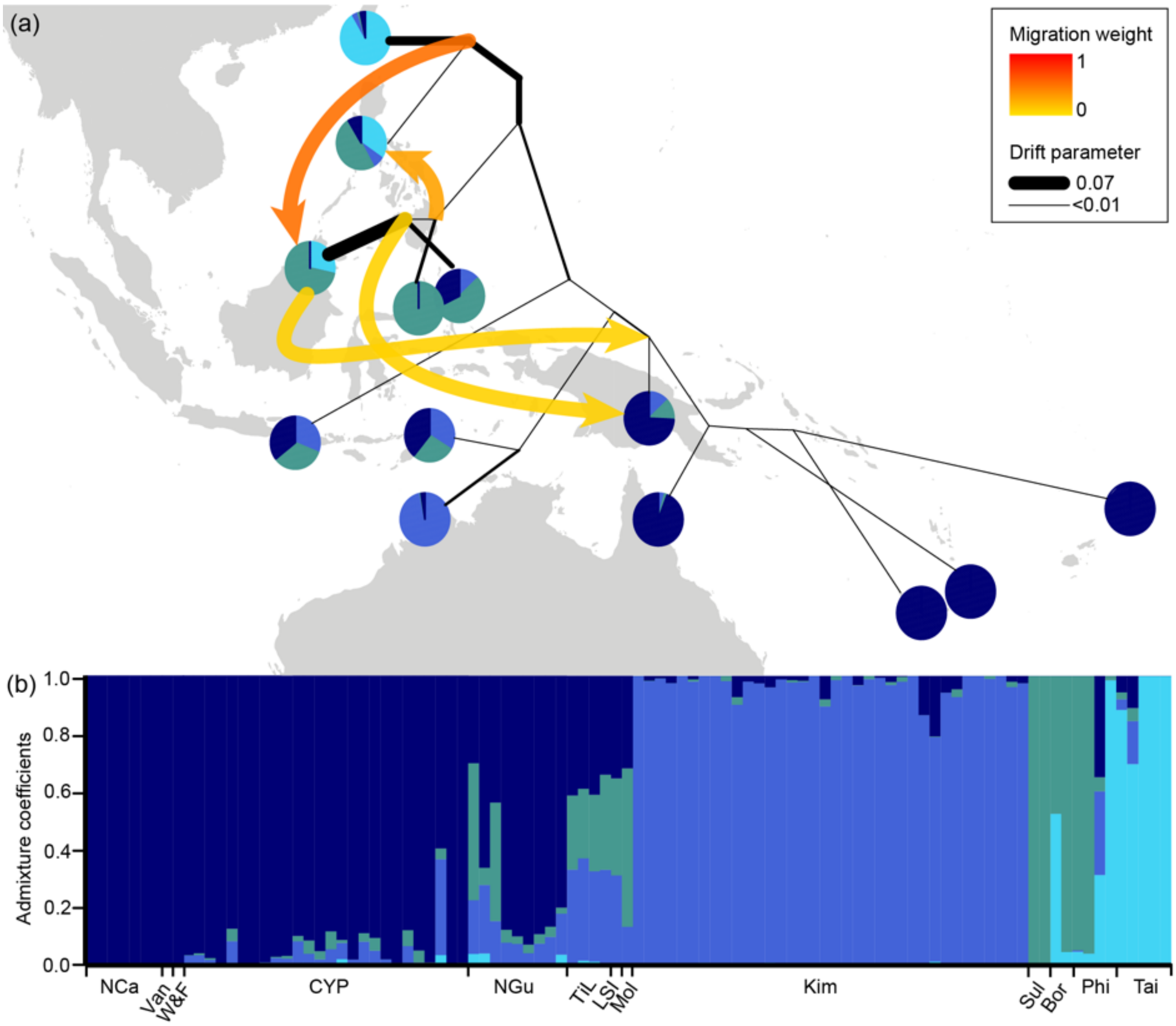

Figure 4.5 Genetic structure of eastern *A. elaeagnoidea*. a) results of TreeMix analysis showing modelled pattern of population splitting, with line thickness proportional to the drift parameter and coloured arrows showing four migration events between populations. Migration event arrow colour is representative of migration weight. For the original TreeMix tree output, see Appendix B5. Pie charts for each population superimposed on the map show mean Q-values for each population from the LEA snmf admixture analysis under four modelled ancestral populations. b) Bar plot of Q values for each individual of eastern *A. elaeagnoidea* from the LEA snmf admixture analysis modelled under four ancestral populations. Populations are indicated on the x-axis of the bar-plot: NCa = New Caledonia; Van = Vanuatu; W&F = Wallis and Futuna; CYP = Cape York Peninsula; NGu = New Guinea; TiL = Timor; LSI = Lesser Sunda Islands; Mol = Moluccas; Kim = Kimberley Plateau; Sul = Sulawesi; Bor = Borneo; Phi = Philippines; Tai = Taiwan. Colours for ancestral populations are the same in (a) and (b).

weight was from Philippines to Borneo, resulting in an estimated 51% shared alleles. A second migration event was modelled from Sulawesi, Borneo and the Moluccas to Philippines, contributing 33% of alleles to the Philippines population. A third migration event was modelled from Borneo to an ancestor of the Australia, New Guinea and Pacific island populations, and the fourth event from an ancestor of the Borneo and Moluccas populations to New Guinea, both contributing 8% of alleles to their respective sink populations.

The results of the LEA analysis suggest that the genetic structure in eastern *A. elaeagnoidea* is best explained by four ancestral populations (Figure 4.5). It revealed that the Australian populations have little shared ancestry. Populations with the highest degree of admixture were from New Guinea, Timor, the Moluccas and Philippines.

Environmental niche modelling

The mean environmental niche models (ENMs) based on eight climatic variables predicted climate suitability maps that broadly reflect the present-day distribution of eastern *A. elaeagnoidea* (mean AUC = 0.978, standard deviation = 0.008; Figure 4.6a). Bio07 (annual temperature range) and Bio03 (isothermality) explained most of the variation, contributing 38.5% and 35.2% to the model respectively. Interestingly, the model indicated high suitability in the Northern Territory of Australia, but *A. elaeagnoidea* has not been recorded there. The model also predicted that much of the landmass at equatorial latitude is currently unsuitable for *A. elaeagnoidea*, while Cape York Peninsula, the Pacific islands and Taiwan are some of the most climatically suitable areas for the species.

The projection of the model onto the LGM data predicted a much expanded distribution of climatic conditions associated with the distribution of eastern *A. elaeagnoidea*; suitable conditions were predicted south along the coast of eastern Australia into subtropical latitudes, into northern New Guinea and the Bird’s Head Peninsula, across equatorial islands and around the coast of Sundaland (Figure 4.6b,c). The Lesser Sunda Islands were predicted to be suitable for *A. elaeagnoidea*, but most of the west coast of the Arafura Shelf (Figure 4.6c) was unsuitable, with the exception of the land-masses along the Sahul Banks and Ashmore Reef in close proximity to Timor.

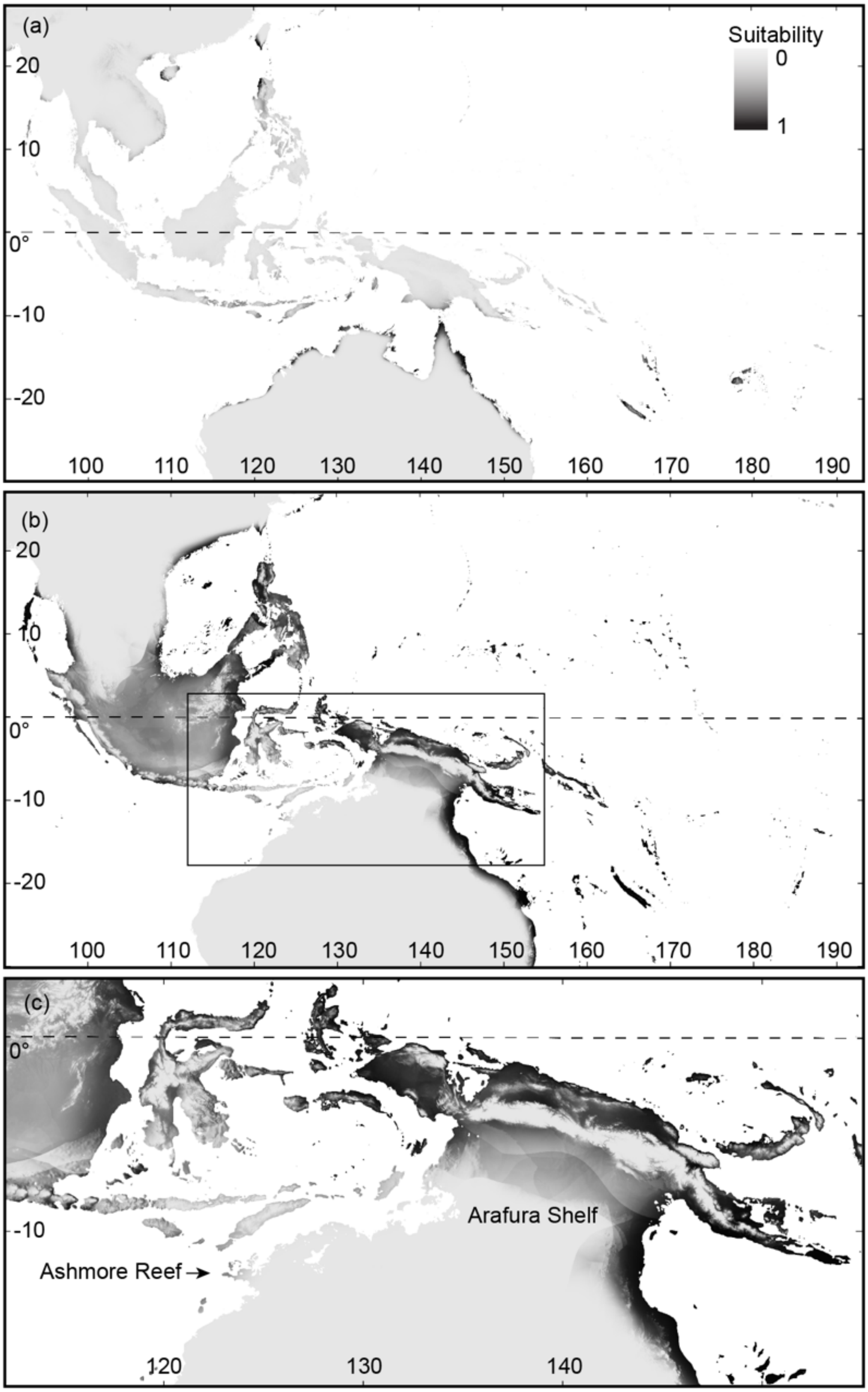

Figure 4.6 Results of Maxent species distribution modelling, predicting suitable climatic conditions for eastern *A. elaeagnoidea* from eight environmental variables (a) at present, and (b-c) during the last LGM, 22 ka. Shading is proportional to modelled habitat suitability.

Discussion

Genetic structure in A. elaeagnoidea

My results strongly suggest that *A. elaeagnoidea* as currently circumscribed comprises multiple genetic entities that are likely to represent different species. The NeighbourNet analysis showed a clear genetic distinction between western individuals (India, Sri Lanka, Bangladesh, Thailand, Java and Lesser Sunda Islands) and eastern individuals (Lesser Sunda Islands, Timor, Sulawesi, Borneo, Philippines, Taiwan, New Guinea, Moluccas, Australia and Pacific islands). Moreover, the SVDquartets analysis indicates that these two groups are not monophyletic: *A. korthalsii* is sister to the eastern *A. elaeagnoidea* group whereas *A. edulis* is sister to the western *A. elaeagnoidea* group.

These findings are congruent with those of Muellner *et al*. (2009), who observed strong genetic differentiation between a small set of 13 samples from eastern and western extremes of the range of *A. elaeagnoidea* based on one nuclear marker (internal transcribed spacer of nrDNA - ITS). Grudinski *et al*. (2014) included two samples of *A. elaeagnoidea* in their ITS phylogeny, which were not retrieved as monophyletic. Furthermore, observations of herbarium specimens indicates that the observed genetic disjunction coincides with morphological differences. I recommend that the taxonomy of *A. elaeagnoidea* is reviewed in light of these results.

Phylogeography of eastern A. elaeagnoidea and Australian-Asian exchange tracks

This paper is the first phylogeographic study to identify floristic exchange tracks between Southeast Asia and Australia. I posited four historical biogeographical scenarios that could explain the current Australian distribution of *A. elaeagnoidea*: 1) a single exchange track between Australia and Asia with vicariance within Australia; 2) a single exchange track between Australia and Asia with long-distance dispersal within Australia; 3) two exchange tracks between Australia and Asia from the same source regions in Asia, and 4) two exchange tracks between Australia and Asia from different source regions in Asia. Scenarios one, two and three are rejected on the basis of the admixture analysis and Fst statistics which indicate that the Cape York Peninsula and Kimberley Plateau populations are highly genetically distinct from each other, and the SVDquartets and TreeMix analyses which indicate that the Cape York Peninsula and Kimberley Plateau populations have greater genetic connectivity with New Guinea and Timor, respectively, than they do with each other. Scenario one is rejected on the basis of the ENM analysis also, which predicts a lack of continuous suitable habitat across northern Australia at the LGM and therefore argues against a widespread northern population between the Cape York Peninsula and Kimberley Plateau that was split vicariantly due to extinction of intervening subpopulations. The results of all analyses are consistent with scenario four, which posits two exchange tracks for *A. elaeagnoidea* in Australia: one between New Guinea and Cape York Peninsula, and one between Timor and the Kimberley Plateau.

The results suggest the exchange track between New Guinea and Cape York Peninsula is contemporary, with an extremely low Fst (Fst = 0.09; Table 4.1) indicating ongoing gene flow between these areas. Phylogeographic studies on birds (Roshier *et al.* 2012; Marki *et al.* 2018; Lamb *et al.* 2019; Joseph *et al.* 2019; Dorrington *et al.* 2019) and reptiles (Pepper *et al.* 2017; Natusch *et al.* 2020) have found shallow to no genetic divergence between Australian and New Guinean lineages, attributable to recent repeated geneflow between New Guinea and Cape York Peninsula populations during periods of low glacial sea levels until c. 17 Ka ago (Voris 2000). Contemporary gene flow has also been inferred for highly mobile fauna species such as the Palm Cockatoo (Keighley *et al.* 2019). The dispersal ecology of eastern *A. elaeagnoidea* is largely unknown; however, Pied Imperial Pigeons (*Duculus bicolor*), which migrate annually between Cape York Peninsula and New Guinea, have been observed eating the fruit (Pannell, 1992). Furthermore, approximately 40 species of birds (not including waterbirds) migrate annually between Cape York Peninsula and the Trans-Fly region of New Guinea. Of these, two are predominantly frugivorous, and the small size of *A. elaeagnoidea* fruits means it is likely to be dispersed between New Guinea and Australia by one or more of these species (Mees 1982; Bishop 2006; Rossetto *et al.* 2015; Joseph *et al.* 2019), maintaining geneflow between these populations.

I am not aware of any other phylogeographic study that has demonstrated exchange track between Timor and the Kimberley Plateau for plants. However, a track between Asia and northwestern Australia has been previously reported for fauna (e.g. Williams *et al*. (2008); Toon *et al*. (2017); Dorrington *et al.* (2019)), and humans (Bird *et al.* 2018). For *Aglaia elaeagnoidea*, I suggest that the Kimberley Plateau population was established by stepping-stone dispersal from Timor during a previous glacial maximum when proximity between the two land masses was substantially greater than at present. Global sea levels dropped to as low as -120 m (below current sea level) at c. 20 Ka (Brooke *et al.* 2017) and -85 m prior to 60 Ka (Lambeck and Chappell 2001). Although Timor has never had a dryland connection to Australia, at sea levels of -75 m, land now represented by the Ashmore Reef and the Sahul Banks was exposed along the Arafura Shelf, with the closest island 87 km away from Roti (Bird *et al.* 2018). Moreover, the results of the ENM analysis suggest that these exposed islands along the Arafura Shelf were likely to be climatically suitable for *A. elaeagnoidea*, being highly seasonal in annual temperature and showing high isothermality (although my model does not take into account other variables that may be of importance for habitat suitability such as edaphic and biotic factors). I suggest that subsequent sea level rise at c. 17 Ka is likely to have isolated the Kimberley Plateau populations from Timor and other *A. elaeagnoidea* populations; this is supported by the high genetic divergence and genetic drift shown between the Kimberley Plateau and other populations. Such a signature of genetic divergence following migration between the Kimberley Plateau and Timor has also been observed in Zebra Finches (Balakrishnan and Edwards 2009). Pied Imperial Pigeons (the most likely major dispersal vector of *A. elaeagnoidea*) occur on the Kimberley Plateau but are sedentary; they are isolated from Cape York Peninsula populations, and do not migrate to Asia like the Cape York Peninsula and Arnhem Land Pied Imperial Pigeon populations (Johnstone 1981; Forshaw 2015). It would be worthwhile investigating whether the phylogeography of Pied Imperial Pigeons shows a similar pattern to that of *A. elaeagnoidea*.

Historical cycles of expansion and contraction of suitable habitat impacted dispersal and connectivity throughout the range of eastern *A. elaeagnoidea*. The ENM suggests that suitable habitat expanded during cooler, drier glacial peaks into equatorial Southeast Asia, and contracted to peripheral islands during interglacials. This agrees with the results of the LEA, which shows greatest admixture in equatorial populations, and greatest genetic differentiation in peripheral populations. In other Australian rainforest taxa, repeated range expansions and contractions coeval with Quaternary climatic fluctuations have been shown to reinforce a pattern of low genetic diversity and high genetic differentiation in peripheral populations (Rossetto *et al.* 2012; Mellick *et al.* 2012, 2013; Fahey *et al.* 2019). This appears particularly relevant for the Kimberley and Taiwan populations of *A. elaeagnoidea*, where the TreeMix analysis modelled a high drift parameter, suggesting pronounced genetic drift following population isolation. However, the Pacific island populations (New Caledonia, Vanuatu and Wallis and Futuna) have a low drift parameter and show little genetic differentiation between islands. This could be explained by recent or ongoing stochastic dispersal events. Pied Imperial Pigeons are highly mobile and may be capable of dispersing *A. elaeagnoidea* seeds over relevant distances. Although it is difficult to unequivocally identify the processes underlying geographic variation based on current sampling, the results strongly suggest that a combination of climate-induced expansion and contraction and stochastic dispersal events have lead to the phylogeographic patterns observed in eastern *A. elaeagnoidea*.

Conclusion: Implications for the phytogeography of Australia and Southeast Asia

My results support a broad conclusion that the monsoon tropics of the Kimberley Plateau and the monsoon and wet tropics of Cape York Peninsula have separate biogeographic histories (Crisp *et al.* 1995; Bowman *et al.* 2010). However, I suggest that the high genetic differentiation between the Kimberley Plateau and Cape York Peninsula was not only driven by the restriction of exchange by biogeographic barriers in northern Australia (González-Orozco *et al.* 2014; Edwards *et al.* 2017), but also by the presence of multiple exchange tracks between Asia and northern Australia.

Future research should test for the presence of an exchange track between Arnhem Land and Asia and its role, together with the Kimberley Plateau and Cape York Peninsula tracks, in shaping northern Australian biogeography. The influence that multiple northern Australian-Asian exchange tracks has on southern Australian biogeography should also be investigated; Brown *et al*. (2011) has previously identified a phylogenetic link in *Paraserianthes* I.C.Nelson (Fabaceae) between the Lesser Sunda Islands and south-west Western Australia. The results suggest that colonisation of south-western Australia by Asian lineages may have occurred via the western Arafura Shelf to the Kimberley Plateau followed by southern expansion and subsequent extinction in northern Australia. Comparison of the phylogenetic and phylogeographic history of Asian lineages in Australia to that of Australian autochthonous lineages provides an exciting opportunity for developing new insights into the evolution of the modern Australian biota.

Data Availability Statement

DArTseq SNP data has been deposited to the James Cook University Research Data data repository and is available at https://doi.org/10.25903/D3AZ-YB02.

Chapter 5

Development of a phylogenomic analytical pipeline to gain novel insights into Sapindalean evolution across the Sunda-Sahul Convergence Zone

Preface

In Chapters 2, 3 and 4 I used floristic, phenetic and phylogeographic methods to investigate patterns and processes in the SSFE. In Chapter 5, I develop a pipeline for integrating next-generation phylogenomic data with legacy Sanger data to investigate dynamics of the SSFE within the angiosperm order Sapindales. Investigation of such dynamics within this phylogenomic framework has the advantage of being able to integrate information about evolutionary history and biology through space and time to enable a more nuanced and detailed investigation into the SSFE.

This chapter will be published in multiple papers according to a publication plan agreed upon by E. Joyce and collaborators.

E. Joyce and D. Crayn conceived the idea for this work, and E. Joyce designed the study, conducted sampling, carried out the majority of laboratory work, developed the analytical pipeline, conducted the analyses and wrote the chapter. J. de Vos, S. Pell and J. Bachelier provided the majority of Anacardiaceae samples, M. Appelhans provided most of the samples for Rutaceae and J. Pirani, G. Alves, and M. Devecchi provided most of the samples for Simaroubaceae. M. Cheek and C. Pannell verified identifications for Meliaceae samples. Most of the Sapindaceae lab work was led and completed by F. Forest and S. Buerki. These researchers also provided expertise on their groups, as did J. Mitchell, M. Groppo, M. Callmander, P. Lowry, J. Munzinger, C. Moriani-Siniscalchi and A. Weeks. Sequencing was coordinated by O. Maurin. A. Zuntini assisted with lab work and analysis, and L. Nauheimer and M. Lee were also consulted for analysis assistance. H. Sauquet and P. Wilf advised on fossil calibrations. All target capture sequencing was conducted as part of the Royal Botanic Gardens Kew's Plants and Fungi Tree of Life (PAFTOL) project led by W. Baker, I. Leitch and F. Forest. K. Thiele, K. Nargar, D. Crayn and J. Holtum advised E. Joyce and provided feedback on earlier drafts of the manuscript. PAFTOL is funded by

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Abstract

The convergence of the Sunda continental shelf (Peninsular Malaysia and parts of Indonesia and the Philippines; Figure 1.1) and the Sahul continental shelf (Australia and New Guinea; Figure 1.1) from c. 25 Mya was a significant event in global biogeography that resulted in the exchange of previously isolated floras (the 'Sunda-Sahul Floristic Exchange'). Despite the importance of the Sunda-Sahul Floristic Exchange in shaping the flora of the region, much remains to be understood about the processes underlying the exchange. Previous studies using phylogenetic, floristic and palaeobotanical approaches have provided limited insight due to methodological and/or data shortcomings. To address this, I used target capture data to generate the most densely sampled genus-level phylogenetic tree of Sapindales with 443 samples and c. 81% of the genera represented. The phylogeny resolves the relationships of the constituent families for the first time: Nitrariaceae, Biebersteiniaceae and Sapindaceae form a basal grade, and the relationship between Meliaceae, Simaroubaceae and Rutaceae is shown to be incongruent with current understanding, with Meliaceae sister to Rutaceae. Bayesian divergence dating estimation with 29 rigorously assessed fossil calibrations indicates that most Sapindales families arose in the Cretaceous. I then developed an analytical pipeline to integrate the target-capture data with legacy Sanger data to produce a species-level phylogenetic tree of Anacardiaceae including 373 samples across 73 genera, representing c. 90% of the generic and 47% of the species diversity. This tree broadly supports the subfamily classification of Anacardiaceae while indicating that the tribal classification is in need of review, and sheds new light on generic and infra-generic relationships. Ancestral range reconstruction of the dated, species-level tree of Anacardiaceae supports an Asian origin for the family, confirms the eastward bias in exchange from Sunda to Sahul, and highlights the importance of the emergence of Wallacea in facilitating the exchange. Most interestingly, the results also indicate that extinction of tropical lineages on Sahul coincident with Miocene aridification may contribute to the observed bias in exchange. This study demonstrates the utility of this novel methodological pipeline for gaining novel insights into biogeography, and particularly the SSFE. Furthermore, my results emphasise the importance of considering ancient evolutionary history when attempting to understand recent and current biogeographic processes.

Introduction

The Sunda-Sahul Convergence Zone (SSCZ), comprising modern-day Southeast Asia and Australia, has an extremely complex geological and biogeographic history that has been the focus of scientific investigation for nearly 200 years. The SSCZ straddles two continental shelves: the Sunda and Sahul continental shelves. Approximately 45 Mya the Sahul shelf rifted from Antarctica at southern latitudes and commenced its northwards drift, colliding with the Sunda shelf from approximately 25 Mya (Lohman *et al.* 2011). The collision triggered a cascade of geological change, including the trapping of terranes of various origins – now referred to as Wallacea – between the shelves, rapid orogenesis in Wallacea and New Guinea, and the torsion of the Sunda plate (Zahirovic *et al.* 2016; Hall 2017). It also facilitated the exchange of biotas that had previously evolved in isolation. Undoubtedly, the exchange of flora (the Sunda–Sahul Floristic Exchange: SSFE) had an impact on the evolution and composition of the flora in the region and beyond (Kooyman *et al.* 2019), but much remains to be understood about the impact, patterns and drivers of the SSFE.

Historically, scientists have relied on comparing the distribution and diversity of extant species to understand the dynamics of the SSFE (e.g. Hooker 1859; Van Steenis 1950; Kalkman 1955; Richardson *et al.* 2012). In these studies, subsets of species for regions across the SSCZ are listed and the origin of each genus is assigned to its centre of diversity ('Age-Area Theory'; Willis, 1922), thus giving an estimate of SSFE directionality (i.e. any Sahulian species without congeners endemic to Sahul but with congeners in Sunda is considered to be an immigrant from Sunda, and vice versa). Although these species-counting studies may give a general indication of SSFE directionality, they are problematic. Age-Area Theory has now been largely discredited as a reliable method for determining the area of origin for a lineage, and is especially dubious in the SSCZ (Webb *et al.* 1984) wherein the complex geological history of the region likely led to unique patterns of diversification and endemism that do not satisfy the theory's assumptions. Other methods are therefore necessary to gain a more accurate and nuanced understanding of SSFE directionality and dynamics. Based on the macrofossil record of Australia, Sniderman and Jordan (2011) reported a nine-fold eastward bias in exchange, suggesting that the majority of immigration of Sundanian flora occurred during the late Neogene and Quaternary. Although providing invaluable insight into the historical changes in the Australian flora, the palynological and macrofossil records of northern Australia and southeast Asia west of Wallacea are depauperate. Reliable data are scanty and fossil sites are biased in their distribution, limiting the number of comparable sites to infer patterns of floristic exchange.

Because the fossil record is imperfect, phylogenies are critical to understanding the SSFE. They enable integration of lineages that are not present in the fossil record and facilitate the investigation of evolutionary dynamics over time. Phylogenies have been used extensively to reconstruct the biogeographic histories of many lineages across the Sunda-Sahul Convergence Zone (e.g. Su and Saunders 2009; Thomas *et al.* 2012; Bacon *et al.* 2012; Grudinski *et al.* 2014). These studies often have a taxonomic focus, or focus on the evolution and biogeography of the lineage of interest; however, comparison of exchange events across multiple phylogenies can give insight into spatio-temporal patterns of exchange at a floristic scale. De Bruyn *et al.* (2014) was the first to undertake a multi-lineage comparative phylogenetic analysis of faunal and floral clades distributed across Southeast Asia. The authors compared the ages of nodes in each clade that represented a biogeographic transition between Sunda and Sahul, and found a bias in the directionality of floristic exchange, with eastward dispersal outweighing westward dispersal by a factor of 1.5; however, the study only included six plant clades. Crayn *et al.* (2015) conducted a larger comparative phylogenetic study of 21 published dated molecular phylogenies across 49 SSCZ plant clades and also reported an eastward bias in exchange (this time by a factor of 2.4). Additionally, Crayn *et al*. (2015) characterised the temporal dynamics of the SSFE, finding that the earliest phylogenetic evidence of an exchange event occurred 33 Mya, from when exchange occurred at a rate of 0.41 My^{-1} until 12 Mya, after which the rate increased substantially to 3.33 Myr^{-1}. Similar multi-lineage comparative phylogenetic analyses have also been used to understand the exchange of flora between South and North America in the Great American Biotic Exchange (GABI; e.g. Bacon *et al.* 2015).

Such comparative phylogenetic meta-analyses have provided the most comprehensive overview of temporal and directional patterns in the SSFE to date; however, the findings of these studies are confounded by methodological limitations. Firstly, in such meta-analyses node ages are taken directly from published chronograms, many of which were generated using different genes, phylogenetic methods, and dating and ancestral area reconstruction analyses. These methodological inconsistencies confound differences in the ages of biogeographic transitions, making it difficult to rigorously infer temporal patterns and underlying explanations of exchange. Secondly, the analytical methods used in some published studies are suboptimal for older lineages, or lineages with many extinct or missing taxa, potentially leading to inaccuracies in some published phylogenies (Linder *et al*. 2005). Finally, most published phylogenetic trees focus on one lineage, usually at the genus-level. This means that only shallow (more recent) nodes and potential biogeographic disjunctions are captured, likely biasing the analysis towards more recent patterns and excluding more ancient patterns of SSFE. The flora of the SSCZ may have been shaped by Gondwanan vicariance prior to the SSFE; there is evidence of Gondwanan taxa immigrating to Sunda from India in the Paleogene (Morley 2002; Kooyman *et al.* 2019), and from Gondwanan fragments (now modern-day Myanmar) in the Middle Eocene (Hall 2012b; Poinar and Chambers 2017). Understanding how ancient Gondwanan patterns may affect patterns of SSFE is impossible with shallow, genus level phylogenies and remains a challenge for understanding the evolution of the flora of the SSCZ.

Recent advances in high-throughput sequencing methods provides new opportunities for investigating spatio-temporal dynamics of the SSFE in a rigorous, consistent phylogenomic framework. Target capture sequencing has become the foremost high-throughput sequencing method for phylogenomics, enabling the reliable retrieval of hundreds or thousands of target loci at an increasingly affordable price (Cronn *et al.* 2012; Barrett *et al.* 2016; Bragg *et al.* 2016; McLay *et al.* in press). The amount of data generated with target capture sequencing, and the recent development of universal bait kits such as the Angiosperms353 bait kit (Johnson *et al.* 2019), has enabled the resolution of phylogenetic relationships with high support at many taxonomic scales, from infra-specific relationships to ordinal and familial relationships (Bossert and Danforth 2018; Dodsworth *et al.* 2019; Johnson *et al.* 2019; Larridon *et al.* 2020; Shee *et al.* 2020). Target capture sequencing therefore offers an opportunity to produce more complete, better-resolved phylogenetic trees to allow study of SSFE dynamics in a consistent and rigorous phylogenomic framework, spanning a long timescale.

In this chapter, I develop a phylogenomic pipeline which enables streamlined analysis of large DNA sequence datasets, that can integrate legacy, publicly available Sanger data with target-capture data, and takes advantage of cutting-edge analytical tools for phylogenomic analysis of high-throughput sequence data, including divergence date estimation and range area analysis. The phylogenomic pipeline facilitates the generation of densely sampled genus- and species-level phylogenetic trees for the purposes of investigating biogeographic patterns and processes spanning deep time in an analytically consistent and rigorous way. Using the angiosperm order Sapindales and sapindalean family Anacardiaceae as case studies, I demonstrate the utility of my phylogenomic pipeline for examining the dynamics of the SSFE. Sapindales comprises 9 families (Anacardiaceae, Biebersteiniaceae, Burseraceae, Kirkiaceae, Nitrariaceae, Meliaceae, Rutaceae, Sapindaceae and Simaroubaceae), c. 467 genera and c. 6550 species. The order is distributed globally, comprises approximately 3% of the world's angiosperm diversity, and is an economically important group of plants including lineages of agricultural, forestry, medicinal, cosmetic and chemical significance. Sapindales was chosen as the focus group of this study due to its high level of diversity in the SSCZ. Furthermore, the order inhabits a variety of biomes and has high morphological diversity, enabling investigation of the influence of environment and plant traits on exchange dynamics. In this study, I generate the most densely-sampled and well-supported genus-level phylogeny of Sapindales to date, and develop a method for integrating this with species level data, focusing on the family Anacardiaceae as an example. I then demonstrate the utility of this analytical pipeline for providing new insights into SSFE dynamics.

Materials and methods

A summary of the entire methodological workflow employed in this project – from sampling to data analysis – is depicted in Figure 5.1. Details of each of the major methodological steps are provided below.

Sampling

A total of 443 samples were included in the ordinal phylogeny, representing all nine families and c. 81% of the generic diversity of Sapindales (Table 5.1). One representative per genus was included, and where possible the type species for the genus was sampled. Multiple species were sampled for genera that were suspected to be polyphyletic by taxonomic experts (listed in preface). Samples were variously sourced from the DNA bank and living collection at the Royal Botanic Gardens Kew, silica-dried field collections and herbarium specimens (Table 5.1).

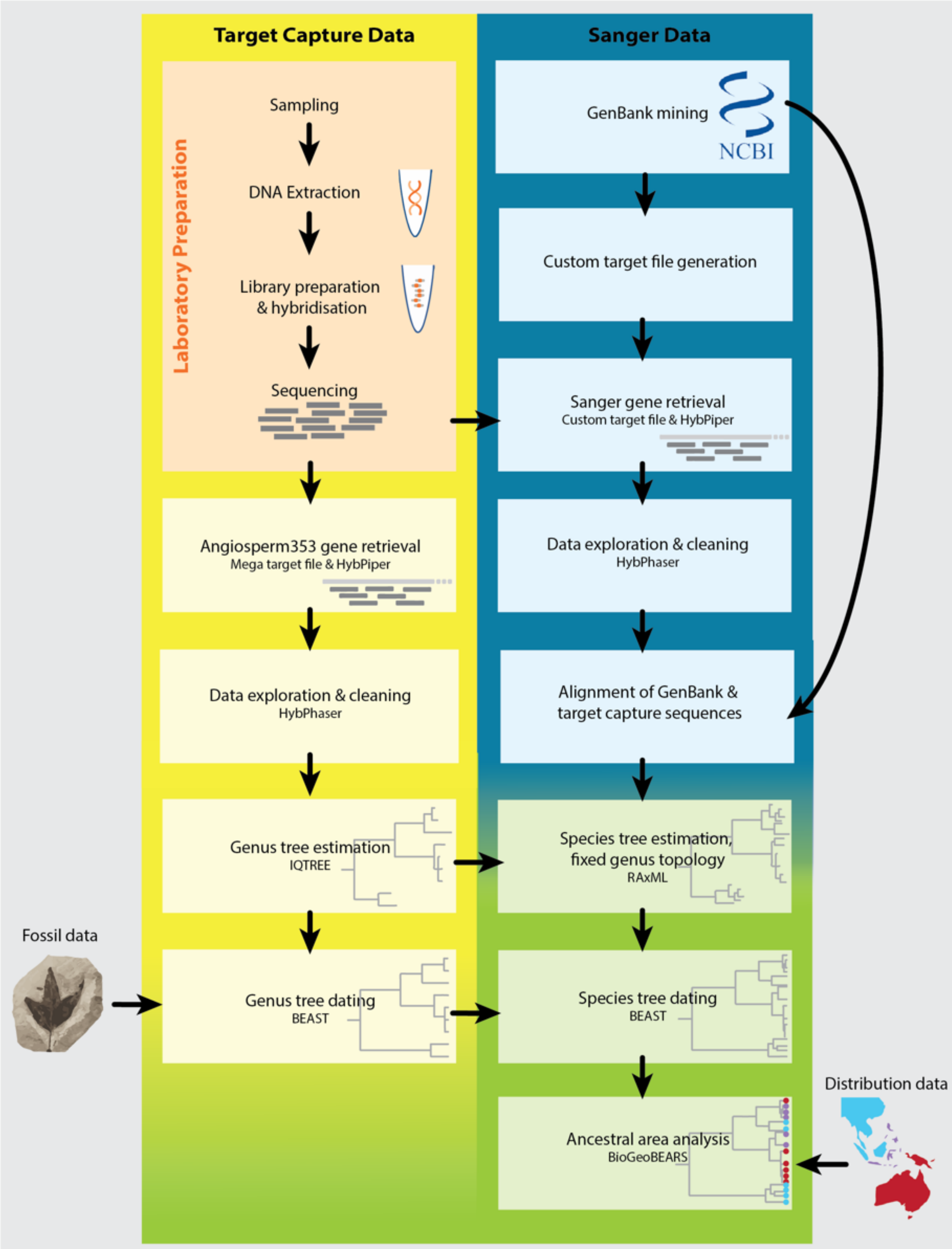

Figure 5.1 Summary of method workflow developed in this chapter outlining the major laboratory and bioinformatic steps taken to integrate target capture data (yellow column) with legacy Sanger data (blue column) for biogeographic analysis.

Table 5.1 List of next generation samples included in the Angiosperms353, genus-level phylogenetic analysis of Sapindales, outlining species and source of each sample. 'I/O' lists whether the sample is an ingroup or outgroup and 'SRA' stands for NCBI's Sequence Read Archive. 'Museum codes' lists herbarium specimen sheet, or DNA bank number or living collection number where specified.

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Anacardiaceae	*Abrahamia ditimena*	DNA	10573		Randrianasolo 781	MO	
I	Anacardiaceae	*Actinocheita potentillifolia*	Herbarium	7484		Salinas 7503	K	
I	Anacardiaceae	*Allospondias lakonensis*	DNA	10575		Pell 1035	NY (BKL)	
I	Anacardiaceae	*Amphipterygium adstringens*	DNA	10577		Pendry 845	E	
I	Anacardiaceae	*Anacardium occidentale*	Herbarium	10459		McKenna, S.G. 363	CNS	CNS131081
I	Anacardiaceae	*Apterokarpos gardneri*	DNA	10583		Pirani 2586	NY	
I	Anacardiaceae	*Astronium* sp.	DNA	10713		Anderson, W.R. 13597	MICH	K DNA bank no. 21936
I	Anacardiaceae	*Baronia taratana*	DNA	10589		Pell 625	NY	
I	Anacardiaceae	*Blepharocarya involucrigera*	DNA	10591		R. Jensen 826	A	
I	Anacardiaceae	*Bonetiella anomala*	DNA	10593		Johnston, Wendt & Chiang	F	
I	Anacardiaceae	*Bouea oppositifolia*	Herbarium	10465		Saw, L.G. FRI48291	CNS	CNS143380
I	Anacardiaceae	*Buchanania obovata*	Silica	10431		Wannan, B.S. 6674	CNS	CNS141235
I	Anacardiaceae	*Campnosperma zeylanicum*	Herbarium	6465				K DNA bank no. 6369
I	Anacardiaceae	*Campylopetalum siamense*	DNA	10597		Garrett 1398	NY	
I	Anacardiaceae	*Cardenasiodendron brachypterum*	DNA	10599		Pendry 691	E	
I	Anacardiaceae	*Choerospondias axillaris*	DNA	10601		JD Mitchell 652	NY	
I	Anacardiaceae	*Cotinus coggygria*	SRA		SRR8298330			
I	Anacardiaceae	*Cotinus obovatus*	Silica	10797		Joyce & Maurin	K	K living collection no.
I	Anacardiaceae	*Cyrtocarpa caatingae*	Herbarium	8429		Ule 7256	K	
I	Anacardiaceae	*Cyrtocarpa procera*	DNA	10605		Torres 1240	NY	
I	Anacardiaceae	*Dobinea vulgaris*	DNA	10607		Delendick 617	NY	
I	Anacardiaceae	*Dracontomelon duperreanum*	DNA	10609		SK Pell 1034	NY	
I	Anacardiaceae	*Drimycarpus racemosus*	DNA	10611		Grierson/Long 4261	A	
I	Anacardiaceae	*Euroschinus papuanus*	Herbarium	7785		Takeuchi, W.; Ama, D. 17126	K	K000618182
I	Anacardiaceae	*Fegimanra africana*	DNA	10617		Reitsma & Reitsma 1257	NY	
I	Anacardiaceae	*Gluta renghas*	Herbarium	6466		Chase, M.W. 2066	K	K DNA bank no. 1953

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Anacardiaceae	*Haplorhus peruviana*	DNA	10621		O. Zöllner 4030	L	
I	Anacardiaceae	*Harpephyllum caffrum*	DNA	10623		Lau 1588	NY	
I	Anacardiaceae	*Heeria argentea*	DNA	10841		Chase, M.W. 6588	K	K DNA bank no. 4855
I	Anacardiaceae	*Laurophyllus capensis*	DNA	10945		Manning, J.C. & Laura 2906	K	K DNA bank no. 29002
I	Anacardiaceae	*Loxopterygium grisebachii*	DNA	10857		Cadrera et al. 27543	K	K DNA bank no. 17824
I	Anacardiaceae	*Loxostylis alata*	DNA	10629		C. Pinheiro 79	NY	
I	Anacardiaceae	*Mangifera indica*	SRA		SRR1562187			
I	Anacardiaceae	*Mangifera odorata*	DNA	10469			CNS	
I	Anacardiaceae	*Mauria simplicifolia*	DNA	10633		Leiva et al. 1552	F	
I	Anacardiaceae	*Melanochyla caesia*	DNA	10635		Ambriansyah & Arifin 903	MO	
I	Anacardiaceae	*Metopium brownei*	DNA	10639		Brokaw 295	NY	
I	Anacardiaceae	*Micronychia macrophylla*	DNA	10641		Pell 643	NY	
I	Anacardiaceae	*Mosquitoxylum jamaicense*	DNA	10643		Rodríguez 736	MO	
I	Anacardiaceae	*Myracrodruon urundeuva*	DNA	10645		Pendry 724	E	
I	Anacardiaceae	*Nothopegia beddomei*	DNA	10891		Samuel, R.	K	K DNA bank no. 21392
I	Anacardiaceae	*Ochoterenaea colombiana*	DNA	10647		Escobar, Folsom, Brand &	F	
I	Anacardiaceae	*Operculicarya decaryi*	DNA	10649		Randrianasolo 627	MO	
I	Anacardiaceae	*Orthopterygium huaucui*	DNA	10651		Smith 5726	NY	
I	Anacardiaceae	*Ozoroa insignis*	DNA	10653		Randrianasolo 680	MO	
I	Anacardiaceae	*Pachycormus discolor*	DNA	10787		Chase, M.W. 3074	K	K DNA bank no. 2873
I	Anacardiaceae	*Parishia insignis*	Silica	10655		Bachelier	NA	
I	Anacardiaceae	*Pegia nitida*	DNA	10657		Zhanhuo 92-254	MO	
I	Anacardiaceae	*Pistacia chinensis*	SRA		SRR8661763			
I	Anacardiaceae	*Pistacia lentiscus*	SRA		SRR5043662			
I	Anacardiaceae	*Pleiogynium timorense*	Herbarium	6468		Chase, M.W. 2069	K	K DNA bank no. 1956
I	Anacardiaceae	*Poupartia borbonica*	Silica	10803		Joyce & Maurin	K	K living collection no.
I	Anacardiaceae	*Poupartia chapelieri*	Herbarium	11873		Dumetz 1294	K	K001275567
I	Anacardiaceae	*Poupartia minor*	DNA	10665		Pell 657	NY	
I	Anacardiaceae	*Poupartiopsis spondiocarpus*	DNA	10667		Randrianasolo 592	MO	
I	Anacardiaceae	*Protorhus longifolia*	DNA	10669		R.Brand 322	NY	

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Anacardiaceae	*Pseudosmodingium andrieuxii*	DNA	10675		Tenorio 17041	F	
I	Anacardiaceae	*Pseudospondias microcarpa*	DNA	10673		RA 809	MO	
I	Anacardiaceae	*Rhodosphaera rhodanthema*	Herbarium	10453		Forster, P.I.; Booth, R. 25343	CNS	QRS128713
I	Anacardiaceae	*Rhus coriaria*	DNA	10679		E. Vitek 2000-301	W	
I	Anacardiaceae	*Rhus perrieri*	DNA	10681		Randrianasolo 629	MO	
I	Anacardiaceae	*Rhus taitensis*	DNA	10637		Pell 841	NY	
I	Anacardiaceae	*Rhus thouarsii*	DNA	10683		Pell 638	NY	
I	Anacardiaceae	*Schinopsis brasiliensis*	DNA	10685		Bridgewater 1012	E	
I	Anacardiaceae	*Schinus patagonicus*	DNA	10939		Kepos 27850	K	K DNA bank no. 28228
I	Anacardiaceae	*Sclerocarya birrea*	DNA	10689		SKP 695	NY (BKL)	
I	Anacardiaceae	*Searsia undulata*	DNA	10691		SKP 692	NY (BKL)	
I	Anacardiaceae	*Semecarpus* sp.	DNA	10861		Johns, R.J. 9795	K	K DNA bank no. 18116
I	Anacardiaceae	*Smodingium argutum*	DNA	10695		Winter 88	MOR	
I	Anacardiaceae	*Sorindeia madagascariensis*	DNA	10697		Randrianasolo 653	MO	
I	Anacardiaceae	*Spondias mombin*	Herbarium	6469		Ameka et al. 213	GC	K DNA bank no. 40825
I	Anacardiaceae	*Swintonia schwenckii*	DNA	10701		C. Herscovitch s.n.	NY	
I	Anacardiaceae	*Tapirira guianensis*	DNA	10703		Daly 13984	NY	
I	Anacardiaceae	*Thyrsodium spruceanum*	DNA	10705		S. Mori 24215	NY	
I	Anacardiaceae	*Toxicodendron pubescens*	DNA	10707		J.D. Mitchell 1501	NY	
I	Anacardiaceae	*Toxicodendron radicans*	SRA		ERR2040463			
I	Anacardiaceae	*Toxicodendron vernicifluum*	SRA		SRR5858884			
I	Anacardiaceae	*Trichoscypha longifolia*	Silica	10935		Burgt, X.M. van der 1856	K, SL, WAG	K001061794; K DNA bank
I	Biebersteiniaceae	*Biebersteinia odora*	DNA	894		Holubec	K	K DNA bank no. 22402
I	Burseraceae	*Aucoumea klaineana*	Herbarium	11011		J.J.F.E. de Wilde et al. 11307	K	K001275407
I	Burseraceae	*Beiselia mexicana*	DNA	10731		Chase, M.W. 639	K	K DNA bank no. 158
I	Burseraceae	*Boswellia sacra*	DNA	10953		Chase, M.W. 34495	K	K DNA bank no. 34950
I	Burseraceae	*bursera simaruba*	SRA		ERR2040465			
I	Burseraceae	*Commiphora habessinica*	DNA	10723		Chase, M.W. 526	K	K DNA bank no. 160
I	Burseraceae	*Crepidospermum rhoifolium*	Herbarium	11015		Miralha 46	K	K001275409
I	Burseraceae	*Dacryodes laxa*	DNA	10761		Chase, M.W. 2087	K	K DNA bank no. 1974

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I	Burseraceae	*Protium copal*	SRA		SRR9107802			
I	Burseraceae	*Protium javanicum*	Herbarium	6471		Chase, M.W. 2089	K	K DNA bank no. 1976
I	Burseraceae	*Tetragastris altissima*	Herbarium	11017		Zappi, D. 1250	K	K000578064
I	Burseraceae	*Trattinnickia rhoifolia*	Herbarium	11019		Mori & Gracie sn	K	K001275410
I	Burseraceae	*Triomma malaccensis*	DNA	10763		Chase, M.W. 2091	K	K DNA bank no. 1978
O	Caricaceae	*Cylicomorpha parviflora*	SRA		ERR4180126			
O	Combretaceae	*Terminalia neotaliala*	SRA		ERR2040313			
O	Crossosomataceae	*Crossosoma californicum*	SRA		SRR7451089			
O	Cyrillaceae	*Cyrilla racemiflora*	SRA		SRR7451102			
O	Dipentodontaceae	*Perrottetia longistylis*	SRA		ERR4297056			
O	Dipterocarpaceae	*Anisoptera marginata*	SRA		ERR4180094			
O	Dipterocarpaceae	*Monotes glaber*	SRA		ERR4180058			
O	Emblingiaceae	*Emblingia calceoliflora*	SRA		ERR4180003			
O	Fabaceae	*Acacia pycnantha*	SRA		ERR2040344			
O	Fabaceae	*Gilbertiodendron ecoukense*	SRA		SRR7451091			
O	Francoaceae	*Francoa appendiculata*	SRA		ERR2040311			
O	Francoaceae	*Greyia sutherlandii*	SRA		ERR2040312			
O	Geraniaceae	*Geranium carolinianum*	SRA		ERR2040309			
O	Geraniaceae	*Geranium maculatum*	SRA		ERR2040310			
I	Kirkiaceae	*Kirkia acuminata*	Silica	10547		Appelhans MA393	GOET	
I	Kirkiaceae	*Kirkia wilmsii*	SRA		ERR2040467			
O	Koeberliniaceae	*Koeberlinia spinosa*	SRA		ERR4180172			
O	Malvaceae	*Gossypium barbadense*	SRA		SRR8878749			
O	Melastomataceae	*Medinilla magnifica*	SRA		ERR2040321			
I	Meliaceae	*Aglaia macrocarpa*	Silica	11875		Trethowan 608	K	
I	Meliaceae	*Aglaia odorata*	SRA		SRR5947159			
I	Meliaceae	*Aglaia tomentosa*	DNA	10863		Greger, H. 689	K	K DNA bank no. 18158
I	Meliaceae	*Anthocarapa nitidula*	Silica	10441		Costion, C. 1335	CNS	CNS131163
I	Meliaceae	*Aphanamixis polystachya*	DNA	10975		Middleton, D.J. et al. 1329	K	K DNA bank no. 41973
I	Meliaceae	*Astrotrichilia asterotricha*	Herbarium	10567		P.B. Phillipson et al. 6139	K	

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I	Meliaceae	*Azadirachta indica*	Silica	10433		McDonald, K.R. 10191	CNS	CNS137932
I	Meliaceae	*Cabralea canjerana*	DNA	10881		Wasum, R. 1196	K	K DNA bank no. 19711
I	Meliaceae	*Calodecaryia crassifolia*	DNA	10873		Croat, T.B. 31521	K	K DNA bank no. 19701
I	Meliaceae	*Capuronianthus mahafalensis*	DNA	10825		Cheek et al. 3254	K	K DNA bank no. 3607
I	Meliaceae	*Carapa procera*	DNA	10903		Senterre, B. & Obiang, D. 4243	K	K DNA bank no. 26675
I	Meliaceae	*Cedrela angustifolia*	DNA	10889		Muellner, A.N. 2054	K	K DNA bank no. 21127
I	Meliaceae	*Cedrela odorata*	SRA		SRR7505213			
I	Meliaceae	*Chukrasia tabularis*	Herbarium	11863		Meijer 320	K	K001275564
I	Meliaceae	*Cipadessa baccifera*	DNA	10715		Chase, M.W. 249	NCU	K DNA bank no. 22012
I	Meliaceae	*Didymocheton* sp.	DNA	10737		Chase, M.W. 1311	K	K DNA bank no. 576
I	Meliaceae	*Ekebergia capensis*	DNA	10837		Chase, M.W. 5807	K	K DNA bank no. 4090
I	Meliaceae	*Entandrophragma bussei*	Herbarium	11865		Bidgood et al. 1156	K	K001275565
I	Meliaceae	*Guarea glomerulata*	DNA	10907		Senterre, B. & Obiang, D. 3650	K	K DNA bank no. 26680
I	Meliaceae	*Guarea laurentii*	DNA	10983		Evrard, C. 3286	K	K DNA bank no. 41997
I	Meliaceae	*Heckeldora staudtii*	DNA	10909		Senterre, B., Obiang, D. &	K	K DNA bank no. 26681
I	Meliaceae	*Heynea trijuga*	DNA	10997		Boyce 870	K	K DNA bank no. 48352
I	Meliaceae	*Humbertioturraea grandidieri*	Herbarium	10569		C.C.H. Jongkind et al. 3605	K	
I	Meliaceae	*Khaya anthotheca*	DNA	10779		Chase, M.W. 2859	K	K DNA bank no. 2666
I	Meliaceae	*Lepidothrichilia volkensii*	Herbarium	10571		I. Friis et al. 9816	K	
I	Meliaceae	*Lovoa sywnnertonii*	DNA	10781		Faden & Evans 70122	K	K DNA bank no. 2667
I	Meliaceae	*Malleastrum maadenense*	DNA	10827		Cheek et al. 3175	K	K DNA bank no. 3608
I	Meliaceae	*Melia azedarach*	SRA		ERR2040470			
I	Meliaceae	*Melia toosendan*	DNA	10961		Leon, C.J., Li Bao-Li, Huang &	K	K DNA bank no. 37230
I	Meliaceae	*Munronia pinnata*	Herbarium	11871		Ridsdale, C.E. 281	K	K001275561
I	Meliaceae	*Naregamia alata*	DNA	10819		K.C.Kanodia 89603	K	K DNA bank no. 3591
I	Meliaceae	*Neobeguea* sp.	DNA	10829		Cheek et al. 3251	K	K DNA bank no. 3609
I	Meliaceae	*Nymania capensis*	DNA	10719		Chase, M.W. 270	NCU	K DNA bank no. 22033
I	Meliaceae	*Owenia reticulata*	Silica	10435		Jensen, R. 1851	CNS	CNS139403
I	Meliaceae	*Pseudobersama mossambicensis*	DNA	10821		Bidgood, Abdallah & Vollesen	K	K DNA bank no. 3595
I	Meliaceae	*Pseudocedrela kotschyi*	DNA	10853		Asase 8	K	K DNA bank no. 17369

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I	Meliaceae	*Pseudoclausena chrysogyne*	Herbarium	6473		Muellner, A.N. et al. 2052		K DNA bank no. 19709
I	Meliaceae	*Pterorhachis zenkeri*	DNA	10817		F.J.Breteler 2741	K	K DNA bank no. 3590
I	Meliaceae	*Quivisianthe papinae*	DNA	10831		Cheek et al. 3192	K	K DNA bank no. 3610
I	Meliaceae	*Reinwardtiodendron celebicum*	Herbarium	6474		Kostermans, A.J.G.H 13776	K	K DNA bank no. 16381
I	Meliaceae	*Ruagea glabra*	DNA	10895		Marten & Herrera 680	K	K DNA bank no. 25687
I	Meliaceae	*Schmardaea microphylla*	Herbarium	11867		Lewis & Lozano 3034	K	K001275563
I	Meliaceae	*Swietenia macrophylla*	DNA	10717		Chase, M.W. 250	NCU	K DNA bank no. 22013
I	Meliaceae	*Synoum glandulosum*	DNA	10877		Schodde, R. 5101	K	K DNA bank no. 19704
I	Meliaceae	*Toona sinensis*	SRA		SRR8474820			
I	Meliaceae	*Trichilia hirta*	DNA	10893		Wallnofer et al. 9676	K	K DNA bank no. 25639
I	Meliaceae	*Turraea virens*	Herbarium	6477		Ralimanana	K	K DNA bank no. 15733
I	Meliaceae	*Turraeanthus manii*	DNA	10823		Cheek, M. 8058	K	K DNA bank no. 3596
I	Meliaceae	*Vavaea amicorum*	Herbarium	6478		Curry, P. 1614	K	K DNA bank no. 48348
I	Meliaceae	*Walsura tubulata*	Herbarium	6479		Chase, M.W. 1314	K	K DNA bank no. 585
I	Meliaceae	*Xylocarpus moluccensis*	Herbarium	6480		Puradyatmika 10417	BO	K DNA bank no. 19996
I	Nitrariaceae	*Malacocarpus crithmifolius*	DNA	10729		Sheahan, M-C. 0	K	K DNA bank no. 916
I	Nitrariaceae	*Nitraria retusa*	DNA	10727		Chase, M.W. 597	K	K DNA bank no. 918
I	Nitrariaceae	*Nitraria sibirica*	SRA		SRR7013771			
I	Nitrariaceae	*Nitraria tangutorum*	SRA		SRR1768462			
I	Nitrariaceae	*Peganum harmala*	DNA	10965		Chase, M.W. 38653.19685	K	K DNA bank no. 39167
O	Onagraceae	*Oenothera rosea*	SRA		ERR706864			
O	Polygalaceae	*Polygala lutea*	SRA		ERR706838			
I	Rutaceae	*Acmadenia kiwanensis*	DNA	10917		JEV 2405	K	K DNA bank no. 26932
I	Rutaceae	*Acradenia euodiiformis*	Herbarium	11877		Forster PIF14620	K	K001275568
I	Rutaceae	*Acronychia sp*	Herbarium	6481		Chase, M.W. 313	NCU	K DNA bank no. 22076
I	Rutaceae	*Adenandra uniflora*	DNA	10751		Chase, M.W. 1769	K	K DNA bank no. 1578
I	Rutaceae	*Aegle marmelos*	SRA		SRR7268533			
I	Rutaceae	*Aeglopsis chevalieri*	Herbarium	11023		Cheek et al. 13878	K	K000615634
I	Rutaceae	*Afraegle asso*	Silica	10937		Tchiengue, B. 3788	B, BR, G, K,	K001243700; K DNA bank
I	Rutaceae	*Agathosma gonaquensis*	Silica	10809		Joyce & Maurin	K	K living collection no.

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I	Rutaceae	*Amyris elemifera*	Herbarium	10479		Breckle 10844	GOET	
I	Rutaceae	*Angostura bracteata*	DNA	10843		Pirani et al. 3570	K	K DNA bank no. 6710
I	Rutaceae	*Atalantia ceylanica*	Herbarium	6482		Chase, M.W. 1341	K	K DNA bank no. 727
I	Rutaceae	*Balfourodendron riedelianum*	Herbarium	11765		Silva, S.M. & Ziller, S.R. 1889	K	K001173910
I	Rutaceae	*Balsamocitrus dawei*	Herbarium	11767		Dawe, M.J. 1042	K	K000199535
I	Rutaceae	*Boenninghausenia albiflora*	Silica	10507		Appelhans MA574	GOET	
I	Rutaceae	*Boronella verticillata*	DNA	10549		Munzinger & McPherson 813	MO	
I	Rutaceae	*Bosistoa medicinalis*	Silica	10437		Sankowsky, G. 4001	CNS	CNS142990
I	Rutaceae	*Bottegoa insignis*	DNA	10767		Fris, Vollesen & Hassan 4824	K	K DNA bank no. 2087
I	Rutaceae	*Brombya platynema*	DNA	10551		Ford AF4819	L	
I	Rutaceae	*Burkillanthus malaccensis*	Herbarium	11769		Jones & Kusen 3287	K	K001275530
I	Rutaceae	*Calodendrum capense*	Herbarium	11771		Chapman et al. 6034	K	K001275531
I	Rutaceae	*Casimiroa sapota*	Herbarium	11773		Estrada et al. 5035	K	K001275532
I	Rutaceae	*Cedrelopsis gracilis*	DNA	10553		Randrianarivelojosia	TAN, DNA sample L	
I	Rutaceae	*Chloroxylum swietinia*	DNA	10735		Chase, M.W. 1291	K	K DNA bank no. 398
I	Rutaceae	*Citropsis articulata*	Herbarium	11775		Bidgood et al. 4797	K	K001275533
I	Rutaceae	*Citrus aurantiifolia*	SRA		SRR10353559			
I	Rutaceae	*Citrus aurantium*	SRA		SRR5807892			
I	Rutaceae	*Citrus cavaleriei*	SRA		SRR4098611			
I	Rutaceae	*Citrus clementina*	SRA		SRR7614640			
I	Rutaceae	*Citrus deliciosa*	SRA		ERR760725			
I	Rutaceae	*Citrus hindsii*	SRA		SRR9016287			
I	Rutaceae	*Citrus hystrix*	Silica	10511			GOET	
I	Rutaceae	*Citrus japonica*	SRA		SRR6357068			
I	Rutaceae	*Citrus junos*	SRA		SRR7230860			
I	Rutaceae	*Citrus limon*	SRA		SRR11128339			
I	Rutaceae	*Citrus macrophylla*	SRA		ERR1994152			
I	Rutaceae	*Citrus maxima*	SRA		SRR6656016			
I	Rutaceae	*Citrus medica*	SRA		SRR4102488			
I	Rutaceae	*Citrus reticulata*	SRA		SRR12053309			

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I	Rutaceae	*Citrus sinensis*	SRA		SRR5581500			
I	Rutaceae	*Citrus suavissima*	SRA		SRR6489423			
I	Rutaceae	*Citrus trifoliata*	SRA		SRR7614648			
I	Rutaceae	*Citrus unshiu*	SRA		SRR9959412			
I	Rutaceae	*Citrus xparadisi*	SRA		ERR2040472			
I	Rutaceae	*Clausena excavata*	Herbarium	6483		Chase, M.W. 1343	K	K DNA bank no. 729
I	Rutaceae	*Cneoridium dumosum*	Silica	10513		Freund 76	RSA	
I	Rutaceae	*Cneorum tricoccon*	Silica	10515			GOET	
I	Rutaceae	*Coatesia paniculata*	Herbarium	10483		Forster PIF29113	NY	
I	Rutaceae	*Coleonema pulchellum*	Silica	10805		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Comptonella microcarpa*	DNA	10555		Porter P. Lowry II 5734	MO	
I	Rutaceae	*Conchocarpus macrophyllus*	Herbarium	11777		Pirani et al. 6078	K	K001266141
I	Rutaceae	*Correa speciosa*	Silica	10517			GOET	
I	Rutaceae	*Crowea exaltata*	Silica	10813		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Decagonocarpus oppositifolius*	Herbarium	11779		Maas et al. 6887	K	K001275534
I	Rutaceae	*Decatropis bicolor*	Herbarium	11781		de Nova et al. AN 451	K	K000341813
I	Rutaceae	*Decazyx macrophyllus*	Herbarium	11783		Estrada & Vega 2415	K	K001275535
I	Rutaceae	*Dictamnus albus*	Silica	10519		Appelhans MA576	GOET	
I	Rutaceae	*Dictyoloma vandellianum*	DNA	10557		Appelhans MA381	L	
I	Rutaceae	*Dinosperma erythrococcum*	Silica	10443		Kilgour, C.D. 523	CNS	CNS135407
I	Rutaceae	*Diosma sabulosa*	DNA	10913		JEV 2409	K	K DNA bank no. 26929
I	Rutaceae	*Drummondita hassellii*	DNA	10765		Chase, M.W. 2188	K	K DNA bank no. 1903
I	Rutaceae	*Dutaillyea trifoliata*	Herbarium	11785		Bernardi, L. LB 12600	K	K001275536
I	Rutaceae	*Empleurum unicapsulare*	Herbarium	11791		Cowell et al. 4057	K	K001275537
I	Rutaceae	*Ertela trifolia*	Herbarium	11787		Sasaki et al. 1535	K	K000447255
I	Rutaceae	*Erythrochiton brasiliensis*	Silica	10795		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Euchaetis albertiana*	DNA	10915		JEV 2408	K	K DNA bank no. 26930
I	Rutaceae	*Euodia hortensis*	Herbarium	10485		Drake 235	US	
I	Rutaceae	*Fagaropsis spec*	Herbarium	10487		Burger 3054	US	
I	Rutaceae	*Flindersia pimenteliana*	Herbarium	7778		Hartley, T.G. 10493	K	K000062298

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I	Rutaceae	*Galipea trifoliata*	Herbarium	11789		Sasaki et al. 2063	K	K000447910
I	Rutaceae	*Geijera linearifolia*	Herbarium	6484		Smith, R.J., Hopper, S.D.,	K	K DNA bank no. 37682
I	Rutaceae	*Glycosmis pentaphylla*	Herbarium	6485		Chase, M.W. 1345	K	K DNA bank no. 731
I	Rutaceae	*Halfordia* sp.	Herbarium	6486				K DNA bank no. 2149
I	Rutaceae	*Haplophyllum bungei*	Silica	10527		Manafzadeh 207	Z	
I	Rutaceae	*Harrisonia abyssinica*	Silica	10529		Appelhans MA313	L	
I	Rutaceae	*Harrisonia brownii*	Herbarium	6487		Dunlop, C., Cowie, I. 9451	K	K DNA bank no. 37057
I	Rutaceae	*Helietta glaziovii*	Herbarium	11793		Pirani et al. 5325	K	K001173941
I	Rutaceae	*Hortia superba*	Herbarium	11795		Groppo et al. 950	K	K001173896
I	Rutaceae	*Ivodea decaryana*	Herbarium	10489		Andriamihajarivo 296	MO	
I	Rutaceae	*Leionema ellipticum*	Silica	10445		Ford, A. 2262	CNS	
I	Rutaceae	*Limnocitrus littoralis*	Herbarium	11797		Clemens & Clemens 3263	K	K001275538
I	Rutaceae	*Limonia acidissima*	Herbarium	11799		Lau, J. SING 2009-272	K	K001275539
I	Rutaceae	*Lubaria aroensis*	Herbarium	11801		Rodriguez 293	K	K001275540
I	Rutaceae	*Lunasia amara*	Herbarium	6488		Chase, M.W. 1347	K	K DNA bank no. 733
I	Rutaceae	*Luvunga monophylla*	Herbarium	10467		Ford, A. 6211	CNS	CNS140290
I	Rutaceae	*Macrostylis decipiens*	Herbarium	11805		Trinder-Smith 663	K	K001275542
I	Rutaceae	*Medicosma cunninghamii*	Herbarium	6489				K DNA bank no. 2152
I	Rutaceae	*Melicope ternata*	Silica	10531		Appelhans MA487	GOET	
I	Rutaceae	*Merope angulata*	Herbarium	11809		Murata et al. J-486	K	K001275544
I	Rutaceae	*Merrillia caloxylon*	Herbarium	11811		Tokilip 143526	K	K000270699
I	Rutaceae	*Metrodorea nigra*	DNA	10747		Kallunki et al 570	NY	K DNA bank no. 1465
I	Rutaceae	*Monanthocitrus oblanceolata*	Herbarium	11813		Sinanggul, H. 57242	K	K001275545
I	Rutaceae	*Muiriantha hassellii*	Herbarium	11921		Thiele, K.R. 4549	PERTH	PERTH 08700510
I	Rutaceae	*Murraya exotica*	Herbarium	6490		Lin Y-L.J. 910	K	K DNA bank no. 39631
I	Rutaceae	*Murraya koenigii*	Silica	10799		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Myrtopsis macrocarpa*	Herbarium	10493		Van Balgooy 6955	L	
I	Rutaceae	*Nematolepis squamea*	Herbarium	11815		Visoiu & Kerr 708	K	K001275546
I	Rutaceae	*Neoraputia alba*	DNA	10749		J.Kallunki et al. 611	NY	K DNA bank no. 1477
I	Rutaceae	*Nycticalanthus speciosus*	Herbarium	11817		Pirani et al. 3659	K	K001240038

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I	Rutaceae	*Orixa japonica*	Silica	10533			GOET	
I	Rutaceae	*Peltostigma guatamalense*	Herbarium	11823		Jimenez et al. 710	K	K001275549
I	Rutaceae	*Pentaceras australe*	Herbarium	10495		Forster PIF28897	NY	
I	Rutaceae	*Perryodendron parviflorum*	Herbarium	7853		Brass, L.J. 3915	K	K000062295
I	Rutaceae	*Phellodendron amurense*	Silica	10535			GOET	
I	Rutaceae	*Phyllosma capensis*	Herbarium	11825		Oliver 4316	K	K001275550
I	Rutaceae	*Picrella glandulosa*	Herbarium	10499		HS McKee 3189	US	
I	Rutaceae	*Pilocarpus pennatifolius*	Silica	10815		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Pitaviaster haplophyllus*	DNA	10561		Ford 4821	L	
I	Rutaceae	*Pleiospermium alatum*	Herbarium	11827		Kostermans 25109	K	K001275551
I	Rutaceae	*Plethadenia granulata*	Herbarium	10501		B Peguero, T Zanoni & E Soto	NY	
I	Rutaceae	*Psilopeganum sinense*	Silica	10537		Wen 12478	US	
I	Rutaceae	*Ptaeroxylon obliquum*	DNA	10845		Fay, M.F.	K	K DNA bank no. 14714
I	Rutaceae	*Ptelea trifoliata*	Silica	10539			GOET	
I	Rutaceae	*Raputia heptaphylla*	Herbarium	11829		Herrera 8783	K	K001275552
I	Rutaceae	*Raputia ulei*	Herbarium	11833		Cid Ferreira 5767	K	K001177894
I	Rutaceae	*Raputiarana subsigmoidea*	Herbarium	11831		Sasaki et al. 2500	K	K001173096
I	Rutaceae	*Rauia nodosa*	Herbarium	11835		Pirani et al. 4685	K	K001177896
I	Rutaceae	*Ravenia infelix*	DNA	10745		J.Kallunki et al. 614	NY	K DNA bank no. 1464
I	Rutaceae	*Raveniopsis ruellioides*	Herbarium	11839		Mutchinck et al. 64	K	K001275553
I	Rutaceae	*Rhadinothamnus rudis*	Silica	10929		Dixon, K. W. 1015	K	K DNA bank no. 36062
I	Rutaceae	*Ruta angustifolia*	SRA		SRR7900860			
I	Rutaceae	*Ruta graveolens*	Silica	10541		Appelhans MA578	GOET	
I	Rutaceae	*Sarcomelicope simplicifolia*	Silica	10791		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Sheilanthera pubens*	Herbarium	11879		Williams 2122	K	K001275569
I	Rutaceae	*Skimmia japonica*	Silica	10543			GOET	
I	Rutaceae	*Sohnreyia terminalioides*	DNA	10563		A. Gentry et al., 31751	MO, DNA sample L	
I	Rutaceae	*Spathelia splendens*	DNA	10565		P Vásquez 2009-2	HAC, L	
I	Rutaceae	*Spiranthera odoratissima*	Herbarium	11881		Guedes et al. 5155	K	K001177777
I	Rutaceae	*Stauranthus perforatus*	Herbarium	11883		Thomsen 82	K	K001275570

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Rutaceae	*Swinglea glutinosa*	Herbarium	11885		Hodgson Lowe 4342	K	K001275571
I	Rutaceae	*Tetractomia tetrandra*	Herbarium	10503		Brambach 1472	GOET	
I	Rutaceae	*Tetradium daniellii*	Silica	10793		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Thamnosma texana*	Herbarium	11841		Halse 4427	K	K001275554
I	Rutaceae	*Toxosiphon lindenii*	Herbarium	11889		Estrada & Vega 2417	K	K001275573
I	Rutaceae	*Triphasia brassii*	Herbarium	7775		Frodin, D.G. 8097	K	K000062297
I	Rutaceae	*Vepris lanceolata*	Silica	10807		Joyce & Maurin	K	K living collection no.
I	Rutaceae	*Zanthoxylum armatum*	SRA		SRR9179742			
I	Rutaceae	*Zanthoxylum bungeanum*	SRA		SRR9179747			
I	Rutaceae	*Zanthoxylum nitidum*	SRA		SRR10861972			
I	Rutaceae	*Zieria alata*	DNA	10425		Crayn, D.M. DMC1169	CNS	CNS135627; ATH DNA
I	Sapindaceae	*Acer campestre*	DNA	994		Fay 407	K	K DNA bank no. 8163
I	Sapindaceae	*Acer miaotaiense*	SRA		SRR7195583			
I	Sapindaceae	*Acer negundo*	SRA		ERR2040475			
I	Sapindaceae	*Acer palmatum*	SRA		SRR1980924			
I	Sapindaceae	*Acer pictum*	SRA		SRR8922645			
I	Sapindaceae	*Acer rubrum*	SRA		SRR11712223			
I	Sapindaceae	*Acer saccharum*	SRA		SRR6134139			
I	Sapindaceae	*Acer spicatum*	SRA		SRR6134129			
I	Sapindaceae	*Acer truncatum*	SRA		SRR3288570			
I	Sapindaceae	*Acer yangbiense*	SRA		SRR8707037			
I	Sapindaceae	*Aesculus chinensis*	SRA		SRR8073719			
I	Sapindaceae	*Aesculus pavia*	SRA		ERR2040474			
I	Sapindaceae	*Alatococcus siqueirae*	Herbarium	4688		Folli 1761	K	
I	Sapindaceae	*Alectryon carinatum*	DNA	1253		Munzinger 6743	NOU	K DNA bank no. 70369
I	Sapindaceae	*Allophylus* sp.	DNA	1111		Buerki, S. 164	K	K DNA bank no. 66869
I	Sapindaceae	*Amesiodendron chinense*	Herbarium	4690		Buerki, S. 117	BM	
I	Sapindaceae	*Aporrhiza paniculata*	Herbarium	4762		Swnowden 1669	BM	
I	Sapindaceae	*Arfeuillea arborescens*	DNA	3035		Chase, M.W. 2122	K	K DNA bank no. 2013
I	Sapindaceae	*Arytera arcuata*	DNA	4782		Munzinger 6728	NOU	K DNA bank no. 70366

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Sapindaceae	*Arytera lepidota*	DNA	4781		Munzinger 6705	MPU	K DNA bank no. 70361
I	Sapindaceae	*Arytera litoralis*	DNA	3060		Chase, M.W. 2123	K	K DNA bank no. 2014
I	Sapindaceae	*Atalaya capensis*	DNA	1120		Ohaeri, A.O s.n.	GCH	K DNA bank no. 40471
I	Sapindaceae	*Athyana weinmannifolia*	DNA	760		Pennington 17581	K	K DNA bank no. 18374
I	Sapindaceae	*Averrhoidium gardnerianum*	Herbarium	4691		Sello s.n.	BM	
I	Sapindaceae	*Beguea apetala*	Unknown	4743		Buerki, S. 149	G	
I	Sapindaceae	*Billia hippocastanum*	DNA	3040		Pennington & Zamora 604		K DNA bank no. 1416
I	Sapindaceae	*Blighia sapida*	DNA	3041		Chase, M.W. 2124	K	K DNA bank no. 2015
I	Sapindaceae	*Blighiopsis pseudostipularis*	Herbarium	4692		Troupin 7717	BM	
I	Sapindaceae	*Blomia prisca*	Herbarium	4693		Martinez et al. 30160	BM	
I	Sapindaceae	*Boniodendron parviflorum*	Herbarium	4694		Ford 291	K	K000701344
I	Sapindaceae	*Bridgesia incisifolia*	DNA	3012		Killip & Pisano 39778		K DNA bank no. 2671
I	Sapindaceae	*Camptolepis ramiflora*	Unknown	4695		Gautier, L. 4373	G	
I	Sapindaceae	*Castanospora alphandi*	Herbarium	4696		Hartley & Hyland 15106	K	
I	Sapindaceae	*Cnesmocarpon dasyantha*	Herbarium	4698		Forbes s.n.	BM	
I	Sapindaceae	*Conchopetalum brachysepalum*	Herbarium	4699		Randriamampionona 637	MO	
I	Sapindaceae	*Cubilia cubili*	DNA	3043		Chase, M.W. 2125	K	K DNA bank no. 2016
I	Sapindaceae	*Cupania rubiginosa*	DNA	923		Mori 8868	NY	K DNA bank no. 3618
I	Sapindaceae	*Cupaniopsis anacardioides*	DNA	856		Chase, M.W. 217	NCU	K DNA bank no. 21980
I	Sapindaceae	*Cupaniopsis macropetala*	DNA	4778		Deby 1227	MO	K DNA bank no. 66952
I	Sapindaceae	*Cupaniopsis squamosa*	Herbarium	4764		MacKee 20428	L	L0469876
I	Sapindaceae	*Cupaniopsis trigonocarpa*	Herbarium	4763		Veillon 7200	L	L0469922
I	Sapindaceae	*Deinbollia pinnata*	DNA	1136		Odewo, T.K s.n.	FHI	K DNA bank no. 40408
I	Sapindaceae	*Delavaya yunnanensis*	DNA	2839		Forrest 20682	K	K DNA bank no. 3623
I	Sapindaceae	*Diatenopteryx sorbifolia*	DNA	900		Tressens 3504	K	K DNA bank no. 2670
I	Sapindaceae	*Dictyoneura obtusa*	Herbarium	6607			BRI	
I	Sapindaceae	*Dilodendron costaricense*	Herbarium	4701		Galdames 5516	BM	
I	Sapindaceae	*Dimocarpus longan*	Unknown	4742		Buerki, S. 113	G	
I	Sapindaceae	*Dimocarpus* sp.	Unknown	3967		Buerki, S. 356	G	
I	Sapindaceae	*Diploglottis campbellii*	DNA	3039		Chase, M.W. 2048	K	K DNA bank no. 1857

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Sapindaceae	*Diplopeltis huegelii*	DNA	985		Chase, M.W. 2192	K	K DNA bank no. 1907
I	Sapindaceae	*Dipteronia dyeriana*	SRA		SRR2127991			
I	Sapindaceae	*Dipteronia sinensis*	DNA	746		Chase, M.W. 19988	K	K DNA bank no. 19861, K
I	Sapindaceae	*Distichostemon dodecarpus*	DNA	10427		Harrington, M. MH291	CNS	CNS141698; ATH DNA
I	Sapindaceae	*Dodonaea viscosa*	SRA		SRR1914335			
I	Sapindaceae	*Eriocoelum rubiginosum*	DNA	3042		Chase, M.W. 1350	K	K DNA bank no. 743
I	Sapindaceae	*Euchorium cubense*	Herbarium	4703		Ekman 18678	K	K000586270
I	Sapindaceae	*Euphoria malaiensis*	DNA	10429			CNS	ATH DNA no. D0278
I	Sapindaceae	*Euphorianthus longifolius*	DNA	971		Chase, M.W. 2126	K	K DNA bank no. 2017
I	Sapindaceae	*Eurycorymbus cavaleriei*	DNA	3069		Chase, M.W. 2127	K	K DNA bank no. 2018
I	Sapindaceae	*Exothea paniculata*	Herbarium	4704		Stafford 172	BM	
I	Sapindaceae	*Filicium decipiens*	DNA	3068		Chase, M.W. 2128	K	K DNA bank no. 2019
I	Sapindaceae	*Gereaua perrieri*	Herbarium	4705		Rakotomalaza 165	MO	
I	Sapindaceae	*Glenniea africanus*	DNA	1137		Adeyemi, T.O. 20	LUH	K DNA bank no. 40403
I	Sapindaceae	*Gongrodiscus sp.*	Unknown	4737		Callmander, M.W. 896	G	
I	Sapindaceae	*Guindilia trinervis*	DNA	3051		Chase, M.W. 802	K	K DNA bank no. 745; K
I	Sapindaceae	*Guioa rhoifolia*	DNA	1113		Buerki, S. 160	K	K DNA bank no. 66859
I	Sapindaceae	*Handeliodendron bodinieri*	Herbarium	4707		Steward & Cheo 498	BM	
I	Sapindaceae	*Haplocoelopsis africana*	Herbarium	4708		Dale 3820	BM	BM000073098
I	Sapindaceae	*Haplocoelum inopleum*	Herbarium	4709		Kassner 287	BM	BM000073104
I	Sapindaceae	*Harpullia* sp.	Unknown	4739		Buerki, S. 366	G	
I	Sapindaceae	*Hippobromus pauciflorus*	Herbarium	4789		Maurin, O. 1551	BNRH	BNRH0002073
I	Sapindaceae	*Hirania rosea*	Herbarium	4710		Kuchar 17237	K	
I	Sapindaceae	*Hornea mauritiana*	Herbarium	4711		Friedmann 3369	K	
I	Sapindaceae	*Hypelate trifoliata*	Herbarium	4748		Visaya M.J. 94	K	
I	Sapindaceae	*Jagera serrata*	DNA	970		Chase, M.W. 2130	K	K DNA bank no. 2021
I	Sapindaceae	*Koelreuteria paniculata*	DNA	3090		Chase, M.W. 115	NCU	K DNA bank no. 21878
I	Sapindaceae	*Lecaniodiscus cupanioides*	DNA	1122		Ameka et al. 221	GC	K DNA bank no. 40835
I	Sapindaceae	*Lepiderema ixiocarpa*	Herbarium	4772		Jensen 883	L	L0784800
I	Sapindaceae	*Lepiderema punctulata*	Herbarium	4770		Forster, P.I. 29953	L	L0784798

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Sapindaceae	*Lepidopetalum*	DNA	1119		s.n. 6926	K	K DNA bank no. 66895
I	Sapindaceae	*Lepisanthes ramiflora*	DNA	1098		Buerki, S. 324	K	K DNA bank no. 66876
I	Sapindaceae	*Litchi chinensis*	DNA	3066		Chase, M.W. 2131	K	K DNA bank no. 2022
I	Sapindaceae	*Llagunoa nitida*	DNA	729		Penningron et al. 17552	K	K DNA bank no. 18373
I	Sapindaceae	*Lophostigma plumosum*	Herbarium	4713		Brooke 5060	BM	
I	Sapindaceae	*Loxodiscus coriaceus*	DNA	869		Bradford 1136	K	K DNA bank no. 21333
I	Sapindaceae	*Macphersonia cauliflora*	Herbarium	4714		Rakotovao 3607	MO	
I	Sapindaceae	*Magonia pubescens*	DNA	921		Mori 16966	NY	K DNA bank no. 3621
I	Sapindaceae	*Majidea zanguebarica*	DNA	922		Verdcourt 2128	K	K DNA bank no. 3620
I	Sapindaceae	*Matayba tenax*	DNA	3065		Chase, M.W. 2132	K	K DNA bank no. 2023
I	Sapindaceae	*Melicoccus bijugatus*	DNA	1135		Ogu	FHI	K DNA bank no. 40422
I	Sapindaceae	*Mischarytera lautereriana*	Herbarium	4715		Gray 4850	K	
I	Sapindaceae	*Mischocarpus pyriformis*	DNA	2855		Chase, M.W. 2059	K	K DNA bank no. 1868
I	Sapindaceae	*Molinaea sessilifolia*	Herbarium	4734		Ravelonarivo 1784	MO	
I	Sapindaceae	*Nephelium lappaceum*	SRA		SRR11613036			
I	Sapindaceae	*Otonephelium stipulaceum*	Herbarium	4717		Hassan Flora Project 2848	K	
I	Sapindaceae	*Pancovia bijuga*	DNA	1134		Juillick s.n.	FHI	K DNA bank no. 40423
I	Sapindaceae	*Pappea capensis*	DNA	1034		Chase, M.W. 6585	K	K DNA bank no. 4852
I	Sapindaceae	*Paranephelium xestophyllum*	Unknown	1184		Buerki, S. 345	G	
I	Sapindaceae	*Paullinia pinnata*	DNA	1130		Adeyemi, T.O. 26	LUH	K DNA bank no. 40481
I	Sapindaceae	*Pavieasia anamensis*	Herbarium	4773		Cuong 415	L	L0405051
I	Sapindaceae	*Pentascyphus thyrsiflorus*	Herbarium	4718		Nee 42461	K	
I	Sapindaceae	*Placodiscus turbinatus*	Herbarium	4750		s.n. 2239	K	K000426281
I	Sapindaceae	*Plagioscyphus jumellei*	Unknown	4746		Buerki, S. 146	G	
I	Sapindaceae	*Podonephelium homei*	DNA	1154		Callmander, M.W. 908	G	K DNA bank no. 41039
I	Sapindaceae	*Pometia pinnata*	Unknown	4740		Buerki, S. 351	G	
I	Sapindaceae	*Pseudopteris decipiens*	DNA	924		Kakazomannjary 12529	K	K DNA bank no. 3617
I	Sapindaceae	*Radlkofera calodendron*	DNA	1127		Adeyemi, T.O. 30	LUH	K DNA bank no. 40496
I	Sapindaceae	*Rhysotoechia robertsonii*	Herbarium	4723		Gray 5134	K	
I	Sapindaceae	*Sapindus mukorossi*	SRA		SRR8302229			

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I	Sapindaceae	*Sapindus saponaria*	DNA	3064		Chase, M.W. 2136	K	K DNA bank no. 2027
I	Sapindaceae	*Sarcopteryx squamosa*	Herbarium	4736		Brass 13801	BM	
I	Sapindaceae	*Sarcotoechia cuneata*	Herbarium	4724		Gray 2798	K	
I	Sapindaceae	*Serjania communis*	DNA	3063		Chase, M.W. 2138	K	K DNA bank no. 2029
I	Sapindaceae	*Sisyrolepis muricata*	Herbarium	4725		Kerr 2187	K	
I	Sapindaceae	*Smelophyllum capense*	DNA	1315			NBG	K DNA bank no. 27946
I	Sapindaceae	*Stadmannia oppositifolia*	DNA	1332		Page, W. 41	MAU	K DNA bank no. 30007
I	Sapindaceae	*Stocksia brahuica*	Herbarium	4726		Popov 231	BM	
I	Sapindaceae	*Storthocalyx chryseus*	Unknown	4741		Callmander, M.W. 918	G	
I	Sapindaceae	*Synima cordieri*	DNA	1101		Gray, B. 9624	K	K DNA bank no. 70328
I	Sapindaceae	*Talisia nervosa*	DNA	3070		Pennington, T 628	K	K DNA bank no. 2120
I	Sapindaceae	*Thinouia myriantha*	Herbarium	4727		Philipson 2197	BM	
I	Sapindaceae	*Thouinia acuminata*	DNA	2801		Liston 6332	NY	K DNA bank no. 3185
I	Sapindaceae	*Thouinidium decandrum*	Herbarium	4728		Monro 1960	BM	BM000564890
I	Sapindaceae	*Tina tamatavensis*	Unknown	4729		Buerki, S. 140	G	
I	Sapindaceae	*Toechima erythrocarpum*	Herbarium	4738		Gray, B. 9084	K	
I	Sapindaceae	*Toulicia reticulata*	Herbarium	4749		Pennington et al. 16988	K	
I	Sapindaceae	*Trigonachras postardanjeisin*	DNA	1108		Buerki, S. 338	K	K DNA bank no. 66883
I	Sapindaceae	*Tristira triptera*	DNA	3052		Chase, M.W. 2139	K	K DNA bank no. 2030
I	Sapindaceae	*Tristiropsis* sp.	Unknown	3970		Buerki, S. 367	G	
I	Sapindaceae	*Tsingya bemarana*	Herbarium	4751		Leandri 1969	K	
I	Sapindaceae	*Ungnadia speciosa*	DNA	3034		Chase, M.W. 2854	K	K DNA bank no. 2661; K
I	Sapindaceae	*Urvillea ulmacea*	Herbarium	4731		Rolando Tn Ohiz 1660	BM	
I	Sapindaceae	*Vouarana guianensis*	Herbarium	4732		Nascimento 624	BM	
I	Sapindaceae	*Xanthoceras sorbifolium*	DNA	5170		Maurin, O. 4384	K	K DNA bank no. 74254
I	Sapindaceae	*Xerospermum noronhianum*	DNA	3061		Chase, M.W. 2140	K	K DNA bank no. 2031
I	Sapindaceae	*Zanha golungensis*	DNA	1141		Adeyemi, T.O. 35	LUH	K DNA bank no. 40482
I	Sapindaceae	*Zollingeria borneensis*	Herbarium	4776		Elmer 21128	BM	
O	Sapotaceae	*Manilkara zapota*	SRA		ERR2040506			
O	Sarcolaenaceae	*Leptolaena cuspidata*	SRA		ERR4180027			

I/O	Family	Species	Material type	PAFTOL ID	SRA ID	Collector	Museum ID	Museum code
I	Simaroubaceae	*Ailanthus altissima*	SRA		ERR2040477			
I	Simaroubaceae	*Ailanthus triphysa*	Silica	10461		Ford, A. 3095	CNS	QRS126785
I	Simaroubaceae	*Amaroria soulameoides*	Herbarium	11843		Prasad et al. EY055	K	K001275555
I	Simaroubaceae	*Castela coccinea*	Silica	11901		Bourdy, G. GB1967	SPF	
I	Simaroubaceae	*Eurycoma longifolia*	DNA	10887		RS.Th. 7.0218	K	K DNA bank no. 20645
I	Simaroubaceae	*Gymnostemon zaizou*	Herbarium	11857		Bamps 2593	K	K001275560
I	Simaroubaceae	*Hannoa klaineana*	Herbarium	11859		van der Burgt 2058	K	K001243682
I	Simaroubaceae	*Holacantha emoryi*	Herbarium	11845		Way et al. WSSB14	K	K001275556
I	Simaroubaceae	*Homalolepis glabra*	Silica	11907		Devecchi, M.F. MFD298	SPF	
I	Simaroubaceae	*Nothospondias staudtii*	Herbarium	11849		Daramola 24	K	K000040900
I	Simaroubaceae	*Odyendea gabunensis*	Herbarium	11851		Cheek et al. 15832	K	K000673044
I	Simaroubaceae	*Perriera madagascariensis*	Herbarium	11853		Phillipson et al. 6271	K	K001275558
I	Simaroubaceae	*Picrasma crenata*	Silica	11893		Alves, G.G.N. 76	SPF	
I	Simaroubaceae	*Pierreodendron africanum*	Herbarium	11855		Ern 2342	K	K001275559
I	Simaroubaceae	*Quassia amara*	DNA	10951		Chase, M.W. 34485	K	K DNA bank no. 34940
I	Simaroubaceae	*Samadera* sp. Tozer Range	Silica	6813		Baba, Y. 579	CNS	CNS135404
I	Simaroubaceae	*Simaba orinocensis*	Silica	11895		Devecchi, M.F. MFD361	SPF	
I	Simaroubaceae	*Simarouba glauca*	DNA	10711		Chase, M.W. 124	NCU	K DNA bank no. 21887
O	Stachyuraceae	*Stachyurus praecox*	SRA		ERR2040307			
O	Staphyleaceae	*Staphylea trifolia*	SRA		ERR2040308			

DNA extraction and quality control

For silica-dried and herbarium samples, DNA was extracted using the CTAB protocol of Doyle and Doyle (1987). The protocol was modified at the isopropanol precipitation step, with samples left to precipitate at -20°C degrees over 24 hours for silica-dried and fresh samples, and a minimum of 72 hours for herbarium samples. Extractions were cleaned using Agencourt AMPureXP beads (Beckman Coulter, Indianapolis, USA) according to the manufacturer's protocol and eluted to 50 μL. Quality and quantity of DNA was ascertained using a NanoDrop 1000 Spectrophotometer (Thermo Fisher Scientific, Massachusetts, USA) and Quantus Fluorometer (Promega Corporation, Wisconsin, USA) and run through a 1% agarose gel with electrophoresis to assess average fragment size. For extractions with a concentration of less than 4 ng/μL, yield was increased by undertaking a second DNA extraction from the same sample, combined with the first and concentrating it by evaporation.

Library preparation and sequencing

Library preparation protocol varied for each sample depending on quality. For higher-quality extractions (i.e. average fragment size > 350 bp), DNA was sonicated in a M220 Focused-ultrasonicator with microTUBES AFA Fiber Pre-slit Snap-caps (Covaris, Massachusetts, USA) following the manufacturer's protocol. Shearing time was varied depending on the DNA fragment size profile to obtain an average fragment size of 350 bp. Highly degraded samples with an average fragment size <350 bp were not sonicated. Sonicated samples were diluted to 200 ng DNA in 50 μL Tris, and non-sonicated samples to 100 ng DNA in 25 μL Tris.

Dual-indexed libraries were prepared using the NEBNext Ultra II Library Preparation Kit and the NEBNext Multiplex Oligos for Illumina (New England BioLabs, Massachusetts, USA) using half the manufacturer's recommended volumes. Library size profiles were evaluated on a 4200 TapeStation System using High Sensitivity D1000 ScreenTapes (Agilent Technologies, California, USA), and library concentrations ascertained using a Quantus Fluorometer (Promega Corporation, Wisconsin, USA). All libraries were of an average fragment size of approximately 500 bp (including adapters). For libraries not meeting these standards, PCR, adaptor cleanup and/or size selection steps of the library preparation protocol were repeated. All libraries were normalised to a concentration of 10 nM and combined in 7.5 µL library pools with 20–24 samples per pool of similar fragment lengths.

Pooled libraries were enriched using the myBaits 'Angiosperms 353 v1' Target Sequence Capture Kit (Arbor Bioscience, Michigan, USA) following the manufacturer's protocol. Hybridisations were performed at 60 or 65°C (depending on average fragment length) for 24 hours in a Hybex Microsample Incubator (SciGene, California, USA) using a volume equivalent to the hybridisation reaction (usually 30 µL) of red Chill-out Liquid Wax (Bio224 Rad, Hercules, CA, USA) to prevent evaporation.

Enriched library pools were amplified with KAPA HiFi 2X HotStart ReadyMix PCR Kit (Roche, Basel, Switzerland) for eight PCR cycles, and subsequently cleaned using Agencourt AMPure XP Beads. Concentrations of pools were quantified with a Quantus Fluorometer and quality and size profiling was conducted on a 4200 TapeStation System using High Sensitivity D1000 ScreenTapes. The hybridised pools were then combined into sequencing runs of approximately 96 libraries in 30 µL and 6 nM concentration. Library pools were multiplexed and sequenced by Macrogen (Macrogen Inc., Seoul, South Korea) on an Illumina HiSeq (Illumina Inc., California, USA) producing 2x 150 bp paired-end reads.

Gene retrieval

Sequence reads for 389 samples were obtained (Table 5.1). Transcriptome reads for 54 sapindalean species were downloaded from the Sequence Read Archive (SRA; NCBI, https://www.ncbi.nlm.nih.gov/sra) to augment the data set. Twenty-three outgroup samples were selected, spanning Malvid orders Brassicales, Malvales, Huerteales, Crossosomatales, Myrtales and Geraniales, as well as samples from Fabid order Fabales and Asterid order Ericales (Table 5.1). Transcriptome data for these outgroup samples were downloaded from the SRA.

Trimmomatic (Bolger *et al.* 2014) was used to remove adapter sequences, poor quality base calls and poor quality reads from sequencing reads with the settings: illuminaclip 2:30:10, leading 30, trailing 30, sliding window 4:2:30 and minimum length 36. Exon sequences were assembled using the HybPiper pipeline for nucleotide data (Johnson *et al.* 2016). Trimmed reads were mapped against the Sapindales subset of the mega target file (McLay *et al.* In press), as recovery was substantially higher for sapindalean taxa than against the standard Angiosperm353 target file. Exons and supercontigs were retrieved using the HybPiper script retrieve_sequences.py, and summary gene recovery statistics for each sample were generated with the HybPiper scripts get_seq_lengths.py and hybpiper_stats.py.

Paralogy is thought to be pervasive in some angiosperm lineages. Due to the independent evolutionary history of gene copies in paralogous loci, paralogous loci can produce conflicting phylogenetic signals that are problematic when trying to elucidate phylogenetic relationships. Although the Angiosperm353 bait kit was designed to target homologous genes, these may have paralogs in some lineages and therefore detection of paralogous loci is important. HybPiper assesses genes for paralogy, but misses many paralogous loci (Nauheimer *et al.* in press). Therefore, the newly developed pipeline HybPhaser (Nauheimer *et al.* in press) was used for further exploration of data, identification of paralogous loci and samples, and cleaning. Reads were remapped to the contig for each gene generated with the HybPhaser script Generate_consensus_sequences.sh. Information on length and coverage of sequences from all samples and loci were collated with the script Rscript_1a_count_snps_in_consensus_seqs.R. HybPhaser scripts R1b_optimize_dataset.R and Configure_1_SNPs_assessment.R were then used to clean the data by removing samples with <30% gene recovery, >50% missing loci, and loci with >100 missing samples, as well as samples and loci with outlying heterozygosity (> 1.5x the inter-quartile range for heterozygosity). Tables of heterozygosity and allele divergence were then collated with the script Rscript_1c_summary_table.R, and the cleaned consensus sequences with ambiguities exported with Rscript_1d_generate_sequence_lists.R. A summary of final sample coverage, sequence length, heterozygosity and allele divergence after cleaning is given in Appendix C1.

Genus-level Angiosperms353 Sapindales tree construction

HybPhaser consensus sequences (i.e. sequences including ambiguity codes) were aligned using MAFFT with the -auto flag to automatically select alignment strategy (Katoh and Standley 2013). Sites with >75% missing data were removed from the alignment using the

–clean option in Phyutility (Smith and Dunn 2008), and exon alignments concatenated with AMAS (Borowiec 2016). A maximum likelihood tree was then estimated from the clean alignment in IQ-TREE, with the appropriate substitution model and partitioning scheme for the alignment chosen using ModelFinder Plus option –MFP+MERGE and 1000 ultrafast bootstrap replicates (Lanfear *et al.* 2012; Nguyen *et al.* 2015; Kalyaanamoorthy *et al.* 2017; Hoang *et al.* 2018).

Divergence date estimation for Sapindales tree

Fossil selection

In total, 29 fossils were selected from the literature as reliable calibrations for the Sapindales Angiosperms353 genus-level phylogeny (Table 5.2). The reliability of each fossil's identification and age was rigorously assessed and scored against the five criteria for fossil calibrations of Parham *et al*. (2012) in eFLOWER's PROTEUS fossil database (Sauquet (2016); Appendix C2). A conservative approach to calibration was employed, with fossils usually assigned to the stem node of the taxon or clade the fossil was assigned to. An exception was made for Melieae; the high quality of the fossil used for this clade and rigour of the total evidence approach to identification gives confidence that this fossil belongs to Meliaeae and as such was assigned to the clade's crown node (Atkinson 2020). Refer to Appendix C2 for further justification of node assignment for each fossil calibration.

Divergence time estimation

Bayesian divergence time dating was implemented in BEAST v2.6.3 (Bouckaert *et al.* 2014). Computational efficiency of the dating analysis was improved by reducing, the alignment to sites with <5% gaps in trimAl (Capella-Gutiérrez *et al.* 2009), resulting in an alignment of 5,825 bp. To ensure that these sites were representative of the full alignment, another Maximum Likelihood tree was produced in IQ-TREE using the reduced alignment with the same parameters as for the tree generated with the full alignment; no difference in topology was observed.

Two BEAST analyses were conducted: one under an uncorrelated log-normal (relaxed) clock, and one under a strict clock model. A Yule model was assumed for both. For all

Table 5.2 Summary of fossils used to calibrate the genus-level molecular dating analysis of Sapindales. See Appendix C2 for more details on each fossil and justification for their placement.

	Family	Taxon	Organ/s	Country	Oldest stratum	Min. age (Ma)	Node calibrated	Reference
C02	Sapindaceae	†*Sapindospermum nitidum* Knobloch & Mai	Seed	Czech Republic	Turonian	89.8	crown Sapindales	Knobloch & Mai (1986)
C03	Sapindaceae	†*Aesculus hickeyi* Manchester	Leaf, fruit, seed	USA	Paleocene	56	crown Sapindaceae	Manchester (2001a)
C04	Sapindaceae	†*Dipteronia brownii* McClain & Manchester	Fruit	USA	Middle Paleocene	60	stem *Dipteronia*	McClain & Manchester (2001)
C05	Sapindaceae	†*Acer* sp.	Leaf		Late Paleocene	56	stem *Acer*	Crane *et al*. (1990)
C06	Sapindaceae	†*Koelreuteria allenii* (Lesq.) W. N. Edwards	Fruit	USA	Eocene	52	stem *Koelreuteria*	Wang *et al*. (2013)
C07	Sapindaceae	†*Allophylus graciliformis* (Berry) Berry	Leaf	Argentina	Early Eocene	46	stem *Allophylus*	Panti (2018)
C08	Burseraceae	†*Bursera inaequalateralis* (Lesq.) MacGintie	Leaf	USA	Eocene	48.5	crown Burserinae	MacGinitie (1969)
C09	Burseraceae	†*Bursericarpum aldwickense* Chandler	Pyrene, seed	UK	Ypresian	47.8	stem *Protium* alliance	Chandler (1961)
C10	Anacardiaceae	†*Coahuiloxylon terrazasiae* Estrada-Ruiz, Martínez-Vabrera & Cevallos-Ferriz	Wood	Mexico	Campanian	72.1	stem Anacardiaceae	Estrada-Ruiz *et al*. (2010)
C11	Anacardiaceae	†*Choerospondias sheppeyensis* (Reid & Chandler) Chandler	Fruit, seed	UK	Ypresian	47.8	crown Anacardiaceae	Reid & Chandler (1933); Chandler (1961)
C12	Anacardiaceae	†*Dracontomelon macdonaldii* (Berry) Herrera, Manchester & Jaramillo	Fruit, seed	Panama	Late Eocene	33.9	crown Spondioideae (-*Campnosperma*)	Herrera *et al.* (2012)
C13	Anacardiaceae	†*Spondias rothwellii* Herrera, Carvalho, Jaramillo & Manchester	Fruit, seed	Panama	Early Miocene	18.5	stem *Spondias* + *Allospondias*	Herrera *et al.* (2019)
C14	Anacardiaceae	†*Anacardium germanicum* Manchester *et al.*	Fruit	Germany	Middle Eocene (Lutetian assumed)	41.2	stem *Fegimanra* + *Anacardium*	Manchester *et al*. (2007)
C15	Anacardiaceae	†*Mangifera paleoindica* Sawangchote, Grote, and Dilcher	Leaf	Thailand	Late Oligocene	23.03	stem *Mangifera*	Sawangchote *et al.* (2009)
C16	Anacardiaceae	†*Cotinus fraterna* (Lesquereux) MacGinitie	Leaf	USA	Late Eocene	33.9	stem *Cotinus*	MacGinitie (1953); Manchester (2001b)
C17	Anacardiaceae	†*Pistacia* sp.	Pollen	Austria	Middle Miocene (Middle to Upper Serravallian)	12.7	stem *Pistacia*	Grímsson *et al*. (2020)

	Family	Taxon	Organ/s	Country	Oldest stratum	Min. age (Ma)	Node calibrated	Reference
C18	Anacardiaceae	†*Loxopterygium laplayense* Burnham and Carranco	Fruit	Ecuador	Middle Miocene	13.0	stem *Loxopterygium*	Burnham & Carranco (2004)
C19	Simaroubaceae	†*Ailanthus confucii* Unger	Fruit	Germany	Middle Eocene (Lutetian assumed)	41.2	stem *Ailanthus*	Collinson *et al*. (2012)
C20	Meliaceae	†*Cedrela sp.*	Leaf	USA	Eocene	51	crown Cedreloideae	Hickey & Hodges (1975)
C21	Meliaceae	†*Cedrela merrilli* (Chaney) Brown	Leaf, seed	USA	Late Eocene	36.21	stem *Cedrela* + *Toona*	Meyer & Manchester (1997); Manchester & McIntosh (2007)
C22	Meliaceae	†*Swietenia miocenica* Castañeda-Posadas & Cevallos-Ferriz	Flower	Mexico	Late Oligocene	22.5	stem *Swietenia*	Castañeda-Posadas & Cevallos-Ferriz (2007)
C23	Meliaceae	†Manchestercarpa vancouverensis Atkinson	Fruit, seed	Canada	Middle Campanian	72.1	crown Melieae	Atkinson (2020)
C24	Rutaceae	†*Rutaspermum biornatum* Knobloch & Mai	Seed	Germany	Maastrichtian	66	crown Rutaceae	Knobloch & Mai (1986)
C25	Rutaceae	†*Clausena* sp.	Leaf	Ethiopia	Late Oligocene	27.23	stem *Clausena* + *Glycosmis*	Pan (2010)
C26	Rutaceae	†*Citrus linczangensis* Xie *et al*.	Leaf	China	Late Miocene	11.6	stem *Citrus*	Xie *et al.* (2013)
C27	Rutaceae	†*Ptelea paliuruoides* (Brown) Manchester & O'Leary	Fruit, seed	USA	Middle Eocene	48.5	stem *Ptelea* + *Peltostigma* + *Plethadenia* + *Decazyx* clade	Manchester & O'Leary (2010)
C28	Rutaceae	†*Zanthoxylum* sp.	Seed	UK	Ypresian	47.8	stem *Zanthoxylum*	Chandler (1961)
C29	Rutaceae	†*Euodia costata* (Chandler) Tiffney	Seed	UK	Latest Paleocene (Thanetian)	56	crown Rutoideae clade	Tiffney (1981)
C30	Rutaceae	†*Vepris* sp.	Leaf	Ethiopia	Late Oligocene	27.23	stem *Vepris*	Pan (2010)

fossil calibrations, a uniform distribution was selected for the most-recent common ancestor prior, with the minimum age of the fossil taken as the minimum age of the distribution (as specified in Table 5.2), and the maximum age assigned as 295 My (which is the estimated stem age for Gnetales according to Ramírez-Barahona (2020)). For the root node, the secondary calibration was taken from the age of crown Ericales according to Ramírez-Barahona (2020) and constrained with a normal distribution.

Both the strict clock analysis and relaxed clock analyses were conducted with a fixed topology to improve the computational efficiency. This was done by assigning the starting tree to the best Maximum Likelihood IQ-TREE, and disabling the topology exchange parameters (Wide Exchange, Narrow Exchange, Wilson Balding and Subtree-slide) in Beauti (Bouckaert *et al.* 2014). Ten runs of the strict clock model and 15 runs of the relaxed clock model were conducted, each with a chain length of 50,000,000 and with trees sampled every 1,000 generations.

Runs from each clock model were combined in logCombiner and every 10,000th tree was sampled after a burn-in of 20%. This resulted in a combined tree exploration space where most priors and statistics reached an ESS (Effective Sampling Size) >200 and all priors and statistics had an ESS >100. The consensus tree was generated in TreeAnnotator.

Species-level Anacardiaceae tree construction

Data mining

Sequences of eight plastid (atpB, matK, ndhF, psbA, rbcL, trnL-trnF, trnL, ycf5) and two nuclear (ETS, ITS) markers from all sapindalean taxa were downloaded from GenBank using the R package rentrez (Winter 2017). These loci were chosen as they are commonly used for phylogenetic analysis. GenBank files for each locus were converted into fasta files, and duplicate taxa were removed at random using a custom R script so that only one sample was retained for each taxon. These fasta files were then aligned in MAFFT and visually inspected in Geneious R11.0.5 (http://www.geneious.com). Spurious samples (i.e. samples with notably longer or shorter sequences, highly divergent sequences, or sequences with blocks of ambiguity characters) were manually removed. Accessions for each species and locus are given in Table 5.3.

Table 5.3 Table of species and accessions used for each gene in the Sanger-Angiosperms353 species-level phylogenetic analysis of Anacardiaceae. Accession numbers with the prefix 'IDS' are samples for which target-capture data was generated for Angiosperms353 loci retrieval; refer to Table 5.1 for more information on specimen source and collector. Accession numbers with prefix 'SRR' and 'ERR' are samples for which transcriptome data was downloaded from the SRA and are SRA accession numbers. All other accession numbers are accessions downloaded from GenBank.

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Abrahamia ditimena	-	AY594405.1	AY594373.1	-	-	-	-	-	AY594436.1	-
Abrahamia elongata	-	AY594394.1	AY594362.1	-	-	-	-	-	AY594430.1	-
Abrahamia ibiyensis	-	AY594397.1	AY594364.1	-	-	-	-	-	-	-
Abrahamia latifolia	-	AY594399.1	AY594366.1	-	-	-	-	-	AY594431.1	-
Abrahamia lenticellata	-	AY594398.1	AY594365.1	-	-	-	-	-	-	-
Abrahamia littoralis	-	AY594400.1	AY594367.1	-	-	-	-	-	AY594434.1	-
Abrahamia nitida	-	AY594401.1	AY594368.1	-	-	-	-	-	AY594432.1	-
Abrahamia phillipsonii	-	AY594392.1	-	-	-	-	-	-	-	-
Abrahamia sericea	-	AY594406.1	AY594374.1	-	-	-	-	-	AY594437.1	-
Abrahamia suarezensis	-	AY594407.1	-	-	-	-	-	-	-	-
Abrahamia thouvenotii	-	AY594408.1	AY594375.1	-	-	-	-	-	-	-
Abrahamia viguieri	-	EF089162.1	EF089147.1	-	-	-	-	-	-	-
Actinocheita filicina	-	KF664494.1	AY641509.1	-	AY643120.1	KF664312.1	AY462007.1	-	AY640460.1	-
Allospondias lakonensis	IDS10575	KP963982.1	IDS10575	MN262105.1	IDS10575	KR075986.1	MN262108.1	-	MN262103.1	IDS10575
Amphipterygium adstringens	GU943752.1	KP055187.1	IDS10577	AY594458.1	IDS10577	-	GU935415.1	IDS10577	GU935415.1	IDS10577
Anacardium corymbosum	-	-	-	MF045476.1	MF045480.1	-	-	-	MF045472.1	-
Anacardium excelsum	-	KP055188.1	KF664193.1	MF045475.1	MF045479.1	GQ982143.1	GQ981661.1	KF664217.1	MF045471.1	-
Anacardium humile	-	KP963984.1	-	MF045477.1	MF045481.1	KR075988.1	-	-	MF045473.1	-
Anacardium nanum	-	-	-	MF045478.1	MF045482.1	-	-	-	MF045474.1	-
Anacardium occidentale	IDS10459	KP963986.1	KF664192.1	AY594459.1	KF664342.1	KR075991.1	MN394900.1	MG584466.1	MK186978.1	-
Anacardium parvifolium	-	KP055190.1	-	-	-	-	-	-	KP055485.1	-
Anacardium spruceanum	-	KP055191.1	-	-	-	FJ038839.2	FJ037949.1	-	KP055486.1	FJ039351.1

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Antrocaryon amazonicum	-	KP963987.1	-	AY594460.1	-	KR075993.1	-	-	KR081697.1	-
Apterokarpos gardneri	GU943753.1	KP963988.1	IDS10583	IDS10583	IDS10583	KR075994.1	GU935416.1	-	KR081698.1	IDS10583
Astronium fraxinifolium	-	KP055193.1	-	-	-	-	-	-	AY594542.1	-
Astronium graveolens	-	KP963990.1	-	JQ586471.1	-	GQ982155.1	MG833420.1	-	KR081700.1	-
Astronium lecointei	-	KP055194.1	-	-	-	-	-	-	KP055487.1	-
Astronium ulei	-	-	-	-	-	-	JQ625995.1	-	-	-
Baronia taratana	IDS10589	KP055195.1	IDS10589	IDS10589	IDS10589	-	IDS10589	IDS10589	IDS10589	IDS10589
Blepharocarya depauperata	-	KP055196.1	-	-	-	-	U38928.2	-	KP055488.1	-
Blepharocarya involucrigera	GU943754.1	KP055197.1	IDS10591	IDS10591	IDS10591	-	GU935417.1	IDS10591	GU935417.1	-
Bonetiella anomala	IDS10593	KP055198.1	IDS10593	IDS10593	IDS10593	-	AY462010.1	IDS10593	AY594543.1	IDS10593
Bouea macrophylla	-	KP055199.1	AB071691.1	-	-	-	-	-	KY392617.1	-
Bouea oppositifolia	IDS10465	KP055200.1	MF444895.1	IDS10465	IDS10465	IDS10465	IDS10465	IDS10465	KP055490.1	IDS10465
Buchanania arborescens	GU943755.1	-	-	MH332536.1	-	-	MH332414.1	-	KY067411.1	-
Buchanania glabra	-	KP055201.1	-	-	-	-	-	-	KP055491.1	-
Buchanania lanzan	-	-	-	-	-	-	KF432041.1	-	-	-
Buchanania latifolia	-	-	-	-	-	-	U39275.2	-	-	-
Buchanania obovata	IDS10431	-	IDS10431	IDS10431	IDS10431	IDS10431	IDS10431	-	IDS10431	IDS10431
Buchanania reticulata	-	KP055202.1	-	-	-	-	KY202633.1	-	KY067409.1	-
Buchanania sessilifolia	-	-	-	MH095571.1	-	-	KJ594631.1	-	-	-
Buchanania siamensis	-	KP055203.1	-	-	-	-	KY202636.1	-	KY067410.1	-
Campnosperma gummiferum	-	KP055204.1	-	-	-	-	-	-	KP055494.1	-
Campnosperma micranteium	-	KP055205.1	-	-	-	-	-	-	KP055495.1	-
Campnosperma schatzii	-	KP055206.1	-	-	-	-	-	-	-	-
Campnosperma zeylanicum	IDS6465	IDS6465	IDS6465	IDS6465	IDS6465	-	-	-	IDS6465	-
Campylopetalum siamense	IDS10597	KP055207.1	-	IDS10597	IDS10597	-	IDS10597	IDS10597	KP055496.1	IDS10597
Cardenasiodendron brachypterum	GU943756.1	KP055208.1	AY594377.1	IDS10599	IDS10599	-	GU935419.1	IDS10599	GU935419.1	IDS10599
Choerospondias axillaris	GU943757.1	KP963997.1	KR531918.1	HQ427341.1	IDS10601	KR076007.1	HQ427193.1	IDS10601	KR081711.1	GQ435690.1
Comocladia dodonaea	-	KP055210.1	-	KJ012544.1	-	KJ426678.1	KJ082234.1	MG584467.1	MG584467.1	-
Comocladia mayana	-	KP055212.1	-	-	-	-	-	-	KP055499.1	-

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Comocladia mollissima	-	KP055213.1	-	-	-	-	AY462011.1	-	KP055500.1	-
Cotinus coggygria	SRR8298330	KF682100.1	MH711074.1	MF349885.1	KF681967.1	KF682067.1	KF681984.1	MG584468.1	MG584468.1	SRR8298330
Cotinus nanus	-	KF682089.1	KF681989.1	-	KF681955.1	KF682055.1	KF681972.1	KF682023.1	KF682023.1	-
Cotinus obovatus	GU943759.1	KF682090.1	KF681990.1	SRR8298331	KF681956.1	KF682056.1	KF681973.1	MG584469.1	MG584469.1	SRR8298331
Cotinus szechuanensis	-	KF682102.1	KF682003.1	-	KF681969.1	KF682057.1	KF681986.1	KF682037.1	KF682037.1	-
Cyrtocarpa caatingae	IDS08429	KP964001.1	IDS08429	IDS08429	IDS08429	KR076017.1	IDS08429	IDS08429	KR081721.1	IDS08429
Cyrtocarpa procera	IDS10605	KP055217.1	IDS10605	AY594464.1	IDS10605	KR076018.1	U39272.2	-	KR081722.1	IDS10605
Cyrtocarpa velutinifolia	-	-	-	-	-	-	-	-	KR081723.1	-
Dobinea delavayi	-	-	EU123468.1	-	-	-	-	-	-	-
Dobinea vulgaris	IDS10607	KP055218.1	EU123467.1	AY594466.1	IDS10607	IDS10607	IDS10607	IDS10607	AY594512.1	-
Dracontomelon dao	-	KP964002.1	-	AY594467.1	-	KR076019.1	FJ976128.1	-	KR081724.1	-
Dracontomelon duperreanum	IDS10609	KP055220.1	IDS10609	IDS10609	IDS10609	-	IDS10609	-	KP055502.1	IDS10609
Dracontomelon vitiense	-	KP055221.1	-	-	-	-	-	-	AY594550.1	-
Drimycarpus racemosus	KX526023.1	KP055223.1	KR531994.1	KR530705.1	KX526856.1	KF664316.1	KR529126.1	KF664219.1	KP055504.1	-
Euroschinus aoupiniensis	-	KP055224.1	-	-	-	-	-	-	KP055505.1	-
Euroschinus elegans	-	KP055225.1	-	-	-	-	-	-	KP055506.1	-
Euroschinus falcatus	-	KP055226.1	-	KM894490.1	-	-	KM895580.1	-	KP055507.1	-
Euroschinus jaffrei	-	KP055227.1	-	-	-	-	-	-	KP055508.1	-
Euroschinus verrucosus	-	KP055229.1	-	-	-	-	-	-	KP055510.1	-
Euroschinus vieillardii	-	KP055230.1	-	-	-	-	-	-	KP055511.1	-
Faguetia falcata	GU943761.1	KP055231.1	EF089142.1	-	-	-	GU935425.1	-	GU935425.1	-
Fegimanra africana	GU943762.1	KP055232.1	IDS10617	AY594489.1	IDS10617	-	GU935427.1	IDS10617	GU935427.1	-
Fegimanra afzelii	-	KP055233.1	-	-	-	-	-	-	KP055513.1	-
Gluta laccifera	-	-	-	-	-	-	KY202637.1	-	KY067412.1	-
Gluta renghas	IDS6466	KP055234.1	IDS6466	-	-	KX304064.1	IDS6466	-	KX365742.1	-
Gluta tourtour	-	KP055236.1	-	-	-	-	-	-	KP055515.1	-
Gluta usitata	-	-	-	-	-	-	KY202641.1	-	KY067416.1	-
Gluta wallichii	-	KP055237.1	-	MH095567.1	-	-	KJ594727.1	-	AY594516.1	-
Haplorhus peruviana	IDS10621	KP055238.1	IDS10621	IDS10621	IDS10621	IDS10621	IDS10621	IDS10621	KP055516.1	IDS10621

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Harpephyllum caffrum	GU943763.1	KP964003.1	KF664197.1	AY594469.1	KF664347.1	KR076020.1	GU935428.1	KF664221.1	KR081725.1	IDS10623
Heeria argentea	IDS10841	KP055240.1	AY594378.1	JX518129.1	IDS10841	-	JX572667.1	IDS10841	KP055517.1	IDS10841
Lannea antiscorbutica	-	-	-	JX518185.1	-	-	JX572709.1	-	-	-
Lannea coromandelica	-	KP055241.1	-	-	-	-	MH113414.1	-	KP055518.1	-
Lannea discolor	-	-	-	JF270843.1	-	-	JF265496.1	-	-	-
Lannea edulis	-	-	-	JX518111.1	-	-	JQ025059.1	-	-	-
Lannea nigritana	-	-	-	MN370321.1	-	-	MN366877.1	-	-	-
Lannea rivae	GU943764.1	KP055242.1	-	-	-	-	GU935429.1	-	GU935429.1	-
Lannea schimperi	-	-	-	KX146220.1	-	-	KU567987.1	-	-	-
Lannea schweinfurthii	-	KP055243.1	-	JX517613.1	-	-	GU935430.1	-	GU935430.1	-
Lannea velutina	-	-	-	MN370320.1	-	-	MN366878.1	-	-	-
Lannea welwitschii	-	KP055244.1	-	MN370322.1	-	-	MN366879.1	-	AY594553.1	-
Laurophyllus capensis	IDS10945	KP055245.1	IDS10945	JX517726.1	IDS10945	IDS10945	JX572714.1	IDS10945	KP055519.1	IDS10945
Lithraea brasiliensis	-	-	-	-	-	-	-	MG584473.1	MG584473.1	-
Lithrea molleoides	-	KP055246.1	KF420989.1	MG718845.1	-	KR076021.1	MG718318.1	MG584475.1	MG584475.1	-
Loxopterygium grisebachii	IDS10857	KP055247.1	AY531207.1	IDS10857	IDS10857	IDS10857	IDS10857	IDS10857	KP055520.1	IDS10857
Loxopterygium huasango	GU943765.1	-	AY531206.1	AY594471.1	-	-	GU935431.1	-	GU935431.1	-
Loxopterygium sagotii	-	KP055248.1	AY531208.1	-	-	-	-	-	KP055521.1	-
Loxostylis alata	GU943766.1	KP055249.1	AY531201.1	JX517988.1	IDS10629	IDS10629	GU935432.1	IDS10629	GU935432.1	IDS10629
Mangifera caloneura	-	-	AB071678.1	-	-	-	-	-	-	-
Mangifera camptosperma	-	AB598032.1	MF444900.1	-	-	-	-	-	AB598010.1	-
Mangifera casturi	-	-	MF678493.1	-	-	-	-	-	-	-
Mangifera cochinchinensis	-	-	AB071677.1	-	-	-	-	-	-	-
Mangifera flava	-	-	AB071679.1	-	-	-	KY202638.1	-	KY067413.1	-
Mangifera foetida	-	KP055250.1	MF678506.1	-	-	-	KY202639.1	-	MF997585.1	-
Mangifera gedebe	-	-	AB071681.1	-	-	-	-	-	-	-
Mangifera gracilipes	-	-	AB071686.1	KJ708995.1	-	-	KJ594789.1	-	-	-
Mangifera griffithii	-	AB598034.1	MF444899.1	-	-	-	-	-	AB598012.1	-
Mangifera indica	GU943767.1	KP964005.1	MN477190.1	LC514288.1	KF664349.1	MH749205.1	MH113363.1	AB817698.1	MN481498.1	SRR1562187

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Mangifera kemanga	-	-	MF990368.1	-	-	-	-	-	MF919594.1	-
Mangifera lalijiwa	-	-	MH037252.1	-	-	-	-	-	MF997587.1	-
Mangifera laurina	-	-	MF990367.1	MH095570.1	-	-	KY202653.1	-	MF997588.1	-
Mangifera macrocarpa	-	-	AB071688.1	-	-	-	-	-	-	-
Mangifera minor	-	KP055251.1	-	-	-	-	-	-	-	-
Mangifera minutifolia	-	-	MN011951.1	-	-	-	-	-	-	-
Mangifera odorata	IDS10469	AB598033.1	MF444901.1	MH095574.1	IDS10469	-	KX148479.1	IDS10469	MF945596.1	IDS10469
Mangifera pajang	-	-	MF444896.1	-	-	-	-	-	-	-
Mangifera pentandra	-	-	AB071684.1	-	-	-	-	-	-	-
Mangifera quadrifida	-	-	MF678511.1	-	-	-	-	-	MF997589.1	-
Mangifera reba	-	-	MN011950.1	-	-	-	KY202640.1	-	KY067415.1	-
Mangifera sumatrana	-	-	MF990366.1	-	-	-	-	-	MF997590.1	-
Mangifera sylvatica	-	-	KR532344.1	KR531149.1	-	-	MH113359.1	-	-	-
Mangifera torquenda	-	-	MF990365.1	-	-	-	-	-	-	-
Mangifera zeylanica	-	AB598031.1	MF444898.1	MG787234.1	-	-	-	-	MF997591.1	-
Mauria heterophylla	-	KP055252.1	FJ945958.1	-	FJ945860.1	-	-	-	KP055523.1	-
Mauria simplicifolia	IDS10633	KP055253.1	IDS10633	IDS10633	IDS10633	IDS10633	IDS10633	IDS10633	AY594556.1	IDS10633
Mauria thaumatophylla	-	KP055254.1	KF664200.1	-	KF664350.1	KF664321.1	-	KF664224.1	KP055524.1	-
Melanochyla angustifolia	-	KP055255.1	-	-	-	-	-	-	KP055525.1	-
Melanochyla bracteata	-	KP055256.1	-	-	-	-	-	-	KP055526.1	-
Melanochyla castaneifolia	-	KP055257.1	-	-	-	-	-	-	KP055527.1	-
Metopium brownei	GU943768.1	KP055258.1	IDS10639	IDS10639	IDS10639	-	AY462013.1	IDS10639	GU935434.1	IDS10639
Metopium toxiferum	-	-	-	KJ772941.1	-	KJ426821.1	KJ773682.1	MG584478.1	MG584478.1	-
Micronychia bemangidiensis	-	KP055259.1	-	-	-	-	-	-	KP055529.1	-
Micronychia macrophylla	GU943769.1	AY594414.1	AY594380.1	IDS10641	IDS10641	IDS10641	GU935435.1	IDS10641	GU935435.1	IDS10641
Mosquitoxylum jamaicense	IDS10643	IDS10643	IDS10643	AY594490.1	IDS10643	-	AY462014.1	IDS10643	AY594558.1	-
Myracrodruon balansae	-	-	-	-	-	-	-	-	AY594559.1	-
Myracrodruon urundeuva	IDS10645	IDS10645	IDS10645	IDS10645	IDS10645	-	IDS10645	IDS10645	IDS10645	IDS10645
Nothopegia beddomei	IDS10891	IDS10891	MG672050.1	MG787235.1	IDS10891	-	-	-	IDS10891	-

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Ochoterenaea colombiana	IDS10647	KP055262.1	IDS10647	IDS10647	IDS10647	-	IDS10647	IDS10647	AY594561.1	IDS10647
Operculicarya decaryi	GU943770.1	KP964009.1	MH766915.1	MH748956.1	IDS10649	MH749206.1	MH749111.1	IDS10649	KR081737.1	IDS10649
Operculicarya pachypus	-	KP055264.1	-	-	-	-	-	-	KP055530.1	-
Orthopterygium huaucui	IDS10651	KP055265.1	IDS10651	IDS10651	IDS10651	-	IDS10651	IDS10651	AY594526.1	IDS10651
Ozoroa barbertonensis	-	-	-	KF147424.1	-	-	KU568020.1	-	-	-
Ozoroa dispar	-	KP055266.1	-	-	-	-	-	-	KP055531.1	-
Ozoroa engleri	-	-	-	JX518126.1	-	-	JF265536.1	-	-	-
Ozoroa homblei	-	-	-	KX146336.1	-	-	KU568118.1	-	-	-
Ozoroa insignis	IDS10653	AY594415.1	AY594381.1	KX146378.1	IDS10653	-	KU568163.1	IDS10653	AY594444.1	-
Ozoroa laetans	-	-	-	KX146255.1	-	-	KF147499.1	-	-	-
Ozoroa longipes	-	-	-	KX146281.1	-	-	KU568058.1	-	-	-
Ozoroa mucronata	-	KP055267.1	-	-	-	-	JQ014164.1	-	KP055532.1	-
Ozoroa nitida	-	-	-	KX146226.1	-	-	KU567995.1	-	-	-
Ozoroa obovata	-	AY594416.1	-	JX517800.1	-	-	JF265537.1	-	AY594445.1	-
Ozoroa paniculosa	-	-	-	JX517435.1	-	-	JX572822.1	-	-	-
Ozoroa pulcherrima	-	KP055268.1	-	-	-	-	-	-	KP055533.1	-
Ozoroa sphaerocarpa	-	-	-	JX517468.1	-	-	JX572823.1	-	-	-
Pachycormus discolor	GU943771.1	KP964010.1	IDS10787	AY594493.1	IDS10787	KR076034.1	GU935437.1	IDS10787	KR081739.1	IDS10787
Parishia insignis	IDS10655	IDS10655	IDS10655	MH095569.1	IDS10655	-	IDS10655	IDS10655	IDS10655	IDS10655
Parishia maingayi	-	-	-	KJ709032.1	-	-	KJ594834.1	-	-	-
Parishia paucijuga	-	-	-	KJ709034.1	-	-	KJ594836.1	-	-	-
Pegia nitida	KX525820.1	KP964013.1	IDS10657	AY594473.1	-	KR076035.1	KR529879.1	-	KR081740.1	-
Pegia sarmentosa	-	KP055270.1	-	-	-	-	-	-	KP055534.1	-
Pentaspadon annamense	-	KP055271.1	-	-	-	-	-	-	KP055535.1	-
Pentaspadon motleyi	IDS10659	IDS10659	IDS10659	IDS10659	IDS10659	-	IDS10659	-	IDS10659	IDS10659
Pentaspadon poilanei	-	KP055272.1	-	-	-	-	-	-	KP055536.1	-
Pistacia aethiopica	-	KF664465.1	KF664185.1	-	KF664335.1	-	-	KF664210.1	KF664210.1	-
Pistacia atlantica	-	KP055273.1	MT113330.1	-	EF193108.1	KF664286.1	KU504612.1	-	KP055537.1	-
Pistacia chinensis	GU943772.1	KP055274.1	MH711767.1	KP089206.1	DQ390462.1	KF664289.1	GU935438.1	MG584480.1	MG584480.1	SRR8661763

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Pistacia cucphuongensis	-	KF664473.1	KF664187.1	-	KF664337.1	KF664291.1	KF664524.1	KF664211.1	KF664211.1	-
Pistacia khinjuk	-	KF664475.1	KJ018024.1	-	EF193112.1	KF664293.1	KY794577.1	-	EF193129.1	-
Pistacia lentiscus	SRR5043662	KP964014.1	MT113331.1	KM527361.1	DQ390463.1	KR076036.1	KU504609.1	DQ390471.1	KR081741.1	SRR5043662
Pistacia mexicana	-	KP055275.1	KF664189.1	-	DQ390464.1	KF664306.1	KF664539.1	MG584482.1	MG584482.1	-
Pistacia terebinthus	-	KF664486.1	KY549579.1	-	EF193119.1	KF664304.1	KF664537.1	MG584481.1	MG584481.1	-
Pistacia vera	AJ132282.1	KP055276.1	MH444724.1	IDS10661	AY677204.1	MK578168.1	MK468869.1	MG584483.1	MG584483.1	IDS10661
Pistacia weinmaniifolia	-	KP055277.1	MF785655.1	KR531362.1	DQ390465.1	MF785959.1	MF786696.1	DQ390473.1	KY067417.1	-
Pleiogynium hapalum	-	KP055278.1	-	-	-	-	-	-	KP055542.1	-
Pleiogynium timoriense	-	KP055279.1	-	AY594474.1	-	KR076037.1	KM896152.1	-	KR081742.1	-
Poupartia borbonica	IDS10803	IDS10803	KX689318.1	IDS10803	IDS10803	KR076038.1	IDS10803	-	KR081743.1	IDS10803
Poupartia chapelieri	IDS11873	IDS11873	IDS11873	IDS11873	IDS11873	IDS11873	IDS11873	IDS11873	IDS11873	IDS11873
Poupartia minor	IDS10665	KP055280.1	MN257832.1	IDS10665	KF664351.1	KF664322.1	KF664555.1	KF664225.1	KF664225.1	IDS10665
Poupartia pubescens	-	-	-	-	-	KR076039.1	-	-	KR081744.1	-
Poupartiopsis spondiocarpus	IDS10667	KP055281.1	EF089145.1	IDS10667	IDS10667	IDS10667	IDS10667	IDS10667	AY594564.1	IDS10667
Protorhus grandidieri	-	KP055282.1	-	-	-	-	-	-	KP055544.1	-
Protorhus longifolia	IDS10669	KP055283.1	AY594382.1	JX517542.1	IDS10669	IDS10669	JX572886.1	IDS10669	KP055545.1	IDS10669
Pseudosmodingium andrieuxii	IDS10675	KP055286.1	IDS10675	IDS10675	IDS10675	IDS10675	IDS10675	IDS10675	AY594566.1	-
Pseudospondias microcarpa	IDS10673	KP964017.1	IDS10673	-	-	KR076042.1	KC628472.1	-	KR081747.1	-
Rhodosphaera rhodanthema	IDS10453	IDS10453	IDS10453	KM894755.1	IDS10453	-	KM895909.1	IDS10453	IDS10453	-
Rhus allophylloides	-	-	HE862264.1	-	-	-	-	-	HE862254.1	-
Rhus andrieuxii	-	-	HE862262.1	-	-	-	-	-	-	-
Rhus aromatica	-	AY594418.1	MG236688.1	AY594486.1	AY643107.1	-	MG248522.1	MG584484.1	MG584484.1	-
Rhus barclayi	-	-	HE862263.1	-	-	-	-	-	HE862253.1	-
Rhus chinensis	FN599843.1	KP055289.1	MH711357.1	KP089290.1	AY643096.1	KF664324.1	KY202643.1	-	KY067418.1	GQ435691.1
Rhus choriophylla	-	FJ945804.1	AY641498.1	-	AY643110.1	-	-	-	AY640450.1	-
Rhus copallinum	-	-	MG236611.1	MH621553.1	-	-	MH549964.1	MG584485.1	MG584485.1	-
Rhus coriaria	IDS10679	KP055291.1	KM210330.1	IDS10679	AY643099.1	-	IDS10679	IDS10679	KP055552.1	IDS10679
Rhus glabra	-	KP055292.1	KY584358.1	MK520522.1	AY643100.1	MF348360.1	MK526498.1	MG584487.1	MG584487.1	-
Rhus hartmanii	-	-	-	-	-	-	-	-	HE862260.1	-

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Rhus hypoleuca	-	-	-	HQ427342.1	-	HQ427036.1	-	-	-	-
Rhus integrifolia	-	FJ945805.1	AY641499.1	-	AY643111.1	-	-	-	AY640451.1	-
Rhus lanceolata	-	KP055293.1	EF682846.1	-	AY643101.1	-	-	-	AY594449.1	-
Rhus michauxii	-	KP055294.1	AY641488.1	-	AY643102.1	-	-	-	KP055554.1	-
Rhus microphylla	-	KF664508.1	KF664203.1	-	AY643108.1	KF664326.1	-	KF664227.1	KF664227.1	-
Rhus oaxacana	-	-	HE862266.1	-	-	-	-	-	HE862256.1	-
Rhus ovata	-	KP055295.1	MF963949.1	MF963575.1	AY643114.1	-	MF963245.1	-	KP055555.1	-
Rhus pachyrrhachis	-	-	AY641503.1	-	AY643115.1	-	-	-	AY640455.1	-
Rhus perrieri	IDS10681	AY594421.1	AY594369.1	IDS10681	IDS10681	IDS10681	IDS10681	IDS10681	KP055556.1	IDS10681
Rhus potaninii	-	-	MH711790.1	KP089291.1	AY643103.1	-	KP088831.1	-	AY640443.1	-
Rhus punjabensis	-	-	AY641490.1	KP089292.1	AY643104.1	-	KP088832.1	-	AY640444.1	-
Rhus rubifolia	-	-	AY641508.1	-	AY643119.1	-	-	-	AY640459.1	-
Rhus sandwicensis	-	KP055296.1	EF682847.1	-	AY643105.1	-	-	MG584489.1	MG584489.1	-
Rhus schiedeana	-	-	AY641504.1	-	AY643116.1	-	-	-	AY640456.1	-
Rhus taitensis	IDS10637	MN158630.1	MN161743.1	IDS10637	MN158640.1	IDS10637	JF739070.1	IDS10637	MN158646.1	IDS10637
Rhus terebinthifolia	-	-	HE862269.1	-	-	-	-	-	HE862259.1	-
Rhus thouarsii	GU943773.1	KP055297.1	AY594386.1	AY594484.1	IDS10683	IDS10683	GU935440.1	IDS10683	GU935440.1	IDS10683
Rhus trilobata	-	FJ945807.1	MG237046.1	-	AY643109.1	-	MG248959.1	-	AY640449.1	-
Rhus typhina	GU943774.1	KP055298.1	MG234618.1	MG220600.1	AY643106.1	-	MK526499.1	MG584491.1	MG584491.1	-
Rhus virens	-	KP055299.1	KF664204.1	-	AY643118.1	KF664327.1	KF664558.1	KF664228.1	KP055558.1	-
Schinopsis balansae	-	-	-	-	-	-	AY462015.1	-	AY594570.1	-
Schinopsis brasiliensis	IDS10685	KP964019.1	AY531203.1	AY594477.1	IDS10685	KR076054.1	KX640880.1	IDS10685	KR081759.1	IDS10685
Schinopsis lorentzii	-	-	-	-	-	-	-	-	AY594571.1	-
Schinopsis marginata	-	KP055301.1	KF664205.1	-	KF664355.1	KF664328.1	-	KF664229.1	KF664229.1	-
Schinus areira	-	KP055302.1	AY531202.1	AY594488.1	-	-	-	-	AY594572.1	-
Schinus fasciculata	-	KP055303.1	-	-	-	-	-	-	KP055560.1	-
Schinus gracilipes	-	KP055304.1	-	-	-	-	-	-	KP055561.1	-
Schinus molle	AF035914.1	KP964020.1	AY641512.1	JX495755.1	AY643123.1	MG947130.1	KU504611.1	MG584494.1	MG584494.1	-
Schinus montanus	-	KF664512.1	KF664206.1	-	KF664356.1	KF664330.1	KF664560.1	KF664230.1	KF664230.1	-

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Schinus myrtifolia	-	KP055305.1	-	-	-	-	-	-	KP055562.1	-
Schinus patagonicus	IDS10939	IDS10939	IDS10939	IDS10939	IDS10939	IDS10939	IDS10939	IDS10939	IDS10939	IDS10939
Schinus polygama	-	-	-	-	-	-	-	MG584497.1	MG584497.1	-
Schinus terebinthifolius	-	-	KF420944.1	GU134992.1	EU002257.1	KF421079.1	GU135156.1	-	-	-
Schinus weinmanniifolius	-	-	-	-	-	-	-	-	AY594573.1	-
Sclerocarya birrea	IDS10689	KP964022.1	IDS10689	MN243452.1	IDS10689	KR076058.1	MN216752.1	MG584502.1	MK187201.1	IDS10689
Sclerocarya gillettii	-	KP964024.1	-	-	-	KR076060.1	-	-	KR081766.1	-
Searsia acocksii	-	-	-	JX517985.1	-	-	JX572962.1	-	-	-
Searsia angustifolia	-	-	-	JX517801.1	-	-	JX572963.1	-	-	-
Searsia chirendensis	-	-	-	JF270931.1	-	-	JF265588.1	-	-	-
Searsia chirindensis	-	-	-	JX517658.1	-	-	JX572964.1	-	-	-
Searsia crenata	-	-	-	JX517881.1	-	-	JX572965.1	-	-	-
Searsia dentata	-	FJ945801.1	FJ945963.1	-	FJ945866.1	-	KF147514.1	-	FJ946018.1	-
Searsia discolor	-	KX360057.1	KX360047.1	KF147442.1	KX360027.1	-	KF147515.1	-	KX360037.1	-
Searsia dissecta	-	-	-	KP110143.1	-	-	KP110462.1	-	-	-
Searsia erosa	GU943775.1	KX360056.1	KX360046.1	-	KX360026.1	-	GU935442.1	-	KX360036.1	-
Searsia fastigiata	-	-	-	JX517893.1	-	-	JX572966.1	-	-	-
Searsia glauca	-	FJ945800.1	FJ945962.1	KF227400.1	FJ945865.1	-	-	-	FJ946017.1	-
Searsia gueinzii	-	-	-	JX517709.1	-	-	JX572967.1	-	-	-
Searsia incisa	-	-	-	JX517587.1	-	-	JX572968.1	-	-	-
Searsia kirkii	-	-	-	KX146286.1	-	-	KU568063.1	-	-	-
Searsia laevigata	-	-	-	JX518086.1	-	-	JX572969.1	-	-	-
Searsia lancea	-	KP055308.1	EF682850.1	JX518157.1	AY643125.1	-	JX572970.1	-	KP055564.1	-
Searsia leptodictya	-	-	AY641515.1	EU214282.1	AY643126.1	-	EU213509.1	-	AY640466.1	EU214114.1
Searsia longipes	-	KP055309.1	-	-	-	-	-	-	KP055565.1	-
Searsia longispina	-	-	-	JX517438.1	-	-	JX572972.1	-	-	-
Searsia lucida	-	KP055310.1	EF682851.1	KM896892.1	-	-	EU042184.1	-	KP055566.1	-
Searsia magalismontana	-	-	-	JF270934.1	-	-	JF265591.1	-	-	-
Searsia natalensis	-	FJ945785.1	MT137492.1	JX518140.1	FJ945850.1	-	JX572973.1	-	FJ946003.1	-

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Searsia nebulosa	-	-	-	JX517862.1	-	-	JX572974.1	-	-	-
Searsia pallens	-	-	-	KM896930.1	-	-	KM894259.1	-	-	-
Searsia paniculata	-	KX360054.1	KX360044.1	-	KX360025.1	-	-	-	KX360034.1	-
Searsia parviflora	-	KX360055.1	KX360045.1	-	-	-	-	-	KX360035.1	-
Searsia pendulina	GU943776.1	KP055311.1	-	JX517444.1	-	-	GU935443.1	-	GU935443.1	-
Searsia pentheri	-	-	-	JX517813.1	-	-	JF265592.1	-	-	-
Searsia pyroides	-	FJ945784.1	FJ945952.1	JX517483.1	AY643127.1	-	JX572977.1	-	FJ946002.1	-
Searsia quartiniana	-	KF664513.1	AY641518.1	-	AY643129.1	KF664331.1	KF664561.1	-	AY640468.1	-
Searsia rimosa	-	-	-	-	-	-	KP110463.1	-	-	-
Searsia scytophylla	-	-	-	-	-	-	KP110465.1	-	-	-
Searsia tenuinervis	-	KX360058.1	KX360048.1	-	KX360028.1	-	-	-	KX360038.1	-
Searsia tomentosa	-	-	-	KP110144.1	-	-	KP110466.1	-	-	-
Searsia transvaalensis	-	-	-	JX518204.1	-	-	JX572930.1	-	-	-
Searsia tumulicola	-	-	-	KF147445.1	-	-	KF147519.1	-	-	-
Searsia undulata	IDS10691	KF664514.1	AY594387.1	AY594483.1	AY643130.1	KF664332.1	JQ025088.1	IDS10691	AY594454.1	-
Searsia wilmsii	-	-	-	KF147446.1	-	-	KF147520.1	-	-	-
Searsia zeyheri	-	-	-	JX905948.1	-	-	JX572979.1	-	-	-
Semecarpus anacardiopsis	-	-	-	-	-	-	KY202647.1	-	KY067422.1	-
Semecarpus anacardium	-	KP055312.1	-	-	-	-	-	-	AY594575.1	-
Semecarpus australiensis	-	-	-	AY594479.1	-	-	KF496691.1	-	-	-
Semecarpus forstenii	GU943777.1	KP055313.1	-	-	-	-	GU935444.1	-	GU935444.1	-
Semecarpus gigantifolia	FN599855.1	-	-	-	-	-	FN599462.1	-	FN599474.1	-
Semecarpus magnificus	-	KP055314.1	-	-	-	-	-	-	KP055567.1	-
Semecarpus neocaledonicus	-	KP055315.1	-	-	-	-	-	-	KP055568.1	-
Semecarpus obscurus	-	KP055316.1	-	-	-	-	-	-	KP055569.1	-
Semecarpus reticulatus	-	KP055317.1	KR532565.1	-	-	-	KY202648.1	-	KY067423.1	-
Semecarpus schlechteri	-	KP055318.1	-	-	-	-	JF738945.1	-	KP055571.1	-
Semecarpus tonkinensis	-	KP055319.1	-	-	-	-	-	-	KP055572.1	-
Smodingium argutum	IDS10695	KP055320.1	IDS10695	IDS10695	IDS10695	IDS10695	AY462016.1	IDS10695	AY594576.1	-

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Sorindeia juglandifolia	-	KP055321.1	-	KC627648.1	-	-	KC628277.1	-	KP055573.1	-
Sorindeia madagascariensis	IDS10697	AY594424.1	AY594388.1	IDS10697	IDS10697	-	IDS10697	KC479213.1	AY594455.1	-
Spondias acida	-	KP964025.1	-	-	-	KR076061.1	-	-	KR081767.1	-
Spondias bahiensis	-	KP964420.1	-	-	-	KR076391.1	-	-	KR081927.1	-
Spondias bipinnata	-	KP964196.1	-	-	-	-	-	-	-	-
Spondias dulcis	-	KP964201.1	-	KP774606.1	-	KJ026800.1	JF739148.1	MG584503.1	MG584503.1	-
Spondias globosa	-	-	-	-	-	KR076209.1	-	-	KR081819.1	-
Spondias macrocarpa	-	KP964206.1	-	-	-	KR076210.1	-	-	KR081824.1	-
Spondias malayana	-	KP964207.1	-	-	-	KR076211.1	-	-	KR081825.1	-
Spondias mombin	IDS6469	KP964416.1	AF445882.1	AY594480.1	IDS6469	GQ982370.1	GQ981882.1	MG584505.1	MG584505.1	-
Spondias pinnata	-	KP964269.1	-	MN262106.1	-	KR076263.1	MN262109.1	-	MN262102.1	-
Spondias purpurea	-	KP964419.1	-	KP774612.1	-	KR076390.1	KU176194.1	MG584506.1	MG584506.1	-
Spondias testudinis	-	KP964280.1	-	-	-	KR076270.1	-	-	KR081875.1	-
Spondias tuberosa	GU943778.1	KP964328.1	-	KP774614.1	-	KR076309.1	KP774626.1	-	KR081884.1	-
Spondias venulosa	-	KP964375.1	-	KP774610.1	-	KR076346.1	KP774632.1	-	KR081921.1	-
Swintonia schwenckii	IDS10701	IDS10701	IDS10701	IDS10701	IDS10701	IDS10701	IDS10701	IDS10701	IDS10701	-
Tapirira bethanniana	GU943779.1	KP055326.1	-	AY594481.1	-	-	GU935445.1	MK797671.1	GU935445.1	-
Tapirira guianensis	IDS10703	KP964422.1	MG217387.1	KF981295.1	IDS10703	KR076396.1	MG718542.1	-	KR081932.1	-
Tapirira mexicana	-	-	-	JQ586479.1	-	-	U39273.2	-	-	-
Tapirira obtusa	GU943780.1	KP055329.1	-	JQ626383.1	-	-	GU935446.1	MK797672.1	GU935446.1	-
Thyrsodium puberulum	-	-	FJ037790.1	FJ514723.1	-	FJ038841.2	GQ428577.1	MK797686.1	-	-
Thyrsodium spruceanum	IDS10705	KP964424.1	IDS10705	IDS10705	-	KR076399.1	IDS10705	-	KR081934.1	-
Toxicodendron acuminatum	-	-	-	KR531578.1	-	-	KR530141.1	-	-	-
Toxicodendron borneense	-	MN158628.1	-	-	MN158639.1	-	-	-	MN158644.1	-
Toxicodendron diversilobum	-	-	MF964008.1	KX676732.1	AY677205.1	-	MF963266.1	-	AY677208.1	-
Toxicodendron fulvum	-	FJ945751.1	FJ945921.1	-	FJ945814.1	-	-	-	FJ945967.1	-
Toxicodendron grandiflorum	-	FJ945791.1	MF785520.1	MF786837.1	FJ945856.1	MF785799.1	MF786557.1	-	FJ946009.1	-
Toxicodendron griffithii	-	KP055332.1	MF785457.1	MF786777.1	FJ945818.1	MF785726.1	MF786461.1	-	FJ945971.1	-
Toxicodendron nodosum	-	MN158626.1	MN161740.1	-	MN158637.1	-	-	-	MN158642.1	-

Name	atpB	ETS	ITS	matK	ndhF	psbA	rbcL	trnL	trnL-trnF	ycf5
Toxicodendron orientale	-	-	-	-	-	-	-	-	AB365016.1	-
Toxicodendron pubescens	IDS10707	KP055333.1	IDS10707	MH552158.1	FJ945853.1	-	KY627337.1	IDS10707	KP055582.1	-
Toxicodendron radicans	ERR2040463	KP055334.1	FJ945949.1	MH551860.1	AY677206.1	ERR2040463	KP643978.1	MG584507.1	MG584507.1	-
Toxicodendron rhetsoides	-	KP055335.1	-	-	-	-	-	-	-	-
Toxicodendron rydbergii	-	KF664515.1	MG235531.1	KX677136.1	FJ945857.1	KF664333.1	MG247072.1	KF664231.1	KF664231.1	-
Toxicodendron striatum	-	FJ945778.1	FJ945948.1	-	FJ945843.1	-	-	-	FJ945996.1	-
Toxicodendron succedaneum	FN599854.1	KP055336.1	MH548389.1	MF786785.1	FJ945864.1	HQ427037.1	LC413474.1	AB817449.1	KY067426.1	-
Toxicodendron sylvestre	-	FJ945780.1	MH813029.1	HQ415319.1	FJ945845.1	-	AY510145.1	-	FJ945998.1	-
Toxicodendron trichocarpum	-	FJ945757.1	LC191586.1	-	FJ945820.1	-	AY510143.1	-	FJ945973.1	-
Toxicodendron vernicifluum	GU943781.1	KP055337.1	MH711200.1	KP089348.1	FJ945848.1	KF664334.1	AY510142.1	KF664232.1	GU935447.1	-
Toxicodendron vernix	-	KP055338.1	MG236574.1	KY607381.1	AY643131.1	-	MK526812.1	MG584508.1	MG584508.1	-
Trichoscypha acuminata	-	AY594425.1	AY594389.1	KC627761.1	-	-	KC628423.1	-	AY594456.1	-
Trichoscypha arborea	-	-	-	KC627512.1	-	-	KC628094.1	-	-	-
Trichoscypha baldwinii	-	-	-	MN370314.1	-	-	MN366881.1	-	-	-
Trichoscypha bijuga	-	-	-	MN370315.1	-	-	MN366882.1	-	-	-
Trichoscypha cavalliensis	-	-	-	MN370316.1	-	-	MN366883.1	-	-	-
Trichoscypha klainei	-	-	-	KC627911.1	-	-	KC628636.1	-	-	-
Trichoscypha longifolia	IDS10935	IDS10935	IDS10935	IDS10935	-	-	-	IDS10935	IDS10935	-
Trichoscypha lucens	-	-	-	MN370318.1	-	-	MN366884.1	-	-	-
Trichoscypha mannii	-	-	-	MN370317.1	-	-	MN366885.1	-	-	-
Trichoscypha patens	-	-	-	KC627727.1	-	-	KC685086.1	-	-	-
Trichoscypha preussii	-	-	-	KC627584.1	-	-	KC628222.1	-	-	-
Trichoscypha smythei	-	-	-	-	-	-	MN366887.1	-	-	-
Trichoscypha ulugurensis	-	AY594426.1	EF089140.1	-	-	-	-	-	EF089140.1	-

Extraction of Sanger loci from target capture samples

To extract the ten Sanger loci from the target capture samples, a custom target file was created. One sample of each genus was selected at random from each cleaned, unaligned locus fasta file. These sequences were formatted as a target file compatible with HybPiper, with the final target file including one sample for every genus for each gene (for which there was a sequence available on GenBank). The trimmed reads of all target capture samples were then run through the HybPiper pipeline against this custom target file, following the same method as for the Mega target file described above.

Alignment and cleaning

All sequences derived from target capture and Sanger data were combined into one fasta file per locus. These files were then split by family, resulting in one fasta file per family per locus. Each family locus file was aligned in MAFFT and visually inspected in Geneious R11.0.5. Alignment was conducted on a family basis, as aligning at the ordinal level resulted in alignments with a high proportion of gaps due to the high divergence of some loci between families. Alignments were then cleaned using phyutility to remove sites with more than 50% gaps, resulting in a final alignment of 8,382 bp.

Tree estimation

Modeltest-NG (Darriba *et al.* 2020) was used to assess the best substitution model for each gene in the concatenated alignment for Anacardiaceae, with GTR+I+G4 found to be optimal for all genes. Alignments were compressed using the –parse command of RAxML-NG, stipulating gene partitions and the substitution model to apply to each gene (Kozlov *et al.* 2019). Partitioned maximum likelihood RAxML-NG analyses were then run on the compressed alignment. Genus topology was constrained to that of the Angiosperms353 Sapindales phylogeny, as the same samples were used in both the Angiosperms353 and Sanger alignments. In a constrained RAxML-NG analysis, the position of samples that were not in the Angiosperms353 tree (i.e. Sanger accessions sourced from GenBank) are estimated around the genus backbone. Ten analyses were conducted, with each run resulting in a tree with slightly different topology. The run estimating the tree with the highest likelihood was chosen. Bootstrapping converged after 200 replicates, and bootstrap values were used to indicate the confidence of the estimated topology of the best tree.

In the best Maximum Likelihood tree, some samples were retrieved on long branches and in 'erroneous' clades. Samples on outlying long branches were pruned from the tree using TreeShrink (Mai and Mirarab 2018) with α set to 0.50. Samples remaining in the tree in 'erroneous' positions (i.e. were placed outside an otherwise monophyletic genus) were pruned from the tree for genera that are generally accepted to be monophyletic according to current phylogenetic and taxonomic work. However, samples from genera that are known to have problematic taxonomy and poorly-defined phylogenetic relationships (e.g. *Rhus*), were retained regardless of their retrieved position. In total, 38 samples were pruned from the tree.

Divergence date estimation for Anacardiaceae

The Anacardiaceae tree was dated using BEAST v2.6.3 (Bouckaert *et al.* 2014) under an uncorrelated log-normal (relaxed) clock and Yule model. The topology of the tree was constrained by assigning the starting tree to the best Maximum Likelihood RAxML-NG tree and disabling the topology exchange parameters (Wide Exchange, Nanon Exchange, Wilson Balding and Subtree-slide) in Beauti. Tree topology was constrained to ensure that deeper relationships of genera were correctly retrieved in accordance with the Angiosperms353 phylogeny (as the Sanger data did not have enough informative sites to resolve relationships at this level), and to ensure convergence of the model in a reasonable time.

The Anacardiaceae tree was calibrated using 17 secondary calibrations taken from the Sapindales Angiosperms353 chronogram estimated under a relaxed clock (Table 5.4). Secondary calibrations were chosen as the ages in the Sapindales tree were estimated with high-quality and highly informative target capture data and a rigorous primary calibration approach, and to give the analysis as much information as possible to reach convergence of ages. For each age calibration prior, a normal distribution was selected with mean and a standard deviation that matched that of the Sapindales chronogram ages 95% HPD interval (Table 5.4).

To further optimise the time-efficiency of the analysis, auto-optimisation of MCMC step size was disabled and step size was increased by deactivating the mean and standard deviation scaler parameters, and increasing the weight of the mean scaler to 3.0. Four runs were conducted in BEAST, each with a chain length of 50 M sampled every 10,000 generations. Runs were combined in logCombiner and every 10,000th tree was sampled after a burn-in of 20%. This resulted in convergence diagnostics where most priors and statistics reached an ESS (Effective Sampling Size) >200 and all priors and statistics had an ESS >100.

Table 5.4 Secondary calibrations used for dating the species-level Anacardiaceae tree as shown in Figure 5.4. All calibrations had a normal distribution with the mean and standard deviation as indicated below.

	Calibration	**Mean (Mya)**	**σ**
A	Root Anacardiaceae	83.5	4.5
B	Stem *Campnosperma*	76.2	7.0
C	Stem *Buchanania*	56.6	6.0
D	Stem *Dracontomelon*	33.6	4.0
E	Crown Dobineae	41.0	6.5
F	Stem *Semecarpus*	24.6	4.0
G	Stem *Gluta*	36.1	3.0
H	Stem *Bouea*	26.4	1.5
I	Stem *Anacardium*	25.8	4.5
J	Stem *Mangifera* + *Anacardium et al*. clade	60.9	3.5
K	Stem *Pistacia*	23.9	3.5
L	Stem *Toxicodendron*	28.4	4.0
M	Stem *Schinus*	26.1	4.0
N	Stem *Searsia*	21.6	3.5
O	Stem *Schinopsis*	21.8	3.0
P	Stem *Abrahamia*	16.1	3.0

Ancestral area analysis

All species included in the Anacardiaceae tree were coded according to their presence in seven biogeographic regions: Sunda, Sahul, Wallacea, Africa, Eurasia, the Pacific and the Americas. Presence of species in Sunda, Sahul and Wallacea was coded by checking names against the Checklist of Vascular Plants of the SSCZ (Joyce *et al*. 2020; Chapter 2). To code species into regions encompassing the rest of the world, occurrence data for each species was downloaded from GBIF using the rgbif v.1.3.0 package in R (Chamberlain *et al*. 2019; GBIF.org 2021). Only herbarium records from after 1960 with a geospatial coordinate uncertainty of <25 km were retrieved. Geospatial coordinates for each species were then coded into Level 2 regions under the World Geographical Scheme for Recording Plant Distributions (TDWG Level 2; Brummitt *et al.* 2001) using the speciesgeocodeR package in R (Töpel *et al.* 2017). Records for TDWG Level 2 regions 'Indo-China', 'Papuasia' and 'Australia' were omitted as they were captured in the initial sorting of species that are found in Sunda, Sahul and Wallacea according to Joyce *et al*. (2020). Records in TDWG Level 2 regions making up TDWG Level 1 botanical continents 'Asia-Temperate', 'Europe' and the TDWG Level 2 region 'Indian Subcontinent' were sunk into the biogeographic region 'Eurasia', records in TDWG Level 2 regions making up the TDWG Level 1 botanical continent 'Africa' were classified in the biogeographic region 'Africa', and records in TDWG Level 2 regions making up the TDWG Level 1 botanical continent 'Pacific' were classified in the biogeographic region 'Pacific'. Records in TDWG Level 2 regions making up TDWG Level 1 botanical continents 'Northern America' and 'Southern America' were coded into the biogeographic region 'Americas'. Biogeographic coding for each species was then manually checked.

Bayesian ancestral area reconstruction for the Anacardiaceae species chronogram was conducted using the seven biogeographic regions using BioGeoBEARS in R (Matzke 2013). All area combinations were allowed in the analysis, and no time-slicing or distance or trait-based weightings were used, to lower the number of assumptions incorporated into the model and enable a pattern-exploration approach to the analysis. The maximum number of areas allowed in the reconstruction was set to five, as this was the maximum number of areas occupied by any extant species. Ancestral area reconstructions were conducted under DEC, DEC+J, DIVALIKE, DIVALIKE+J, BAYAREALIKE and BAYAREALIKE+J models (Landis *et al.* 2013; Matzke 2014). The Akaike Information Criterion (AIC) was used to compare the relative model probabilities, and DEC+J was found to be the best model, with an AIC of 1,135 (Appendices C3 and C4).

Biogeographic stochastic mapping was then conducted in BioGeoBEARS under the DEC+J model to simulate ancestral range transitions along branches as well as at nodes. A total of 100 stochastic maps were generated. A linear regression of the Maximum Likelihood ancestral range probabilities against the mean biogeographic stochastic models was conducted to assess the confidence of the biogeographic stochastic model. Source areas were simulated for each cladogenetic and anagenetic event, and the number of events for each source, sink and event type summarised across all 100 simulations. To investigate dispersal patterns between Sunda, Sahul and Wallacea, the mean number of dispersal events between these regions (with simulated source areas) was calculated in 2 My time bins.

Results

Sapindales Angiosperms353 genus tree

Phylogenetic relationships

The final Sapindales dataset comprised 466 samples (including 23 outgroup representatives) with an average of 324 loci and 74.74% target coverage (Appendix C1). Following cleaning of highly paralogous loci in HybPhaser, samples had an average of 14.98 (0–46) paralogous loci, and a mean of 60.56% (8.81%–99.09%) of heterozygous sites with allele divergence averaging 1.22 (0.09–7.52). The variation in these paralogy and heterozygosity statistics was unevenly spread across the order, with higher values grouped in some clades and families (particularly Meliaceae).

The concatenated alignment was 199,268 bp and comprised 137,780 parsimony-informative sites and 16.47% gaps or ambiguities. IQ-TREE identified the best partition scheme and merged the alignment into 44 partitions (LnL = 10,415,060, df = 1,800), all of which were ascribed an optimal substitution model with the inbuilt ModelTest function of IQ-TREE, resulting in an alignment with 0.02% missing data. After 124 iterations and 1000 bootstrap trees, IQ-TREE produced a consensus tree with a log-likelihood of -10,413,850 (Figure 5.2).

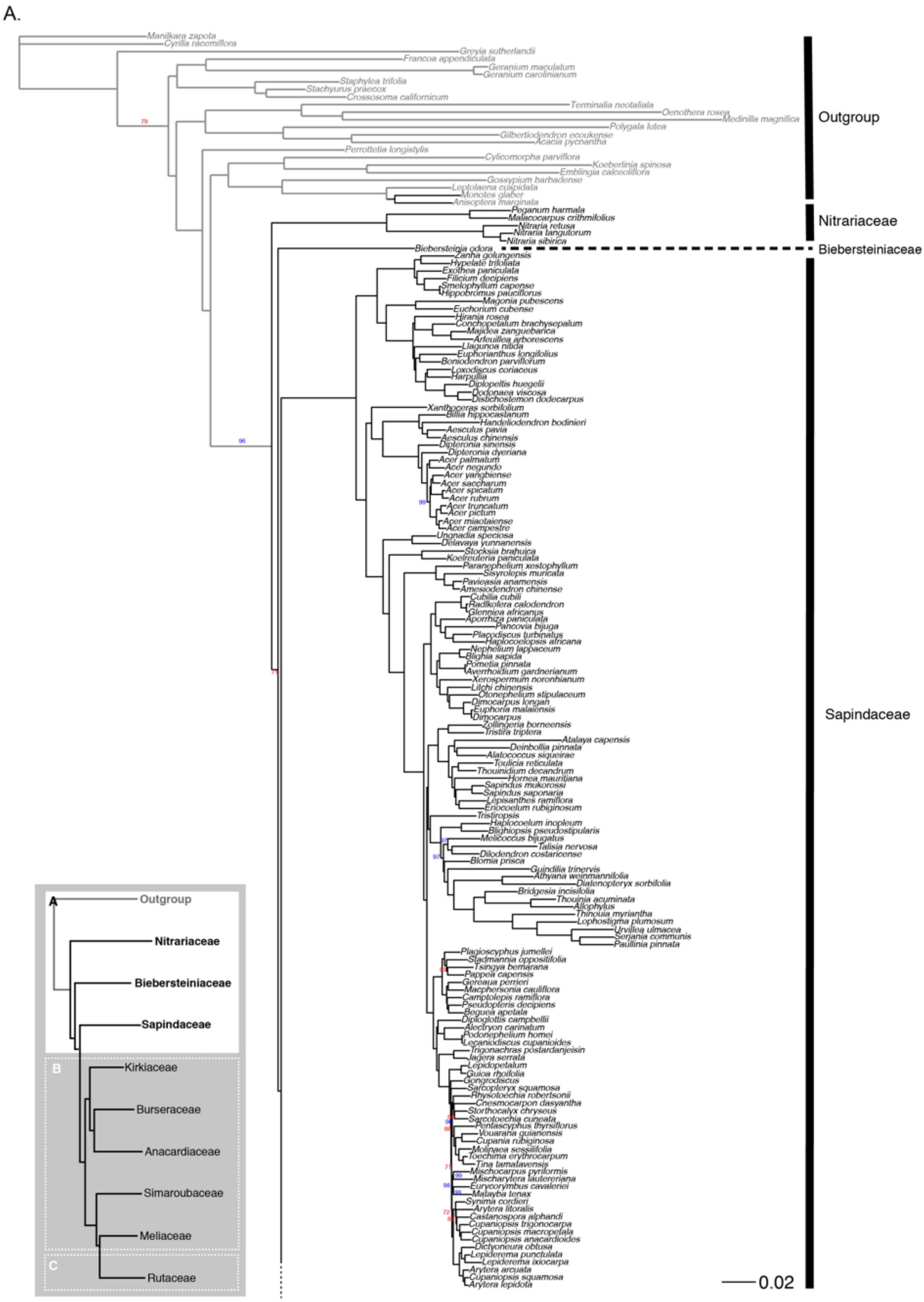
All sapindalean families were retrieved as monophyletic with maximum support, with the exception of Nitrariaceae and Biebersteiniaceae which were recovered with 96% and 71% bootstrap support, respectively (Figure 5.2). Nitrariaceae, Biebersteiniaceae and Sapindaceae formed an early-diverging grade within the order. The remaining families grouped into two clades: (Kirkiaceae (Burseraceae + Anacardiaceae)), and (Simaroubaceae (Meliaceae + Rutaceae)).

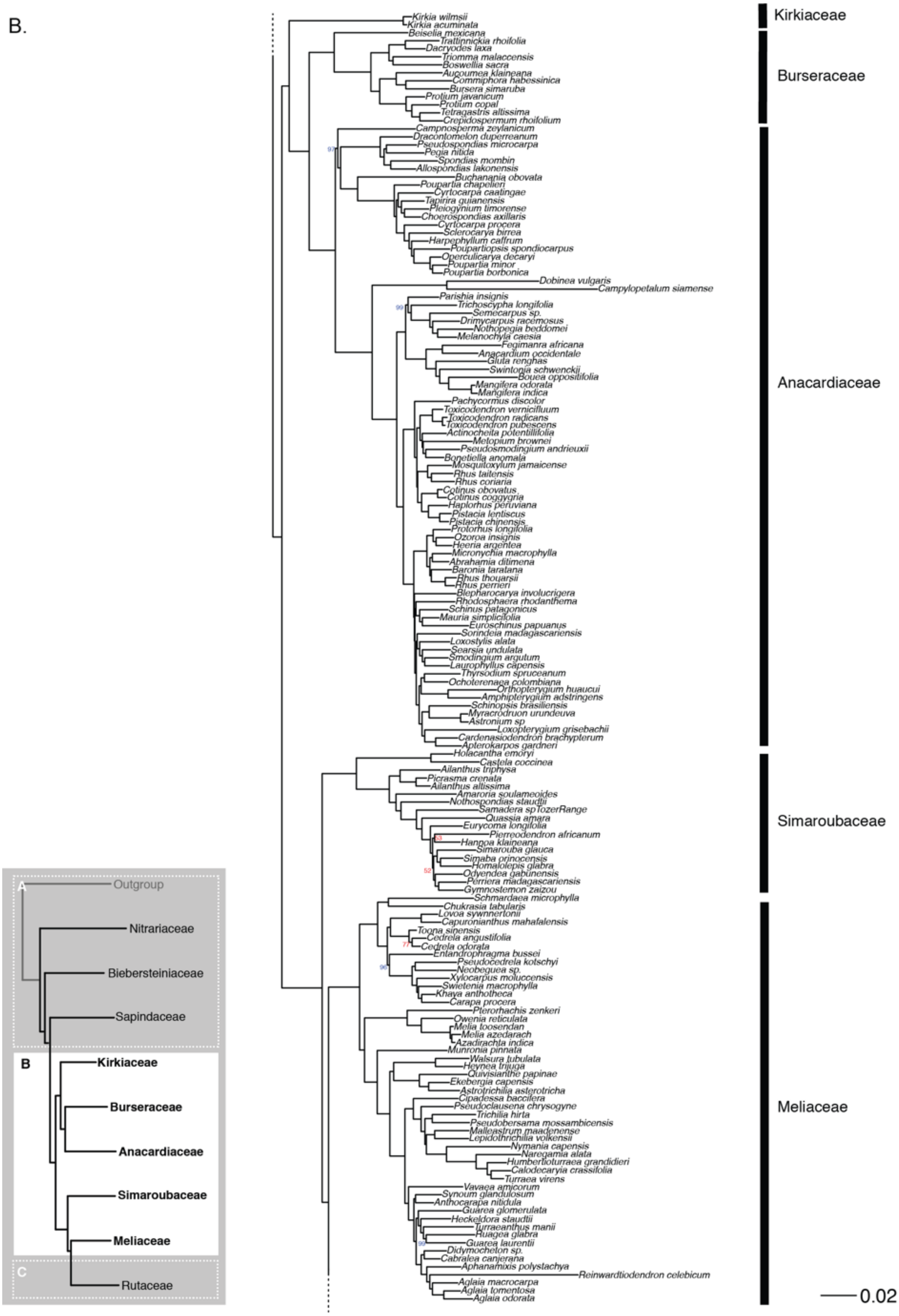
Three major clades were retrieved in Sapindaceae: one comprising 20 genera including *Dodonaea*, *Harpullia*, *Euchoria* and *Smelophyllum*; the second comprising 6 genera including *Acer*, *Aesculus*, *Billia* and *Xanthoceras*; and the third comprising 94 genera including *Delavaya*, *Koelreuteria*, *Nephelium*, *Litchi*, *Sapindus*, *Serjania* and *Cupaniopsis* (Figure 5.2A). These major clades had maximum bootstrap support, as did most generic relationships within the family. The greatest uncertainty in generic relationships was found in the third, large clade, particularly in the branch leading to the clades containing *Mischocarpus* and *Cupaniopsis* (bs = 72%), and in the relationship between these clades and the clade containing *Cupania* (bs = 71%). A sister relationship between *Sarcotoechia* and *Storthocalyx* was also poorly supported (bs = 66%).

In Burseraceae, *Beiselia* was placed as sister to the rest of the family (Figure 5.2B). The remainder of Burseraceae comprised three main clades: the first with *Trattinnickia*, *Dacryodes*, *Triomma* and *Boswellia*; the second containing *Aucoumea*, *Commiphora* and *Bursera*; and the third made up of *Protium*, *Tetragastris* and *Crepidospermum*. All infra-familial relationships in Burseraceae were retrieved with maximum support.

Anacardiaceae was retrieved with two major clades of genera (Figure 5.2B). One clade, recovered with high support (bs = 97%), comprises 19 genera with *Campnosperma* as the earliest diverging genus sister to a clade with the remaining genera including *Dracontomelon*, *Spondias*, *Buchanania*, *Poupartia* and *Choerospondias*. Two accessions of *Cyrtocarpa* in this clade (*C. procera* and *C. caatingae*) were not monophyletic. The second major Anacardiaceous clade received maximum support, with *Campylopetalum* + *Dobinea* recovered (on long branches) as sister to the remaining 49 genera including *Semecarpus*, *Anacardium*, *Mangifera*, *Toxicodendron*, *Rhus*, *Cotinus*, *Mauria* and *Searsia*. Most genera for which multiple accessions were included (*Mangifera, Toxicodendron, Cotinus* and *Pistacia*) were retrieved as monophyletic; however, *Rhus* was polyphyletic, with *R. taitensis* + *R. coriaria* grouping separately from *R. thouarsii* + *R. perrieri*. All generic relationships were recovered with maximum or very high support in this clade (bs ≥99%).

Three main clades were recovered in Simaroubaceae, the first comprising *Holacantha* + *Castela*, which is the earliest-diverging clade sister to the rest of the family (Figure 5.2B). The second major clade in Simaroubaceae comprised *Ailanthus* and *Picrasma*, although the two accessions of *Ailanthus* were not retrieved as monophyletic. The third major clade comprises 13 genera (*Amaroria*, *Quassia*, *Hannoa*, *Samadera* and *Simarouba,* amongst


A.
Outgroup
Nitrariaceae
Biebersteiniaceae
Sapindaceae
0.02
Outgroup
Nitrariaceae
Biebersteiniaceae
Sapindaceae
Kirkiaceae
Burseraceae
Anacardiaceae
Simaroubaceae
Meliaceae
Rutaceae


B.
Kirkia wilmsii
Kirkia acuminata
Beiselia mexicana
Trattinnickia rhoifolia
Dacryodes laxa
Triomma malaccensis
Boswellia sacra
Aucoumea klaineana
Commiphora habessinica
Bursera simaruba
Protium javanicum
Protium copal
Tetragastris altissima
Crepidospermum rhoifolium
Campnosperma zeylanicum
Dracontomelon duperreanum
Pseudospondias microcarpa
Pegia nitida
Spondias mombin
Allospondias lakonensis
Buchanania obovata
Poupartia chapelieri
Cyrtocarpa caatingae
Tapirira guianensis
Pleiogynium timorense
Choerospondias axillaris
Cyrtocarpa procera
Sclerocarya birrea
Harpephyllum caffrum
Poupartiopsis spondiocarpus
Operculicarya decaryi
Poupartia minor
Poupartia borbonica
Dobinea vulgaris
Campylopetalum siamense
Parishia insignis
Trichoscypha longifolia
Semecarpus sp.
Drimycarpus racemosus
Nothopegia beddomei
Melanochyla caesia
Fegimanra africana
Anacardium occidentale
Gluta renghas
Swintonia schwenckii
Bouea oppositifolia
Mangifera odorata
Mangifera indica
Pachycormus discolor
Toxicodendron vernicifluum
Toxicodendron radicans
Toxicodendron pubescens
Actinocheita potentillifolia
Metopium brownei
Pseudosmodingium andrieuxii
Bonetiella anomala
Mosquitoxylum jamaicense
Rhus taitensis
Rhus coriaria
Cotinus obovatus
Cotinus coggygria
Haplorhus peruviana
Pistacia lentiscus
Pistacia chinensis
Protorhus longifolia
Ozoroa insignis
Heeria argentea
Micronychia macrophylla
Abrahamia ditimena
Baronia taratana
Rhus thouarsii
Rhus perrieri
Blepharocarya involucrigera
Rhodosphaera rhodanthema
Schinus patagonicus
Mauria simplicifolia
Euroschinus papuanus
Sorindeia madagascariensis
Loxostylis alata
Searsia undulata
Smodingium argutum
Laurophyllus capensis
Thyrsodium spruceanum
Ochoterenaea colombiana
Orthopterygium huaucui
Amphipterygium adstringens
Schinopsis brasiliensis
Myracrodruon urundeuva
Astronium sp
Loxopterygium grisebachii
Cardenasiodendron brachypterum
Apterokarpos gardneri
Holacantha emoryi
Castela coccinea
Ailanthus triphysa
Picrasma crenata
Ailanthus altissima
Amaroria soulameoides
Nothospondias staudtii
Samadera spTozerRange
Quassia amara
Eurycoma longifolia
Pierreodendron africanum
Hannoa klaineana
Simarouba glauca
Simaba orinocensis
Homalolepis glabra
Odyendea gabunensis
Perriera madagascariensis
Gymnostemon zaizou
Schmardaea microphylla
Chukrasia tabularis
Lovoa swynnertonii
Capuronianthus mahafalensis
Toona sinensis
Cedrela angustifolia
Cedrela odorata
Entandrophragma bussei
Pseudocedrela kotschyi
Neobeguea sp.
Xylocarpus moluccensis
Swietenia macrophylla
Khaya anthotheca
Carapa procera
Pterorhachis zenkeri
Owenia reticulata
Melia toosendan
Melia azedarach
Azadirachta indica
Munronia pinnata
Walsura tubulata
Heynea trijuga
Quivisianthe papinae
Ekebergia capensis
Astrotrichilia asterotricha
Cipadessa baccifera
Pseudoclausena chrysogyne
Trichilia hirta
Pseudobersama mossambicensis
Malleastrum maadenense
Lepidotrichilia volkensii
Nymania capensis
Naregamia alata
Humbertioturraea grandidieri
Calodecaryia crassifolia
Turraea virens
Vavaea amicorum
Synoum glandulosum
Anthocarapa nitidula
Guarea glomerulata
Heckeldora staudtii
Turraeanthus manii
Ruagea glabra
Guarea laurentii
Didymocheton sp.
Cabralea canjerana
Aphanamixis polystachya
Reinwardtiodendron celebicum
Aglaia macrocarpa
Aglaia tomentosa
Aglaia odorata
Kirkiaceae
Burseraceae
Anacardiaceae
Simaroubaceae
Meliaceae
0.02
A
Outgroup
Nitrariaceae
Biebersteiniaceae
Sapindaceae
B
Kirkiaceae
Burseraceae
Anacardiaceae
Simaroubaceae
Meliaceae
C
Rutaceae

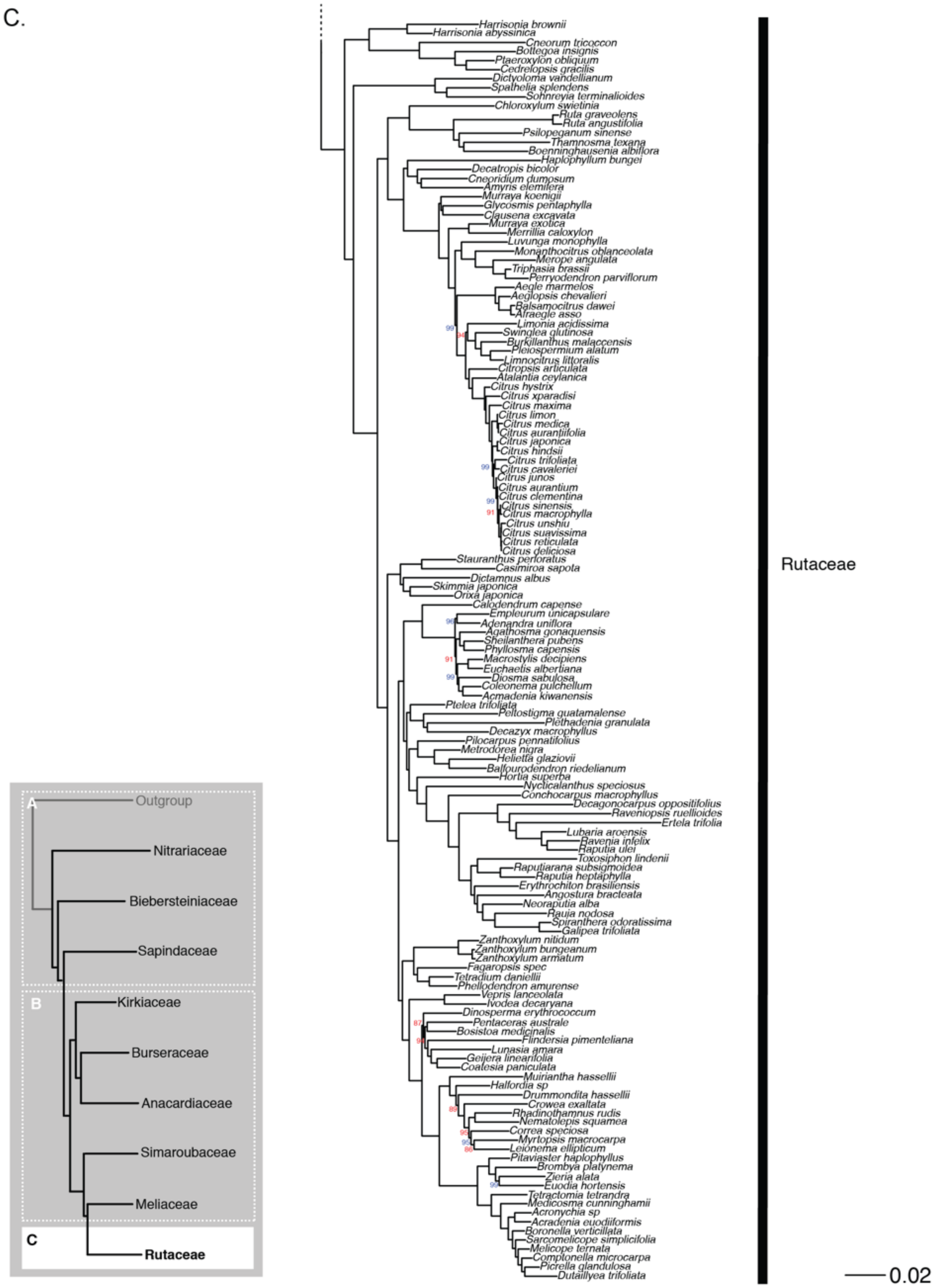


Figure 5.2 Genus-level phylogenetic tree of Sapindales, displayed in three sections showing: (A) Nitrariaceae, Biebersteiniaceae, Sapindaceae; (B) Kirkiaceae, Burseraceae, Anacardiaceae, Simaroubaceae, Meliaceae, and (C) Rutaceae. The phylogeny was

estimated by maximum likelihood analysis (using IQ-TREE) of target capture sequences generated using the Angiosperms353 bait kit. Numbers on branches indicate support for nodes with low support (<91%; red) or moderate to high support (>91%; blue). Branches without bootstrap values annotated have maximum bootstrap support (bs = 100%).

others). Generic relationships in this third clade were less well-resolved than for the rest of the family, with a sister relationship of *Pierreodendron* + *Hannoa* receiving poor support (bs = 53%), as well as the branch leading to the clades (*Simarouba* (*Simaba* + *Homalolepis*)) and (*Odyendea* (*Perriera* + *Gymnostemon*)) (bs = 52%).

In Meliaceae, two major clades of genera were recovered (Figure 5.2B). The first comprises 13 genera including *Chukrasia, Lovoa, Toona, Cedrela, Swietenia* and *Khaya*, amongst others. The second major clade comprises 33 genera, with an early-diverging sub-clade of (*Pterorhachis* (*Owenia* (*Melia* + *Azadirachta*))), and a larger sub-clade including *Munronia*, *Astrotrichilia*, *Naregamia, Cipadessa, Guarea* and *Aglaia,* amongst others. All relationships are recovered with strong support (bs ≥ 96%), except the *Cedrela* clade, which received moderate support (bs = 77%). *Aglaia* was retrieved as monophyletic, but *Melia* and *Guarea* were not. *Reinwardtiodendron* was retrieved on a particularly long branch.

Rutaceae has two early-diverging clades, the first of which comprises (*Harrisonia* (*Cneorum* (*Bottegoa* (*Ptaeroxylon* + *Cedrelopsis*)))), and the second of which comprises (*Dictyoloma* (*Spathelia* + *Sohnreynia*)) (Figure 5.2C). The remainder of the family is made up of two sister clades, the first comprising 30 genera including (but not limited to) *Ruta, Cneoridium, Murraya, Glycosmis, Clausena, Merope* and *Citrus*, and the second comprising 77 genera including *Casimiroa*, *Skimmia*, *Agathosma*, *Ptelea*, *Raputia*, *Zanthoxylum*, *Correa*, *Acronychia* and *Melicope,* amongst others. All relationships within Rutaceae were retrieved with at least moderate support (bs >85%), and most were retrieved with maximum support.

Divergence time estimation

Sapindales genus-level tree

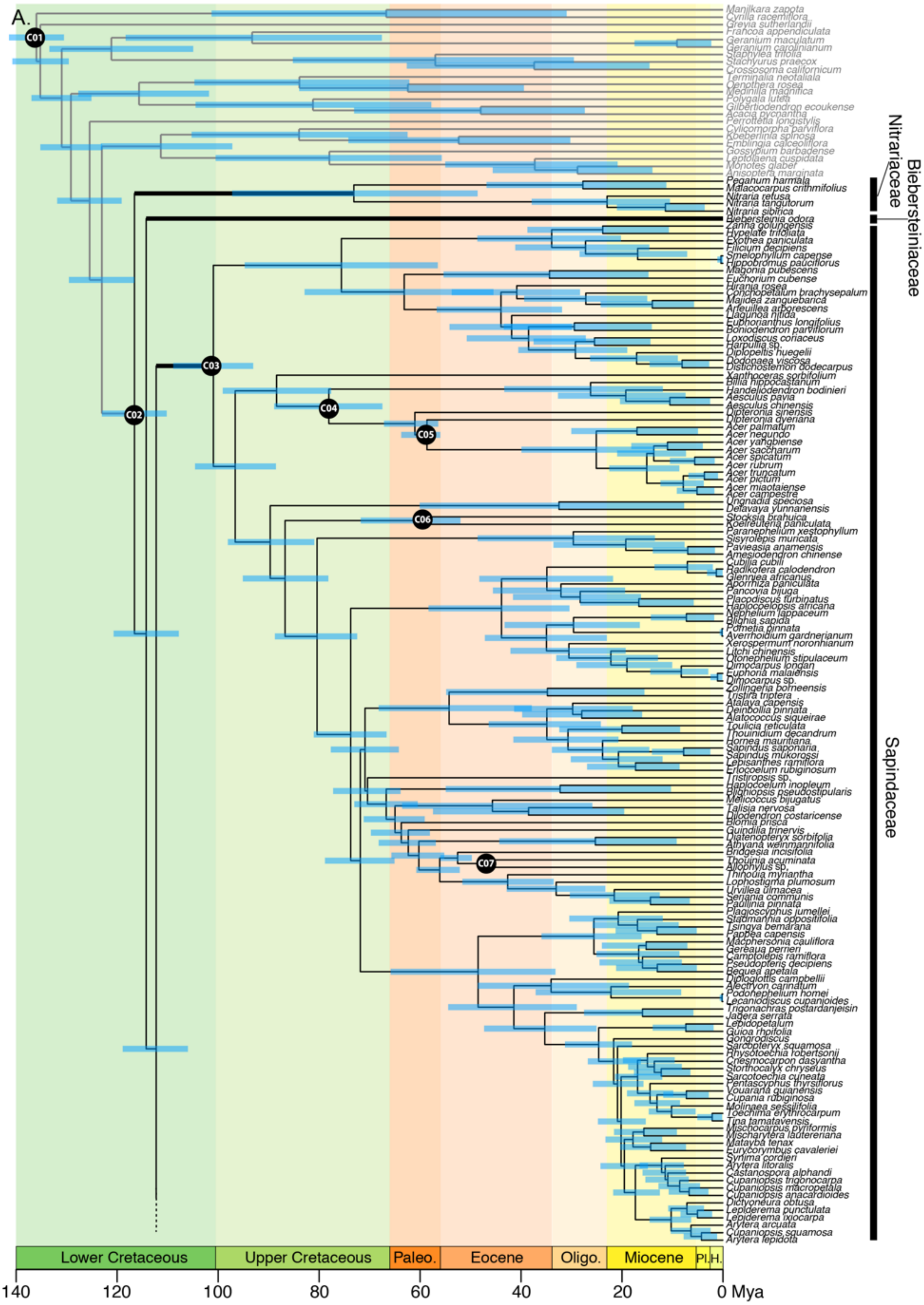
Ages for nodes of Sapindales estimated under a strict clock model were substantially older than those estimated under a relaxed clock. The ages of lineages as estimated under a relaxed clock are more similar to those estimated in previous angiosperm and ordinal phylogenetic analyses (e.g. Magallón *et al*. 2015; Muellner-Riehl *et al*. 2016; Ramírez-Barahona *et al*. 2020) and are closer to the ages of fossils within the order. Therefore, the ages estimated by the relaxed clock model are regarded here as being more likely to be accurate.

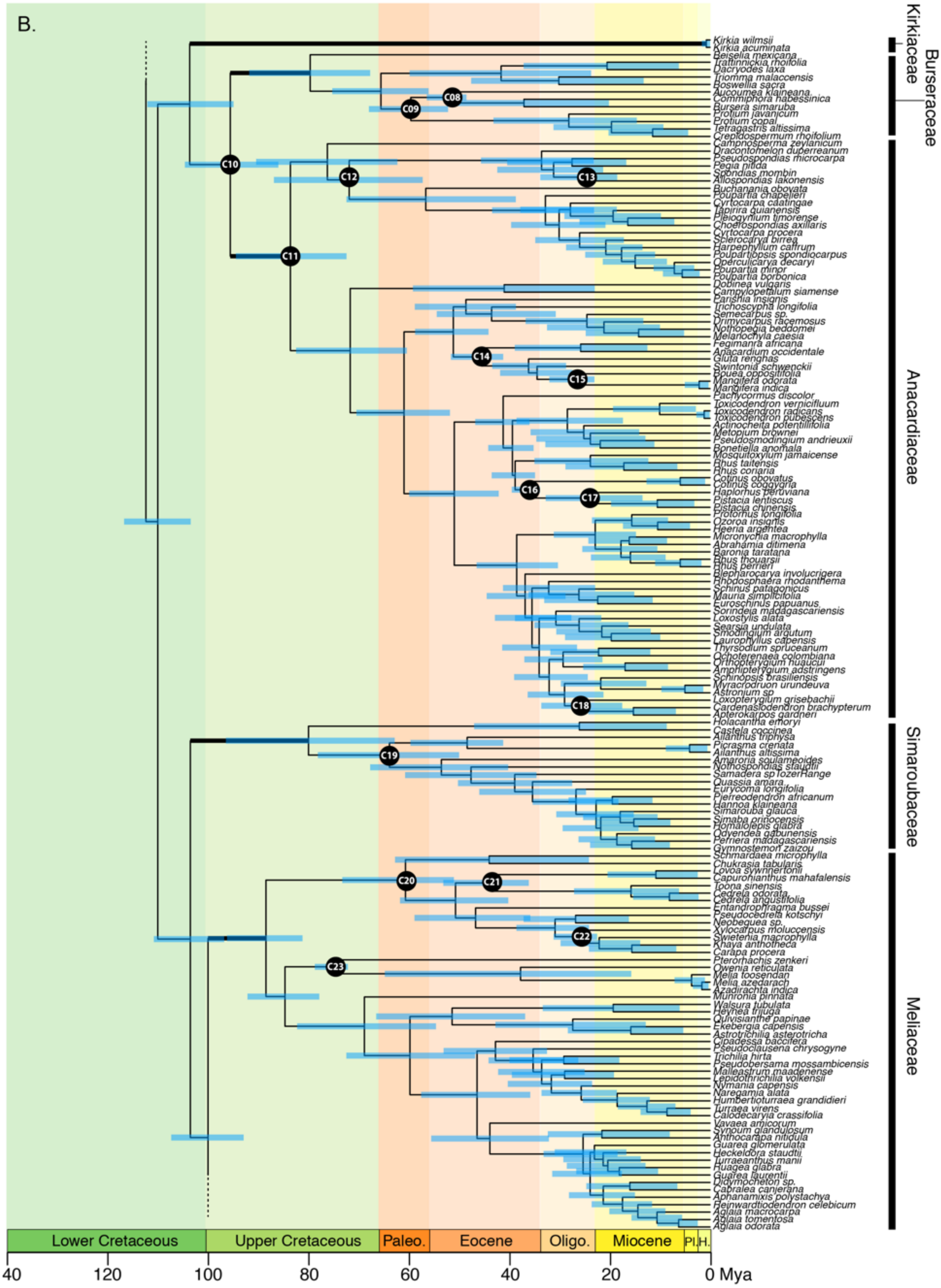
The stem node of Sapindales estimated to an age of 123.03 (116.59 – 129.55) Mya (Figure 5.3). Nitrariaceae, Biebersteiniaceae, Sapindaceae diverged in the Lower Cretaceous with stem ages of 116.57 (110.19 – 123.01) Mya, 114.25 (107.79 – 120.65) Mya and 112.27 (105.99 – 118.87) Mya, respectively (Figure 5.3A). The remaining families were estimated to have diverged at the Lower-Upper Cretaceous boundary. Kirkiaceae emerged at 103.56 (94.84 – 111.99) Mya, and the derived Burseraceae and Anacardiaceae split from their most recent common ancestor at 95.48 (85.92 – 104.52) Mya (Figure 5.3B). Simaroubaceae diverged at 103.43 (96.70 – 110.67) Mya, and Meliaceae and Rutaceae diverged from their most recent common ancestor at 99.91 (92.84 – 107.23) Mya (Figure 5.3B, C). A figure with all estimated node ages and 95% HPD intervals is given in Appendix C5.

Anacardiaceae species-level phylogeny

The final Anacardiaceae alignment comprised 373 accessions (73 genera = c. 90% generic diversity; 373 species = c. 47% species diversity) and ten genes comprising 4,795 base pairs. RaxML analysis resulted in a tree with a log likelihood of -82,591.03 (Appendix C6).

Care must be taken when interpreting the bootstrap support values of the species-level phylogeny. Generic relationships were usually recovered without bootstrap support. This is likely to be due to a combination of the use of Sanger data with limited information most appropriate for resolving shallower, species-level relationships, and the fact that these generic relationships were constrained in the analysis. However, because these generic relationships were elucidated with target capture data with very high to maximum support, the estimates of deeper relationships within the family are likely to be accurate.


A.
C01
C02
C03
C04
C05
C06
C07
Manilkara zapota
Cyrilla racemiflora
Greyia sutherlandii
Francoa appendiculata
Geranium maculatum
Geranium carolinianum
Staphylea trifolia
Stachyurus praecox
Crossosoma californicum
Terminalia neotaliala
Oenothera rosea
Medinilla magnifica
Polygala lutea
Gilbertiodendron ecoukense
Acacia pycnantha
Perrottetia longistylis
Cylicomorpha parviflora
Koeberlinia spinosa
Emblingia calceoliflora
Gossypium barbadense
Leptolaena cuspidata
Monotes glaber
Anisoptera marginata
Peganum harmala
Malacocarpus crithmifolius
Nitraria retusa
Nitraria tangutorum
Nitraria sibirica
Biebersteinia odora
Zanha golungensis
Hypelate trifoliata
Exothea paniculata
Filicium decipiens
Smelophyllum capense
Hippobromus pauciflorus
Magonia pubescens
Euchorium cubense
Hirania rosea
Conchopetalum brachysepalum
Majidea zanguebarica
Arfeuillea arborescens
Llagunoa nitida
Euphorianthus longifolius
Boniodendron parviflorum
Loxodiscus coriaceus
Harpullia sp.
Diplopeltis huegelii
Dodonaea viscosa
Distichostemon dodecarpus
Xanthoceras sorbifolium
Billia hippocastanum
Handeliodendron bodinieri
Aesculus pavia
Aesculus chinensis
Dipteronia sinensis
Dipteronia dyeriana
Acer palmatum
Acer negundo
Acer yangbiense
Acer saccharum
Acer spicatum
Acer rubrum
Acer truncatum
Acer pictum
Acer miaotaiense
Acer campestre
Ungnadia speciosa
Delavaya yunnanensis
Stocksia brahuica
Koelreuteria paniculata
Paranephelium xestophyllum
Sisyrolepis muricata
Pavieasia anamensis
Amesiodendron chinense
Cubilia cubili
Radikofera calodendron
Glenniea africanus
Aporrhiza paniculata
Pancovia bijuga
Placodiscus turbinatus
Haplocoelopsis africana
Nephelium lappaceum
Blighia sapida
Pometia pinnata
Averrhoidium gardnerianum
Xerospermum noronhianum
Litchi chinensis
Otonephelium stipulaceum
Dimocarpus longan
Euphoria malaiensis
Dimocarpus sp.
Zollingeria borneensis
Tristira triptera
Atalaya capensis
Deinbollia pinnata
Alatococcus siqueirae
Toulicia reticulata
Thouinidium decandrum
Hornea mauritiana
Sapindus saponaria
Sapindus mukorossi
Lepisanthes ramiflora
Eriocoelum rubiginosum
Tristiropsis sp.
Haplocoelum inopleum
Blighiopsis pseudostipularis
Melicoccus bijugatus
Talisia nervosa
Dilodendron costaricense
Blomia prisca
Guindilia trinervis
Diatenopteryx sorbifolia
Athyana weinmannifolia
Bridgesia incisifolia
Thouinia acuminata
Allophylus sp.
Thinouia myriantha
Lophostigma plumosum
Urvillea ulmacea
Serjania communis
Paullinia pinnata
Plagioscyphus jumellei
Stadmannia oppositifolia
Tsingya bemarana
Pappea capensis
Macphersonia cauliflora
Gereaua perrieri
Camptolepis ramiflora
Pseudopteris decipiens
Bequea apetala
Diploglottis campbellii
Alectryon carinatum
Podonephelium homei
Lecaniodiscus cupanioides
Trigonachras postardanjeisin
Jagera serrata
Lepidopetalum
Guioa rhoifolia
Gongrodiscus
Sarcopteryx squamosa
Rhysotoechia robertsonii
Cnesmocarpon dasyantha
Storthocalyx chryseus
Sarcotoechia cuneata
Pentascyphus thyrsiflorus
Vouarana guianensis
Cupania rubiginosa
Molinaea sessilifolia
Toechima erythrocarpum
Tina tamatavensis
Mischocarpus pyriformis
Mischarytera lautereriana
Matayba tenax
Eurycorymbus cavaleriei
Synima cordieri
Arytera litoralis
Castanospora alphandi
Cupaniopsis trigonocarpa
Cupaniopsis macropetala
Cupaniopsis anacardioides
Dictyoneura obtusa
Lepiderema punctulata
Lepiderema ixiocarpa
Arytera arcuata
Cupaniopsis squamosa
Arytera lepidota
Nitrariaceae
Biebersteiniaceae
Sapindaceae
Lower Cretaceous
Upper Cretaceous
Paleo.
Eocene
Oligo.
Miocene
Pl.
H.
140
120
100
80
60
40
20
0 Mya


B.
C08
C09
C10
C11
C12
C13
C14
C15
C16
C17
C18
C19
C20
C21
C22
C23
Kirkiaceae
Burseraceae
Anacardiaceae
Simaroubaceae
Meliaceae
Lower Cretaceous
Upper Cretaceous
Paleo.
Eocene
Oligo.
Miocene
Pl.
H.
140
120
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40
20
0 Mya

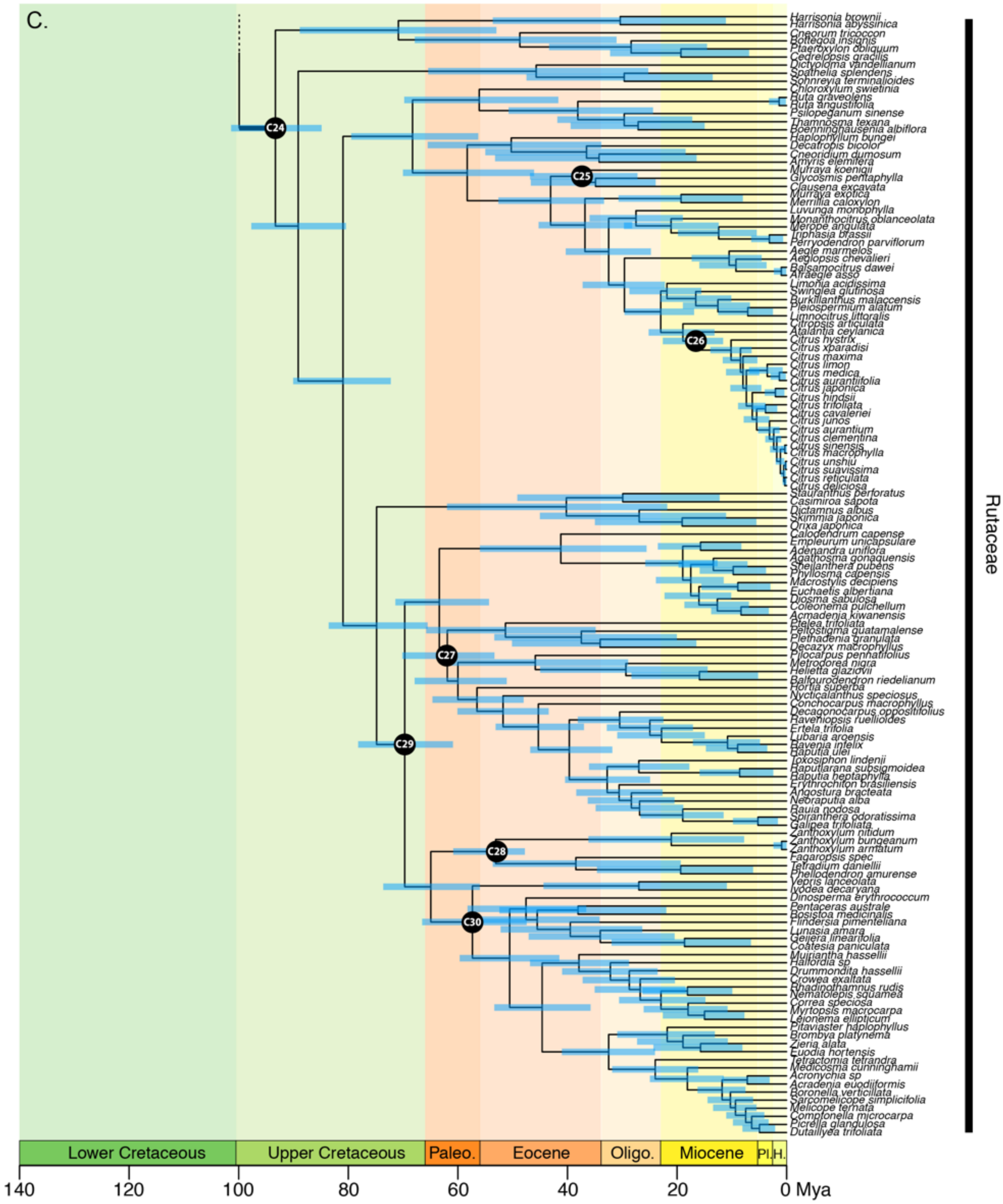


Figure 5.3 Chronogram of Sapindales. Black circles on calibrated nodes show the 30 calibrations C01-C30 (refer to Table 5.2) used for dating. Blue bars represent 95% HPD confidence intervals. Thickened branches indicate the stem branch of families.

As the topology of the Anacardiaceae species-level tree was constrained to match that of the Sapindales Angiosperms353 genus tree, the same generic relationships were retrieved (Figure 5.4). Six genera included in the species-level tree were not included in the genus-level Sapindales tree: *Antrocaryon*, *Comocladia*, *Faguetia*, *Lannea*, *Lithraea* and *Pentaspadon*. *Antrocaryon amazonicum* was retrieved as sister to *Poupartia pubescens* with low support (bs = 52%). The three species of *Comocladia* (*C. dodonaea, C. mollissima* and *C. mayana*) were recovered as monophyletic, albeit without support (bs = 9%), and as sister to the clade well-supported in the Angiosperms353 phylogeny containing *Sorindeia*, *Loxostylis*, *Smodingium*, *Laurophyllus* and *Searsia*. The placement of *Faguetia* was unresolved in a clade comprising *Baronia*, some *Rhus* species, *Micronychia* and *Abrahamia*, which had high support in the Angiosperms353 genus-level Sapindales phylogeny. The ten species of *Lannea* included in the species tree were recovered as monophyletic but without support (bs = 34%) and as sister to *Sclerocarya*. The two species of *Lithraea* (*L. brasiliensis* and *L. molleoides*) were also recovered as monophyletic with low support (bs = 53%) and as sister to *Mauria*. *Pentaspadon* was recovered as monophyletic with high support (bs = 83%), as sister to the clade containing *Dracontomelon*, *Pseudospondias*, *Pegia*, *Spondias* and *Allospondias*.

In the BEAST analysis, the crown age of Anacardiaceae was estimated to be 84.52 (77.11 – 91.72) Mya (Figure 5.4; Appendix C9). The crown ages of the two major clades in Anacardiaceae (as identified in the genus-level Angiosperms353 phylogeny) were similar, at 73.06 (62.75 – 82.56) and 73.46 (63.30 – 84.56) Mya.

Biogeographic analysis

In the Bayesian ancestral area analysis under a DEC+J model, the origin for Anacardiaceae was reconstructed to most likely be in Sunda, or in Sunda + Eurasia (probabilities = 30.2% and 34.60%, respectively; Figure 5.4; Appendices C7-C8). These were also reconstructed as the most probable areas of origin for the two major clades in the family.

The Bayesian ancestral area reconstruction indicated that most biogeographic transitions across the SSCZ in Anacardiaceae occurred in the Miocene from Sunda to Sahul. The first major clade within Anacardiaceae was reconstructed as most likely having its ancestor in Sunda + Eurasia (probability = 40.78%). Within this clade, *Buchanania* was reconstructed

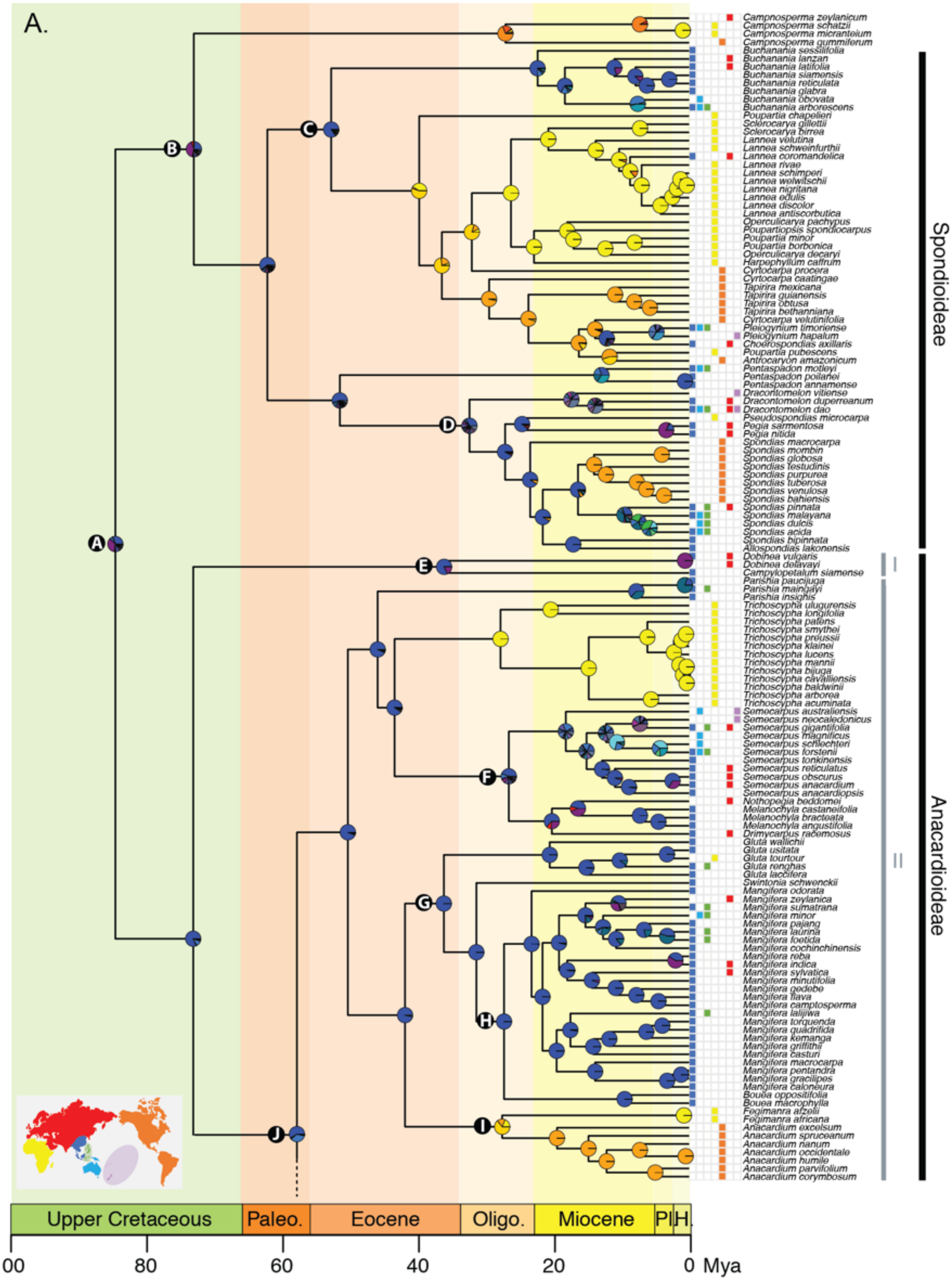
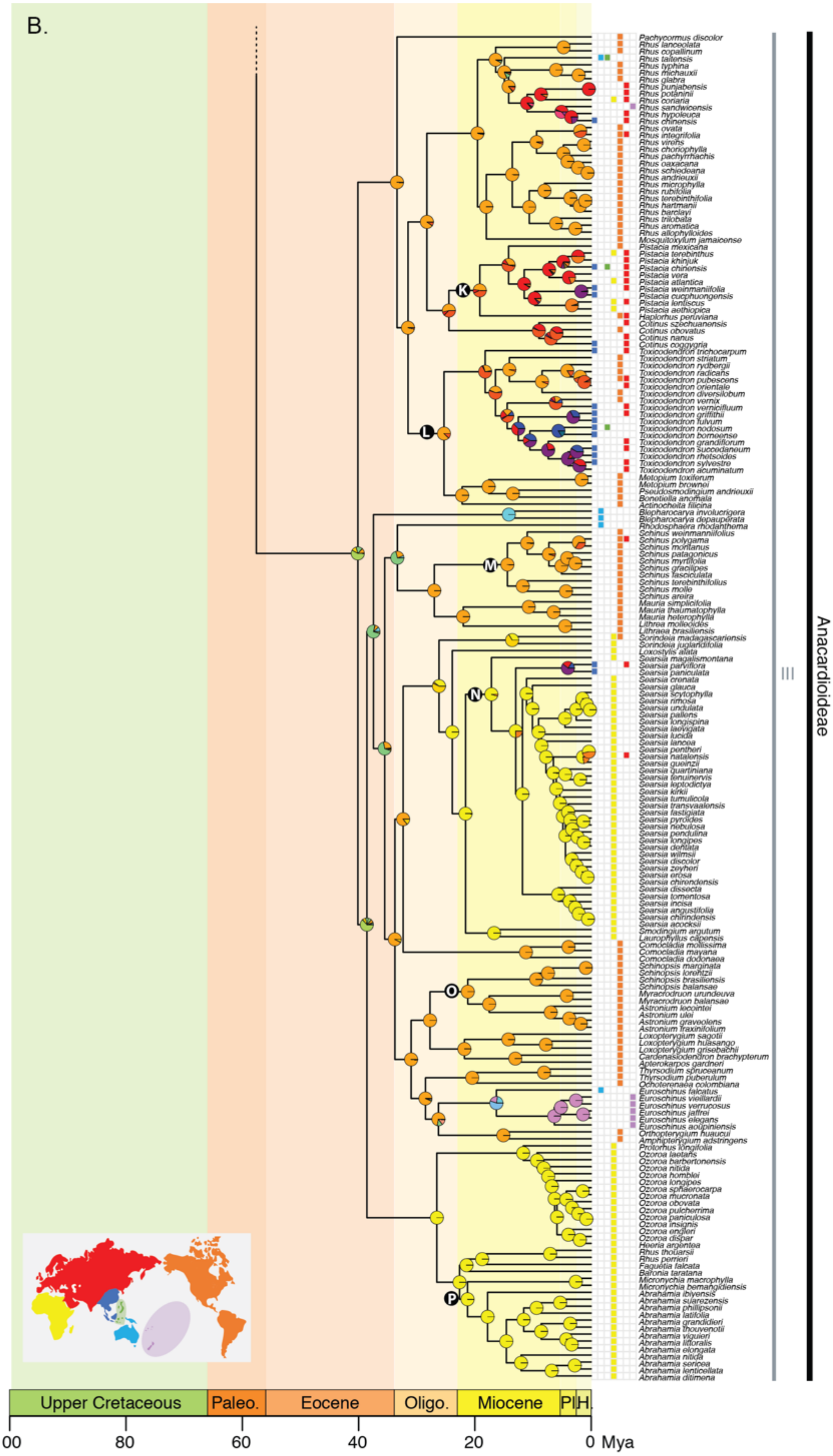


Figure 5.4 Anacardiaceae chronogram, on this page (A) and the next (B), with probability of ancestral areas at each node reconstructed with BioGeoBEARS at nodes under a DEC+J model. Subfamilies according to Pell *et al*. 2011 are indicated on the right in black, and the three major clades in Anacardioideae are labelled (I, II, III) in grey. Refer to Appendices C6 for node support values, C7 and C8 for area probabilities at each node, and C9 for mean ages and 95% HPD confidence intervals.


B.
K
L
M
N
O
P
III
Anacardioideae
Upper Cretaceous
Paleo.
Eocene
Oligo.
Miocene
Pl
H.
100
80
60
40
20
0 Mya

as having persisted in Sunda and Eurasia, with *B. arborescens* and *B. obovata* transitioning to Sahul and Wallacea in the Late Miocene. *Pentaspadon* persisted in Sunda, with *P. motleyi* moving to Sahul and Wallacea in the mid-Miocene. *Pleiogynium* and *Choerospondias* are nested in an American clade, with a transition to Sunda reconstructed as the most likely scenario in the mid-Miocene followed by an expansion to Sahul, Wallacea and the Pacific islands occurring with the divergence of *Pleiogynium* in the Late Miocene to Early Pliocene. In the clade comprising *Dracontomelon, Pseudospondias, Pegia, Spondias* and *Allospondias*, the American *Spondias* species are nested in the predominantly SSCZ/Eurasian/Pacific clade, with a transition to the Americas occurring in the mid-Miocene. *Dracontomelon* was reconstructed as transitioning from Sunda to Sahul and Wallacea in the Miocene although the timing in the Bayesian analysis is ambiguous given that Sunda + Sahul + Wallacea + Eurasia + Pacific was the most likely ancestral area for the crown of *Dracontomelon* 17.27 (8.79 – 26.67) Mya). For *Spondias* + *Allospondias*, the results indicate transitions across the SSCZ occurred from Sunda to Sahul in the Late Miocene. The most likely ancestral area of *Parishia* was reconstructed to Sunda, with exchange from Sunda to Wallacea occurring in the last million years (0.55 [0.20 – 0.81] Mya).

The second major clade of Anacardiaceae was reconstructed to have its origins in Sunda under a DEC+J model (probability = 81.30%; Appendix C8). For the most recent common ancestor of *Semecarpus, Nothopegia, Melanochyla* and *Drimycarpus*, Sunda was reconstructed as the most likely area of origin in the DEC+J model (probability = 44.49%). *Semecarpus* is the only genus in this clade that has been exchanged across the SSCZ; *S. australiensis*, which is only species present in Sahul and the Pacific, was retrieved as the earliest diverging species, likely driving an ambiguous area of origin for the crown of the genus. *Semecarpus australiensis* is sister to two clades of *Semecarpus*, one that is distributed across the SSCZ, Eurasia and the Pacific, and one that is exclusively present in Sunda + Eurasia. In the clade distributed across the SSCZ, my Bayesian analysis suggests transitions between Sunda, Sahul and Wallacea occurred in multiple directions throughout the Middle–Late Miocene. *Gluta*, *Swintonia, Mangifera* and *Bouea* are a clade of predominantly Sundanian genera. One transition from Sunda to Wallacea occurred in *Gluta* and three in *Mangifera* in the Late Miocene, and two transitions from Sunda to Wallacea occurred in *Mangifera* in the Late Miocene–Early Pliocene. *Mangifera minor* is the only species of *Mangifera* included in this study to reach Sahul. The most likely area for the

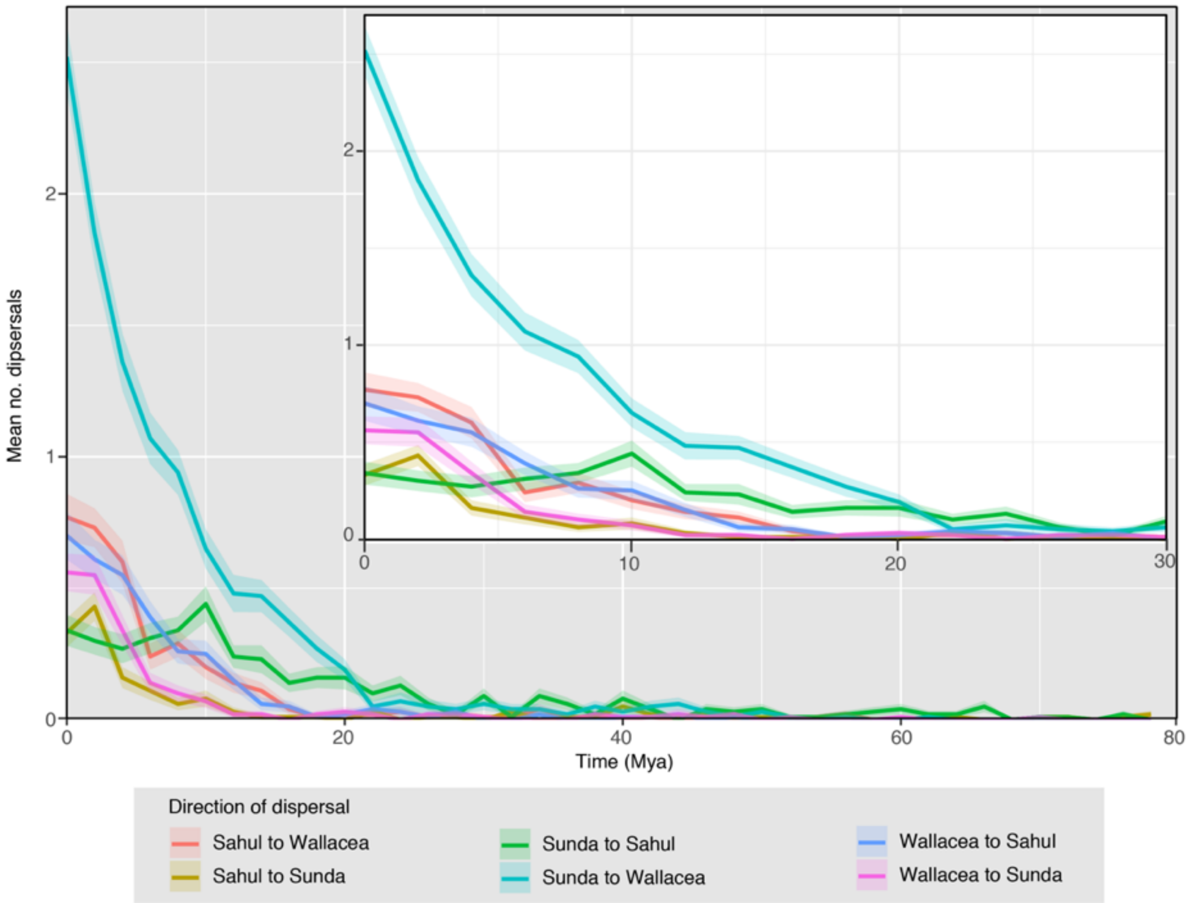


Figure 5.5 Mean number of dispersals between Sunda, Sahul and Wallacea throughout the evolutionary history of Anacardiaceae according to a biogeographic stochastic model under a DEC+J model and 100 permutations. Inset shows magnification of the last 30 Mya. The shaded area bounding the lines represents the standard error.

most recent common ancestor of *Mangifera minor* was in Sunda, thus the exchange across the SSCZ was eastward with a minimum age of 12.61 (8.46 – 16.96) Mya. The rest of the second major clade was reconstructed as having originated in Sahul + the Americas + Africa (probability = 57.58%). The ancestral area of the clade containing *Rhus, Mosquitoxylum, Pistacia, Cotinus, Toxicodendron, Metopium, Pseudosmodingium, Bonetiella* and *Actinocheita* has a high probability of being in the Americas (probability = 98.29%). Some lineages within *Rhus, Pistacia*, and *Cotinus* spread to Eurasia at around the Oligocene–Miocene boundary, and then to Sunda from the mid-Miocene. One transition along the branch of *Pistacia chinensis* occurred in the last 4.88 (2.13 – 8.00) Ma (most likely from Sunda to Wallacea given that the ancestral area is reconstructed to Eurasia, which is adjacent to Sunda). A second transition in this major clade occurred on the branch of *Toxicodendron nodosum* from Sunda to Wallacea in the last 5.66 (1.94 – 9.99) Mya.

Biogeographic stochastic mapping indicated that across Sunda, Sahul and Wallacea, the mean number of dispersals increased from 22 Mya until the present (Figure 5.5). From 22 Mya, the number of dispersals was greatest from Sunda to Wallacea. Globally, most dispersal events in Anacardiaceae occurred from Sunda to Eurasia (19.56), from Sunda to Wallacea (11.12), from Africa to the Americas (9.68) and from the Americas to Eurasia (7.75) (Figure 5.6).

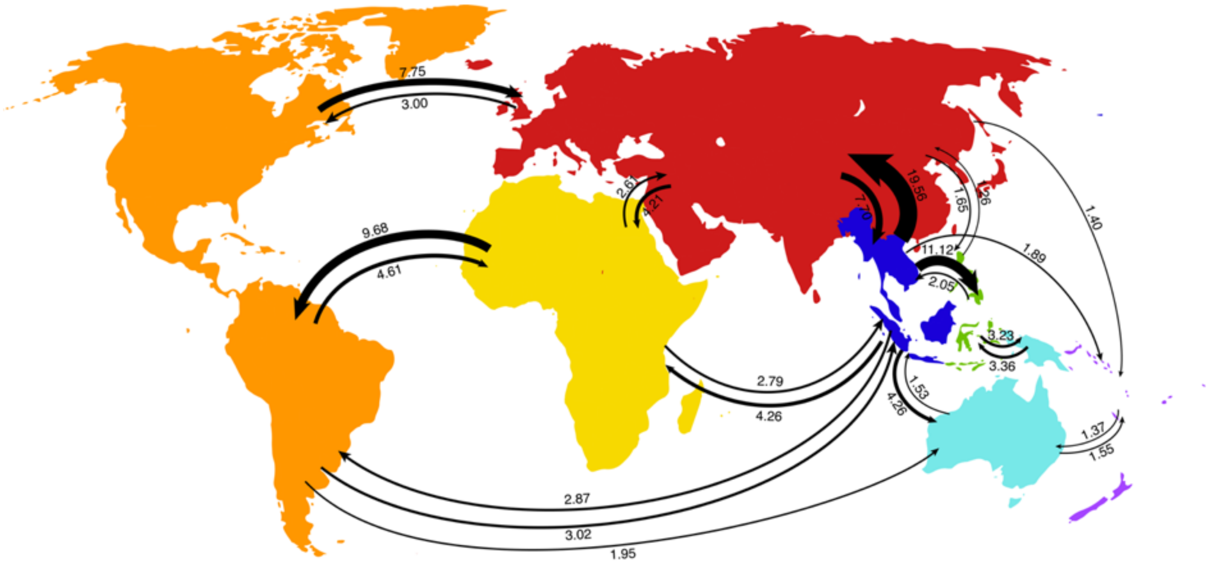


Figure 5.6 Mean number of dispersal events between biogeographic regions throughout the evolutionary history of Anacardiaceae according to a biogeographic stochastic model under a DEC+J model and 100 permutations. Arrows indicate the direction of dispersal events, and arrow thickness is proportional to the mean number of dispersals.

Discussion

Evolution of Sapindales and Anacardiaceae

This analysis of genus-level Angiosperms353 data of Sapindales has estimated family relationships within the order with strong support for the first time, and has provided a rigorous framework for studying sapindalean evolution. Historically, the relationships of sapindalean families have been difficult to resolve, particularly in regards to the relationship of Biebersteiniaceae and Nitrariaceae with the rest of the order, the placement of Sapindaceae, and the topology of the Rutaceae, Meliaceae and Simaroubaceae clade (Gadek *et al.* 1996; Stevens 2001; Muellner *et al.* 2007; Wang *et al.* 2009). The most well-sampled study of Sapindales by Muellner-Riehl *et al*. (2016) included three plastid genes, and suggested that Biebersteiniaceae and Nitrariaceae form a basal grade, with Biebersteiniaceae being the earliest-diverging family. The position of Sapindaceae was unresolved, but was placed as the sister family to the clade containing (Rutaceae (Simaroubaceae + Meliaceae)) (Muellner-Riehl *et al.* 2016). Incongruously, the more recent next-generation plastid phylogenies of Li *et al*. (2019) and Lin *et al*. (2018) (that both used 80 plastid loci but only included 9 and 29 samples, respectively) found strong support for a Simaroubaceae + Rutaceae sister family relationship rather than Simaroubaceae + Meliaceae as in Muellner-Riehl *et al*. (2016). The position of Sapindaceae was also weakly supported in these next-generation plastid phylogenies (Lin *et al.* 2018; Li *et al.* 2019). In contrast to these previous studies, my results suggest that Nitrariaceae is the earliest diverging family in Sapindales, followed by Biebersteiniaceae (although the placement of Biebersteiniaceae was only moderately supported; bs = 71%) and then Sapindaceae, these three together forming an early-diverging grade in the order (Figure 5.2). The families in this grade diverge before the emergence of two well-supported clades of families: (Kirkiaceae (Burseraceae + Anacardiaceae)) and (Simaroubaceae ((Meliaceae + Rutaceae)). The difference in topology in the present phylogeny compared to previous work – particularly in regards to the placement of Sapindaceae and topology of Simaroubaceae, Meliaceae and Rutaceae – is likely to be driven by the vast difference in sampling; my study uses an order of magnitude more data than previous studies on Sapindales relationships (Gadek *et al.* 1996; Muellner *et al.* 2007; Wang *et al.* 2009; Muellner-Riehl *et al.* 2016; Lin *et al.* 2018; Li *et al.* 2019). There is the possibility that differences in previous topologies compared to that in the present study is due to the use of plastid data as opposed to the use of nuclear data in this study, and this deserves further examination with a densely sampled plastid phylogeny of the order. Nevertheless, given that my phylogeny was achieved with the densest sampling and most data to date, and generally has very high to maximum bootstrap support, I am confident that it is currently the best representation of Sapindales family relationships. How our new understanding of sapindalean topology from this study may influence our interpretation of trait evolution warrants further investigation, as does the interesting pattern of uneven distribution of paralogous genes across the order.

The stem ages for Sapindales and sapindalean families were slightly older (mean = 12.21 Mya older) than those estimated by Muellner-Riehl *et al*. (2016) (Figure 5.3, Table 5.5). For Rutaceae, Meliaceae, Kirkiaceae, Burseraceae and Anacardiaceae these ages fall within the 95% HPD confidence intervals of Muellner-Riehl *et al*. (2016). However, for Sapindales, Simaroubaceae, Nitrariaceae and Biebersteiniaceae, mean stem ages are 11.51, 14.76, 22.03 and 19.71 Mya older than those estimated by Muellner-Riehl *et al*. (2016) and fall outside the 95% HPD confidence intervals (Table 5.5). The order and family stem ages were also similar to those estimated in the angiosperm-wide study by Ramírez-Barahona *et al*. (2020), with only Biebersteiniaceae and Nitrariaceae not having overlapping 95% HPD confidence intervals, estimated as 33.19 and 35.51 Mya older, respectively, in the present study (Table 5.5). I think that the broad congruence of family stem ages in these recent studies supports the ages estimated in my study, with the major difference in ages likely being predominantly driven by the different family topology retrieved by Ramírez-Barahona *et al*. (2020) and Muellner-Riehl *et al*. (2016)[1]. Crown ages estimated in my study were within the confidence intervals of the most recent family-specific studies for Anacardiaceae, Burseraceae, Meliaceae and Simaroubaceae (Anacardiaceae crown = 97.00 (83–128) Mya (Weeks *et al.* 2014) vs. 83.52 (72.37–94.38) Mya (this study); Burseraceae crown = 91.00 (78–106) Mya (Weeks *et al.* 2014) vs. 79.59 (67.68–91.71) Mya (this study); Meliaceae crown = 80.40 (69.10–91.60) Mya (Koenen *et al.* 2015) vs. 88.38 (81.12–96.13) Mya (this study); Simaroubaceae crown = 69.80 (62.10–78.60) Mya (Clayton *et al.* 2009) vs. 79.93 (62.79–96.35) Mya (this study)). However, the crown age estimated for Rutaceae (93.31 (84.90–101.38) Mya) was older than that estimated by Appelhans *et al*. (2012; 81.92 Ma), and the crown age estimated for Sapindaceae (100.94 (93.05–108.88) Mya) was younger than that estimated by Buerki *et al.* (2011; 109.90 Mya). The results add to the growing body of evidence (e.g. Ramírez-Barahona *et al.* 2020) that the Cretaceous was a key period for the emergence of angiosperm families. Given the similarity of ages to

[1] I am aware of the recent study by Silvestro *et al*. (2021) where family ages were estimated using a novel Bayesian analysis of the angiosperm fossil record that accounts for incomplete sampling. However, I share the concerns of other scientists (e.g. Budd *et al*. (2021)) about the validity of the method employed, as well as the quality of the fossils included for Sapindalean families. As such, I have opted not to discuss the results of this study in the context of the ages estimated by Silvestro *et al*. (2021).

Table 5.5 Comparison of family ages calculated in the present study's Angiosperms353 genus-level Sapindales chronogram with those estimated by the recent studies of Muellner-Riehl *et al.* (2016) and Ramírez-Baharona *et al.* (2020). Ages of Muellner-Riehl *et al.* (2016) taken from the chronogram with three maximum age constraints at deeper nodes; ages from the Ramírez-Baharona *et al.* (2020) study taken from the relaxed clock analysis with the complete suite of fossils.

Stem node	**This study**	**Muellner-Riehl *et al.* (2016): 3 max. constraints**	**Ramírez-Baharona *et al.* (2020): RC, complete set**
Sapindales	123.03 (116.59-129.55)	111.52 (106.19-116.86)	127.47 (121.99-133.28)
Sapindaceae	112.27 (105.99-118.87)	100.45 (94.39-106.50)	104.25 (94.45-113.14)
Rutaceae	99.91 (92.84-107.23)	93.51 (86.56-100.25)	87.62 (77.57-97.01)
Meliaceae	99.91 (92.84-107.23)	88.67 (81.01-96.67)	91.79 (81.75-102.66)
Simaroubaceae	103.43 (96.70-110.67)	88.67 (81.01-96.67)	87.62 (77.57-97.01)
Kirkiaceae	103.56 (94.84-111.99)	94.63 (85.64-102.89)	93.95 (80.28-104.99)
Burseraceae	95.48 (85.92-104.52)	87.38 (78.27-97.04)	82.18 (72.11-93.40)
Anacardiaceae	95.48 (85.92-104.52)	87.38 (78.27-97.04)	82.18 (72.11-93.40)
Nitrariaceae	116.57 (110.19-123.01)	94.54 (79.44-107.59)	81.06 (57.35-102.26)
Biebersteiniaceae	114.25 (107.79-120.69	94.54 (79.44-107.59)	81.06 (57.35-102.26)

previous studies, the large amount of data included, evenness and density of sampling across the order, high support for the retrieved family topology and rigour of the calibration scheme, I suggest that the present results represent the best available estimate of sapindalean ages. This chronogram therefore provides a sound framework for investigating the evolution of sapindalean groups in this study and in future research.

The genus and species-level Anacardiaceae phylogenetic trees are in broad agreement with the latest subfamily classification of Anacardiaceae (with the exception of the placement of *Campnosperma*), but challenges current tribal classification (Figures 5.2, 5.3 and 5.4). Pell (2004), in a family phylogenetic analysis based on three plastid loci, formally circumscribed two subfamilies: Anacardioideae and Spondioideae. Each of Engler's (1892) Anacardiaceae tribes (*sensu* Mitchell and Mori 1987) were assigned to a subfamily, with Anacardieae, Dobineae, Rhoeae and Semecarpeae grouped into Anacardioideae, and Spondiadeae grouped into Spondioideae (although it was noted that some tribes were polyphyletic in some gene trees). This subfamilial classification was altered in Pell *et al.* (2011), where *Buchanania* was recognised as a member of Spondioideae on the basis of unpublished molecular data, in line with the morphological groupings of Wannan and Quinn (1990, 1991), and later supported by the molecular phylogeny of Weeks *et al*. (2014). It was also noted in Pell *et al*. (2011) that the unpublished molecular analysis retrieved Spondioideae as polyphyletic, but because Anacardiaceae relationships were incompletely resolved the two-subfamily classification was maintained in the treatment. This study also challenged the tribal classification of Anacardiaceae, with only Dobineae and Semecarpeae retrieved as monophyletic. The present phylogenetic estimate supports the subfamilial classification of Pell *et al*. (2011) in that Spondioideae (including *Buchanania*) is monophyletic, but suggests that Anacardioideae is polyphyletic, retrieving *Campnosperma* as an early-diverging lineage in Spondioideae (Figure 5.4). The placement of *Campnosperma* in Spondioideae is supported by the molecular study of Weeks *et al*. (2014) and the anatomical studies of Wannan and Quinn (1990, 1991) and suggests that the subfamilial classification of this genus should be reassigned.

The subfamilial classification of *Pentaspadon* is controversial. Morphological studies have placed the genus contrastingly in Anacardioideae (Mitchell and Mori 1987) and Spondioideae (Wannan *et al.* 1987; Wannan and Quinn 1991), and the molecular study of Weeks *et al*. (2014) retrieved it as sister to all Anacardiaceae. The present analysis using Sanger data for three species of *Pentaspadon* integrated into the Angiosperms353 backbone (that did not include *Pentaspadon*) supports the morphology-based assignment of Wannan (1987) and Wannan and Quinn (1991), and places it within Spondioideae. In the Sanger species-level tree, *Pentaspadon* is retrieved on a long branch as sister to the well supported clade (Angiosperms353 genus tree bs = 100) containing *Dracontomelon* + *Pseudospondias* + *Pegia* + *Spondias* + *Allospondias* with moderate support (species tree bs = 83). Target capture sequencing of *Pentaspadon* is required to verify the appropriate subfamilial classification of this genus.

As in the analyses of Pell (2004) and Weeks *et al*. (2014), the present analysis suggest that all tribes are polyphyletic with the exception of Dobineae (*Campylopetalum* + *Dobinea*) and Semecarpeae (with the present study sampling *Semecarpus*, *Drimycarpus*, *Nothopegia* and *Melanochyla* species but missing *Holigarna*). These results add to the growing body of evidence that the current tribal classification of Anacardiaceae is artificial and is in need of revision. *Androtium*, *Holigarna*, *Malosma*, *Haematostaphis*, *Haplospondias*, *Koordersiodendron* and *Solenocarpus* have never been included in molecular studies and their subfamilial and tribal classifications within Anacardiaceae are yet to be corroborated.

With respect to infra-generic topology, the Angiosperms353 tree strongly suggests that *Cyrtocarpa* and *Poupartia* are polyphyletic, and confirms that *Rhus* is polyphyletic and is in urgent need of taxonomic revision (Miller *et al.* 2001; Pell 2004; Yi *et al.* 2004, 2007; Moffett 2007; Pell *et al.* 2008, 2011). The polyphyly of these genera was maintained in the species tree. *Allospondias* was placed within a clade including all species of *Spondias*, rendering the latter paraphyletic. Within this clade, *S. macrocarpa*, *S. bipinnata* and *A. lakonensis* were weakly supported as early diverging. In their latest revision of Neotropical *Spondias*, Mitchell and Daly (2015) considered that morphology supports the recognition of *Allospondias* as distinct from *Spondias*, but noted that the placement of *Spondias bipinnata* 'presents a challenge', having shared morphological characters with both *Spondias* and *Allospondias lakonensis*. My results support the affinity of *S. bipinnata* with *A. lakonensis*, but because support for relationships is weak, a more in-depth phylogenetic study of Asian *Spondias* and allied genera is needed to test this phylogenetic estimate.

Novel insights into the SSFE from a new methodological pipeline

Like the study by Weeks *et al*. (2014), my study suggests that Sunda (analogous to 'Southeast Asia' in Weeks *et al*. 2014) is the most likely area of origin for Anacardiaceae. Along with the strong representation of pre-Eocene Anacardiaceous fossils in the Northern Hemisphere, my study supports the idea that the family originated in Laurasia rather than Gondwana (Weeks *et al*. 2014). Throughout the Cenozoic and Cretaceous, Eurasia had varying levels of connectivity with North America, with land bridges linking the continents at stages (e.g., via the North Atlantic land bridges and Bering land bridge), and intrusive seas presenting barriers to gene migration and gene flow (e.g. the northward incursion of the Atlantic Ocean during the Cretaceous) (Tiffney 1985a; b; Wen 2001; Wen *et al.* 2010; Seton *et al.* 2012; Weeks *et al.* 2014; Scotese 2016). This dynamic Laurasian landscape likely influenced early diversification within the family.

While my analysis supports a Laurasian origin for the family, there is a signal of Gondwanan diversification in subfamily Anacardioideae driven by range expansion coincident with the Palaeocene-Eocene thermal maximum (PETM). The common ancestor

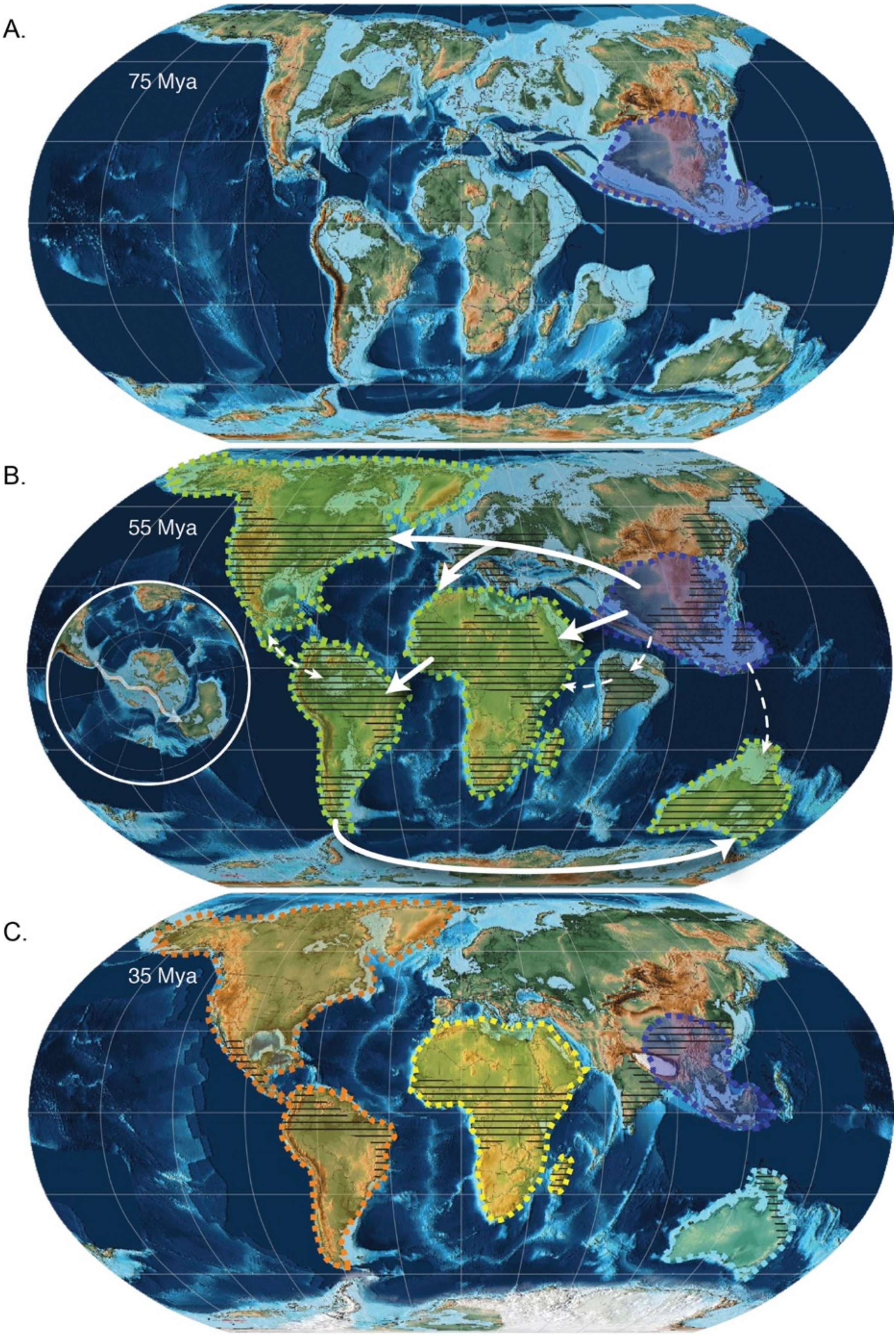

A.
75 Mya
B.
55 Mya
C.
35 Mya

Figure 5.7 Biogeography of Anacardioideae clade III and its expansion into southern Gondwanan continents (A) before (75 Mya); (B) during (55 Mya), and (C) after (35 Mya) the Paleocene-Eocene thermal maximum. Shading colours correspond to the ancestral areas as modelled under a DEC+J model in BioGeoBEARS shown in Figure 5.5; dark blue indicates Sundanian lineages, green represents the common ancestor widespread across Africa, the Americas and Sahul between 57.74 (51.66–63.7) and 40.23 (33.56–48.29) Mya; orange, yellow and light blue represent the divergence of American, African, and Sahulian lineages evident at 35 Mya, respectively. The inset in (C) shows the connectivity of South America to Sahul through Antarctica at 55 Mya and the potential route of expansion by Anacardioideae clade III. The arrows in (C) represent potential routes of expansion at the Paleocene-Eocene thermal maximum, with solid lines representing the most likely route of expansion and dashed lines indicating alternative routes. The paleogeographic reconstruction was generated from Scotese (2016). The hatched areas show the extent of tropical rainforest at the Paleocene-Eocene thermal maximum and in the Oligocene according to Morley (2003).

of Anacardioideae clade III (Figure 5.4B) was reconstructed as having a widespread distribution across the Americas + Sahul + Africa in the mid-Eocene. Anacardioideae clade III is sister to clade II, and these share an ancestor that was most likely in Sunda at the Palaeocene boundary. The transition of the ancestral range of Anacardioideae clade III from Sunda to the Americas + Sahul + Africa is coincident with the PETM (c. 55.5 Mya). Recent evidence suggests that during the PETM the global mean surface temperature was 31.6°C, 17.6°C higher than modern (pre-industrial) temperatures (Inglis *et al.* 2020). The warm climate and tectonic connectivity during this time is known to have encouraged global expansion of megathermal lineage distributions (Morley 2003). In line with this, I suggest that the PETM provided ideal conditions for the ancestor of Anacardioideae clade III to expand its range from Sunda into the southern hemisphere and across the Gondwanan continents (Figure 5.7A–B). Subsequent global cooling and tectonic separation then induced the divergence of major Anacardioideae clade III lineages (Figure 5.7C).

Although my chronogram gives good evidence for the expansion of the ancestral range of Anacardioideae clade III coincident with the PETM, the route of expansion is less clear. At the Palaeocene-Eocene boundary there was potentially a minimum distance of c. 1000 km between Africa and South America (minimum distance calculated using modern shorelines and according to the tectonic model of Zahirovic *et al.* (2016)), and a land bridge connected South America, Antarctica and Sahul (Morley 2003). India was part way through its northwards drift and at that time was placed between Sunda and Africa (Zahirovic *et al.* 2016). Tropical rainforests were extensive at this time, having expanded across most of South America, Africa, India, Sunda and Sahul, and extending across Europe, North America and north-east Asia (Morley 2003; Figure 5.7). Thus, connectivity for megathermal lineages was high, and many possible routes for the expansion of the Anacardioideae clade III are possible. It is very possible that the ancestor of the clade migrated across Europe and into North America via the North Atlantic land bridge and possibly into Africa, as Anacardiaceae lineages including those in the Anacardioideae III clade (e.g. *Rhus* and *Cotinus*) are represented in the Eocene floras of Europe and North America[2] (Reid and Chandler 1933; Manchester 1994; Manchester *et al.* 2007; Flynn *et al.* 2019). Most explicitly, Manchester *et al*. (2007) presented fossil evidence supporting an expansion of *Anacardium* and *Fegimanra* (in Anacardioideae clade II) into Africa and North America in the Eocene, facilitated by migration across Europe and the North Atlantic land bridge. Palynological evidence also suggests that some megathermal lineages dispersed directly from Sunda to Africa (Morley 2003), or that India may have acted as a stepping stone between them. India is suggested to have facilitated the movement of tropical angiosperms between Africa and Sunda – including members of sapindalean family Sapindaceae – in the Upper Cretaceous, too early to be a plausible explanation for the expansion of Anacardioideae clade III into Africa according to my chronogram (Morley 1998). Movement of lineages into South America could have occurred via dispersal from North America, as has been suggested for the Anacardioideae clade II genus *Anacardium* (Manchester *et al.* 2007), or South America could have been reached directly by long-distance dispersal from Africa. Long-distance dispersal across the Atlantic Ocean between Africa and South America has previously been suggested by Pell (2004), and my biogeographic stochastic mapping analysis does indicate that the number of dispersal

[2] Fossils of *Rhus* are well represented in the fossil record; however, the taxonomy *Rhus* is problematic and many studies, including the present one, suggest that the genus is polyphyletic. As such, assigning *Rhus* fossils to nodes with confidence is not possible until the relationships in the genus are resolved and fossils are reassessed against the revised taxonomy. Given the high representation of *Rhus* in the fossil record, resolution of the group could give key information needed to better understand the biogeographic history of Anacardiaceae.

events from Africa to South America was relatively high (Figure 5.6). Range expansion of the Anacardioideae clade III ancestor into Sahul may have occurred via overland dispersal from South America and across Antarctica. Alternatively, simultaneous with the northern expansion into Africa and the Americas, the ancestor of Anacardioideae clade III could have colonised Sahul via direct, long-distance dispersal from Sunda, being one of the earliest Sunda-Sahul exchange events. However, given the physical connection of South America with Sahul via Antarctica, I posit that the former is the more likely scenario to explain the establishment of the ancestral lineage in Sahul. Further insight into the routes of expansion of Anacardioideae clade III can be gained through a more detailed biogeographic coding scheme including India and a separate North and South American area, as well as further palaeobotanical evidence.

The sister relationship of Anacardioideae clades II and III demonstrates that most of the extant Anacardiaceae diversity in Sunda is likely to have evolved and persisted there since the Cretaceous. Based on my results, the only exceptions to this are *Pleiogynium* and *Choerospondias* in the Spondioideae, and *Rhus*, *Pistacia*, *Cotinus*, *Toxicodendron* and *Searsia* in the Anacardioideae clade III. My biogeographic analyses indicate that members of these lineages secondarily colonised Sunda in the Miocene by stepping-stone or long distance dispersal from the Americas and Africa. Interestingly, none of the genera in Anacardioideae clade III that are extant on Sahul – *Euroschinus*, *Blepharocarya and Rhodosphaera* – have dispersed to Sunda following its collision with Sunda, and all are species-poor (*Euroschinus* has nine species, *Blepharocarya* has two, and *Rhodosphaera* has one). According to my analysis, *Euroschinus* arrived on Sahul or New Caledonia from the Americas at the Oligocene-Miocene boundary, and is therefore likely to represent a case of secondary colonisation of Sahul by long-distance dispersal. In contrast, *Blepharocarya* and *Rhodosphaera* are reconstructed as having persisted on Sahul since the Eocene, diverging from ancestors that were distributed across the Americas + Africa + Sahul, and the Americas + Sahul, respectively. When contrasted against lineages in this clade that persisted in Africa and the Americas from the Eocene, there is a distinct lack of diversification in *Blepharocarya* and *Rhodosphaera* in the same time period.

There are three potential reasons for the lack of diversification in the autochthonous Sahulian lineages *Blepharocarya* and *Rhodosphaera* – a history of (a) low speciation, (b) high extinction, or (c) both low speciation and high extinction. Given that these genera shared an ancestor with other Anacardioideae clade III genera that diversified relatively extensively in Africa and North and South America, there does not seem to be any clear reason why *Blepharocarya* and *Rhodosphaera* would both have sudden, independent reductions in speciation rate. Rather, I posit that these lineages experienced a much higher rate of extinction than their African and American relatives. Following the separation of Sahul from Antarctica c. 45 Mya, the effects of the initiation of the Antarctic circumpolar current and associated changed global wind systems, compounded by the northwards drift of Sahul, drove aridification on the continent from the mid-Miocene (Locker and Martini 1989; Flower and Kennett 1994; Pichon *et al.* 2019; Stotz *et al.* 2021). The rapid aridification of Sahul is likely to have caused the retraction of rainforest and extinction of megathermal plant lineages (Hill 1994; Macphail *et al.* 1994; Byrne *et al.* 2008). I suggest that it is the major aridification of Sahul compared to Africa and North and South America during the Miocene that caused greater extinction on Sahul and reduced the extant diversity of *Blepharocarya* and *Rhodosphaera*.

The evidence for an ancient history of extinction of Sahulian Anacardiaceae lineages gives a key new insight into the potential drivers of SSFE dynamics. None of the Sahulian Anacardiaceous lineages that are likely to have experienced extinction through the aridification of Sahul (*Blepharocarya*, *Rhodosphaera* and *Euroschinus*) successfully dispersed into and established in Sunda after collision with the continent. However, lineages from Anacardioideae clade III that evolved in Africa and the Americas were able to secondarily disperse back into Sunda (e.g. *Searsia* and *Cotinus*). As with all ancestral area reconstruction methods, the uncertainty of the reconstructed area increases at older nodes. However, given the congruence of the ancestral area analysis results with tectonic, climatic and palaeobotanical information, it is likely that my results present a reasonable picture of the biogeographic history of Anacardiaceae. Future work could incorporate further scruitiny of the biogeographic models and the incorporation of additional parameters, such as distance between areas, to inform the reconstruction.

The generation of a well-supported, family-level phylogeny has enabled a direct comparison of dispersal and diversification of these lineages with differing biogeographic histories, and suggests that colonisation of Sunda may be affected by the diversity of the colonising lineage and its adaptation to climate. The present analysis indicates that it is plausible that by the time Sahul reached Sunda, any Sahulian lineages – even if their ancestors were tropical Sundanian megatherms – had undergone such extensive extinction that only a small pool of lineages remained and were available for colonisation of Sunda. Therefore, the chance of successful dispersal to Sunda from Sahul was low. Further, it is possible that any lineages that were able to persist on Sahul as it underwent its northwards drift had to adapt to drying conditions, and as such, may no longer be able to invade and persist in perhumid Sunda. Indeed, *Blepharocarya* is usually found at the edge of seasonally-dry, secondary rainforests. Finally, when Sahul reached equatorial, tropical climates, it may have had many unfilled ecological niches caused by extinction that could be filled by tropical Sundanian lineages, further compounding the bias of exchange directionality. The likely ancient history of extinction on Sahul is likely to be a major reason for the eastward bias in SSFE directionality detected in this study and by previous authors (Sniderman and Jordan 2011; Richardson *et al.* 2012; De Bruyn *et al.* 2014; Crayn *et al.* 2015).

As intimated above, my biogeographic stochastic modelling further emphasises the bias in directionality of exchange between Sunda, Sahul and Wallacea. Overall, eastward dispersal (Sunda to Wallacea to Sahul) outweighed westward dispersal in Anacardiaceae by a factor of 2.68. This is in agreement with previous estimates of the bias in directionality, where eastward exchange was estimated to dominate westward dispersal by 2.4x (Crayn *et al.* 2015), 1.5x (De Bruyn *et al.* 2014) and 9x (Sniderman and Jordan 2011). In light of the ancestral area analysis, however, the bias in directionality is compounded further, as it suggests that any exchange that did occur from Sahul to Sunda is actually recent dispersal of a lineage that originated in Sunda, spread to Sahul upon the collision of the shelves, and secondarily spread back into Sunda. My analysis also sheds new insight on the importance of the emergence of Wallacea in facilitating the exchange; it suggests that in Anacardiaceae the bias in exchange was predominantly driven by dispersal from Sunda to Wallacea, with 5.42 as many dispersal events from Sunda to Wallacea than the reverse, and 3.31 times more dispersal events from Sunda to Wallacea than from Sahul to Wallacea.

My results suggest that dispersal between Sunda, Sahul and Wallacea was low to non-existent up until 20 Mya, when the rate of dispersal events increased between all biogeographic areas. The increase in dispersal at this time is coincident with the timing of the collision of the biogeographic regions, with the increased proximity likely facilitating more regular exchange. Dispersal events from Sunda to Wallacea show the largest increase and a step-change in the number of dispersal events is observed c. 12.5 Mya. This correlates with a period of great geological change in the region; from 12.5 Mya rapid orogenesis was occurring throughout the region. It is possible that the emergence of land masses throughout Wallacea and Sahul decreased the dispersal distance for lineages across the SSCZ and facilitated stepping-stone dispersal across the region. It also created new biomes, particularly upland and montane ones, for lineages to step along. Interestingly, the number of dispersal events modelled directly from Sunda to Sahul in Anacardiaceae remains low throughout most of the Cenozoic, but for a distinct peak at 10 Mya (Fig. 5.5). This peak is contemporaneous with the rapid orogenesis of the central ranges of New Guinea in Sahul which generated new habitat. However, it is interesting that the number of dispersals drops again after this time, contrasting with the results of the meta-analysis of Crayn *et al*. (2015) which showed a sharp increase in dispersal from Sunda to Sahul at this time, remaining high to the present. However, Crayn *et al*. (2015) did not include disjunctions with Wallacea, so the drop in number of dispersals between Sunda and Sahul after 10 Mya could be explained by dispersal from Sunda being stopped at Wallacea rather than being dispersed directly to Sahul. Alternatively, this pattern could be an artefact of small sample size – the reliability and generality of this pattern should be tested by repeating this analysis on other families, particularly the other families in Sapindales.

Future directions

The new insights gained using this novel pipeline emphasises the use and importance of considering ancient evolutionary history when trying to understand more recent biogeographic phenomena such as the SSFE. Integration of diverse data to generate one, large phylogenetic tree has enabled direct comparison of evolutionary histories of lineages that would otherwise be impossible to compare. For example, under the current method of comparing separate phylogenies in phylogenetic meta-analyses, comparing a phylogeny of *Blepharocarya* with a phylogeny of *Mangifera* would be pointless, as *Blepharocarya* does not have any disjunctions with Sunda. But by including it in the context of the deeper evolutionary history of the family, it has given the new insight that extinction in Sahul has likely played a major role in influencing the SSFE.

This methodological pipeline can and should be more broadly utilised to gain even more insight into the SSFE. Firstly, it should be applied to the other families in Sapindales to provide independent tests for the patterns of SSFE observed in. Secondly, formal tests of diversification rate could be used to further test the hypothesis that ancient extinction has had a major effect on SSFE dynamics. It will be interesting to test if lineages that have exchanged across the SSCZ demonstrate higher rates of speciation than those that are not exchanged. Thirdly, trait information should be integrated to examine whether lineages with certain traits are more likely to be exchanged across the SSCZ; Sapindales is an ideal group for this given the diversity of its morphology and dispersal syndromes. Likewise, information about biomes can be used to empirically investigate the influence of phylogenetic niche conservatism on SSFE dynamics. Finally, the biogeographic model used in this chapter can be extended to integrate information about distances between tectonic plates over time.

Conclusion

The generation of target capture sequence data has enabled resolution of family and genus relationships within Sapindales and the timing and geography of lineage origins and diversification. Given the large amount of data, thorough and even sampling, rigorous calibration scheme and broad agreement with other morphological and molecular studies, the resultant genus-level chronogram of Sapindales provides the best available framework for further evolutionary studies. The development of a pipeline to combine Angiosperms353 data with legacy Sanger data provides a useful method for investigating historical biogeography, particularly in the SSCZ. The new insights gained into the SSFE by deployment of this pipeline using Anacardiaceae as a test case emphasises the importance of considering ancient evolutionary history when attempting to understand recent and current biogeographic processes.

Chapter 6

General discussion

Introduction

In this thesis I have employed floristic, phenetic, phylogeographic and phylogenomic methods to investigate aspects of the Sunda-Sahul Floristic Exchange (SSFE) and its effect on the evolution of the flora of the Sunda-Sahul Convergence Zone (SSCZ). In this chapter, I synthesise the key findings of my research, discuss the new insights it has given into how the SSFE has shaped the region's flora, and highlight key areas for future research.

Scale of the Sunda-Sahul Floristic Exchange

From the outset of this work, it was clear that a necessary precursor to understanding the assembly of the Sunda-Sahul Convergence Zone flora was a comprehensive checklist of the region's plant species and their distributions. For this reason, in Chapter 2 (Joyce *et al.* 2020) I compiled the first systematic synthesis of current knowledge of the region's flora and presented it as a digital checklist. Analysis of this checklist quantified the diversity of the SSCZ within a global context, concluding that the SSCZ is one of the most floristically diverse regions on Earth – with species richness comparable to that of the neotropics – and harbours c. 16.2% of Earth's vascular plant species. This highlights the importance of the region for understanding the evolutionary processes that lead to the accumulation of global biodiversity.

The baseline data provided by the checklist allowed a thorough examination of the patterns of plant distribution in the region, an assessment of the importance of well-known biogeographical lines (e.g. Lydekker's and Wallace's Lines), and a better understanding of the scale of the SSFE. I found that at the species level, 11.9% of species are distributed across two or more biogeographical regions, and at the genus level almost half of the genera (46.2%) in the region have crossed either or both Lydekker's and Wallace's Line (Chapter 3; Joyce *et al*. 2021a). The species distributions are likely to represent relatively recent floristic exchange patterns, while the distributions of genera likely represent older exchange events, probably from the mid-Miocene. Most plant families are shared across biogeographic lines (77.5%), although given the age of most families, these patterns could reflect ancient vicariance that predates collision of the Sunda and Sahul shelves c. 25 Mya. The high proportion of species, but particularly genera, that are shared across Wallace's and Lydekker's Lines is indicative of the strong influence that the SSFE has had on the assembly of the region's flora, and strongly suggests that deep sea channels alone are not effective biogeographical barriers for many plants.

The effect of the Sunda-Sahul collision on the flora of the SSCZ

In Chapter 3, I reported that shelf endemism is uneven in the SSCZ, with Sahul having a larger number and higher proportion of endemic species than Sunda, and Sunda sharing more species and genera with Wallacea than does Sahul (Joyce *et al*. 2021a). Studying patterns of endemism is at the heart of understanding the effects of Sunda-Sahul continental shelf convergence on the assembly of the flora of the SSCZ and provides direct evidence of exchange (with high exchange leading to decreased shelf endemism) and *in situ* diversification (with high *in situ* diversification leading to increased shelf endemism). Based on the results of my research, I suggest that the convergence of the Sunda and Sahul shelves contributed to the uneven patterns of endemism across the SSCZ in two main ways: 1) there was a directionally biased SSFE in which Sundanian lineages dispersed and established in other biogeographic regions at higher rates than Sahulian lineages, and 2) collisional orogenesis led to much recent *in situ* evolutionary diversification in Sahul. In this way, I posit that the convergence of the Sunda and Sahul shelves has made a major contribution to the megadiversity of the region, not only through admixture of lineages facilitated by the SSFE, but also by triggering floristic diversification.

Directional bias in the Sunda-Sahul Floristic Exchange

The results of my research support previous floristic, phylogenetic and palaeobotanical studies reporting a strong bias in favour of exchange from Sunda into Sahul (e.g. (Kalkman 1955; Van Welzen *et al.* 2005, 2011; Sniderman and Jordan 2011; Richardson *et al.* 2012; Crayn *et al.* 2015). Moreover, my results add nuance to this bias in exchange, indicating that the bias is mainly in the exchange of Sundanian lineages into Wallacea rather than Sahul, and that most westward exchange may have actually been secondary exchange of lineages that originated in Sunda back into Sunda, rather than autochthonous Sahulian lineages. In Chapter 3, my phytogeographic analysis indicated that Sunda shares almost twice as many species and genera with Wallacea as does Sahul and that species endemism in Sunda is lower than in Sahul (Joyce *et al.* 2020; Joyce *et al*. 2021a). Further, in Chapter 5, my biogeographic analysis of Anacardiaceae indicates that Sundanian lineages dispersed into Wallacea three times more frequently than did Sahulian lineages. It also showed that in Anacardiaceae, any lineages originating on Sahul are likely to have undergone extensive extinction, and did not successfully expand to Wallacea or Sunda. Any lineages in the family that did move from Sahul to Sunda or Wallacea were secondary movements of Sundanian lineages. Available evidence hence strongly supports the notion that there was an eastward bias in exchange, and my research has given new insight into the potential drivers of exchange.

A long-standing explanation for the eastward bias in exchange is that Sundanian lineages possess traits that confer an advantage in invading new territory, evident both in explicit statements and in the anthropomorphication of flora as ‘invasive’ and ‘aggressive’ (Hooker 1859; Burbidge 1960; Richardson *et al.* 2012). Some support for this hypothesis is provided in a recent study (Yap *et al.* 2018), which shows that immigrant Sundanian species in Sahul are more likely than co-occurring Sahulian natives to possess functional traits that are advantageous in novel and unstable environments. However, this hypothesis requires further testing. Comparison of traits thought to be important for invasion success between immigrant Sahulian species in Sunda and immigrant Sundanian species in Sahul would be a critical step in understanding whether there is in fact a difference in the intrinsic invasiveness of Sundanian and Sahulian lineages.

Contrastingly, my research suggests that a major driver of the eastward bias in exchange is the pre-adaptation of Sundanian taxa to the perhumid climates that characterised the newly-emergent landmasses in Wallacea and Sahul, rather than the presence of superior invasive traits. The collision of the Sunda and Sahul shelves caused the emergence and uplift of islands including Sulawesi (in Wallacea), and most of New Guinea (in Sahul), both of which have equatorial perhumid climates similar to those in which Sundanian species had evolved throughout the Cenozoic. As such, any new landmass in Wallacea was likely to be more suitable for Sundanian lineages. In contrast, Sahulian lineages had evolved at higher latitudes and experienced dramatic environmental change during Sahul’s northwards drift. My analyses in Chapter 5 indicate that this is likely to have caused a high rate of extinction in megathermal Sahulian lineages, and adaptation of persistent lineages to increasingly arid conditions. This is in line with my findings in Chapter 3, that climate and available land mass are major influences on the phytogeography and SSFE in the region, supporting the idea that pre-adaptation to climate could be a major driver of the eastward bias of exchange (Joyce *et al*. 2021a). A recent ecological study by Brambach *et al*. (2020) also supports this concept, finding that across the SSCZ Sahulian species tend to establish at higher altitudes and in drier, more seasonal conditions than species of Sundanian origin, which predominate in wetter, less seasonal lowlands. The evidence that lineages generally expand their range within the same biome gives insight into the underlying mechanism of phylogenetic niche conservatism. The importance of the interaction of environment and available land mass with the SSFE is discussed further below.

Following from my work in Chapter 5, I suggest that along with the difference in suitability of Sundanian and Sahulian lineages to novel Wallacean landmasses, historical extinction on Sahul may have played a major role in driving the eastward bias in the SSFE. My biogeographic analysis of Anacardiaceae supports the idea that major aridification of Sahul during the Miocene caused extinction and reduced the extant diversity of *Blepharocarya*, *Rhodosphaera* and *Euroschinus*. Further, none of these Sahulian Anacardiaceous lineages successfully dispersed into and established in Sunda after collision with the continent. However, lineages from Anacardioideae clade III that evolved in Africa and the Americas were able to secondarily disperse back into Sunda (e.g. *Searsia* and *Cotinus*). This possibly indicates that by the time Sahul reached Sunda, any Sahulian lineages – even if their ancestors were tropical Sundanian megatherms – had undergone such extensive extinction that only a small pool of lineages remained and were available for colonisation of Sunda. Therefore, the chance of successful dispersal to Sunda from Sahul was low. Further, when Sahul reached equatorial, tropical climates, it may have had many unfilled ecological niches caused by extinction that could be filled by tropical Sundanian lineages, further compounding the bias of exchange directionality. The probable ancient history of extinction on Sahul is therefore likely to be a major reason for the eastward bias in SSFE directionality detected in this research and by previous authors (Sniderman and Jordan 2011; Richardson *et al.* 2012; De Bruyn *et al.* 2014; Crayn *et al.* 2015).

In situ radiation of lineages in Sahul

A second driver for the higher species endemism on Sahul is higher rates of *in situ* diversification there, particularly in New Guinea. Van Welzen (2005) found higher species endemism in New Guinea than in Sundanian islands, attributing this to the persistence of more ancient lineages on New Guinea. This may have played a role, but the higher ratio of species endemism to generic and familial endemism in Sahul relative to Sunda reported in Chapter 3 is best explained by recent speciation rather than persistence of old lineages. Recent, rapid diversification coincident with the uplift of the New Guinea Central Ranges has been inferred in both animal and plant lineages (Thomas *et al.* 2012; Toussaint *et al.* 2014; Tallowin *et al.* 2018). As well as rapid orogeny in New Guinea promoting speciation, there may have been less opportunity for diversification in Sunda given the stable geomorphology and climate of the region relative to Sahul (Morley and Morley 2011; Hall 2017). Another possibility is that Sahul is now undergoing rapid diversification to fill empty niches following the apparent extinction in Sahul coincident with Miocene aridification (Chapter 5). Comparative phylogenetic studies, particularly the analysis of lineage-through-time plots in concert with geology are needed to test this hypothesis further.

The impact of taxonomic concepts

A caveat in any biogeographical analysis is that some patterns may be an artefact of discrepant taxonomic concepts and survey efforts across the geographical units studied. For the SSCZ, it is possible that the difference in endemism between Sunda, Sahul and Wallacea could be skewed by such disparities. Taxonomic concepts may be narrower in Australia, and survey efforts greater, leading to a higher number of recognized species endemic to Sahul; however, I am not aware of direct evidence for this affecting the general patterns reported in this thesis. Moreover, evidence for a bias in directionality of exchange is now overwhelming and comes from a variety of study types, indicating that these patterns are indeed real and are unlikely to be an artefact of taxonomic bias.

The influence of environment and available landmass on the Sunda-Sahul Floristic exchange

Based on my results I conclude that climate and available landmass had a crucial influence on the dynamics of the SSFE. As intimated in the previous section, climate and available landmass are likely to be key factors driving the directional bias in the SSFE; however, my results also suggest that climate and available landmass also explain temporal patterns of exchange and, at a smaller scale, define spatially-reticulated migration routes for exchanged lineages. Further, I suggest that the reticulated nature of these migration routes may perpetuate speciation.

The multivariate analysis of floristic composition in Chapter 3 suggests that geographical proximity is not the main driver of phytogeography in the SSCZ, as regions that are geographically closer do not always have more similar floras. My analyses did not retrieve Lydekker's and Wallace's Lines delineating major disjunctions in floristic composition, suggesting that overwater dispersal is not strongly limited for plants and that other factors are more important determinants of floristic composition. Instead, I found that climate – particularly annual precipitation and seasonality – were most strongly correlated with floristic composition across the SSCZ. The idea that environment rather than dispersal is the major determinant of phytogeographical patterns in the region has also recently been suggested in the conceptual work of Trethowan (2021). It is also supported by the ecological study of Brambach *et al.* (2020), who found that the proportion of Sundanian and Sahulian species changes along environmental gradients. The greatest disparity in annual precipitation in the region is between Australia and Asia, and this is likely to be the main determinant of exchanges involving New Guinea, in line with previous hypotheses (van Steenis 1950; Van Welzen *et al.* 2005).

The connectivity analysis in Chapter 3 indicates that phytogeographical connectivity tracks throughout the SSCZ have changed through time, influenced by changing landmass availability. At the species level, relatively even connectivity was observed between most pairs of islands or island groups. However, at the genus and family levels, the relative connectivity between the large landmasses of mainland Asia, Borneo, Australia, New Guinea and the Philippines is very high, while very little connectivity is inferred between the smaller Lesser Sunda Islands, Maluku Islands, Sulawesi and Sumatra. I suggest that this change in connectivity tracks through time correlates with the availability of landmass across the SSCZ over time. Mainland Asia, Borneo, Australia and the Philippines have all maintained substantial emergent landmass available to support vegetation since the Eocene (De Bruyn *et al.* 2014); parts of New Guinea were also probably emergent from the Late Jurassic (Hill and Hall 2003; Cloos *et al.* 2005; Jonsson *et al.* 2011; Harrington *et al.* 2017). Further, mainland Asia, Borneo, the Philippines and parts of New Guinea were historically geographically closer than they are today. Recent tectonic models suggest that from 43 Mya, the Philippine Arc, Melanesian Arc and proto-Caroline Arc (which make up modern-day mainland Asia, Borneo, the Philippines and parts of New Guinea) formed a continuous island arc (Zahirovic *et al.* 2016). The long-term persistence of these emergent landmasses and their historical connectivity is likely to explain the signature of exchange between these landmasses at higher taxonomic levels – an idea that is supported by studies of lizards that show signatures of long-term persistence on these ancient arcs (Oliver *et al*. 2018). In contrast, Sumatra and Java on the Sunda shelf were mostly submerged during the mid-Miocene (De Bruyn *et al.* 2014), and most of Sulawesi, the Lesser Sunda Islands and the Maluku Islands did not become emergent until the Pliocene (Nugraha and Hall 2018), helping explain why signatures of plant exchange between these islands are mainly detectable at the species level.

The phylogeographic study of *Aglaia elaeagnoidea* reported in Chapter 4, which by characterising in detail the migration of a single species across the SSCZ, also gives insights into how these general floristic patterns are driven by environment and available landmass. It is evident that historical cycles of expansion and contraction of suitable habitat impacted dispersal and connectivity throughout the range of *A. elaeagnoidea*. Environmental niche modelling suggested that suitable habitat expanded into equatorial Southeast Asia during cooler, drier glacial periods, and contracted to peripheral islands during interglacials. I suggest that this resulted in the strong genetic structuring observed in *A. elaeagnoidea*, with equatorial populations showing high admixture and peripheral populations showing strong genetic differentiation. A similar pattern has also been observed in Australian rainforest taxa, where repeated range expansions and contractions coincident with Quaternary climatic fluctuations reinforced a pattern of low genetic diversity and high genetic differentiation in peripheral populations (Rossetto *et al.* 2012; Mellick *et al.* 2012, 2013; Fahey *et al.* 2019).

My research is the first study to my knowledge that shows this pattern in a plant species across Southeast Asia. This study on *A. elaeagnoidea* therefore gives insight into how exchange may occur spatially at the species scale across the SSCZ; at a phylogenetic or floristic level exchange may be observed simply as unidirectional movement of a lineage from one shelf to another, while at a phylogeographic level exchange may be multidirectional, reticulate and iterative. This complex pattern of movement across the SSCZ is likely to have led to genetic differentiation and the accumulation of the region’s diversity. Complex phylogeographic history as shown for *A. elaeagnoidea* as it moved from one shelf to the other in concert with changing environment and available landmass is likely to have stimulated speciation in peripheral populations, and therefore contribute to the high diversity of the region.

Asian-Australian exchange tracks

A key finding of this PhD research is the identification of two floristic exchange tracks between Southeast Asia and Australia, one between New Guinea and Cape York Peninsula, and one between Timor and the Kimberley Plateau. It had been previously suggested, based on observational, palaeobotanical and phylogenetic evidence, that plant lineages were exchanged between Australia and Southeast Asia, but substantial additional evidence is provided in Chapters 2 and 3 of this thesis. These chapters conclude that more than 2300 species of vascular plants are shared between Australia and Southeast Asia (Joyce *et al.* 2020a). Of these, 635 are found in the northern Australian phytogeographic subregions of Kimberley Plateau, Arnhem Land, Cape York Peninsula and Atherton (*sensu* Ebach *et al.* 2015; Figure 4.1), representing approximately 10% of the plant species in northern Australia (Chapters 2 & 3; Joyce *et al.* 2020, 2021a). These chapters document the locations of past and present exchange tracks, which were previously unclear and generally assumed to be primarily between New Guinea and Cape York Peninsula (e.g. van Steenis 1934; Burbidge 1960). My results indicate that at least some lineages in northern Australia of Southeast Asian origin entered northwestern Australia via dispersal tracks in what is now the Timor Sea (Joyce *et al.* 2021b).

As well as being spatially separated, the findings of Chapter 4 suggests that the exchange tracks are also temporally separated. The New Guinea-Cape York Peninsula track appears to be contemporary for *A. elaeagnoidea*, with ongoing gene flow implied by low genetic differentiation between New Guinea and Cape York Peninsula populations, while the Kimberley-Timor (Timor Sea) track is historical, with strong genetic differentiation between populations indicating little or no apparent ongoing gene flow. These findings are consistent with patterns observed in animals; ongoing or recent (up to c. 17 Ka ago; Voris 2000) gene flow between New Guinea and Cape York Peninsula has been reported in birds (Roshier *et al.* 2012; Marki *et al.* 2018; Lamb *et al.* 2019; Joseph *et al.* 2019; Dorrington *et al.* 2019; Keighley *et al.* 2019) and reptiles (Pepper *et al.* 2017; Natusch *et al.* 2020). A track between Asia and northwestern Australia has been previously suggested for fauna (e.g. Williams *et al*. 2008; Toon *et al*. 2017; Dorrington *et al.* 2019), and humans (Bird *et al.* 2018), and a signature of genetic divergence following migration between the Kimberley Plateau and Timor has also been reported in Zebra Finches (Balakrishnan and Edwards 2009).

The discovery of these two spatially and temporally separated floristic exchange tracks between Southeast Asia and northern Australia has major implications for our understanding of the phytogeography and evolution of the northern Australian flora. The results support a broad conclusion that the monsoon tropics of the Kimberley Plateau and the monsoon and wet tropics of Cape York Peninsula have separate biogeographic histories (Crisp *et al.* 1995; Bowman *et al.* 2010). Biogeographic barriers separating the Kimberley from the Top End and Cape York are well known (González-Orozco *et al.* 2014; Edwards *et al.* 2017), and floristic studies show that each region has a high proportion of endemic species (Wannan 2014; Joyce *et al*. 2021a). However, the findings of my thesis indicate that separate biogeographic histories of the northern Australian regions have been driven not only by restriction of exchange by biogeographic barriers in northern Australia, but also by independent colonisations of Southeast Asian lineages during the SSFE. This again emphasises the importance of the SSFE in influencing the flora of Australia, calls into question anecdotal assumptions that northern Australia's flora is relatively homogenous, and suggests that management and conservation practices should be considered separately for each region. How the largely independent evolutionary histories of the three northern Australian regions have interacted with the evolution of the southern Australia flora remains to be understood; investigating this question provides exciting opportunities not only to understand the evolution of southern Australia's flora but also how Australia's biogeography changed with the aridification of central Australia.

The role of phylogenomics in understanding the SSFE

Recent advancements such as target capture sequencing have great promise for providing further insights into dynamics of the SSFE. Previously, comparative phylogenetic techniques have been used to understand dynamics of the SSFE by comparing published chronograms from independent studies and counting the number of biogeographic transitions between Sunda and Sahul (e.g. Crayn *et al*. 2015, de Bruyn *et al*. 2014). However, comparison of phylogenies produced with different – and often outdated –

methods may lead to inaccurate results. Further, counting the number of nodes representing biogeographic transitions often yields a low sample size from which only general patterns can be inferred. Comparing individual phylogenies (usually at genus level) also means that deeper nodes of transition may be excluded, and could lead to a bias in favour of more recent transitions. In Chapter 5 I developed a solution to these limitations by integrating new target-sequence capture data with legacy Sanger data to cost-efficiently produce a densely sampled and robust phylogeny of Sapindales for the purposes of investigating the dynamics of the SSFE.

The method described overcomes important previous limitations of comparative phylogenetic biogeographic studies. The generation of a single phylogeny with the latest tree-building and dating methods, with comprehensive taxon sampling, ensures that all biogeographic transitions are consistently compared across the phylogeny. It also means that deeper biogeographic transitions are able to be detected, reducing potential bias of timings of exchange. Furthermore, the method enables custom biogeographic coding instead of being reliant on the areas coded in published studies. This problem limited Crayn *et al*. 2015 to scoring biogeographic disjunctions between Sunda and Sahul and ignoring Wallacea due to the varied biogeographic areas coded in different included studies.

The biogeographic analysis conducted on Anacardiaceae (Chapter 5) demonstrates the utility of the method in being able to code species into Sunda, Sahul and Wallacea in one large analysis. It enabled direct comparison of evolutionary histories of lineages that would otherwise be impossible to compare. For example, under the current method of comparing separate phylogenies in phylogenetic meta-analyses, comparing a phylogeny of *Blepharocarya* with a phylogeny of *Mangifera* would be pointless, as *Blepharocarya* does not have any disjunctions with Sunda. But by including it in the context of the deeper evolutionary history of the family, it has given the new insight that extinction in Sahul has likely played a major role in influencing the SSFE. Additionally, the Biogeographic Stochastic Mapping analysis provided new insights into the exchange, suggesting that exchange between Sunda and Sahul is relatively even but exchange between the continental shelves and Wallacea is not. In Anacardiaceae, the cause of a bias of exchange between Sunda and Sahul (as suggested by previous authors) is likely due to the filtering effect of Wallacea: Sundanian lineages are three times more likely to enter Wallacea than Sahulian ones, but once in Wallacea, dispersal to Sahul and Sunda is approximately equally likely.

Whether this pattern holds for the remainder of the Sapindales remains to be seen; extending the analysis to the whole of the Sapindales will substantially increase its power. Exciting lines of future research will come from investigating differences in exchange dynamics and the effect of biogeography on diversification between families, times, and biomes within Sapindales.

Future directions

Despite a long history, understanding the full extent and nature of the SSFE and its effect on the flora of the region remains in its infancy. One of the challenges (and joys) of researching the subject is the multi-disciplinary, multi-scale approach required to understand the SSFE's complex dynamics. Further research will benefit greatly from collaborations between multi-disciplinary teams of ecologists, bioinformaticians, population biologists, taxonomists, phylogeneticists, zoologists, botanists, geologists, archaeologists and palaeobotanists. Several lines of research that build directly on the research presented in this thesis I think will be particularly enlightening.

Firstly, it is essential that further work is conducted on the checklist of vascular plants of the SSCZ. As emphasised throughout my thesis, the work of Chapter 2 was intended as a preliminary systematic synthesis of current knowledge of the region's flora, presented in a digital format. The next step is to incorporate expert verification into the reviewing process. This is vital for keeping the list up to date, reliable and useful in the face of new discoveries and changing nomenclatures. Ultimately, I hope that the checklist will provide a key resource to enable researchers to generate and test biogeographic, ecological and evolutionary hypotheses in the SSCZ.

Secondly, it has become clear from my research – and from growing evidence in the literature – that establishment conditions (particularly annual rainfall, seasonality and available landmass) have had a major influence on the SSFE and therefore the composition of the SSCZ flora, which means that phylogenetic niche conservatism (Crisp *et al.* 2009; Donoghue and Edwards 2014) has a major influence on the evolution of the region's flora. This has important implications for future studies on the evolution of the region. One such implication is that environmental units such as biomes, rather than geographical units such as continental shelves, should be considered as the areas coded for biogeographic ancestral area reconstruction in phylogenetic studies, as dynamics between biomes may differ from the overall floristic trends. It also emphasises the novelty and importance of lineages that have managed to switch biomes or invade suboptimal areas. It will be useful to determine which traits are associated with which biomes, and which traits have enabled some lineages to expand into suboptimal environmental conditions while most are restricted to their ancestral niches. This will also have implications for conservation of lineages in certain biomes in the face of climate change. Although it is clear that establishment conditions have a major impact on the SSFE, the role of soils were not assessed in this research and are also likely to have an important influence (Slik *et al.* 2011; Kooyman *et al.* 2019). Further, although these results suggest that dispersal is not a major limiting factor influencing floristic patterns in the region overall, there is some evidence that dispersal syndrome may still play a role (e.g. Crayn *et al*. 2015), and this should be investigated further to achieve a more comprehensive and nuanced understanding of the relative roles of establishment conditions and dispersal in explaining the dynamics of the SSFE. The implications for plant traits as dispersal causes lineages to encounter different communities of dispersal verctors across Wallace's Line (e.g. primates are absent from Sahul), is one tantalising question yet to be explored.

Thirdly, additional research into the timing and location of Asian-Australian exchange tracks will be important in understanding the evolution of Australia's flora. Of particular interest will be investigating the location and timing of exchange routes between Australia's Top End and Asia and any interaction this may have with the Kimberley and Cape York Peninsula. Additionally, investigating the timing of dispersal of key immigrant plant groups that may have had a substantial impact on the ecology of northern Australia will be illuminating. The family Poaceae will be a key one for this, as the majority of Australian lineages are likely to have immigrated to Australia from Southeast Asia in the Miocene (S. Bryceson, M. Barrett, pers. comm. 2021) and their arrival and establishment would have had a profound influence on fire and other ecological drivers. Another major advancement in our understanding of Australian-Asian exchange would be a greater understanding of the dispersal and pollination ecology of shared Southeast Asian-Australian plants and the dispersal ecology of key animal dispersers such as Pied Imperial Pigeons and fruit bats.

As touched on previously, the influence that multiple northern Australian-Asian exchange tracks has had on southern Australian biogeography should also be investigated; Brown *et al*., (2011) has previously identified a phylogenetic link between the Lesser Sunda Islands and south-west Western Australia in *Paraserianthes* I.C.Nelson (Fabaceae). Our results suggest that colonisation of south-western Australia by Asian lineages may have occurred via the western Arafura Shelf to the Kimberley Plateau followed by southern expansion and subsequent extinction in northern Australia. Comparison of the phylogenetic and phylogeographic history of Asian lineages in Australia to that of Australian autochthonous lineages provides an exciting opportunity for developing new insights into the evolution of the modern Australian biota.

Fourthly, one of the most exciting areas of future research on the SSFE lies in making use of major advancements in phylogenomics. I suggest the phylogenomic method developed to produce a biogeographic analysis of Sapindales using integrated phylogenomic and legacy Sanger data in this thesis holds particular promise. This method will enable the integration of traits and biogeography in a consistent and rigorous framework; its application to other families in Sapindales will augment the sample size of dispersal events between Sunda and Sahul, with many insights likely if there are differences in exchange dynamics between families. The diverse range of traits (such as dispersal syndrome and lifeform) exhibited in sapindalean lineages and the diversity of biomes they inhabit will enable investigation of the relative roles of traits and phylogenetic niche conservatism on the SSFE. This method also enables investigation not only of how sapindalean lineages were exchanged, but also how the exchange affected sapindalean evolution. In particular, it will be very worthwhile investigating whether biogeographic exchange of sapindalean lineages between Sunda and Sahul leads to a change in their diversification rates; the phylogeographic study of *A. elaeagnoidea* (Chapter 4) suggests that reticulate migration patterns across the region could lead to speciation. I also suggest that a more complex model of biogeography is used in future research to investigate patterns of exchange across the SSCZ; reconsideration of the areas coded could enable the integration of time, distance, and island emergence into the model, and this is likely to lead to a more nuanced and detailed picture of exchange dynamics.

Finally, and reiterating the opening paragraph of this section, this work has emphasised the importance of taking a collaborative and interdisciplinary approach to this subject. In particular, it is clear that a major challenge for future research in understanding the effect of the SSFE on the evolution of the SSCZ, and particularly northern Australia, is untangling anthropogenic influences on the modern flora from more ancient biological processes. Extricating these processes can only be done by working with archaeologists and Traditional Owners.

Conclusion

My work contributes to our understanding of the Sunda-Sahul Floristic Exchange and its impact on the evolution of the northern Australian and Southeast Asian floras. I have emphasised the scale and importance of the collision in shaping the region's flora and the dynamic, complex nature of the exchange through space and time. Overall, the collision of the Sunda and Sahul shelves has contributed to the accumulation of diversity in the region, both through the admixture of previously separated floras and through diversification stimulated by geological and climatic changes and reticulate migration patterns of plant lineages as they move between shelves. It is clear that the presence of suitable establishment conditions has played a major role in the spatio-temporal dynamics of the exchange (with further work needed on the importance of edaphic conditions), and on the interaction of plant functional traits and dispersal ecology on exchange dynamics. I have also showed that the ancient history of extinction on Sahul is likely to be a major explanation for the eastward bias of exchange. Phylogeographic evidence presented in this thesis shows that movement across the SSCZ by plant lineages is likely to be reticulate rather than unidirectional, largely controlled by the availability of suitable establishment conditions, and it likely to have led to speciation. I have also highlighted the presence of multiple exchange tracks between Southeast Asia and Australia, and these are likely to played a role in the independent evolutionary histories of the Kimberley, Top End and Cape York Peninsula regions of northern Australia. Finally, recent advancements in sequencing technology and computational power herald an exciting time for improving our understanding of the SSFE within a phylogenetic framework. The development of a bioinformatic pipeline integrating target capture data with legacy Sanger data to produce an ordinal-level phylogeny enables the investigation of questions previously unanswerable.

I hope that future work building on the research presented in this thesis can continue to complete the picture of how the SSFE has helped shape the flora of this megadiverse and unique part of the planet.

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Appendix A

Chapter 3 Supplementary Information

Appendix A1 Values for each environmental variable for each island group. bio01_mean = Annual Mean Temperature; bio02_mean = Mean Diurnal Range); bio03_mean = Isothermality; bio04_mean = Temperature Seasonality; bio05_mean = Max Temperature of Warmest Month; bio06_mean = Min Temperature of Coldest Month; bio07_mean = Temperature Annual Range; bio08_mean = Mean Temperature of Wettest Quarter; bio09_mean = Mean Temperature of Driest Quarter; bio10_mean = Mean Temperature of Warmest Quarter; bio11_mean = Mean Temperature of Coldest Quarter; bio12_mean = Annual Precipitation; bio13_mean = Precipitation of Wettest Month; bio14_mean = Precipitation of Driest Month; bio15_mean = BIO15 = Precipitation Seasonality; bio16_mean = Precipitation of Wettest Quarter; bio17_mean = BIO17 = Precipitation of Driest Quarter; bio18_mean = Precipitation of Warmest Quarter; bio19_mean = Precipitation of Coldest Quarter; xcoord = longitude coordinate of centroid; ycoord = latitude coordinate of centroid; alt_mean = mean altitude of island group. Island group abbreviations are as follows: MAS, Mainland Asia; Sum, Sumatra; Bor, Borneo; Jav, Java; Phi, Philippines; Sul, Sulawesi; LSI, Lesser Sunda Islands; Mlk, Maluku Islands; NGu, New Guinea; AKP, Kimberley Plateau; AAL, Arnhem Land; ACY, Cape York Peninsula; AAP, Atherton Plateau; AGS, Great Sandy Desert Interzone; ACD, Central Desert; ACQ, Central Queensland; AEQ, Eastern Queensland; AWD, Western Desert; AED, Eastern Desert; ASe, Southeastern; ASw, Southwestern; ASI, Southwest Interzone; AHa, Hampton; ANu, Nullarbor; AEP, Eyre Peninsula; AAd, Adelaide; AVi, Victoria; ATa, Tasmania.

Region	bio01_mean	bio02_mean	bio03_mean	bio04_mean	bio05_mean	bio06_mean	bio07_mean	bio08_mean	bio09_mean	bio10_mean	bio11_mean	bio12_mean	bio13_mean	bio14_mean	bio15_mean	bio16_mean	bio17_mean	bio18_mean	bio19_mean	xcoord	ycoord	alt_mean
AAd	15.2	9.9	47.5	383.1	25.0	4.2	20.7	11.6	19.6	20.1	10.7	556.7	83.2	16.1	47.4	235.3	62.5	65.9	232.6	140.6	-35.5	140.3
AAL	26.9	10.4	62.0	227.4	34.5	17.8	16.8	28.4	23.9	29.2	23.6	1319.4	301.3	1.9	110.3	846.9	9.7	440.3	11.8	133.8	-14.4	37.7
AAP	23.0	8.9	53.1	273.8	30.7	14.0	16.7	25.4	20.5	25.9	19.2	2279.5	485.4	40.1	86.1	1254.7	150.0	1002.4	209.5	145.8	-17.3	237.9
Bor	26.3	9.4	87.4	33.9	31.7	20.9	10.8	26.1	26.3	26.7	25.9	3025.2	336.0	165.7	22.8	938.7	548.9	753.4	817.0	114.2	0.9	251.8
ACY	25.6	12.6	62.2	269.4	35.2	14.9	20.3	27.8	22.7	28.5	21.9	1107.1	285.3	3.9	115.5	749.7	16.3	510.9	21.3	143.3	-16.1	202.9
ACD	26.2	15.1	54.1	476.6	39.0	11.0	28.0	30.5	20.2	31.1	19.6	497.2	132.2	1.7	107.9	327.2	11.6	246.7	12.2	132.4	-19.1	286.2
ACQ	23.6	14.7	52.8	489.8	36.6	8.7	27.9	28.7	18.4	28.8	16.9	516.1	112.1	8.7	81.5	286.2	34.7	271.4	38.8	144.3	-22.0	298.9

Region	bio01_mean	bio02_mean	bio03_mean	bio04_mean	bio05_mean	bio06_mean	bio07_mean	bio08_mean	bio09_mean	bio10_mean	bio11_mean	bio12_mean	bio13_mean	bio14_mean	bio15_mean	bio16_mean	bio17_mean	bio18_mean	bio19_mean	xcoord	ycoord	alt_mean
AED	20.8	14.0	45.8	609.0	35.2	4.5	30.7	26.1	16.0	28.0	13.0	305.4	45.6	13.3	38.9	116.3	47.7	112.3	52.9	140.9	-28.2	205.5
AEQ	21.1	12.3	51.4	421.9	32.3	8.5	23.8	25.8	16.0	25.8	15.4	848.8	142.4	24.3	57.4	387.1	87.4	382.5	93.3	150.1	-24.1	212.1
AEP	17.6	12.7	48.5	492.0	29.9	3.7	26.2	12.7	22.3	23.6	11.5	290.0	37.6	12.6	33.0	105.2	44.5	49.5	102.4	136.1	-32.6	154.6
AGD	27.0	15.4	52.4	492.9	40.5	11.1	29.4	31.6	25.3	32.1	20.3	396.4	108.1	1.5	104.4	259.8	8.6	205.9	35.0	120.6	-20.7	224.1
AHa	17.5	13.2	55.3	377.9	28.7	4.8	23.9	13.9	21.2	21.9	12.6	259.5	30.3	14.0	22.7	82.7	48.4	52.3	75.5	126.4	-32.1	88.6
Jav	24.7	8.5	84.0	49.2	29.8	19.7	10.1	24.5	24.4	25.2	24.1	2419.8	368.9	57.1	58.8	1012.3	209.0	547.5	557.2	109.9	-7.3	325.9
AKP	27.0	14.4	62.3	317.6	37.5	14.4	23.1	29.1	23.2	30.2	22.5	899.9	240.7	0.9	118.9	622.7	8.1	296.2	10.4	126.4	-16.1	222.5
LSI	25.0	8.6	78.2	81.1	30.4	19.4	11.1	25.2	24.2	25.9	23.9	1577.5	296.8	15.5	80.1	808.9	70.0	454.5	108.2	121.2	-8.6	393.4
MAs	24.5	8.7	56.5	249.7	31.8	15.8	16.0	25.9	21.7	27.1	21.0	1825.8	371.3	14.5	85.3	988.3	62.5	594.1	120.2	101.1	16.9	430.4
Mlk	25.8	7.5	77.4	58.6	30.5	20.7	9.8	25.8	25.8	26.3	25.0	2290.0	313.6	90.9	38.3	850.7	321.7	550.5	603.4	129.5	-3.2	282.9
NGu	24.1	9.2	79.5	61.8	29.7	18.1	11.6	24.4	23.7	24.7	23.3	3044.9	348.4	171.0	25.5	974.7	559.0	818.0	647.7	140.9	-5.3	547.2
ANu	18.5	14.5	51.9	475.8	31.5	3.5	28.0	18.3	18.3	24.1	12.4	204.0	23.6	11.1	21.7	63.2	39.2	47.3	53.3	129.0	-30.9	153.6
Phi	25.9	8.2	70.5	105.1	31.7	20.0	11.7	25.8	25.5	27.1	24.5	2524.5	393.2	78.7	52.1	1048.5	269.9	573.9	482.5	122.4	11.2	325.5
ASe	14.9	11.3	46.1	481.3	26.5	1.9	24.6	17.6	12.5	20.7	8.8	913.1	117.2	43.5	28.6	315.0	150.3	285.5	179.5	150.4	-32.8	539.4
ASI	17.2	12.9	48.9	493.2	29.7	3.2	26.5	12.9	20.5	23.2	11.1	329.2	42.3	15.5	31.8	117.3	53.7	60.6	112.4	120.7	-32.0	309.6
ASw	17.5	12.3	49.2	470.6	29.4	4.2	25.2	12.5	22.1	23.3	11.9	483.9	83.0	11.6	59.5	227.3	44.3	51.6	223.2	117.0	-31.9	246.1
Sul	24.4	8.4	82.7	45.1	29.5	19.3	10.2	24.5	24.4	24.9	23.9	2161.4	277.6	93.4	33.3	752.3	320.5	460.1	522.3	121.1	-2.0	537.8
Sum	25.2	8.8	87.4	35.8	30.4	20.3	10.0	25.0	25.2	25.7	24.8	2672.8	324.2	123.9	30.9	899.8	416.3	653.2	794.5	101.5	-0.4	285.3
ATa	12.5	7.9	48.8	294.1	20.2	4.1	16.1	9.6	16.0	16.2	9.0	1024.8	122.4	44.2	28.1	344.2	165.3	168.5	337.3	146.6	-41.9	159.1
AVi	12.9	9.9	45.3	427.8	23.2	1.3	21.9	9.9	16.8	18.3	7.7	890.1	100.8	45.1	22.8	284.6	159.6	165.4	263.6	146.1	-37.4	386.0
AWD	22.4	14.5	46.1	614.5	37.1	5.8	31.3	26.6	19.5	29.5	14.5	263.9	48.9	6.2	56.1	116.5	24.3	106.1	50.7	123.2	-25.9	421.4

Appendix A2 Draftsman plot of every environmental variable for each island group, with correlation coefficients and significance. Environmental variable codes are as per Table B.1. For full resolution version please see Supplementary Information S2 of (Joyce *et al.* 2020).

Appendix B

Chapter 4 Supplementary Information

Appendix B1 List of all *Aglaia elaeagnoidea* and outgroup species (*A. chittagonga, A. edulis, A. korthalsii, A. spectabilis* and *A. leucophylla*) samples included in this study, whether they were a field or herbarium specimen, the herbarium from which they were sampled and their locality and GPS coordinates. Full details for herbarium codes are listed in Appendix B2. CYP locality stands for Cape York Peninsula.

DNA no.	Species	Collector	Collection number	Collection date	Herbarium or field	Herbarium code	Locality	Latitude	Longitude
G08343	*A. elaeagnoidea*	A. Ford	5776	15/9/2010	Herbarium	CNS	CYP, Australia	-17.74	146.16
G08344	*A. elaeagnoidea*	A. Ford	6502	14/12/2015	Herbarium	CNS	CYP, Australia	-18.18	146.17
G08345	*A. elaeagnoidea*	B.M. Waterhouse	4846	27/3/1998	Herbarium	CNS	CYP, Australia	-9.75	143.42
G08346	*A. elaeagnoidea*	B. Hyland	16029	6/5/1998	Herbarium	CNS	CYP, Australia	-17.67	146.17
G08347	*A. elaeagnoidea*	J.R. Croft & Y. Lelean	LAE68526	28/7/1976	Herbarium	CNS	New Guinea	-7.52	147.35
G08348	*A. elaeagnoidea*	D.I. Nicholson	AFO04853	5/5/1975	Herbarium	CNS	CYP, Australia	-16.50	145.48
G08349	*A. elaeagnoidea*	B. Hyland	1204RFK	20/10/1967	Herbarium	CNS	CYP, Australia	-17.83	146.08
G08351	*A. elaeagnoidea*	L.J. Webb	13773	1/7/1973	Herbarium	CNS	Kimberley, Australia	-14.53	125.82
G08352	*A. elaeagnoidea*	J.G. Tracey	15234	26/5/1981	Herbarium	CNS	Kimberley, Australia	-14.88	125.77
G08353	*A. elaeagnoidea*	J.G. Tracey	15124	25/5/1981	Herbarium	CNS	Kimberley, Australia	-14.65	125.70
G08354	*A. elaeagnoidea*	J.G. Tracey	15064	27/5/1981	Herbarium	CNS	Kimberley, Australia	-14.80	125.70
G08356	*A. elaeagnoidea*	Greger	HG753	25/11/2000	Herbarium	FHO	Bangladesh	22.11	89.63
G08357	*A. elaeagnoidea*	Greger	HG502	15/2/1998	Herbarium	FHO	Thailand	13.07	102.22
G08359	*A. elaeagnoidea*	Kenneally & Hyland	10853	26/01/1989	Herbarium	FHO	Kimberley, Australia	-14.60	125.30
G08360	*A. elaeagnoidea*	Greger	HG650	3/2/1999	Herbarium	FHO	CYP, Australia	-17.60	146.30
G08361	*A. elaeagnoidea*	Pennington	8130	18/2/1964	Herbarium	FHO	New Caledonia	-20.40	164.30
G08362	*A. elaeagnoidea*	Mabberley	2012	25/8/1984	Herbarium	FHO	New Caledonia	-20.59	164.72
G08363	*A. elaeagnoidea*	K.M. Matthew	RHT27482	11/4/1980	Herbarium	GH/A	India	12.94	74.90
G08364	*A. elaeagnoidea*	McDonald & Ismail	4976	8/2/1994	Herbarium	GH/A	Bali	-8.84	115.10

DNA no.	Species	Collector	Collection number	Collection date	Herbarium or field	Herbarium code	Locality	Latitude	Longitude
G08365	*A. elaeagnoidea*	W. Takeuchi	16203	26/4/2001	Herbarium	GH/A	New Guinea	-7.51	147.30
G08366	*A. elaeagnoidea*	W. Takeuchi	16205	26/4/2001	Herbarium	GH/A	New Guinea	-7.51	147.30
G08367	*A. elaeagnoidea*	W. Takeuchi	16208	26/4/2001	Herbarium	GH/A	New Guinea	-7.51	147.30
G08368	*A. elaeagnoidea*	W. Takeuchi	16210A	26/4/2001	Herbarium	GH/A	New Guinea	-7.51	147.30
G08438	*A. elaeagnoidea*	Wight	140	April 1835	Herbarium	NY	India	8.93	77.28
G08441	*A. elaeagnoidea*	Wight	418	-	Herbarium	NY	India	11.59	76.28
G08442	*A. elaeagnoidea*	E. M. Joyce, R. Butcher & K.R. Thiele	EMJ011	9/5/2018	Field	PERTH	Kimberley, Australia	-14.66	125.76
G08443	*A. elaeagnoidea*	E. M. Joyce, R. Butcher & K.R. Thiele	EMJ012	9/5/2018	Field	PERTH	Kimberley, Australia	-14.74	125.80
G08444	*A. elaeagnoidea*	Ambriansyah *et al.*	AA 2634	Nov 2003	Herbarium	L	Sulawesi	1.38	125.10
G08445	*A. elaeagnoidea*	B. Hyland	3725RFK	12/7/1978	Herbarium	CNS	CYP, Australia	-16.75	145.97
G08446	*A. elaeagnoidea*	B. Hyland	15784	5/5/1998	Herbarium	CNS	CYP, Australia	-17.74	146.16
G08447	*A. elaeagnoidea*	J. Le Cussan	767	31/10/1997	Herbarium	CNS	CYP, Australia	-16.93	146.00
G08448	*A. elaeagnoidea*	K. Freebody	105	20/10/1999	Herbarium	CNS	CYP, Australia	-9.52	141.57
G08449	*A. elaeagnoidea*	P.I. Forster	6432	1/3/1990	Herbarium	CNS	CYP, Australia	-10.92	142.25
G08450	*A. elaeagnoidea*	E. Cameron	2338	31/7/1975	Herbarium	CNS	CYP, Australia	-9.42	142.50
G08453	*A. elaeagnoidea*	B. Hyland	7431	12/9/1974	Herbarium	CNS	CYP, Australia	-12.17	143.08
G08455	*A. elaeagnoidea*	H. Heatwole & E. Cameron	787	29/7/1974	Herbarium	CNS	CYP, Australia	-9.94	144.03
G08456	*A. elaeagnoidea*	R. Mazlin	s.n.	5/5/1969	Herbarium	CNS	CYP, Australia	-16.33	145.50
G08457	*A. elaeagnoidea*	D.G. Fell	2869	25/2/1993	Herbarium	CNS	CYP, Australia	-15.50	145.30
G08458	*A. elaeagnoidea*	B.M. Waterhouse	2797B	26/3/1993	Herbarium	CNS	CYP, Australia	-9.28	142.18
G08459	*A. elaeagnoidea*	Fell, D.G.	2999	29/3/1993	Herbarium	CNS	CYP, Australia	-14.17	144.52

DNA no.	Species	Collector	Collection number	Collection date	Herbarium or field	Herbarium code	Locality	Latitude	Longitude
G08461	*A. elaeagnoidea*	A. Ford, P. Green. & P. Williams	4213	8/12/2003	Herbarium	CNS	CYP, Australia	-19.07	146.35
G08462	*A. elaeagnoidea*	Hyland, B.	13814	26/1/1989	Herbarium	CNS	Kimberley, Australia	-14.38	125.95
G08463	*A. elaeagnoidea*	Hyland, B.	25486RFK	10/6/1988	Herbarium	CNS	Kimberley, Australia	-14.38	125.95
G08464	*A. elaeagnoidea*	K.F. Kenneally	10175	5/6/1987	Herbarium	CNS	Kimberley, Australia	-14.62	125.25
G08465	*A. elaeagnoidea*	Volck, H.E.	AFO04304		Herbarium	CNS	CYP, Australia	-15.95	145.33
G08466	*A. elaeagnoidea*	M.R. O'Reilly	470	5/12/1989	Herbarium	CNS	CYP, Australia	-12.67	141.83
G08467	*A. elaeagnoidea*	B. Hyland	15865	5/5/1998	Herbarium	CNS	CYP, Australia	-17.75	146.16
G08468	*A. elaeagnoidea*	B. Hyland	15916	6/5/1998	Herbarium	CNS	CYP, Australia	-17.68	146.18
G08469	*A. elaeagnoidea*	Anonymous	s.n.	-	Herbarium	PERTH	Kimberley, Australia	-14.09	126.20
G08470	*A. elaeagnoidea*	J.S. Beard	7006	8/6/1974	Herbarium	PERTH	Kimberley, Australia	-14.49	125.83
G08471	*A. elaeagnoidea*	G.J. Keighery	10149	8/6/1988	Herbarium	PERTH	Kimberley, Australia	-13.90	126.08
G08472	*A. elaeagnoidea*	E.A. Chesterfield	388	28/5/1984	Herbarium	PERTH	Kimberley, Australia	-14.09	126.20
G08473	*A. elaeagnoidea*	P.G. Wilson	11401	6/7/1973	Herbarium	PERTH	Kimberley, Australia	-15.08	125.17
G08474	*A. elaeagnoidea*	P.G. Wilson	10662	12/5/1972	Herbarium	PERTH	Kimberley, Australia	-15.42	124.58
G08475	*A. elaeagnoidea*	K.F. Kenneally	5099	17/6/1976	Herbarium	PERTH	Kimberley, Australia	-14.67	125.75
G08476	*A. elaeagnoidea*	F. Lullfitz	L 6116	16/6/1968	Herbarium	PERTH	Kimberley, Australia	-13.97	126.05
G08477	*A. elaeagnoidea*	K.F. Kenneally	5234	21/6/1976	Herbarium	PERTH	Kimberley, Australia	-14.61	125.80
G08478	*A. elaeagnoidea*	K.F. Kenneally	8969	10/6/1984	Herbarium	PERTH	Kimberley, Australia	-15.03	125.35
G08479	*A. elaeagnoidea*	K.F. Kenneally	7946	24/1/1982	Herbarium	PERTH	Kimberley, Australia	-14.83	125.84
G08480	*A. elaeagnoidea*	K.F. Kenneally	9671	16/5/1986	Herbarium	PERTH	Kimberley, Australia	-15.98	124.65
G08481	*A. elaeagnoidea*	K.F. Kenneally	8147	27/4/1982	Herbarium	PERTH	Kimberley, Australia	-14.81	125.88
G08482	*A. elaeagnoidea*	K.F. Kenneally & B.P.M. Hyland	s.n.	10/6/1988	Herbarium	PERTH	Kimberley, Australia	-14.38	125.95

DNA no.	Species	Collector	Collection number	Collection date	Herbarium or field	Herbarium code	Locality	Latitude	Longitude
G08483	*A. elaeagnoidea*	K.F. Kenneally	8128	25/4/1982	Herbarium	PERTH	Kimberley, Australia	-14.59	125.76
G08484	*A. elaeagnoidea*	A.V. Milewski	102	22/5/1983	Herbarium	PERTH	Kimberley, Australia	-16.27	124.98
G08485	*A. elaeagnoidea*	K.F. Kenneally & B.P.M. Hyland	KFK10175	5/6/1987	Herbarium	PERTH	Kimberley, Australia	-14.62	125.25
G08486	*A. elaeagnoidea*	N.G. Marchant	72/379	14/6/1972	Herbarium	PERTH	Kimberley, Australia	-14.25	126.00
G08487	*A. elaeagnoidea*	T. Handasyde	TH 3494	26/5/2008	Herbarium	PERTH	Kimberley, Australia	-15.36	125.00
G08488	*A. elaeagnoidea*	T. Handasyde	TH 3488	26/5/2008	Herbarium	PERTH	Kimberley, Australia	-15.36	125.00
G08489	*A. elaeagnoidea*	T. Willing	321	5/4/1991	Herbarium	PERTH	Kimberley, Australia	-14.38	125.95
G08490	*A. elaeagnoidea*	T. Willing	386	23/5/1991	Herbarium	PERTH	Kimberley, Australia	-14.67	125.85
G08491	*A. elaeagnoidea*	A.A. Mitchell	5428	18/5/1998	Herbarium	PERTH	Kimberley, Australia	-13.94	125.63
G08492	*A. elaeagnoidea*	A.A. Mitchell & A.J. Williams	7392	25/2/2003	Herbarium	PERTH	Kimberley, Australia	-13.94	125.63
G08493	*A. elaeagnoidea*	A.A. Mitchell	7128	21/3/2002	Herbarium	PERTH	Kimberley, Australia	-14.48	125.86
G08494	*A. elaeagnoidea*	R.P.S. - BBG consultants	356	18/4/2007	Herbarium	PERTH	Kimberley, Australia	-14.52	124.98
G08495	*A. elaeagnoidea*	P.L. Comanor	1165	28/3/1968	Herbarium	GH/A	India	6.32	81.43
G08496	*A. elaeagnoidea*	D.D. Soejarto et al.	6026	22/4/1987	Herbarium	GH/A	Thailand	14.50	102.00
G08498	*A. elaeagnoidea*	Kostermans	24392	2/6/1971	Herbarium	GH/A	India	7.16	81.22
G08500	*A. elaeagnoidea*	D.D. Soejarto & F.C. Ho	6688	6/12/1989	Herbarium	GH/A	Taiwan	21.95	120.78
G08501	*A. elaeagnoidea*	C.C. Chuang	2210	3/5/1962	Herbarium	GH/A	Taiwan	21.94	120.79
G08502	*A. elaeagnoidea*	T. Tanaka	10329	9/9/1930	Herbarium	GH/A	Taiwan	21.90	120.86
G08504	*A. elaeagnoidea*	G. Murata et al.	37072	2/10/1984	Herbarium	GH/A	Thailand	14.33	101.82
G08508	*A. elaeagnoidea*	D.D. Soejarto & E. Reynoso	6302	1/8/1988	Herbarium	GH/A	Philippines	9.94	118.65
G08514	*A. elaeagnoidea*	J.T. Buchholz	1403	20/11/1947	Herbarium	GH/A	New Caledonia	-22.31	166.46

DNA no.	Species	Collector	Collection number	Collection date	Herbarium or field	Herbarium code	Locality	Latitude	Longitude
G08515	*A. elaeagnoidea*	J.H. Taylor	35	3/2/1946	Herbarium	GH/A	New Caledonia	-22.30	166.44
G08516	*A. elaeagnoidea*	M.G. Baumann-Bodenheim	5222	8/8/1950	Herbarium	GH/A	New Caledonia	-22.30	166.44
G08518	*A. elaeagnoidea*	J.F. Maxwell	01-359	3/9/2001	Herbarium	GH/A	Thailand	14.44	101.37
G08519	*A. elaeagnoidea*	O. Petrmitr	516	22/5/2002	Herbarium	GH/A	Thailand	14.44	101.37
G08521	*A. elaeagnoidea*	Madulid, Gaerlan, *et al*.	23751	21/4/1996	Herbarium	GH/A	Philippines	20.38	121.92
G08522	*A. elaeagnoidea*	Ambriansyah *et al*.	AA 2634	Nov 2003	Herbarium	GH/A	Sulawesi	1.38	125.10
G08527	*A. elaeagnoidea*	D. Mueller-Dombois & R.G. Cooray	67120614	6/12/1967	Herbarium	US	India	6.32	81.43
G08528	*A. elaeagnoidea*	D. Mueller-Dombois & R.G. Cooray	68013012A	30/1/1968	Herbarium	US	India	6.32	81.43
G08530	*A. elaeagnoidea*	S. Ripley	469	22/11/1971	Herbarium	US	India	8.58	81.24
G08532	*A. elaeagnoidea*	J.W. Nowicke & M. Jayasuriya	392	18/7/1973	Herbarium	US	India	6.34	81.47
G08536	*A. elaeagnoidea*	F.R. Fosberg	39687	18/12/1958	Herbarium	US	Java	-6.74	105.26
G08537	*A. elaeagnoidea*	H.S. McKee	3317	23/10/1955	Herbarium	US	New Caledonia	-22.30	166.44
G08538	*A. elaeagnoidea*	J.T. Buchholz	1402	20/11/1947	Herbarium	US	New Caledonia	-22.31	166.45
G08540	*A. elaeagnoidea*	R.G. Cooray	69111624R	16/11/1969	Herbarium	US	India	6.40	81.49
G08541	*A. elaeagnoidea*	Kostermans	26000	5/6/1976	Herbarium	US	India	8.94	77.28
G08542	*A. elaeagnoidea*	W. Meijer	188	28/6/1970	Herbarium	US	India	6.44	81.14
G08544	*A. elaeagnoidea*	S. Ripley	151	14/4/1969	Herbarium	US	India	7.91	80.99
G08545	*A. elaeagnoidea*	S. Ripley	259	31/1/1969	Herbarium	US	India	7.91	80.99
G08550	*A. elaeagnoidea*	W. Dittus	WD71090303	3/9/1971	Herbarium	US	India	7.95	81.01

DNA no.	Species	Collector	Collection number	Collection date	Herbarium or field	Herbarium code	Locality	Latitude	Longitude
G08551	*A. elaeagnoidea*	W. Meijer	766	8/7/1971	Herbarium	US	India	9.31	80.78
G08560	*A. elaeagnoidea*	D.J. Collins	1132	11/3/1926	Herbarium	US	Thailand	13.14	100.90
G08561	*A. elaeagnoidea*	D.J. Collins	802	Apr 1922	Herbarium	US	Thailand	13.14	100.90
G08562	*A. elaeagnoidea*	S. Ripley	232	24/9/1968	Herbarium	US	India	7.95	81.00
G08563	*A. elaeagnoidea*	P.L. Comanor	674	10/12/1967	Herbarium	US	India	6.32	81.43
G08564	*A. elaeagnoidea*	H. Streimann and A. Kairo	NGF 39426	-	Herbarium	BRI	New Guinea	-7.50	147.25
G08566	*A. elaeagnoidea*	B.M. Waterhouse	BMW 4148	16/2/1997	Herbarium	BRI	New Guinea	-9.18	141.91
G08568	*A. elaeagnoidea*	R.T.	T12	13/3/1991	Herbarium	BRI	Wallis and Futuna	-14.30	-178.11
G08569	*A. elaeagnoidea*	W. Cooper	WWC2559	1/11/2018	Field	CNS	CYP, Australia	-12.25	141.75
G08570	*A. elaeagnoidea*	W. Cooper	WWC2564	1/11/2018	Field	CNS	CYP, Australia	-12.25	141.75
G08609	*A. elaeagnoidea*	C.G.G.J. van Steenis	7573	1/4/1936	Herbarium	NY	Lesser Sunda Islands	-8.21	114.46
G08613	*A. elaeagnoidea*	J.A.R. Anderson	S16032	5/6/1962	Herbarium	GH/A	Borneo	4.40	113.99
G08614	*A. elaeagnoidea*	M. bin Samsudin	A169	15/12/1950	Herbarium	GH/A	Borneo	4.48	118.61
G08625	*A. elaeagnoidea*	A. Kostermans	1567	20/6/1949	Herbarium	GH/A	Moluccas	2.32	128.42
G08638	*A. elaeagnoidea*	Kostermans	24308	30/5/1971	Herbarium	GH/A	India	7.93	81.00
G08646	*A. elaeagnoidea*	M.T. Kao	9719	12/5/1982	Herbarium	GH/A	Taiwan	21.92	120.73
G08648	*A. elaeagnoidea*	A. Boonkongchart	206	12/5/2003	Herbarium	GH/A	Thailand	14.44	101.37
G08651	*A. elaeagnoidea*	A.W. Herre	1240	6/8/1931	Herbarium	GH/A	Philippines	4.73	119.41
G08652	*A. elaeagnoidea*	M. van Balgooy & J. Mamesah	6348	17/4/1993	Herbarium	GH/A	New Guinea	-6.74	134.39
G08653	*A. elaeagnoidea*	R. Kanehira & S. Hatusima	13317	31/3/1940	Herbarium	GH/A	New Guinea	-1.84	134.18
G08657	*A. elaeagnoidea*	Madulid, Gaerlan, *et al*.	23848	27/4/1996	Herbarium	GH/A	Philippines	20.77	121.83
G08662	*A. elaeagnoidea*	J.P. Wilson	987	Sep 1929	Herbarium	US	Vanuatu	-20.16	169.88
G08665	*A. elaeagnoidea*	H. Keng	s.n.	31/10/1950	Herbarium	US	Taiwan	21.98	120.78
G08723	*A. elaeagnoidea*	I.D. Cowie	IDC11230	19/10/2006	Herbarium	DNA	Timor	-8.50	127.21

DNA no.	Species	Collector	Collection number	Collection date	Herbarium or field	Herbarium code	Locality	Latitude	Longitude
G08724	*A. elaeagnoidea*	I.D. Cowie	IDC13853	6/5/2015	Herbarium	DNA	Timor	-8.20	125.59
G08726	*A. elaeagnoidea*	I.D. Cowie	IDC14565	16/5/2015	Herbarium	DNA	Timor	-8.20	125.59
G08727	*A. elaeagnoidea*	I.D. Cowie	IDC14566	17/5/2015	Herbarium	DNA	Timor	-8.20	125.59
G08523	*A. chittagonga*	A.F.G. Kerr	18931	11/4/1930	Herbarium	GH/A	Thailand		
G08525	*A. korthalsii*	E.L. Bynum	7023	23/10/1990	Herbarium	GH/A	Sulawesi		
G08555	*A. edulis*	S.K. Lau	58	10/6/1932	Herbarium	US	Hainan		
G08556	*A. edulis*	N.K. Chun.& C.L. Tso	44404	Dec 1932-33	Herbarium	US	Hainan		
G08558	*A. leucophylla*	J.H. Beaman	10643	9/7/1984	Herbarium	US	Borneo		
G08721	*A. spectabilis*	W. Cooper & C.M. Pannell	WWC2351	8/10/2016	Field	CNS	Australia		
G08722	*A. spectabilis*	W. Cooper & C.M. Pannell	WWC2356	8/10/2016	Field	CNS	Australia		

Appendix B2 List of herbaria from which *Aglaia* specimens were sampled

Herbarium Code	**Herbarium Name**	**Institution**	**Country**
A	Arnold Arboretum Herbarium	Harvard University	USA
BO	Herbarium Bogoriense	Research Centre for Biology, LIPI	Indonesia
BRI	Queensland Herbarium	Queensland Government	Australia
CNS	Australian Tropical Herbarium	James Cook University, Queensland Government and CSIRO	Australia
DNA	Northern Territory Herbarium	Department of Environment and Natural Resources	Australia
FHO	Daubeny Herbarium	Oxford University	UK
GH	Gray Herbarium	Harvard University	USA
K	Kew Herbarium	Royal Botanic Gardens, Kew	UK
L	Nationaal Herbarium Nederland	Naturalis Biodiversity Center	The Netherlands
MICH	University of Michigan Herbarium	University of Michigan	USA
NY	William and Lynda Steere Herbarium	The New York Botanic Garden	USA
PERTH	Western Australian Herbarium	Department of Biodiversity, Conservation and Attractions	Australia
SING	Singapore Herbarium	Singapore Botanic Gardens	Singapore
US	United States National Herbarium	Smithsonian Institute	USA

Appendix B3 List of 344 presence data points of eastern *A. elaeagnoidea* used to train the MaxEnt ENM. Data were high quality herbarium records downloaded from GBIF, as well as samples included for sequencing in this study.

Species	**Latitude**	**Longitude**
Aglaia elaeagnoidea	-6.75	105.2
Aglaia elaeagnoidea	-15.923604	145.375845
Aglaia elaeagnoidea	-6.733333	105.25
Aglaia elaeagnoidea	3.8	113.8
Aglaia elaeagnoidea	-10.840302	142.409202
Aglaia elaeagnoidea	-22.2667	166.4497
Aglaia elaeagnoidea	-22.30528	166.43833
Aglaia elaeagnoidea	-22.166667	166.383333
Aglaia elaeagnoidea	-20.333333	164.5
Aglaia elaeagnoidea	-10.845	142.370833
Aglaia elaeagnoidea	-20.273575	148.842482
Aglaia elaeagnoidea	-20.248576	148.750817
Aglaia elaeagnoidea	-20.49167	164.30472
Aglaia elaeagnoidea	-17.8333	146.0833
Aglaia elaeagnoidea	-17.84026	146.092508
Aglaia elaeagnoidea	21.965278	120.804444
Aglaia elaeagnoidea	-20.833333	167.216667
Aglaia elaeagnoidea	-13.968333	126.045
Aglaia elaeagnoidea	21.9025	120.845833
Aglaia elaeagnoidea	-20.70389	167.17056
Aglaia elaeagnoidea	-16.3333	145.5
Aglaia elaeagnoidea	-16.3	145.5
Aglaia elaeagnoidea	-15.95	145.3333
Aglaia elaeagnoidea	-15.808333	145.325
Aglaia elaeagnoidea	-15.921389	145.352778
Aglaia elaeagnoidea	-7.416667	147.166667
Aglaia elaeagnoidea	-22.25111	167.02944
Aglaia elaeagnoidea	-9.756975	143.425857
Aglaia elaeagnoidea	-6.016389	106.193056
Aglaia elaeagnoidea	-22.25	166.483333
Aglaia elaeagnoidea	-6.7333	105.25
Aglaia elaeagnoidea	-15.416667	124.583333
Aglaia elaeagnoidea	-14.25	126
Aglaia elaeagnoidea	-16.5	145.4667
Aglaia elaeagnoidea	-15.116667	145.283333

Species	Latitude	Longitude
Aglaia elaeagnoidea	-15.016667	145.45
Aglaia elaeagnoidea	-15.083333	145.383333
Aglaia elaeagnoidea	-14.5333	125.8167
Aglaia elaeagnoidea	-15.083333	125.166667
Aglaia elaeagnoidea	-15.123608	145.29251
Aglaia elaeagnoidea	-15.632222	145.263889
Aglaia elaeagnoidea	-14.740276	145.192511
Aglaia elaeagnoidea	-15.023608	145.442508
Aglaia elaeagnoidea	-15.093889	145.379444
Aglaia elaeagnoidea	-15.02	145.45
Aglaia elaeagnoidea	-14.73	145.18
Aglaia elaeagnoidea	-15.12	145.28
Aglaia elaeagnoidea	-15.08	145.38
Aglaia elaeagnoidea	-12.166667	143.083333
Aglaia elaeagnoidea	-14.581949	125.884591
Aglaia elaeagnoidea	-14.781947	125.834586
Aglaia elaeagnoidea	-14.494722	125.829722
Aglaia elaeagnoidea	-10.2081	142.8244
Aglaia elaeagnoidea	-9.9433	144.0261
Aglaia elaeagnoidea	-14.611389	125.801389
Aglaia elaeagnoidea	-14.6333	125.85
Aglaia elaeagnoidea	-14.8011	125.8253
Aglaia elaeagnoidea	-12.1667	143.0833
Aglaia elaeagnoidea	-16.723599	145.64251
Aglaia elaeagnoidea	-12.173627	143.09253
Aglaia elaeagnoidea	-20.11583	164.21139
Aglaia elaeagnoidea	-19.666667	163.65
Aglaia elaeagnoidea	-16.5	145.4833
Aglaia elaeagnoidea	-19.69333	163.66417
Aglaia elaeagnoidea	-8.833333	115.166667
Aglaia elaeagnoidea	-7.75	147.583333
Aglaia elaeagnoidea	-8.333333	114.516667
Aglaia elaeagnoidea	-20.666667	164.933333
Aglaia elaeagnoidea	-7.516667	147.35
Aglaia elaeagnoidea	-14.666667	125.75
Aglaia elaeagnoidea	-14.65	125.8
Aglaia elaeagnoidea	-7.5167	147.35
Aglaia elaeagnoidea	-18.556924	146.192509
Aglaia elaeagnoidea	-8.33	114.52

Species	Latitude	Longitude
Aglaia elaeagnoidea	-7.51667	147.35
Aglaia elaeagnoidea	-12.4167	143.2667
Aglaia elaeagnoidea	-12.5	143.2667
Aglaia elaeagnoidea	-12.423625	143.275861
Aglaia elaeagnoidea	-12.506958	143.275862
Aglaia elaeagnoidea	-16.7594	145.9744
Aglaia elaeagnoidea	-14.6667	145.45
Aglaia elaeagnoidea	-11.9833	141.8667
Aglaia elaeagnoidea	-11.990296	141.875876
Aglaia elaeagnoidea	-24.248551	151.917457
Aglaia elaeagnoidea	-19.140253	146.85917
Aglaia elaeagnoidea	-14.8833	125.7667
Aglaia elaeagnoidea	-10.9167	142.25
Aglaia elaeagnoidea	-14.65	125.7
Aglaia elaeagnoidea	-14.8	125.7
Aglaia elaeagnoidea	-14.5833	125.7167
Aglaia elaeagnoidea	-14.585	125.755
Aglaia elaeagnoidea	-12.666667	143.4
Aglaia elaeagnoidea	-14.831944	125.844444
Aglaia elaeagnoidea	-10.7833	142.5833
Aglaia elaeagnoidea	-12.6667	143.4
Aglaia elaeagnoidea	-14.808333	125.883333
Aglaia elaeagnoidea	-12.673624	143.409194
Aglaia elaeagnoidea	-18.9202	169.13359
Aglaia elaeagnoidea	-18.88753	169.03395
Aglaia elaeagnoidea	-20.533333	164.316667
Aglaia elaeagnoidea	-16.2667	124.9833
Aglaia elaeagnoidea	-16.266667	124.983333
Aglaia elaeagnoidea	-14.081943	126.18458
Aglaia elaeagnoidea	-14.0875	126.1958
Aglaia elaeagnoidea	-14.0833	126.2
Aglaia elaeagnoidea	-14.086111	126.197222
Aglaia elaeagnoidea	-14.0861	126.1972
Aglaia elaeagnoidea	-15.033333	125.35
Aglaia elaeagnoidea	-20.4667	148.7333
Aglaia elaeagnoidea	-20.10691	148.725816
Aglaia elaeagnoidea	-20.547222	149.113056
Aglaia elaeagnoidea	-20.441667	149.041667
Aglaia elaeagnoidea	-20.162222	149.032222

Species	Latitude	Longitude
Aglaia elaeagnoidea	-20.473575	148.742484
Aglaia elaeagnoidea	-20.273575	148.942481
Aglaia elaeagnoidea	-18.92592	169.11205
Aglaia elaeagnoidea	-15.983333	124.65
Aglaia elaeagnoidea	-20.881978	149.617539
Aglaia elaeagnoidea	-15.9833	124.65
Aglaia elaeagnoidea	-20.873571	149.609141
Aglaia elaeagnoidea	-20.790239	149.292478
Aglaia elaeagnoidea	-20.486667	149.076667
Aglaia elaeagnoidea	-14.6167	125.25
Aglaia elaeagnoidea	-14.6208	125.2542
Aglaia elaeagnoidea	-14.5833	125.1833
Aglaia elaeagnoidea	-14.620833	125.254167
Aglaia elaeagnoidea	9.933333	118.666667
Aglaia elaeagnoidea	-14.3833	125.95
Aglaia elaeagnoidea	-15.6	145.3167
Aglaia elaeagnoidea	-13.9	126.083333
Aglaia elaeagnoidea	-18.1	146.3
Aglaia elaeagnoidea	-14.35	125.95
Aglaia elaeagnoidea	-14.383333	125.95
Aglaia elaeagnoidea	-24.156885	151.892457
Aglaia elaeagnoidea	-15.606939	145.325844
Aglaia elaeagnoidea	-18.106925	146.309173
Aglaia elaeagnoidea	-23.161389	151.074722
Aglaia elaeagnoidea	-14.67361	145.475841
Aglaia elaeagnoidea	-14.692222	145.446111
Aglaia elaeagnoidea	-14.381946	125.951252
Aglaia elaeagnoidea	-12.6667	141.8333
Aglaia elaeagnoidea	-12.661667	141.835278
Aglaia elaeagnoidea	-12.467427	143.266404
Aglaia elaeagnoidea	-21.673566	150.275802
Aglaia elaeagnoidea	-21.756898	150.342468
Aglaia elaeagnoidea	-20.940238	149.442477
Aglaia elaeagnoidea	-20.923572	149.042482
Aglaia elaeagnoidea	-14.007639	167.588505
Aglaia elaeagnoidea	9.833333	118.633333
Aglaia elaeagnoidea	-19.266667	147.033333
Aglaia elaeagnoidea	-10.915233	142.251086
Aglaia elaeagnoidea	-20.255833	148.813889

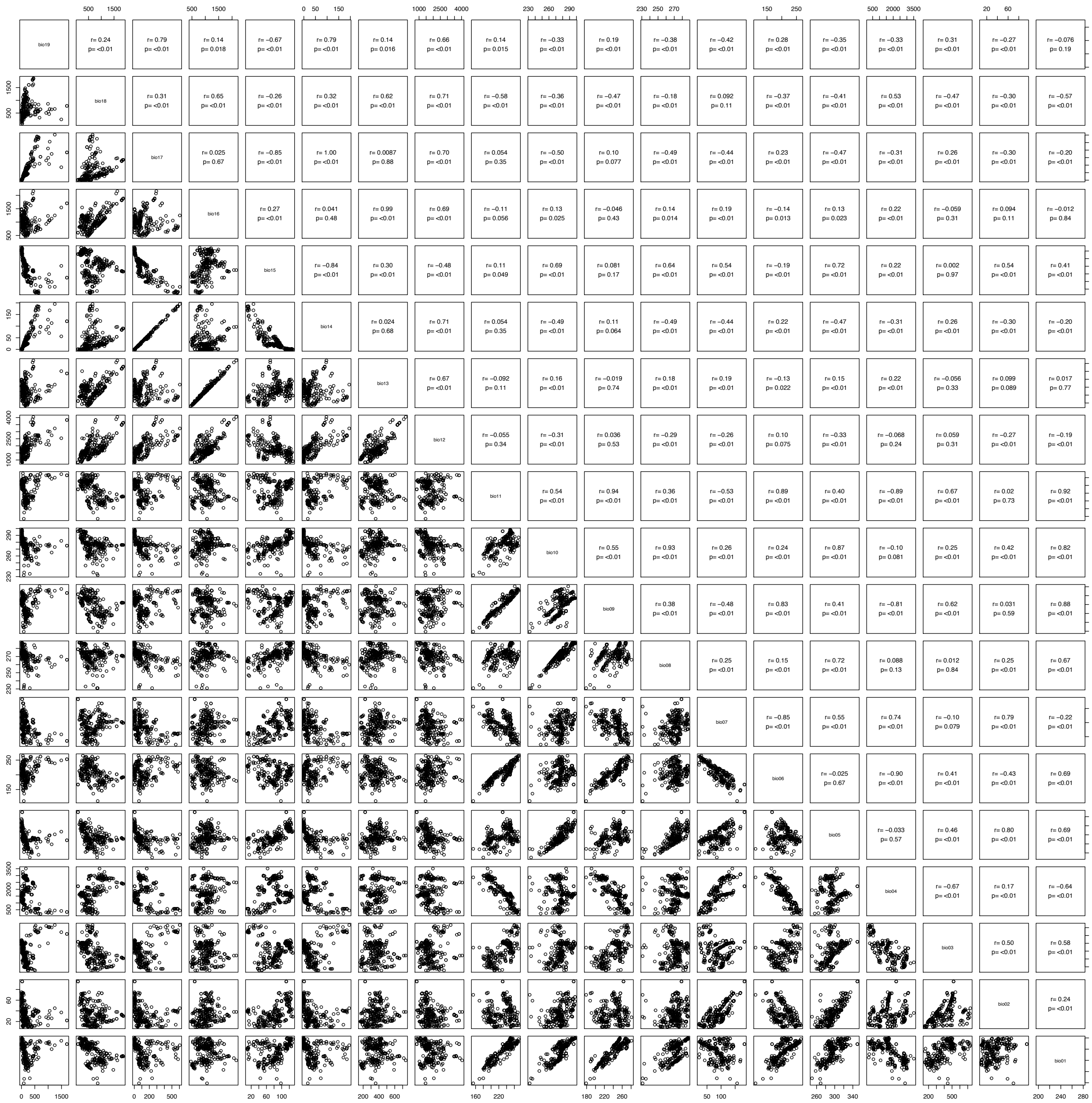
Species	Latitude	Longitude
Aglaia elaeagnoidea	-10.911691	142.245593
Aglaia elaeagnoidea	-19.273585	147.042501
Aglaia elaeagnoidea	-14.666667	125.85
Aglaia elaeagnoidea	-21.063278	149.09751
Aglaia elaeagnoidea	-13.883333	143.516667
Aglaia elaeagnoidea	-13.8833	143.5167
Aglaia elaeagnoidea	-21.315311	149.684206
Aglaia elaeagnoidea	-13.8167	143.45
Aglaia elaeagnoidea	-20.873573	148.942483
Aglaia elaeagnoidea	-21.323569	149.692475
Aglaia elaeagnoidea	-8.433333	112.7
Aglaia elaeagnoidea	-9.281946	142.18417
Aglaia elaeagnoidea	-14.1667	144.5167
Aglaia elaeagnoidea	-15.498606	145.252245
Aglaia elaeagnoidea	-11.648929	142.85519
Aglaia elaeagnoidea	-9.290312	142.192537
Aglaia elaeagnoidea	-14.283115	144.587637
Aglaia elaeagnoidea	-14.172781	144.522517
Aglaia elaeagnoidea	-21.123571	149.209147
Aglaia elaeagnoidea	-20.257581	148.949615
Aglaia elaeagnoidea	-15.498606	145.252234
Aglaia elaeagnoidea	-19.2557	169.59978
Aglaia elaeagnoidea	-8.833333	115.083333
Aglaia elaeagnoidea	-9.3833	142.65
Aglaia elaeagnoidea	-9.7333	143.4333
Aglaia elaeagnoidea	-9.7519	143.4042
Aglaia elaeagnoidea	-12.331852	142.534389
Aglaia elaeagnoidea	-12.34327	142.540905
Aglaia elaeagnoidea	-20.923573	149.009149
Aglaia elaeagnoidea	-18.490257	146.309174
Aglaia elaeagnoidea	-12.0333	143.3
Aglaia elaeagnoidea	-11.168056	143.015833
Aglaia elaeagnoidea	-20.898646	149.400875
Aglaia elaeagnoidea	-12.238627	143.081419
Aglaia elaeagnoidea	-20.906905	149.409144
Aglaia elaeagnoidea	-9.1833	141.9011
Aglaia elaeagnoidea	-16.9333	146
Aglaia elaeagnoidea	-16.940264	146.009173
Aglaia elaeagnoidea	-13.936111	125.632778

Species	Latitude	Longitude
Aglaia elaeagnoidea	-17.6761	146.1797
Aglaia elaeagnoidea	-9.7522	143.4161
Aglaia elaeagnoidea	-17.6744	146.1689
Aglaia elaeagnoidea	-17.7378	146.1597
Aglaia elaeagnoidea	-17.7453	146.1606
Aglaia elaeagnoidea	-9.611667	143.302222
Aglaia elaeagnoidea	-9.752222	143.416111
Aglaia elaeagnoidea	-16.263172	168.020543
Aglaia elaeagnoidea	-16.91667	145.76667
Aglaia elaeagnoidea	-13.34029	141.775879
Aglaia elaeagnoidea	-13.87362	141.909212
Aglaia elaeagnoidea	-15.990251	145.433201
Aglaia elaeagnoidea	-15.253814	144.996626
Aglaia elaeagnoidea	-7.483333	147.283333
Aglaia elaeagnoidea	-14.478056	125.856944
Aglaia elaeagnoidea	-14.4781	125.8569
Aglaia elaeagnoidea	-7.4833	147.2833
Aglaia elaeagnoidea	-7.48	147.28
Aglaia elaeagnoidea	-20.32222	164.39444
Aglaia elaeagnoidea	1.383333	125.1
Aglaia elaeagnoidea	-13.9364	125.6322
Aglaia elaeagnoidea	-13.936389	125.632167
Aglaia elaeagnoidea	-19.0667	146.35
Aglaia elaeagnoidea	-19.077119	146.353044
Aglaia elaeagnoidea	-24.149941	151.885235
Aglaia elaeagnoidea	-8.4959	127.21256
Aglaia elaeagnoidea	-14.520183	124.982343
Aglaia elaeagnoidea	-15.3577	124.99675
Aglaia elaeagnoidea	-9.7517	143.3775
Aglaia elaeagnoidea	-9.751667	143.3775
Aglaia elaeagnoidea	-17.1967	145.4544
Aglaia elaeagnoidea	-17.7383	146.1572
Aglaia elaeagnoidea	-17.738333	146.157222
Aglaia elaeagnoidea	-9.271121	142.138542
Aglaia elaeagnoidea	-9.259253	142.211262
Aglaia elaeagnoidea	-9.091907	124.054282
Aglaia elaeagnoidea	-10.254722	142.831111
Aglaia elaeagnoidea	-10.254801	142.831034
Aglaia elaeagnoidea	-8.94578	126.46695

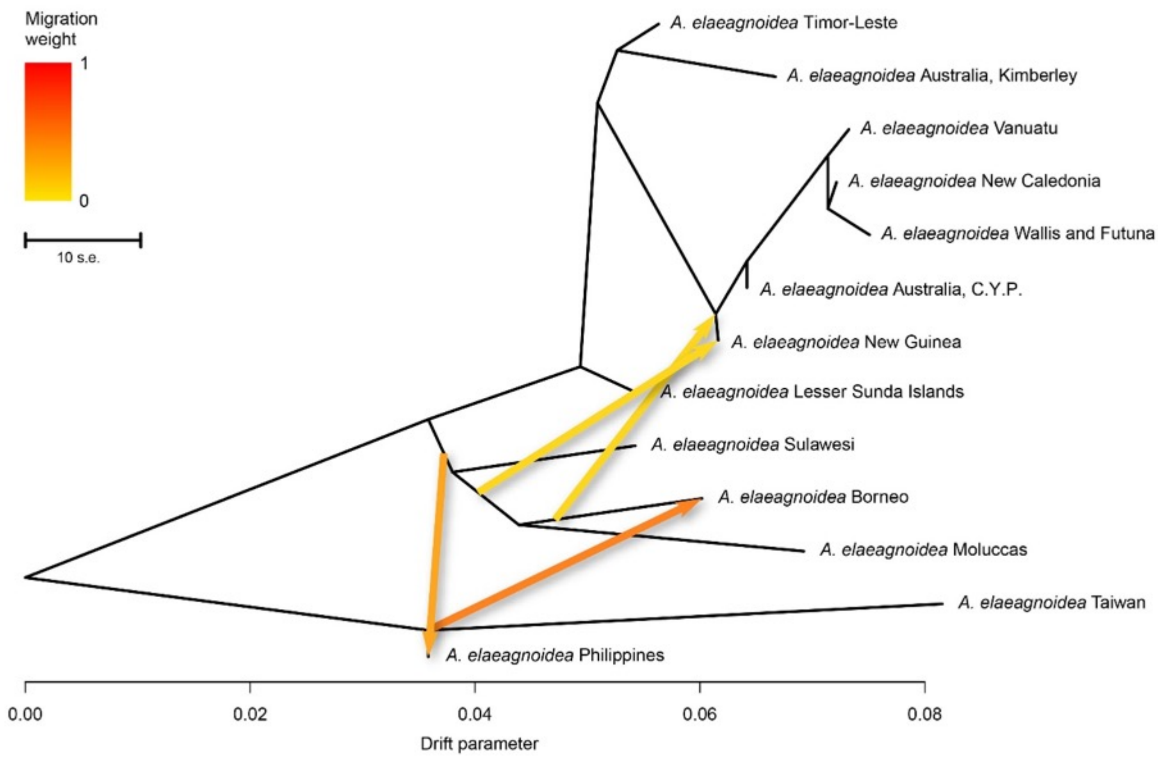
Species	Latitude	Longitude
Aglaia elaeagnoidea	-8.19973	125.59258
Aglaia elaeagnoidea	-18.1778	146.1706
Aglaia elaeagnoidea	-8.2625	125.5763
Aglaia elaeagnoidea	-15.651083	145.305361
Aglaia elaeagnoidea	-14.013533	126.18765
Aglaia elaeagnoidea	-6.583333	110.65
Aglaia elaeagnoidea	-1.684356	124.868546
Aglaia elaeagnoidea	-5.883333	105.516667
Aglaia elaeagnoidea	-2.833333	107.916667
Aglaia elaeagnoidea	-6.031667	106.202778
Aglaia elaeagnoidea	-6.118056	106.861389
Aglaia elaeagnoidea	13.833333	121.983333
Aglaia elaeagnoidea	-7.5	147.25
Aglaia elaeagnoidea	-5.349404	132.496901
Aglaia elaeagnoidea	-5.95	105.85
Aglaia elaeagnoidea	7.066667	122.1
Aglaia elaeagnoidea	-1.717678	124.360986
Aglaia elaeagnoidea	-1.85	106.133333
Aglaia elaeagnoidea	-22.266667	166.45
Aglaia elaeagnoidea	-18.0833	146
Aglaia elaeagnoidea	-15.45	145.2167
Aglaia elaeagnoidea	-18.15	146.2667
Aglaia elaeagnoidea	-19.5	146.9833
Aglaia elaeagnoidea	-14.0875	126.195833
Aglaia elaeagnoidea	-21.1167	149.2167
Aglaia elaeagnoidea	-11.9667	143.2167
Aglaia elaeagnoidea	-21.755556	150.331944
Aglaia elaeagnoidea	-20.415242	148.584153
Aglaia elaeagnoidea	-24.1503	151.886
Aglaia elaeagnoidea	-24.15	151.89
Aglaia elaeagnoidea	-7.52	147.35
Aglaia elaeagnoidea	-19.72139	163.66028
Aglaia elaeagnoidea	22.0975	120.860278
Aglaia elaeagnoidea	22.75	121.15
Aglaia elaeagnoidea	22.45	120.45
Aglaia elaeagnoidea	21.915278	120.850556
Aglaia elaeagnoidea	22.008333	120.866667
Aglaia elaeagnoidea	22.0375	120.786111
Aglaia elaeagnoidea	22.0225	120.831389

Species	**Latitude**	**Longitude**
Aglaia elaeagnoidea	21.969444	120.8
Aglaia elaeagnoidea	-12.248781	141.745394
Aglaia elaeagnoidea	-17.7383	146.1572
Aglaia elaeagnoidea	-17.6744	146.1689
Aglaia elaeagnoidea	-17.6	146.3
Aglaia elaeagnoidea	-16.75	145.9667
Aglaia elaeagnoidea	-9.4167	142.5
Aglaia elaeagnoidea	-9.9433	144.0292
Aglaia elaeagnoidea	-15.5	145.3
Aglaia elaeagnoidea	-9.2819	142.1842
Aglaia elaeagnoidea	-17.7378	146.1597
Aglaia elaeagnoidea	-16.9333	146
Aglaia elaeagnoidea	-9.5181	141.5708
Aglaia elaeagnoidea	-14.1667	144.5167
Aglaia elaeagnoidea	-19.0667	146.35
Aglaia elaeagnoidea	-15.95	145.3333
Aglaia elaeagnoidea	-17.7453	146.1606
Aglaia elaeagnoidea	-17.6833	146.1833
Aglaia elaeagnoidea	-14.38333333	125.95
Aglaia elaeagnoidea	-15.98333333	124.65
Aglaia elaeagnoidea	-15.41666667	124.5833333
Aglaia elaeagnoidea	-14.80833333	125.8833333
Aglaia elaeagnoidea	-15.08333333	125.1666667
Aglaia elaeagnoidea	-14.52018285	124.9823432
Aglaia elaeagnoidea	-14.83194444	125.8444444
Aglaia elaeagnoidea	-13.9	126.0833333
Aglaia elaeagnoidea	-13.93611111	125.6327778
Aglaia elaeagnoidea	-14.47805556	125.8569444
Aglaia elaeagnoidea	-14.66666667	125.85
Aglaia elaeagnoidea	-14.585	125.755
Aglaia elaeagnoidea	-14.0875	126.1958333
Aglaia elaeagnoidea	-16.26666667	124.9833333
Aglaia elaeagnoidea	-13.96833333	126.045
Aglaia elaeagnoidea	-14.49472222	125.8297222
Aglaia elaeagnoidea	-13.93638889	125.6321667
Aglaia elaeagnoidea	-14.62083333	125.2541667
Aglaia elaeagnoidea	-15.3577	124.99675
Aglaia elaeagnoidea	-14.66666667	125.75
Aglaia elaeagnoidea	-15.03333333	125.35

Species	**Latitude**	**Longitude**
Aglaia elaeagnoidea	-14.08611111	126.1972222
Aglaia elaeagnoidea	-14.61138889	125.8013889
Aglaia elaeagnoidea	-14.5333	125.8167
Aglaia elaeagnoidea	-14.6	125.3
Aglaia elaeagnoidea	-14.6208	125.2542
Aglaia elaeagnoidea	-14.6643	125.76241
Aglaia elaeagnoidea	-14.74231505	125.79743
Aglaia elaeagnoidea	4.398238881	113.9917583
Aglaia elaeagnoidea	4.479393648	118.6115472
Aglaia elaeagnoidea	-8.838788	115.095923
Aglaia elaeagnoidea	2.315786325	128.4248716
Aglaia elaeagnoidea	-22.301169	166.437271
Aglaia elaeagnoidea	-22.298012	166.443729
Aglaia elaeagnoidea	-22.30766	166.454931
Aglaia elaeagnoidea	-20.4	164.3
Aglaia elaeagnoidea	-20.588902	164.722491
Aglaia elaeagnoidea	-22.31073	166.456369
Aglaia elaeagnoidea	-1.843055	134.182282
Aglaia elaeagnoidea	-6.738642	134.392355
Aglaia elaeagnoidea	-9.183333	141.908333
Aglaia elaeagnoidea	-7.513192	147.298706
Aglaia elaeagnoidea	-7.5167	147.35
Aglaia elaeagnoidea	1.383470095	125.0999162
Aglaia elaeagnoidea	20.766667	121.833333
Aglaia elaeagnoidea	20.381667	121.92
Aglaia elaeagnoidea	4.730262	119.412448
Aglaia elaeagnoidea	9.935567	118.64636
Aglaia elaeagnoidea	21.980142	120.778407
Aglaia elaeagnoidea	21.897205	120.859019
Aglaia elaeagnoidea	21.944774	120.785456
Aglaia elaeagnoidea	21.948241	120.779878
Aglaia elaeagnoidea	21.919962	120.734773
Aglaia elaeagnoidea	-8.199729	125.59258
Aglaia elaeagnoidea	-8.4959	127.21256
Aglaia elaeagnoidea	-20.159939	169.876527
Aglaia elaeagnoidea	-14.304989	-178.108721



Appendix B4 Draftsman plot of the value of every environmental variable for each sample of eastern *A. elaeagnoidea*, with correlation coefficients and significance. bio01 = Annual Mean Temperature; bio02 = Mean Diurnal Range; bio03 = Isothermality; bio04 = Temperature Seasonality; bio05 = Max Temperature of Warmest Month; bio06 = Min Temperature of Coldest Month; bio07 = Temperature Annual Range; bio08 = Mean Temperature of Wettest Quarter; bio09 = Mean Temperature of Driest Quarter; bio10 = Mean Temperature of Warmest Quarter; bio11 = Mean Temperature of Coldest Quarter; bio12 = Annual Precipitation; bio13 = Precipitation of Wettest Month; bio14 = Precipitation of Driest Month; bio15 = Precipitation Seasonality; bio16 = Precipitation of Wettest Quarter; bio17 = Precipitation of Driest Quarter; bio18 = Precipitation of Warmest Quarter; bio19 = Precipitation of Coldest Quarter.



Appendix B5 Original tree output from TreeMix analysis. Drift parameter is represented along the x axis, and coloured arrows showing migration events with colour representative of migration weight.

Appendix C

Chapter 5 Supplementary Information

Appendix C1 Output of HybPhaser summarising sequence length (bp), coverage (%) before and after HybPhaser cleaning, number of paralogs detected, the number of loci recovered, percentage heterozygosity and allele divergence for each sample in the final Angiosperms353 Sapindales dataset. Sample name includes first four letters of the family, the species, and accession number separated by underscores.

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
ANAC_Abrahamia_ditimena_IDS10573	244860	79.6	237939	80.3	30	331	77.64	0.84
ANAC_Actinocheita_potentillifolia_IDS07484	255399	83	248220	83.8	23	336	59.23	0.50
ANAC_Allospondias_lakonensis_IDS10575	244683	79.5	237564	80.2	21	335	62.39	0.45
ANAC_Amphipterygium_adstringens_IDS10577	244269	79.4	237600	80.2	21	332	66.27	0.44
ANAC_Anacardium_occidentale_IDS10459	247788	80.6	240096	81.1	7	331	66.47	1.79
ANAC_Apterokarpos_gardneri_IDS10583	232383	75.5	227049	76.7	18	331	35.05	0.33
ANAC_Astronium_sp_IDS10713	248322	80.7	241845	81.7	22	334	66.77	0.51
ANAC_Baronia_taratana_IDS10589	245352	79.8	237978	80.4	21	334	46.11	0.40
ANAC_Blepharocarya_involucrigera_IDS10591	233163	75.8	226491	76.5	30	332	63.25	0.62
ANAC_Bonetiella_anomala_IDS10593	251682	81.8	244761	82.6	19	332	46.69	0.40
ANAC_Bouea_oppositifolia_IDS10465	114918	37.4	110715	37.4	3	276	10.87	0.22
ANAC_Buchanania_obovata_IDS10431	226968	73.8	221346	74.7	16	330	53.33	0.30
ANAC_Campnosperma_zeylanicum_IDS6465	255588	83.1	248229	83.8	21	334	39.52	0.32
ANAC_Campylopetalum_siamense_IDS10597	217509	70.7	211305	71.3	15	318	30.82	0.19
ANAC_Cardenasiodendron_brachypterum_IDS10599	247470	80.5	241299	81.5	27	332	70.78	0.51
ANAC_Choerospondias_axillaris_IDS10601	256356	83.3	249669	84.3	18	335	58.81	0.30
ANAC_Cotinus_coggygria_SRR8298330	273990	89.1	263739	89	13	328	54.57	0.35
ANAC_Cotinus_obovatus_IDS10797	256815	83.5	248958	84.1	18	333	65.77	0.45
ANAC_Cyrtocarpa_caatingae_IDS08429	240417	78.2	233733	78.9	20	334	60.18	0.30
ANAC_Cyrtocarpa_procera_IDS10605	241353	78.5	235035	79.4	14	334	38.32	0.20
ANAC_Dobinea_vulgaris_IDS10607	166419	54.1	161529	54.5	4	309	13.27	0.16
ANAC_Dracontomelon_duperreanum_IDS10609	248136	80.7	239925	81	22	334	55.69	0.42
ANAC_Drimycarpus_racemosus_IDS10611	211857	68.9	204714	69.1	0	324	74.38	3.01
ANAC_Euroschinus_papuanus_IDS7785	153414	49.9	148917	50.3	16	310	45.81	0.41
ANAC_Fegimanra_africana_IDS10617	190545	61.9	185085	62.5	0	323	34.98	1.53
ANAC_Gluta_renghas_IDS6466	245817	79.9	237936	80.3	0	330	49.70	1.60
ANAC_Haplorhus_peruviana_IDS10621	254700	82.8	246645	83.3	27	335	51.34	0.45
ANAC_Harpephyllum_caffrum_IDS10623	244596	79.5	238947	80.7	19	333	45.35	0.18
ANAC_Heeria_argentea_IDS10841	247329	80.4	240264	81.1	21	333	67.87	0.57
ANAC_Laurophyllus_capensis_IDS10945	229116	74.5	223008	75.3	16	336	38.99	0.44
ANAC_Loxopterygium_grisebachii_IDS10857	167466	54.4	161619	54.6	10	328	21.65	0.24
ANAC_Loxostylis_alata_IDS10629	246939	80.3	240393	81.2	24	333	60.06	0.39

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
ANAC_Mangifera_indica_SRR1562187	249204	81	240351	81.2	36	312	64.74	1.28
ANAC_Mangifera_odorata_IDS10469	246549	80.2	239202	80.8	33	331	94.26	2.80
ANAC_Mauria_simplicifolia_IDS10633	255057	82.9	248115	83.8	23	332	55.12	0.44
ANAC_Melanochyla_caesia_IDS10635	224352	72.9	217647	73.5	0	322	86.02	3.34
ANAC_Metopium_brownei_IDS10639	165057	53.7	160806	54.3	15	197	63.96	0.44
ANAC_Micronychia_macrophylla_IDS10641	244587	79.5	237870	80.3	19	332	43.07	0.39
ANAC_Mosquitoxylum_jamaicense_IDS10643	243198	79.1	236865	80	17	333	37.24	0.29
ANAC_Myracrodruon_urundeuva_IDS10645	250002	81.3	243264	82.1	18	334	73.05	0.51
ANAC_Nothopegia_beddomei_IDS10891	205173	66.7	199023	67.2	0	325	79.69	2.73
ANAC_Ochoterenaea_colombiana_IDS10647	254280	82.7	247407	83.5	22	335	39.70	0.34
ANAC_Operculicarya_decaryi_IDS10649	246141	80	239025	80.7	13	331	81.27	0.72
ANAC_Orthopterygium_huaucui_IDS10651	211533	68.8	205473	69.4	13	329	25.84	0.21
ANAC_Ozoroa_insignis_IDS10653	238077	77.4	231840	78.3	24	331	47.13	0.45
ANAC_Pachycormus_discolor_IDS10787	232680	75.6	226455	76.5	22	331	67.98	0.47
ANAC_Parishia_insignis_IDS10655	217287	70.6	210687	71.1	3	326	79.75	4.12
ANAC_Pegia_nitida_IDS10657	186699	60.7	181218	61.2	18	310	40.32	0.34
ANAC_Pistacia_chinensis_SRR8661763	283485	92.2	272730	92.1	17	335	60.00	0.43
ANAC_Pistacia_lentiscus_SRR5043662	275424	89.5	264912	89.4	10	324	48.77	0.38
ANAC_Pleiogynium_timorense_IDS6468	254475	82.7	248742	84	16	334	52.69	0.32
ANAC_Poupartia_borbonica_IDS10803	257022	83.6	250974	84.7	13	335	72.24	0.35
ANAC_Poupartia_chapelieri_IDS11873	248307	80.7	242331	81.8	16	334	58.68	0.32
ANAC_Poupartia_minor_IDS10665	241203	78.4	235557	79.5	13	331	63.75	0.40
ANAC_Poupartiopsis_spondiocarpus_IDS10667	237216	77.1	231150	78	15	332	34.34	0.17
ANAC_Protorhus_longifolia_IDS10669	249906	81.2	242808	82	24	335	57.91	0.39
ANAC_Pseudosmodingium_andrieuxii_IDS10675	226239	73.6	220794	74.5	26	333	49.55	0.42
ANAC_Pseudospondias_microcarpa_IDS10673	238917	77.7	233169	78.7	19	331	67.07	0.52
ANAC_Rhodosphaera_rhodanthema_IDS10453	225912	73.4	220002	74.3	15	332	31.93	0.25
ANAC_Rhus_coriaria_IDS10679	213156	69.3	207246	70	14	333	34.53	0.27
ANAC_Rhus_perrieri_IDS10681	249957	81.3	242985	82	24	331	78.25	0.74
ANAC_Rhus_taitensis_IDS10637	255840	83.2	248178	83.8	13	331	53.78	0.34
ANAC_Rhus_thouarsii_IDS10683	245667	79.9	238656	80.6	26	332	61.14	0.58
ANAC_Schinopsis_brasiliensis_IDS10685	245094	79.7	238962	80.7	20	335	69.85	0.55
ANAC_Schinus_patagonicus_IDS10939	260214	84.6	253041	85.4	21	332	70.18	0.57
ANAC_Sclerocarya_birrea_IDS10689	248184	80.7	242283	81.8	19	335	71.34	0.50
ANAC_Searsia_undulata_IDS10691	243549	79.2	236952	80	22	333	59.16	0.49
ANAC_Semecarpus_sp._IDS10861	208530	67.8	202104	68.2	0	323	69.35	2.58
ANAC_Smodingium_argutum_IDS10695	247323	80.4	240738	81.3	21	335	41.49	0.39
ANAC_Sorindeia_madagascariensis_IDS10697	248913	80.9	241299	81.5	22	330	45.45	0.51
ANAC_Spondias_mombin_IDS6469	253404	82.4	245082	82.7	20	333	72.37	0.46

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
ANAC_Swintonia_schwenckii_IDS10701	229200	74.5	223005	75.3	19	326	68.71	1.77
ANAC_Tapirira_guianensis_IDS10703	249657	81.2	243186	82.1	22	332	69.28	0.45
ANAC_Thyrsodium_spruceanum_IDS10705	247071	80.3	239865	81	17	331	67.07	0.54
ANAC_Toxicodendron_pubescens_IDS10707	258849	84.2	251544	84.9	23	330	70.61	0.63
ANAC_Toxicodendron_radicans_ERR2040463	256371	83.3	247113	83.4	9	299	66.56	0.30
ANAC_Toxicodendron_vernicifluum_SRR5858884	272835	88.7	262623	88.7	15	326	73.93	0.56
ANAC_Trichoscypha_longifolia_IDS10935	209364	68.1	202977	68.5	2	323	55.11	2.62
BIEB_Biebersteinia_odora_IDS894	203637	66.2	198909	67.2	9	321	75.39	2.72
BURS_Aucoumea_klaineana_IDS11011	237339	77.2	230835	77.9	32	334	72.46	0.78
BURS_Beiselia_mexicana_IDS10731	262935	85.5	254154	85.8	18	335	46.57	0.42
BURS_Boswellia_sacra_IDS10953	256128	83.3	248922	84	26	334	63.77	0.76
BURS_Bursera_simaruba_ERR2040465	186633	60.7	178584	60.3	12	291	57.04	0.31
BURS_Commiphora_habessinica_IDS10723	233562	75.9	227421	76.8	20	333	88.29	1.22
BURS_Crepidospermum_rhoifolium_IDS11015	251268	81.7	244269	82.5	24	332	55.12	0.60
BURS_Dacryodes_laxa_IDS10761	233001	75.8	225861	76.3	5	331	92.75	4.15
BURS_Protium_copal_SRR9107802	268647	87.3	257796	87	16	329	45.29	0.23
BURS_Protium_javanicum_IDS6471	243054	79	235557	79.5	14	332	96.08	2.54
BURS_Tetragastris_altissima_IDS11017	238227	77.4	231807	78.3	29	329	72.64	0.74
BURS_Trattinnickia_rhoifolia_IDS11019	208230	67.7	203274	68.6	5	331	77.34	3.26
BURS_Triomma_malaccensis_IDS10763	251229	81.7	244608	82.6	32	332	71.69	0.80
KIRK_Kirkia_acuminata_IDS10547	252606	82.1	245970	83	12	333	72.67	0.49
KIRK_Kirkia_wilmsii_ERR2040467	257277	83.6	248784	84	9	332	56.33	0.31
MELI_Aglaia_macrocarpa_IDS11875	201930	65.6	196581	66.4	1	330	95.76	5.60
MELI_Aglaia_odorata_SRR5947159	265998	86.5	256194	86.5	1	328	72.87	2.08
MELI_Aglaia_tomentosa_IDS10863	232245	75.5	226320	76.4	1	328	89.02	4.49
MELI_Anthocarapa_nitidula_IDS10441	220296	71.6	214407	72.4	1	323	94.74	5.76
MELI_Aphanamixis_polystachya_IDS10975	211842	68.9	206175	69.6	3	327	86.85	5.40
MELI_Astrotrichilia_asterotricha_IDS10567	200457	65.2	195024	65.8	1	328	88.41	3.86
MELI_Azadirachta_indica_IDS10433	244407	79.5	238473	80.5	16	335	51.34	0.32
MELI_Cabralea_canjerana_IDS10881	213942	69.6	209259	70.7	2	328	92.38	5.40
MELI_Calodecaryia_crassifolia_IDS10873	223533	72.7	217752	73.5	40	332	76.51	1.24
MELI_Capuronianthus_mahafalensis_IDS10825	232359	75.5	226656	76.5	0	331	90.03	3.65
MELI_Carapa_procera_IDS10903	206211	67	199872	67.5	1	327	85.32	3.87
MELI_Cedrela_angustifolia_IDS10889	214065	69.6	209790	70.8	3	324	91.98	4.27
MELI_Cedrela_odorata_SRR7505213	265878	86.4	257808	87	0	335	84.78	3.24
MELI_Chukrasia_tabularis_IDS11863	238719	77.6	232287	78.4	22	334	55.09	0.34
MELI_Cipadessa_baccifera_IDS10715	243894	79.3	237435	80.2	22	332	37.95	0.33
MELI_Didymocheton_sp._IDS10737	212007	68.9	208320	70.3	2	322	88.51	5.13
MELI_Ekebergia_capensis_IDS10837	209916	68.2	204957	69.2	2	329	86.63	3.24

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
MELI_Entandrophragma_bussei_IDS11865	203634	66.2	199086	67.2	0	324	93.21	6.64
MELI_Guarea_glomerulata_IDS10907	202701	65.9	197256	66.6	0	324	76.23	3.94
MELI_Guarea_laurentii_IDS10983	173739	56.5	168732	57	8	323	82.04	4.33
MELI_Heckeldora_staudtii_IDS10909	218676	71.1	212298	71.7	1	329	93.62	5.24
MELI_Heynea_trijuga_IDS10997	229926	74.8	223731	75.5	16	332	37.35	0.43
MELI_Humbertioturraea_grandidieri_IDS10569	230721	75	225051	76	40	332	75.30	1.50
MELI_Khaya_anthotheca_IDS10779	246723	80.2	239061	80.7	0	330	87.88	4.10
MELI_Lepidothrichilia_volkensii_IDS10571	217287	70.6	211140	71.3	0	317	65.93	2.74
MELI_Lovoa_sywnnertonii_IDS10781	221976	72.2	216594	73.1	0	328	82.01	3.83
MELI_Malleastrum_maadenense_IDS10827	194433	63.2	187899	63.4	3	327	77.37	2.97
MELI_Melia_azedarach_ERR2040470	238785	77.6	230400	77.8	8	324	20.06	0.14
MELI_Melia_toosendan_IDS10961	247479	80.5	241236	81.5	12	335	63.28	0.46
MELI_Munronia_pinnata_IDS11871	185409	60.3	179904	60.7	4	330	90.61	7.52
MELI_Naregamia_alata_IDS10819	214959	69.9	207852	70.2	1	324	28.40	0.69
MELI_Neobeguea_sp._IDS10829	233547	75.9	228489	77.1	1	332	90.66	3.53
MELI_Nymania_capensis_IDS10719	235731	76.6	229869	77.6	29	328	53.96	0.91
MELI_Owenia_reticulata_IDS10435	252987	82.2	247062	83.4	20	335	58.81	0.53
MELI_Pseudobersama_mossambicensis_IDS10821	211053	68.6	206376	69.7	0	331	84.89	3.30
MELI_Pseudocedrela_kotschyi_IDS10853	228639	74.3	222876	75.3	0	330	80.30	2.46
MELI_Pseudoclausena_chrysogyne_IDS6473	221049	71.9	214494	72.4	3	329	88.45	4.52
MELI_Pterorhachis_zenkeri_IDS10817	202986	66	196806	66.4	8	331	18.73	0.16
MELI_Quivisianthe_papinae_IDS10831	247275	80.4	240513	81.2	29	332	55.12	0.51
MELI_Reinwardtiodendron_celebicum_IDS6474	143688	46.7	137973	46.6	5	312	62.18	2.36
MELI_Ruagea_glabra_IDS10895	177540	57.7	171585	57.9	8	321	67.91	3.29
MELI_Schmardaea_microphylla_IDS11867	237723	77.3	230781	77.9	12	333	52.25	0.21
MELI_Swietenia_macrophylla_IDS10717	235215	76.5	229746	77.6	0	333	80.48	3.50
MELI_Synoum_glandulosum_IDS10877	199602	64.9	193944	65.5	0	320	91.88	5.42
MELI_Toona_sinensis_SRR8474820	272022	88.4	261717	88.4	0	333	89.49	3.04
MELI_Trichilia_hirta_IDS10893	191226	62.2	186405	62.9	0	327	74.31	3.03
MELI_Turraea_virens_IDS6477	241971	78.7	234813	79.3	2	328	44.82	0.96
MELI_Turraeanthus_manii_IDS10823	193686	63	188016	63.5	2	329	77.51	4.69
MELI_Vavaea_amicorum_IDS6478	235284	76.5	229038	77.3	0	330	82.42	3.50
MELI_Walsura_tubulata_IDS6479	248883	80.9	241188	81.4	17	333	52.55	0.38
MELI_Xylocarpus_moluccensis_IDS6480	240846	78.3	233469	78.8	0	331	73.11	2.73
NITR_Malacocarpus_crithmifolius_IDS10729	218904	71.2	211941	71.6	14	323	43.34	0.28
NITR_Nitraria_retusa_IDS10727	218232	70.9	211326	71.4	16	324	68.52	0.51
NITR_Nitraria_sibirica_SRR7013771	271977	88.4	261306	88.2	16	323	75.85	0.59
NITR_Nitraria_tangutorum_SRR1768462	109605	35.6	104364	35.2	3	232	86.21	1.17
NITR_Peganum_harmala_IDS10965	238668	77.6	231120	78	18	324	39.20	0.26

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
OGpB_Cylicomorpha_parviflora_ERR4180126	201012	65.4	194553	65.7	8	310	16.13	0.23
OGpB_Emblingia_calceoliflora_ERR4180003	220992	71.8	212637	71.8	2	312	9.62	0.12
OGpB_Koeberlinia_spinosa_ERR4180172	156915	51	151503	51.2	12	281	30.25	0.81
OGpC_Crossosoma_californicum_SRR7451089	202821	65.9	197958	66.8	14	326	78.83	0.96
OGpC_Stachyurus_praecox_ERR2040307	171180	55.7	164934	55.7	17	296	50.34	0.36
OGpC_Staphylea_trifolia_ERR2040308	225585	73.3	216723	73.2	21	304	86.84	0.96
OGpE_Cyrilla_racemiflora_SRR7451102	187740	61	182463	61.6	27	321	79.44	1.27
OGpE_Manilkara_zapota_ERR2040506	210261	68.4	201939	68.2	11	297	42.42	0.34
OGpF_Acacia_pycnantha_ERR2040344	187911	61.1	182034	61.5	15	302	34.44	0.26
OGpF_Gilbertiodendron_ecoukense_SRR7451091	179307	58.3	173544	58.6	14	308	56.82	1.39
OGpF_Polygala_lutea_ERR706838	145452	47.3	140220	47.3	0	247	53.44	1.28
OGpG_Francoa_appendiculata_ERR2040311	212958	69.2	205023	69.2	10	297	95.29	1.55
OGpG_Geranium_carolinianum_ERR2040309	203442	66.1	196296	66.3	23	285	91.23	2.13
OGpG_Geranium_maculatum_ERR2040310	156717	50.9	150831	50.9	13	263	82.51	1.51
OGpG_Greyia_sutherlandii_ERR2040312	104949	34.1	101544	34.3	10	237	47.68	0.37
OGpH_Perrottetia_longistylis_ERR4297056	217107	70.6	210783	71.2	21	330	38.79	0.38
OGpM_Anisoptera_marginata_ERR4180094	206448	67.1	199113	67.2	4	314	67.83	2.26
OGpM_Gossypium_barbadense_SRR8878749	250647	81.5	242271	81.8	25	322	94.41	2.11
OGpM_Leptolaena_cuspidata_ERR4180027	212808	69.2	205446	69.4	1	323	53.56	1.75
OGpM_Medinilla_magnifica_ERR2040321	138552	45	134436	45.4	20	241	78.84	1.29
OGpM_Monotes_glaber_ERR4180058	196419	63.9	189651	64	6	308	56.17	1.81
OGpM_Oenothera_rosea_ERR706864	174489	56.7	167436	56.5	6	262	74.43	1.09
OGpM_Terminalia_neotaliala_ERR2040313	105129	34.2	100839	34	6	197	52.28	0.24
RUTA_Acmadenia_kiwanensis_IDS10917	232116	75.5	225906	76.3	11	333	69.07	1.76
RUTA_Acradenia_euodiiformis_IDS11877	216717	70.5	210627	71.1	10	327	51.99	1.20
RUTA_Acronychia_sp_IDS6481	240657	78.2	232350	78.5	33	332	59.64	1.06
RUTA_Adenandra_uniflora_IDS10751	239055	77.7	232431	78.5	2	330	51.82	1.32
RUTA_Aegle_marmelos_SRR7268533	268053	87.1	257463	86.9	9	333	44.44	0.28
RUTA_Aeglopsis_chevalieri_IDS11023	236238	76.8	228570	77.2	20	334	71.56	0.58
RUTA_Afraegle_asso_IDS10937	230715	75	223674	75.5	15	334	52.69	0.37
RUTA_Agathosma_gonaquensis_IDS10809	236229	76.8	229569	77.5	21	332	69.28	1.62
RUTA_Amyris_elemifera_IDS10479	232290	75.5	225561	76.2	0	330	62.12	3.00
RUTA_Angostura_bracteata_IDS10843	221262	71.9	215061	72.6	31	331	72.51	1.52
RUTA_Atalantia_ceylanica_IDS6482	244707	79.6	237267	80.1	20	335	38.51	0.35
RUTA_Balfourodendron_riedelianum_IDS11765	215982	70.2	210528	71.1	1	330	76.06	2.94
RUTA_Balsamocitrus_dawei_IDS11767	234906	76.4	227817	76.9	18	335	31.04	0.26
RUTA_Boenninghausenia_albiflora_IDS10507	242388	78.8	235410	79.5	17	329	33.74	0.34
RUTA_Boronella_verticillata_IDS10549	202485	65.8	195867	66.1	8	331	95.77	4.47
RUTA_Bosistoa_medicinalis_IDS10437	230970	75.1	224211	75.7	0	332	89.76	4.14

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
RUTA_Bottegoa_insignis_IDS10767	216984	70.5	210264	71	30	332	51.20	0.72
RUTA_Brombya_platynema_IDS10551	213699	69.5	207927	70.2	36	327	77.37	1.29
RUTA_Burkillanthus_malaccensis_IDS11769	209127	68	202413	68.3	18	330	33.94	0.32
RUTA_Calodendrum_capense_IDS11771	210384	68.4	204738	69.1	1	328	57.93	2.50
RUTA_Casimiroa_sapota_IDS11773	112173	36.5	108153	36.5	8	286	32.52	0.96
RUTA_Cedrelopsis_gracilis_IDS10553	229926	74.8	223614	75.5	41	332	75.00	1.17
RUTA_Chloroxylum_swietinia_IDS10735	243852	79.3	236181	79.7	19	334	63.47	0.37
RUTA_Citropsis_articulata_IDS11775	233073	75.8	225786	76.2	21	333	53.15	0.44
RUTA_Citrus_aurantiifolia_SRR10353559	266256	86.6	255867	86.4	8	329	94.22	1.08
RUTA_Citrus_aurantium_SRR5807892	263985	85.8	253077	85.4	19	327	88.99	0.97
RUTA_Citrus_cavaleriei_SRR4098611	255456	83.1	247392	83.5	15	326	57.98	0.40
RUTA_Citrus_clementina_SRR7614640	259449	84.3	249507	84.2	16	326	96.01	1.05
RUTA_Citrus_deliciosa_ERR760725	272040	88.4	262083	88.5	17	335	59.40	0.49
RUTA_Citrus_hindsii_SRR9016287	267564	87	256953	86.8	15	329	46.20	0.37
RUTA_Citrus_hystrix_IDS10511	239355	77.8	232698	78.6	26	334	88.62	0.97
RUTA_Citrus_japonica_SRR6357068	176376	57.3	167949	56.7	6	206	67.48	0.38
RUTA_Citrus_junos_SRR7230860	270963	88.1	260202	87.9	15	332	93.67	1.00
RUTA_Citrus_limon_SRR11128339	270795	88	259995	87.8	14	334	95.81	1.11
RUTA_Citrus_macrophylla_ERR1994152	232143	75.5	222027	75	10	295	66.10	0.57
RUTA_Citrus_maxima_SRR6656016	256035	83.2	245244	82.8	24	319	51.72	0.48
RUTA_Citrus_medica_SRR4102488	268338	87.2	257718	87	6	333	11.11	0.12
RUTA_Citrus_reticulata_SRR12053309	264669	86	253923	85.7	17	327	65.75	0.60
RUTA_Citrus_sinensis_SRR5581500	258783	84.1	249219	84.1	15	324	82.41	0.80
RUTA_Citrus_suavissima_SRR6489423	269148	87.5	258609	87.3	15	334	62.28	0.51
RUTA_Citrus_trifoliata_SRR7614648	258972	84.2	248883	84	14	326	57.98	0.33
RUTA_Citrus_unshiu_SRR9959412	261681	85.1	251175	84.8	7	322	55.28	0.52
RUTA_Citrus_xparadisi_ERR2040472	133827	43.5	127722	43.1	14	260	59.23	0.48
RUTA_Clausena_excavata_IDS6483	240129	78.1	233334	78.8	26	335	94.93	1.24
RUTA_Cneoridium_dumosum_IDS10513	216576	70.4	210846	71.2	0	330	81.21	3.45
RUTA_Cneorum_tricoccon_IDS10515	229719	74.7	222711	75.2	22	326	34.36	0.56
RUTA_Coatesia_paniculata_IDS10483	218277	71	212196	71.6	2	308	94.81	4.31
RUTA_Coleonema_pulchellum_IDS10805	227349	73.9	221601	74.8	20	330	82.12	2.11
RUTA_Comptonella_microcarpa_IDS10555	213603	69.4	206850	69.8	35	329	77.20	1.43
RUTA_Conchocarpus_macrophyllus_IDS11777	200178	65.1	194889	65.8	19	329	70.21	1.46
RUTA_Correa_speciosa_IDS10517	218967	71.2	214026	72.3	12	323	41.80	1.20
RUTA_Crowea_exaltata_IDS10813	196146	63.8	190539	64.3	2	312	30.13	0.99
RUTA_Decagonocarpus_oppositifolius_IDS11779	200826	65.3	194997	65.8	19	321	43.93	0.43
RUTA_Decatropis_bicolor_IDS11781	215049	69.9	209547	70.8	2	330	72.12	2.89
RUTA_Decazyx_macrophyllus_IDS11783	215877	70.2	209700	70.8	2	331	65.26	2.22

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RUTA_Dictamnus_albus_IDS10519	200511	65.2	196548	66.4	1	321	55.76	1.76
RUTA_Dictyoloma_vandellianum_IDS10557	229317	74.6	223257	75.4	12	328	36.59	0.25
RUTA_Dinosperma_erythrococcum_IDS10443	236853	77	229854	77.6	0	331	87.01	3.98
RUTA_Diosma_sabulosa_IDS10913	221490	72	216183	73	7	333	59.16	1.79
RUTA_Drummondita_hassellii_IDS10765	220560	71.7	215637	72.8	23	330	60.30	1.26
RUTA_Dutaillyea_trifoliata_IDS11785	162627	52.9	157488	53.2	6	313	23.64	0.70
RUTA_Empleurum_unicapsulare_IDS11791	206070	67	201114	67.9	13	328	62.50	1.54
RUTA_Ertela_trifolia_IDS11787	186357	60.6	180672	61	19	315	47.94	0.59
RUTA_Erythrochiton_brasiliensis_IDS10795	220281	71.6	214302	72.4	32	331	94.26	2.99
RUTA_Euchaetis_albertiana_IDS10915	233124	75.8	225276	76.1	17	327	73.39	1.73
RUTA_Euodia_hortensis_IDS10485	215448	70	207606	70.1	5	324	36.73	0.86
RUTA_Fagaropsis_spec_IDS10487	223530	72.7	217407	73.4	1	331	79.76	3.12
RUTA_Flindersia_pimenteliana_IDS7778	95223	31	92682	31.3	2	277	46.21	2.02
RUTA_Galipea_trifoliata_IDS11789	146529	47.6	140805	47.5	7	252	32.94	0.85
RUTA_Geijera_linearifolia_IDS6484	239982	78	231717	78.2	5	333	91.29	5.72
RUTA_Glycosmis_pentaphylla_IDS6485	244080	79.4	236847	80	26	335	97.61	1.75
RUTA_Halfordia_sp_IDS6486	244806	79.6	237942	80.3	13	331	80.97	2.20
RUTA_Haplophyllum_bungei_IDS10527	210642	68.5	204495	69	12	328	64.33	0.61
RUTA_Harrisonia_abyssinica_IDS10529	232113	75.5	226293	76.4	18	331	97.58	2.81
RUTA_Harrisonia_brownii_IDS6487	230814	75	223932	75.6	22	334	93.71	1.10
RUTA_Helietta_glaziovii_IDS11793	177333	57.7	172530	58.3	3	304	56.58	2.16
RUTA_Hortia_superba_IDS11795	221481	72	215382	72.7	19	330	81.52	2.00
RUTA_Ivodea_decaryana_IDS10489	228894	74.4	223347	75.4	3	335	74.33	2.05
RUTA_Leionema_ellipticum_IDS10445	233805	76	227022	76.7	16	329	71.12	1.59
RUTA_Limnocitrus_littoralis_IDS11797	226914	73.8	220830	74.6	24	334	39.82	0.43
RUTA_Limonia_acidissima_IDS11799	233217	75.8	225870	76.3	20	335	59.40	0.28
RUTA_Lubaria_aroensis_IDS11801	192105	62.5	186201	62.9	14	325	88.31	3.00
RUTA_Lunasia_amara_IDS6488	238620	77.6	231615	78.2	0	328	73.48	2.34
RUTA_Luvunga_monophylla_IDS10467	221307	71.9	214335	72.4	18	333	38.74	0.46
RUTA_Macrostylis_decipiens_IDS11805	228972	74.4	222351	75.1	37	332	93.98	2.43
RUTA_Medicosma_cunninghamii_IDS6489	237429	77.2	230268	77.7	37	332	71.69	1.44
RUTA_Melicope_ternata_IDS10531	233100	75.8	226554	76.5	14	329	53.50	0.93
RUTA_Merope_angulata_IDS11809	115743	37.6	112494	38	4	286	23.78	0.52
RUTA_Merrillia_caloxylon_IDS11811	199446	64.8	192996	65.2	12	330	32.12	0.22
RUTA_Metrodorea_nigra_IDS10747	218190	70.9	212484	71.7	3	329	85.11	3.94
RUTA_Monanthocitrus_oblanceolata_IDS11813	183294	59.6	177624	60	14	322	36.65	0.36
RUTA_Muiriantha_hassellii_IDS11921	235968	76.7	229920	77.6	38	331	65.86	0.91
RUTA_Murraya_exotica_IDS6490	248925	80.9	241524	81.5	21	335	51.34	0.33
RUTA_Murraya_koenigii_IDS10799	243570	79.2	236751	79.9	18	332	86.45	0.76

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
RUTA_Myrtopsis_macrocarpa_IDS10493	207447	67.4	202917	68.5	1	328	56.71	1.76
RUTA_Nematolepis_squamea_IDS11815	215817	70.2	209820	70.8	0	326	93.87	7.51
RUTA_Neoraputia_alba_IDS10749	195336	63.5	189615	64	2	327	67.89	2.18
RUTA_Nycticalanthus_speciosus_IDS11817	167658	54.5	161727	54.6	1	319	34.17	1.42
RUTA_Orixa_japonica_IDS10533	188370	61.2	182322	61.6	1	322	66.15	3.06
RUTA_Peltostigma_guatamalense_IDS11823	171660	55.8	167130	56.4	7	316	56.01	1.92
RUTA_Pentaceras_australe_IDS10495	225609	73.3	219744	74.2	1	332	81.33	3.49
RUTA_Perryodendron_parviflorum_IDS7853	170007	55.3	164523	55.5	19	318	52.20	0.61
RUTA_Phellodendron_amurense_IDS10535	206208	67	200271	67.6	2	319	67.71	2.72
RUTA_Phyllosma_capensis_IDS11825	215586	70.1	209949	70.9	18	329	76.90	1.96
RUTA_Picrella_glandulosa_IDS10499	212223	69	206205	69.6	9	336	45.24	1.04
RUTA_Pilocarpus_pennatifolius_IDS10815	221874	72.1	215550	72.8	0	334	79.04	3.42
RUTA_Pitaviaster_haplophyllus_IDS10561	205524	66.8	199671	67.4	18	327	93.88	4.42
RUTA_Pleiospermium_alatum_IDS11827	205140	66.7	199908	67.5	22	331	46.53	0.46
RUTA_Plethadenia_granulata_IDS10501	223797	72.8	217230	73.3	29	329	63.53	0.75
RUTA_Psilopeganum_sinense_IDS10537	212385	69	206409	69.7	11	333	17.72	0.23
RUTA_Ptaeroxylon_obliquum_IDS10845	243450	79.1	236637	79.9	42	336	62.20	1.10
RUTA_Ptelea_trifoliata_IDS10539	236175	76.8	229926	77.6	0	333	83.48	3.81
RUTA_Raputia_heptaphylla_IDS11829	176772	57.5	170511	57.6	2	317	34.07	1.41
RUTA_Raputia_ulei_IDS11833	188745	61.4	183390	61.9	8	313	38.66	0.65
RUTA_Raputiarana_subsigmoidea_IDS11831	218331	71	211698	71.5	1	329	62.31	2.18
RUTA_Rauia_nodosa_IDS11835	173925	56.5	168414	56.9	15	318	58.81	1.20
RUTA_Ravenia_infelix_IDS10745	189768	61.7	183084	61.8	25	318	57.55	0.81
RUTA_Raveniopsis_ruellioides_IDS11839	141627	46	136740	46.2	19	300	34.67	0.51
RUTA_Rhadinothamnus_rudis_IDS10929	225204	73.2	221334	74.7	34	331	69.18	1.49
RUTA_Ruta_angustifolia_SRR7900860	194409	63.2	188208	63.5	18	273	34.80	0.56
RUTA_Ruta_graveolens_IDS10541	221169	71.9	214329	72.4	44	326	98.47	3.28
RUTA_Sarcomelicope_simplicifolia_IDS10791	222816	72.4	216648	73.1	22	330	99.09	3.77
RUTA_Sheilanthera_pubens_IDS11879	217431	70.7	212550	71.8	2	330	61.52	1.80
RUTA_Skimmia_japonica_IDS10543	219216	71.3	212703	71.8	2	331	82.78	3.64
RUTA_Sohnreyia_terminalioides_IDS10563	111357	36.2	107688	36.4	1	261	8.81	0.15
RUTA_Spathelia_splendens_IDS10565	223419	72.6	217023	73.3	23	324	54.94	0.57
RUTA_Spiranthera_odoratissima_IDS11881	186930	60.8	181395	61.2	19	316	66.46	1.55
RUTA_Stauranthus_perforatus_IDS11883	200316	65.1	195510	66	3	328	74.39	3.41
RUTA_Swinglea_glutinosa_IDS11885	236976	77	229632	77.5	23	335	31.64	0.37
RUTA_Tetractomia_tetrandra_IDS10503	236019	76.7	229533	77.5	40	330	71.52	1.24
RUTA_Tetradium_daniellii_IDS10793	217257	70.6	211053	71.3	2	329	69.30	3.04
RUTA_Thamnosma_texana_IDS11841	217965	70.9	211305	71.3	21	323	57.59	0.41
RUTA_Toxosiphon_lindenii_IDS11889	92256	30	88374	29.8	2	255	15.29	0.35

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
RUTA_Triphasia_brassii_IDS7775	198462	64.5	192279	64.9	20	332	66.27	0.55
RUTA_Vepris_lanceolata_IDS10807	239766	77.9	233385	78.8	1	331	69.49	2.21
RUTA_Zanthoxylum_armatum_SRR9179742	270303	87.9	259734	87.7	46	332	97.29	2.27
RUTA_Zanthoxylum_bungeanum_SRR9179747	259545	84.4	249888	84.4	43	323	94.12	2.47
RUTA_Zanthoxylum_nitidum_SRR10861972	266772	86.7	256233	86.5	43	330	78.18	1.95
RUTA_Zieria_alata_IDS10425	226269	73.6	219339	74.1	23	331	93.05	2.01
SAPI_Acer_campestre_IDS994	254913	82.9	247476	83.6	21	330	63.64	0.84
SAPI_Acer_miaotaiense_SRR7195583	281430	91.5	270705	91.4	27	334	79.64	0.97
SAPI_Acer_negundo_ERR2040475	278733	90.6	268110	90.5	17	332	45.48	0.30
SAPI_Acer_palmatum_SRR1980924	276477	89.9	266124	89.9	21	332	92.17	1.36
SAPI_Acer_pictum_SRR8922645	199755	64.9	191805	64.8	12	269	52.79	0.50
SAPI_Acer_rubrum_SRR11712223	176202	57.3	171396	57.9	3	221	54.30	0.36
SAPI_Acer_saccharum_SRR6134139	274305	89.2	263715	89	21	325	64.00	0.65
SAPI_Acer_spicatum_SRR6134129	270744	88	260637	88	23	327	78.29	0.73
SAPI_Acer_truncatum_SRR3288570	266778	86.7	256416	86.6	19	326	72.09	0.90
SAPI_Acer_yangbiense_SRR8707037	281601	91.6	270846	91.4	13	331	24.47	0.38
SAPI_Aesculus_chinensis_SRR8073719	276186	89.8	265494	89.6	0	331	40.18	1.88
SAPI_Aesculus_pavia_ERR2040474	237261	77.1	227667	76.9	12	317	61.51	1.07
SAPI_Alatococcus_siqueirae_IDS4688	218073	70.9	212154	71.6	14	327	25.99	0.20
SAPI_Alectryon_carinatum_IDS1253	255573	83.1	249132	84.1	19	334	69.46	0.50
SAPI_Allophylus__IDS1111	224397	73	217539	73.4	23	318	49.69	0.45
SAPI_Amesiodendron_chinense_IDS4690	251781	81.9	245892	83	21	331	67.37	0.51
SAPI_Aporrhiza_paniculata_IDS4762	249213	81	242994	82	25	332	67.47	0.48
SAPI_Arfeuillea_arborescens_IDS3035	248775	80.9	241362	81.5	12	329	22.80	0.22
SAPI_Arytera_arcuata_IDS4782	252618	82.1	246528	83.2	24	331	63.75	0.53
SAPI_Arytera_lepidota_IDS4781	256542	83.4	250398	84.5	30	333	55.56	0.52
SAPI_Arytera_litoralis_IDS3060	248088	80.7	241896	81.7	21	329	41.64	0.54
SAPI_Atalaya_capensis_IDS1120	220092	71.6	213597	72.1	14	331	65.86	1.14
SAPI_Athyana_weinmannifolia_IDS760	249261	81	243594	82.2	20	331	58.01	0.40
SAPI_Averrhoidium_gardnerianum_IDS4691	252294	82	246132	83.1	24	329	74.16	0.65
SAPI_Beguea_apetala_IDS4743	252321	82	245877	83	22	331	62.84	0.40
SAPI_Billia_hippocastanum_IDS3040	256428	83.4	247686	83.6	1	332	73.19	2.31
SAPI_Blighia_sapida_IDS3041	258795	84.1	252723	85.3	20	331	51.06	0.53
SAPI_Blighiopsis_pseudostipularis_IDS4692	239811	78	233058	78.7	23	330	63.64	0.48
SAPI_Blomia_prisca_IDS4693	252066	81.9	245820	83	18	332	66.87	0.45
SAPI_Boniodendron_parviflorum_IDS4694	246879	80.3	239964	81	23	332	59.34	0.56
SAPI_Bridgesia_incisifolia_IDS3012	243225	79.1	236484	79.8	28	328	67.07	0.72
SAPI_Camptolepis_ramiflora_IDS4695	251850	81.9	245901	83	14	331	79.15	0.69
SAPI_Castanospora_alphandi_IDS4696	250398	81.4	244179	82.4	28	330	44.85	0.40

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
SAPI_Cnesmocarpon_dasyantha_IDS4698	214782	69.8	209229	70.6	19	326	57.67	0.47
SAPI_Conchopetalum_brachysepalum_IDS4699	261801	85.1	252849	85.4	22	333	62.16	0.50
SAPI_Cubilia_cubili_IDS3043	249471	81.1	241086	81.4	18	331	28.40	0.30
SAPI_Cupania_rubiginosa_IDS923	241314	78.5	235689	79.6	17	329	71.12	0.62
SAPI_Cupaniopsis_anacardioides_IDS856	246423	80.1	240864	81.3	7	329	19.76	0.32
SAPI_Cupaniopsis_macropetala_IDS4778	248793	80.9	242373	81.8	24	329	47.42	0.34
SAPI_Cupaniopsis_squamosa_IDS4764	248064	80.6	242112	81.7	27	328	64.33	0.55
SAPI_Cupaniopsis_trigonocarpa_IDS4763	251040	81.6	245259	82.8	25	332	64.76	0.56
SAPI_Deinbollia_pinnata_IDS1136	185835	60.4	179778	60.7	13	318	36.79	0.32
SAPI_Delavaya_yunnanensis_IDS2839	238473	77.5	232521	78.5	10	332	28.92	0.15
SAPI_Diatenopteryx_sorbifolia_IDS900	238554	77.6	232644	78.5	6	327	52.60	1.43
SAPI_Dictyoneura_obtusa_IDS6607	252228	82	245694	83	23	331	48.94	0.48
SAPI_Dilodendron_costaricense_IDS4701	250860	81.6	244623	82.6	26	333	55.56	0.40
SAPI_Dimocarpus__IDS3967	256062	83.2	249798	84.3	23	331	58.91	0.48
SAPI_Dimocarpus_longan_IDS4742	254007	82.6	247833	83.7	15	331	57.10	0.51
SAPI_Diploglottis_campbellii_IDS3039	255669	83.1	247521	83.6	14	329	55.93	0.34
SAPI_Diplopeltis_huegelii_IDS985	240834	78.3	232341	78.4	11	328	77.44	0.68
SAPI_Dipteronia_dyeriana_SRR2127991	273750	89	263715	89	3	327	20.80	0.42
SAPI_Dipteronia_sinensis_IDS746	250068	81.3	243396	82.2	19	328	44.51	0.60
SAPI_Distichostemon_dodecarpus_IDS10427	239229	77.8	232557	78.5	22	327	55.96	0.41
SAPI_Dodonaea_viscosa_SRR1914335	273870	89	263295	88.9	13	329	82.37	0.58
SAPI_Eriocoelum_rubiginosum_IDS3042	241164	78.4	234489	79.2	14	325	32.62	0.26
SAPI_Euchorium_cubense_IDS4703	223047	72.5	216243	73	16	329	50.15	0.26
SAPI_Euphoria_malaiensis_IDS10429	247869	80.6	242271	81.8	17	331	49.55	0.39
SAPI_Euphorianthus_longifolius_IDS971	222735	72.4	216714	73.2	15	332	41.57	0.29
SAPI_Eurycorymbus_cavaleriei_IDS3069	253155	82.3	246942	83.4	19	331	48.64	0.38
SAPI_Exothea_paniculata_IDS4704	261981	85.2	254847	86	15	331	52.27	0.31
SAPI_Filicium_decipiens_IDS3068	250272	81.4	242823	82	16	329	27.66	0.20
SAPI_Gereaua_perrieri_IDS4705	251556	81.8	246165	83.1	32	333	72.97	0.84
SAPI_Glenniea_africanus_IDS1137	253827	82.5	248118	83.8	23	328	66.16	0.59
SAPI_Gongrodiscus__IDS4737	257319	83.7	250629	84.6	19	332	60.24	0.36
SAPI_Guindilia_trinervis_IDS3051	226047	73.5	221406	74.8	11	322	28.88	0.28
SAPI_Guioa_rhoifolia_IDS1113	258516	84	249396	84.2	21	328	46.65	0.28
SAPI_Handeliodendron_bodinieri_IDS4707	123861	40.3	119766	40.4	5	284	34.51	0.81
SAPI_Haplocoelopsis_africana_IDS4708	193089	62.8	187674	63.4	17	323	38.08	0.29
SAPI_Haplocoelum_inopleum_IDS4709	242037	78.7	235362	79.5	24	330	66.67	0.49
SAPI_Harpullia__IDS4739	251697	81.8	243258	82.1	18	331	45.02	0.37
SAPI_Hippobromus_pauciflorus_IDS4789	256566	83.4	248592	83.9	11	332	68.07	0.49
SAPI_Hirania_rosea_IDS4710	235683	76.6	229011	77.3	24	332	59.94	0.61

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
SAPI_Hornea_mauritiana_IDS4711	116034	37.7	112080	37.8	11	293	29.35	0.37
SAPI_Hypelate_trifoliata_IDS4748	259653	84.4	250854	84.7	16	334	48.50	0.37
SAPI_Jagera_serrata_IDS970	255639	83.1	247959	83.7	16	331	32.63	0.30
SAPI_Koelreuteria_paniculata_IDS3090	257421	83.7	249450	84.2	21	333	41.44	0.35
SAPI_Lecaniodiscus_cupanioides_IDS1122	247947	80.6	242394	81.8	18	329	33.43	0.25
SAPI_Lepiderema_ixiocarpa_IDS4772	192384	62.5	186750	63.1	14	321	37.38	0.40
SAPI_Lepiderema_punctulata_IDS4770	252315	82	246126	83.1	23	330	57.58	0.57
SAPI_Lepidopetalum__IDS1119	250674	81.5	244449	82.5	14	330	36.67	0.29
SAPI_Lepisanthes_ramiflora_IDS1098	245682	79.9	240351	81.2	18	331	51.66	0.38
SAPI_Litchi_chinensis_IDS3066	239535	77.9	233958	79	17	326	45.71	0.54
SAPI_Llagunoa_nitida_IDS729	232476	75.6	224163	75.7	4	328	92.07	2.30
SAPI_Lophostigma_plumosum_IDS4713	238488	77.5	232455	78.5	16	328	50.00	0.27
SAPI_Loxodiscus_coriaceus_IDS869	262578	85.4	253392	85.6	20	332	57.53	0.41
SAPI_Macphersonia_cauliflora_IDS4714	258447	84	252192	85.1	17	334	63.17	0.45
SAPI_Magonia_pubescens_IDS921	117984	38.4	114417	38.6	3	232	14.66	0.16
SAPI_Majidea_zanguebarica_IDS922	248442	80.8	241647	81.6	11	327	22.94	0.22
SAPI_Matayba_tenax_IDS3065	242418	78.8	236736	79.9	4	328	22.87	0.21
SAPI_Melicoccus_bijugatus_IDS1135	180633	58.7	174681	59	5	318	77.99	2.77
SAPI_Mischarytera_lautereriana_IDS4715	211803	68.9	205599	69.4	18	325	36.31	0.32
SAPI_Mischocarpus_pyriformis_IDS2855	248958	80.9	242988	82	14	329	36.78	0.32
SAPI_Molinaea_sessilifolia_IDS4734	249213	81	242814	82	24	328	57.62	0.48
SAPI_Nephelium_lappaceum_SRR11613036	274542	89.3	263709	89	27	329	66.26	0.70
SAPI_Otonephelium_stipulaceum_IDS4717	212718	69.2	207756	70.1	13	327	29.66	0.26
SAPI_Pancovia_bijuga_IDS1134	153552	49.9	148725	50.2	12	311	51.77	0.73
SAPI_Pappea_capensis_IDS1034	254865	82.9	248547	83.9	12	332	62.05	0.44
SAPI_Paranephelium_xestophyllum_IDS1184	247005	80.3	239913	81	32	329	67.78	0.64
SAPI_Paullinia_pinnata_IDS1130	208842	67.9	202659	68.4	19	309	51.78	0.66
SAPI_Pavieasia_anamensis_IDS4773	228741	74.4	222861	75.2	28	329	62.92	0.53
SAPI_Pentascyphus_thyrsiflorus_IDS4718	246360	80.1	239592	80.9	25	332	60.84	0.48
SAPI_Placodiscus_turbinatus_IDS4750	197832	64.3	192402	65	20	314	51.27	0.44
SAPI_Plagioscyphus_jumellei_IDS4746	256638	83.4	250485	84.6	16	333	75.38	0.58
SAPI_Podonephelium_homei_IDS1154	254079	82.6	247911	83.7	23	332	40.96	0.32
SAPI_Pometia_pinnata_IDS4740	257544	83.7	250968	84.7	28	330	79.39	0.72
SAPI_Pseudopteris_decipiens_IDS924	237723	77.3	231966	78.3	17	330	63.33	0.39
SAPI_Radlkofera_calodendron_IDS1127	252099	82	245928	83	19	330	72.73	0.61
SAPI_Rhysotoechia_robertsonii_IDS4723	255627	83.1	249540	84.3	22	333	54.05	0.45
SAPI_Sapindus_mukorossi_SRR8302229	270627	88	260586	88	7	330	21.52	0.24
SAPI_Sapindus_saponaria_IDS3064	251268	81.7	245406	82.9	16	333	33.03	0.23
SAPI_Sarcopteryx_squamosa_IDS4736	258615	84.1	251715	85	30	331	69.79	0.53

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
SAPI_Sarcotoechia_cuneata_IDS4724	247710	80.5	241380	81.5	25	331	53.17	0.43
SAPI_Serjania_communis_IDS3063	201081	65.4	194805	65.8	15	301	52.16	0.95
SAPI_Sisyrolepis_muricata_IDS4725	205446	66.8	199773	67.5	13	323	28.48	0.25
SAPI_Smelophyllum_capense_IDS1315	262527	85.3	253560	85.6	15	331	62.84	0.44
SAPI_Stadmannia_oppositifolia_IDS1332	257259	83.6	251049	84.8	23	332	57.53	0.30
SAPI_Stocksia_brahuica_IDS4726	230250	74.9	223602	75.5	30	328	64.02	0.69
SAPI_Storthocalyx_chryseus_IDS4741	256608	83.4	248988	84.1	28	332	63.86	0.54
SAPI_Synima_cordieri_IDS1101	252243	82	246039	83.1	25	332	75.30	0.72
SAPI_Talisia_nervosa_IDS3070	240471	78.2	234366	79.1	8	331	66.16	1.62
SAPI_Thinouia_myriantha_IDS4727	224925	73.1	218697	73.8	16	323	53.56	0.39
SAPI_Thouinia_acuminata_IDS2801	257469	83.7	248793	84	23	332	59.34	0.45
SAPI_Thouinidium_decandrum_IDS4728	258495	84	251151	84.8	26	333	65.17	0.52
SAPI_Tina_tamatavensis_IDS4729	225990	73.5	220179	74.3	19	322	50.00	0.41
SAPI_Toechima_erythrocarpum_IDS4738	238434	77.5	231936	78.3	11	329	97.26	2.45
SAPI_Toulicia_reticulata_IDS4749	180225	58.6	175425	59.2	8	312	46.15	0.75
SAPI_Trigonachras_postardanjeisin_IDS1108	256581	83.4	249939	84.4	18	333	48.05	0.29
SAPI_Tristira_triptera_IDS3052	248052	80.6	242337	81.8	17	330	37.88	0.32
SAPI_Tristiropsis__IDS3970	256062	83.2	249783	84.3	15	330	26.67	0.22
SAPI_Tsingya_bemarana_IDS4751	232230	75.5	226023	76.3	13	332	29.22	0.18
SAPI_Ungnadia_speciosa_IDS3034	258804	84.1	250815	84.7	19	334	52.69	0.24
SAPI_Urvillea_ulmacea_IDS4731	219618	71.4	213747	72.2	13	322	92.86	2.13
SAPI_Vouarana_guianensis_IDS4732	249771	81.2	244059	82.4	18	331	75.53	0.59
SAPI_Xanthoceras_sorbifolium_IDS5170	259623	84.4	251235	84.8	19	331	61.33	0.41
SAPI_Xerospermum_noronhianum_IDS3061	254187	82.6	248856	84	22	332	52.71	0.52
SAPI_Zanha_golungensis_IDS1141	254466	82.7	248622	83.9	18	334	70.06	0.44
SAPI_Zollingeria_borneensis_IDS4776	218400	71	212784	71.8	15	328	42.68	0.30
SIMA_Ailanthus_altissima_ERR2040477	258279	84	249336	84.2	0	331	81.27	2.33
SIMA_Ailanthus_triphysa_IDS10461	223665	72.7	218853	73.9	0	330	75.45	3.64
SIMA_Amaroria_soulameoides_IDS11843	217698	70.8	211290	71.3	0	328	86.59	3.40
SIMA_Castela_coccinea_IDS11901	177039	57.6	171612	57.9	4	322	21.74	0.09
SIMA_Eurycoma_longifolia_IDS10887	245064	79.7	237774	80.3	20	334	79.34	0.67
SIMA_Gymnostemon_zaizou_IDS11857	245337	79.8	238830	80.6	13	333	88.29	0.83
SIMA_Hannoa_klaineana_IDS11859	249285	81	241986	81.7	18	336	68.75	0.47
SIMA_Holacantha_emoryi_IDS11845	229578	74.6	223656	75.5	20	329	72.64	0.48
SIMA_Homalolepis_glabra_IDS11907	243969	79.3	236931	80	23	333	69.67	0.60
SIMA_Nothospondias_staudtii_IDS11849	237462	77.2	230547	77.8	19	333	56.76	0.35
SIMA_Odyendea_gabunensis_IDS11851	252750	82.2	245151	82.8	20	334	50.60	0.28
SIMA_Perriera_madagascariensis_IDS11853	252180	82	245439	82.9	20	335	50.75	0.32
SIMA_Picrasma_crenata_IDS11893	222087	72.2	216552	73.1	0	332	84.94	4.19

Sample	Bp (original)	Coverage (original)	Bp (clean)	Coverage (clean)	No. paralogs	No. loci	Heterozygosity (%)	AD
SIMA_Pierreodendron_africanum_IDS11855	182889	59.5	177012	59.8	10	323	20.74	0.21
SIMA_Quassia_amara_IDS10951	258804	84.1	251004	84.7	7	332	40.36	0.17
SIMA_Samadera_spTozerRange_IDP6813	216804	70.5	209739	70.8	1	330	74.24	1.87
SIMA_Simaba_orinocensis_IDS11895	252567	82.1	245193	82.8	15	335	77.01	0.55
SIMA_Simarouba_glauca_IDS10711	257565	83.7	249582	84.3	13	336	50.00	0.34

Appendix C2 Profiles of each fossil used for calibration of the Angiosperms353 genus-level Sapindales tree, scored according to Parham *et al*. (2012) and the eFLOWER PROTEUS database of Sauquet (2016).

Calibration no.	C02
Family	Sapindaceae
Full taxon name	†*Sapindospermum nitidum* Knobloch & Mai
Reference (first description)	Knobloch & Mai (1986)
Reference (latest description)	
Organs	Seed
Specimens	Holotype: UUG EK 39618
Locality	Trebec Tj-4a, 76-77 m, graue Schluffe, Klikov-Schichtenfolge
Formation	
Country	Czech Republic
Reference (age)	Knobloch & Mai (1986)
Oldest stratum	Turonian
Age quality	Unrevised (old source < 2000)
Age justification	Paleocarpological evidence places the Klikov layer sequence in the Oberturon to Santon.
Reference (fossil relationships)	Knobloch & Mai (1986)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Pre-molecular era (before 1990)
Min. age (Mya)	89.8
Calibration	crown Sapindales
Node justification	This seed is thought to be attributable to Sapindoideae, and was placed in the extinct genus *Sapindospermum*. Other *Sapindospermum* seeds are known from the Cretaceous of North America, Greenland, Europe, and Siberia, and Sapindaceae fossil wood (*Sapindoxylum*) has been recovered from Cretaceous beds in Egypt (Knobloch and Mai 1986). However, given the age of the fossil and inability to assign it to an extant taxon, I use this fossil conservatively to calibrate the minimum age for the crown of Sapindales.
Calibration no.	C03
Family	Sapindaceae
Full taxon name	†*Aesculus hickeyi* Manchester

Reference (first description)	Manchester (2001a)
Reference (latest description)	
Organs	Leaf, fruit, seed
Specimens	Holotype: UF 30618
Locality	Farmers Butte, North Dakota (UF locality 18744)
Formation	Fort Union Formation
Country	USA
Reference (age)	Belt (2004)
Oldest stratum	Paleocene
Age quality	Revised (stratigraphic)
Age justification	Stratigraphy
Reference (fossil relationships)	Magallón *et al.* (2015)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	56
Calibration	crown Sapindaceae
Node justification	The leaves of *Aesculus hickeyi* were previously assigned to *Carya antiquorum* (Juglandaceae; Hickey, 1977) and initially known from isolated leaflets in the Golden Valley Formation and Farmers Butte locality. Manchester (2001) was the first to recognise the affinity of the leaves with *Aesculus* (Sapindaceae). I accept the assignment by Manchester (2001) and use this fossil taxon to calibrate the crown node of Sapindaceae.
Calibration no.	C04
Family	Sapindaceae
Full taxon name	†*Dipteronia brownii* McClain & Manchester
Reference (first description)	McClain & Manchester (2001)
Reference (latest description)	
Organs	Fruit
Specimens	Holotype: UWBM 39729
Locality	Hell's Half Acre, Wyoming
Formation	Fort Union Formation
Country	USA

Reference (age)	Belt (2004)
Oldest stratum	Middle Paleocene
Age quality	Revised (stratigraphic)
Age justification	Based on palynological evidence, the *Dipteronia* fruits were found in a pollen zone P-4 that is considered to be middle Paleocene (60–63 Mya)."
Reference (fossil relationships)	McClain & Manchester (2001)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	60
Calibration	stem *Dipteronia*
Node justification	The venation is the same in the fossils as in modern *Dipteronia*, complete with fine reticulation on the wing. The fossil *Dipteronia* fruits were assigned to *D. brownii* sp. nov., and most closely resemble extant species *D. sinensis* (McClain & Manchester, 2001). I accept the assignment of this fossil to *Dipteronia*, however do not know when in the evolution of the genus this species evolved. Therefore I take the conservative approach of using this fossil to calibrate the stem node of *Dipteronia*.
Calibration no.	C05
Family	Sapindaceae
Full taxon name	†*Acer* sp.
Reference (first description)	Crane *et al*. (1990)
Reference (latest description)	
Organs	Leaf
Specimens	
Locality	
Formation	
Country	
Reference (age)	
Oldest stratum	Late Paleocene
Age quality	Unrevised (old source < 2000)
Age justification	
Reference (fossil relationships)	Magallón & Castillo (2009)

Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	56
Calibration	stem *Acer*
Node justification	*Acer* fruits first occur in the late Paleocene of North America, and are well represented in the Eocene and later Tertiary of North America, Europe and Asia (Manchester 1999). I accept the assignment of this fossil to *Acer* and take the conservative approach of using it to constrain the stem node of *Acer* to a minimum age of 56 Mya.

Calibration no.	C06
Family	Sapindaceae
Full taxon name	†*Koelreuteria allenii* (Lesq.) W. N. Edwards
Reference (first description)	Wang et al (2013)
Reference (latest description)	
Organs	Fruit
Specimens	Holotype: USNM P1617
Locality	Wyoming
Formation	Green River Formation
Country	USA
Reference (age)	Smith *et al*. (2003)
Oldest stratum	Eocene
Age quality	Revised (radioisotropic)
Age justification	Radioisotropic evidence (Smith *et al*. 2003).
Reference (fossil relationships)	Wang *et al*. (2013)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	52
Calibration	stem *Koelreuteria*
Node justification	This is the oldest known specimen of a capsular valve of *Koelreuteria* Wang *et al.* (2013). I accept the assignment of the fossil to *Koelreuteria* and use it conservatively to constrain the stem node of the genus to a minimum age of 52 Mya.

Calibration no.	C07

Family	Sapindaceae
Full taxon name	†*Allophylus graciliformis* (Berry) Berry
Reference (first description)	Panti (2018)
Reference (latest description)	
Organs	Leaf
Specimens	MPM PB 3079–3088
Locality	Santa Cruz Province, Patagonia
Formation	Río Turbio Formation
Country	Argentina
Reference (age)	Panti (2018)
Oldest stratum	Early Eocene
Age quality	Revised (stratigraphic)
Age justification	The unit was divided into upper and lower informal members. Evidence for the age of the formation comes mainly from dinoflagellates and detrital zircon U/Pb. Dinoflagellate data suggests the age of Early/Middle Eocene for the lower member and Middle/Late Eocene for the upper member. Detrital zircon U/Pb evidence restricts the lower member to the Early Eocene and indicate an Oligocene age for the upper member. Specimens of this fossil were found in the upper and lower members, and so the minimum age of the lower member is used.
Reference (fossil relationships)	
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	46
Calibration	stem *Allophylus*
Node justification	These fossils match with *Allophylus graciliformis* (Berry) as described by Hünicken (1967), particularly with respect to the shape of the base and apex.This species is thought to be related to the extant *Allophylus edulis* (A. St.– Hil., A. Juss. & Cambess.) Hieron. ex Niederl. of northern Argentina (Panti, 2018). I therefore accept the assignment of this fossil to *Allophylus*, and use it conservatively to constrain the stem node of the genus.
Calibration no.	C08
Family	Burseraceae
Full taxon name	†*Bursera inaequalateralis* (Lesq.) MacGintie
Reference (first description)	MacGinitie (1969)

Reference (latest description)	
Organs	Leaf
Specimens	Hypotypes: PA20624, PA20722
Locality	Locality PA106, Wardell Ranch, Utah
Formation	Green River Flora
Country	USA
Reference (age)	Smith *et al*. (2003)
Oldest stratum	Eocene
Age quality	Revised (radioisotropic)
Age justification	The Green River Formation is thought to encompass a ~5 My period between ca. 53.5 and 48.5 Ma, based on the global marine O isotope record.
Reference (fossil relationships)	MacGinitie (1969)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Pre-molecular era (before 1990)
Min. age (Mya)	48.5
Calibration	crown Burserinae
Node justification	*Bursera inaequalateralis* (Lesq.) MacGinitie is similar to several extant *Bursera* species (MacGinitie, 1969), namely *B. penicillata* in *B*. subg. *Elaphrium* and *B. tomentosa*. I therefore assign this fossil conservatively to the stem of *Bursera* (= crown of Burserinae).

Calibration no.	C09
Family	Burseraceae
Full taxon name	†*Bursericarpum aldwickense* Chandler
Reference (first description)	Chandler (1961)
Reference (latest description)	
Organs	Pyrene, seed
Specimens	Holotype: v.30054
Locality	Upper Fish Tooth Bed, Bognor, Sussex
Formation	London Clay Flora
Country	UK
Reference (age)	Chandler (1961)
Oldest stratum	Ypresian
Age quality	Unrevised (old source < 2000)

Age justification	Chandler (1961) places the London Clay Flora in the Ypresian, an age that has apparently not been challenged since.
Reference (fossil relationships)	Magallón *et al*. (2015)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	47.8
Calibration	stem Protium alliance
Node justification	*Bursericarpum aldwickense* is thought to be a relative of the Protium alliance based on the number of pyrenes per fruit (Weeks et al., 2005; Daly et al., 2011). I therefore use this fossil to calibrate the stem of the Protium alliance of Burseraceae.

Calibration no.	C10
Family	Anacardiaceae
Full taxon name	†*Coahuiloxylon terrazasiae* Estrada-Ruiz, Martínez-Vabrera & Cevallos-Ferriz
Reference (first description)	Estrada-Ruiz *et al*. (2010)
Reference (latest description)	
Organs	Wood
Specimens	Holotype: IGM-PB 1295, LPB 4679-4693
Locality	Atascoso Ranch, 7 km N of Melchor Mu´zquiz town, Mu´zquiz Municipality, Coahuila
Formation	Olmos Formation
Country	Mexico
Reference (age)	Estrada-Ruiz *et al*. (2010)
Oldest stratum	Campanian
Age quality	Revised (stratigraphic)
Age justification	The Olmos Formation has been placed in the early Maastrichtian based on foraminifers, dinoflagellates, acritarchs, bivalve fauna and pollen. Ammonite evidence suggests places the formation in the late Campanian age based on ammonites. Therefore, I use late Campanian-early Maastrichtian for this calibration.
Reference (fossil relationships)	Estrada-Ruiz *et al*. (2010)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only

Min. age (Mya)	72.1
Calibration	stem Anacardiaceae
Node justification	The wood structure of *Coahuiloxylon terrazasiae* resembles that of Anacardiaceae and Burseraceae based on the presence of indistinct growth rings, septate and/or nonseptate fibers, alternate intervessel pits and vessel-ray parenchyma pits with reduced borders, simple perforation plates, scanty paratracheal, vasicentric and apotracheal diffuse axial parenchyma, and heterocellular rays (Estrada-Ruiz *et al*., 2010). This is also supported by molecular and anatomical analyses (Terrazas 1994). There is no single wood anatomical character separating these two families; however, the combination of type IIA rays and absence of radial canals place the fossil in *Coahuiloxylon* or *Mauria* in Anacardiaceae (Terrazas, 1994; Estrada-Ruiz et al., 2010). *Coahuiloxylon* and *Mauria* share other diagnostic features of Anacardiaceae such as presence of both nonseptate and septate fibers, paratracheal and apotracheal parenchyma, and heterogeneous type IIA rays (Estrada-Ruiz *et al*., 2010). I therefore use this fossil conservatively to calibrate the stem node of Anacardiaceae to a minimum age of 72.1 Mya.

Calibration no.	C11
Family	Anacardiaceae
Full taxon name	†*Choerospondias sheppeyensis* (Reid & Chandler) Chandler
Reference (first description)	Reid & Chandler (1933)
Reference (latest description)	Chandler (1961)
Organs	Fruit, seed
Specimens	Holotype: V.22554
Locality	Island of Sheppey
Formation	London Clay Flora
Country	UK
Reference (age)	Chandler (1961)
Oldest stratum	Ypresian
Age quality	Unrevised (old source < 2000)
Age justification	Chandler (1961) places the London Clay Flora in the Ypresian, an age that has apparently not been challenged since.
Reference (fossil relationships)	Chandler (1961)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Pre-molecular era (before 1990)
Min. age (Mya)	47.8

Calibration	crown Anacardiaceae
Node justification	These fruits most resemble *Sclerocarya* and *Choerospondias*, but can be separated from extant *Sclerocarya* on the higher number of locules and the absence of woody plugs in their apices (Reid & Chandler, 1933). *Choerospondias* has a similar number of locules but a larger endocarp, and the longitudinal rows of holes on the lateral surfaces between the locules in extant species are fewer and more irregular in the fossils. The fossils are thought to be most closely realted to the extant *C. axillaris* (Roxb.) (Chandler 1961). However, due to the similarity to *Sclerocarya* and broad age range for the Flora I will use this fossil conservatively to date the crown node of Anacardiaceae to a minimum of 47.8 Mya.

Calibration no.	C12
Family	Anacardiaceae
Full taxon name	†*Dracontomelon macdonaldii* (Berry) Herrera, Manchester & Jaramillo
Reference (first description)	Herrera *et al*. (2012)
Reference (latest description)	
Organs	Fruit, seed
Specimens	Lectotype: USNM 35316b
Locality	Tonosí River, Punta Búcaro, Los Santos State, Azuero Peninsula
Formation	Búcaro Formation
Country	Panama
Reference (age)	Herrera *et al*. (2012)
Oldest stratum	Late Eocene
Age quality	Revised (stratigraphic)
Age justification	Mollusc and foraminifera evidence variously suggest an early to late Eocene age for this sequence.
Reference (fossil relationships)	Herrera *et al*. (2012)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	33.9
Calibration	crown Spondioideae (-*Campnosperma*)
Node justification	The fossil endocarps resemble most genera of the Spondioideae subfamily of Anacardiaceae, and particularly the extant genus *Dracontomelon* (Herrera *et al*. 2012). The combination of the presence of endocarps with five single-seeded locules, radially-arranged convex-dorsal-apical germination valves without median longitudinal slits, five

	lacunae, ten peripheral equatorial apertures connected to lacunae, and the tissue organisation of the endocarp is unique to *Dracontomelon* (Herrera *et al*. 2012). However, due to the presence of characters also featuring in other Spondioid genera I use this fossil conservatively to calibrate the crown of Spondioideae, excluding *Campnosperma*.
Calibration no.	C13
Family	Anacardiaceae
Full taxon name	†*Spondias rothwellii* Herrera, Carvalho, Jaramillo & Manchester sp. nov.
Reference (first description)	Herrera *et al*. (2019)
Reference (latest description)	
Organs	Fruit, seed
Specimens	Holotype: UF60773. Other specimens: UF60774, UF60775, UF60776, UF60784, UF60777, UF60778–UF60783.
Locality	Gaillard Cut section (Lirio East outcrop) of the southeastern part of the Panama Canal
Formation	Lower Cucaracha Formation
Country	Panama
Reference (age)	Herrera *et al*. (2019)
Oldest stratum	Early Miocene
Age quality	Revised (radioisotropic)
Age justification	The age of this formation has been deduced from mammals, pollen, marine invertebrates, magnetostratigraphy, and radiometric dating evidence, all of which indicate an age of ca. 19– 18.5 Ma for the Cucaracha Formation.
Reference (fossil relationships)	Herrera *et al*. (2019)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	18.5
Calibration	stem *Spondias* + *Allospondias*
Node justification	Fruits of *S. rothwellii* are thought to be indistinguishable from some extant species of *Spondias* based on endocarp features - particularly the deer antler–like outline of the in transverse section and ventral rows of orbicules within the lacunae that align the fossils with extant Neotropical species (Herrera *et al*. 2019). Hence, the fossil is most similar morphologically to the extant New World representatives of *Spondias*. However, I use this fossil conservatively to calibrate the stem of *Spondias* and *Allospondias* to a minimum age of 18.5 Mya.

Calibration no.	C14
Family	Anacardiaceae
Full taxon name	†*Anacardium germanicum* Manchester *et al.*
Reference (first description)	Manchester *et al*. (2007)
Reference (latest description)	
Organs	Fruit
Specimens	Holotype: SM.B Me 7139. Paratypes: SM.BMe1770,2034,7156,18095.
Locality	Messel Pit, Messel oil shale, Messel
Formation	Messel Formation
Country	Germany
Reference (age)	Manchester *et al*. (2007)
Oldest stratum	Middle Eocene (Lutetian assumed)
Age quality	Revised (stratigraphic)
Age justification	Radiometric dating of the underlying volcaniclastic material suggests a Middle Eocene age for the Messel Formation.
Reference (fossil relationships)	Manchester *et al*. (2007)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	41.2
Calibration	stem *Fegimanra* + *Anacardium*
Node justification	The hypocarp is a specialised structure known only in from Anacardiaceae and the presence of a hypocarp in the fossil specimens aligns the fossil to *Semecarpus*, *Fegimanra* and *Anacardium* (Manchester *et al*. 2007). Based on the shape and surfaces of the drupe and the attachment position of the pedicel, the assignment of the fossil was narrowed to either *Fegimanra* or *Anacardium*; based on the shape of the hypocarp it was decided that this fossil belongs to *Anacardium* (Manchester *et al*. 2007). Although I accept the assignment of this fossil to *Anacardium*, based on the shared characters with *Fegimanra*, I take a conservative approach and use this fossil to calibrate the stem of *Anacardium* and *Fegimanra*.
Calibration no.	C15
Family	Anacardiaceae
Full taxon name	†*Mangifera paleoindica* Sawangchote, Grote, and Dilcher
Reference (first description)	Sawangchote *et al.* (2009)

Reference (latest description)	
Organs	Leaf
Specimens	Holotype: SUT083
Locality	Ban Pa Kha mine, Li Basin, Li District, Lamphun Province
Formation	Ban Pa Kha Subbasin
Country	Thailand
Reference (age)	Sawangchote *et al.* (2009)
Oldest stratum	Late Oligocene
Age quality	Revised (stratigraphic)
Age justification	The age determination of the Ban Pa Kha Subbasin is uncertain and ranges from Paleogene to early Miocene, on the basis of leaf fossils and pollen. However, the leaf evidence has been discredited and pollen evidence is considered to be more reliable. Therefore age determined by pollen evidence of Oligocene to early Miocene is taken.
Reference (fossil relationships)	Sawangchote *et al.* (2009)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	23.03
Calibration	stem Mangifera
Node justification	Leaf architecture was studied in detail for multiple genera in Anacardiaceae and the authors are confident that the specimens belong to the modern genus *Mangifera*. Comparison of leaf architecture to many extant *Mangifera* species indicates this species is most similar to extant species *Mangifera indica* (Sawangchote *et al.* 2009). I accept the assignment of this fossil to *Mangifera*, however take a conservative approach to dating and use this fossil to calibrate the stem of *Mangifera*.
Calibration no.	C16
Family	Anacardiaceae
Full taxon name	†*Cotinus fraterna* (Lesquereux) MacGinitie
Reference (first description)	MacGinitie (1953)
Reference (latest description)	Manchester (2001)
Organs	Leaf
Specimens	Syntypes: USNM 405894, USNM 405895
Locality	Florissant, Colorado
Formation	Florissant Formation

Country	USA
Reference (age)	Manchester (2001)
Oldest stratum	Late Eocene
Age quality	Revised (radioisotropic)
Age justification	Most recently, potassium Argon dating dates the Florissant Formation at 35.0 ± 0.8 Ma, and 40Ar/39Ar dating places the formation at 34.07 ± 0.10 Ma. As such, the Florissant beds could either be late Eocene or early Oligocene.
Reference (fossil relationships)	MacGinitie (1953)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Pre-molecular era (before 1990)
Min. age (Mya)	33.9
Calibration	stem *Cotinus*
Node justification	Assignment to *Cotinus fraterna* by MacGinitie (1953) does not seem to have been disputed since its publication and revision by Manchester; I therefore accept its placement in *Cotinus* and use this fossil to calibrate the stem node of the genus.

Calibration no.	C17
Family	Anacardiaceae
Full taxon name	*†Pistacia* sp.
Reference (first description)	Grímsson *et al*. (2020)
Reference (latest description)	
Organs	Pollen
Specimens	NA
Locality	Lavanttal Basin
Formation	Lavanttal Basin
Country	Austria
Reference (age)	Grímsson *et al*. (2011)
Oldest stratum	Middle Miocene (middle to upper Serravallian)
Age quality	Unrevised (recent source)
Age justification	The stratigraphical position within the sequence, the thickness of the sediments surrounding the coals seems, estimated accumulation rates, and hiatus events above the seams suggests the basin is most likely between 12.6 and 12.5 Ma.
Reference (fossil relationships)	Grímsson *et al*. (2020)

Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	12.7
Calibration	stem Pistacia
Node justification	*Pistacia* is characterised by unique pollen that has been described in detail (Grímsson *et al*., 2020). The apertures of the fossil pollen from Lavanttal correspond to the colpi of *P. terebinthus* L. as described by Halbritter and Weis (2016). Many debatable *Pistacia* fossils have been identified up to the Cretaceous (Edwards and Wonnacott 1935; Grímsson *et al.* 2020). Based on the unique and well-described morphology of *Pistacia* pollen and potential presence of *Pistacia* pollen in the Cretaceous fossil record, I think it is reasonable to apply a middle Miocene age as a minimum constraint on the stem node of *Pistacia*.

Calibration no.	C18
Family	Anacardiaceae
Full taxon name	†*Loxopterygium laplayense* Burnham and Carranco
Reference (first description)	Burnham & Carranco (2004)
Reference (latest description)	
Organs	Fruit
Specimens	Holotype: EPN 1054
Locality	RJB 9602 (‘‘Azogues View’’), Cuenca Basin
Formation	Azogues Formation
Country	Ecuador
Reference (age)	Hungerbühler *et al*. (2002)
Oldest stratum	Middle Miocene
Age quality	Unrevised (recent source)
Age justification	Deposits of the Azogues or Guapan Members of the Azogues Formation have been dated at 13.0–10.2 Ma.
Reference (fossil relationships)	Burnham & Carranco (2004)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	13.0

Calibration	stem *Loxopterygium*
Node justification	This fossil is distinctive in its medially placed stigma remnant on the backbone of the wing, its small size, the remnant calyx at the proximal end of the locule, and the frequently erose to serrate wing tip. This combination of characters assigns the specimens in the genus Loxopterygium of the Anacardiaceae, however it cannot be assigned to any of the extant species of *Loxopterygium* (Burnham & Carranco 2004). I therefore use this fossil to constrain the stem node of *Loxopterygium.*
Calibration no.	C19
Family	Simaroubaceae
Full taxon name	†*Ailanthus confucii* Unger
Reference (first description)	Collinson *et al.* (2012)
Reference (latest description)	
Organs	Fruit
Specimens	Specimens: SM.B Me 4006, 4232, 4233, 4747, 4785, 4786, 16837, 21808, 23395, 24010.
Locality	Messel Pit, Messel oil shale, Messel
Formation	Messel Formation
Country	Germany
Reference (age)	Collinson *et al.* (2012)
Oldest stratum	Middle Eocene (Lutetian assumed)
Age quality	Revised (stratigraphic)
Age justification	Radiometric dating of the underlying volcaniclastic material suggests a Middle Eocene age for the Messel Formation.
Reference (fossil relationships)	Collinson *et al.* (2012)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	41.2
Calibration	stem *Ailanthus*
Node justification	These specimens belong to a widespread morphospecies which is also known from North America and Asia (Corbett and Manchester 2004). Comparisons with extant species indicate the closest similarity with *Ailanthus altissima* of China (Collinson *et al*. 2012). I accept the assignment of these specimens to *Ailanthus* and use them to calibrate the stem node of the genus.
Calibration no.	C20

Family	Meliaceae
Full taxon name	†*Cedrela* sp.
Reference (first description)	Hickey & Hodges (1975)
Reference (latest description)	
Organs	Leaf
Specimens	U.S. National Museum specimen 208538
Locality	Dubois, Wyoming
Formation	Wind River Formation
Country	USA
Reference (age)	Fan *et al*. (2011)
Oldest stratum	Eocene
Age quality	Revised (radioisotropic)
Age justification	Petrographic, detrital zircon U-Pb geochronology, and paleocurrent analyses date the Wind River Range at ca. 53–51 Ma.
Reference (fossil relationships)	Hickey & Hodges (1975)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Pre-molecular era (before 1990)
Min. age (Mya)	51
Calibration	crown Cedreloideae
Node justification	The combination of entire-margined, pinnately compound leaves with an indeterminate leaflet arrangement, angular brochidodromous arches with an outer secondary branch merging with prominent looped marginal venation is restricted to the family Meliaceae. Within extant Meliaceae brochidodromous secondaries are common in *Swietenia* and relatively rare in the closely related genus *Cedrela*. However, only *Cedrela* shows the same pattern of intercostal venation (Hickey & Hodges 1975). Given the similarity of this leaf to *Cedrela* and *Swietenia*, I have chosen to use this fossil as the minimum crown age for Cedreloideae in Meliaceae.

Calibration no.	C21
Family	Meliaceae
Full taxon name	†*Cedrela merrilli* (Chaney) Brown
Reference (first description)	Meyer & Manchester (1997)
Reference (latest description)	Manchester & McIntosh (2007)

Organs	Leaf, seed
Specimens	UF278-50012
Locality	Crooked River Valley, Post, Oregon
Formation	John Day Formation
Country	USA
Reference (age)	Manchester & McIntosh (2007)
Oldest stratum	Late Eocene
Age quality	Revised (radioisotropic)
Age justification	40Ar/39Ar radioisotopic dating gives the formation a date of 36.21 ± 0.26 Ma.
Reference (fossil relationships)	Meyer & Manchester (1997)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	36.21
Calibration	stem *Cedrela* + *Toona*
Node justification	The five locules and numerous imbricately positioned winged seeds of this fruit aligns this fossil with the extant Meliaceae genera of *Cedrela* and *Toona* (Manchester & McIntosh, 2007; Meyer & Manchester, 1997). Although the authors suggest the the elongated shape is more consistent with *Cedrela*, I take a conservative approach and use the fossil to calibrate the stem node of *Cedrela* + *Toona*.

Calibration no.	C22
Family	Meliaceae
Full taxon name	†*Swietenia miocenica* Castañeda-Posadas & Cevallos-Ferriz
Reference (first description)	Castañeda-Posadas & Cevallos-Ferriz (2007)
Reference (latest description)	
Organs	Flower
Specimens	Holotype: Collection of the Museo de Paleontologia Eliseo Palacios Aguilera, sample no. 6114, Tuxtla Gutierrez, Chiapas
Locality	Simojovel de Allende, Chiapas
Formation	Simojovel Group
Country	Mexico
Reference (age)	Castañeda-Posadas & Cevallos-Ferriz (2007)
Oldest stratum	Late Oligocene
Age quality	Revised (stratigraphic)

Age justification	Foraminifera evidence suggest an age of 22.5–26.0 Ma (Early Miocene–Late Oligocene) for the group.
Reference (fossil relationships)	Castañeda-Posadas & Cevallos-Ferriz (2007)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	22.5
Calibration	stem *Swietenia*
Node justification	The complete fusion of the staminal tube, 5-mery, contorted insertion of floral segments and the presence of ciliolated petals and sepals clearly place this fossil flower in Meliaceae. It is most similar to the genus *Swietenia* based on the cylindrical to urceolated staminal tube with a spiny or teethed tip and exposed anthers alternating with the spines (Castañeda-Posadas & Cevallos-Ferriz 2007). I accept the assignment of this fossil to *Swietenia* and use it to calibrate the minimum age for the stem of the genus.

Calibration no.	C23
Family	Meliaceae
Full taxon name	†*Manchestercarpa vancouverensis* Atkinson
Reference (first description)	Atkinson (2020)
Reference (latest description)	
Organs	Fruit, seed
Specimens	Holotype: SH790 B1 bot
Locality	Shelter Point, Vancouver Island, British Columbia
Formation	Spray Formation
Country	Canada
Reference (age)	Ward *et al*. (2012)
Oldest stratum	Middle Campanian
Age quality	Unrevised (recent source)
Age justification	Stratigraphic and magnetochrons C33n and C33r of the global polarity time scale suggest an age range for Shelter Point of 79–72 Ma.
Reference (fossil relationships)	Atkinson (2020)
Node assignment method	Phylogenetic analysis

Reconciliation method	Combined morphological and molecular analysis (total evidence)
Min. age (Mya)	72.1
Calibration	crown Melieae
Node justification	In the total-evidence analysis of Atkinson (2020), *Manchestercarpa vancouverensis* was recovered within the Melioideae in a clade consisting of *Melia azedarach* L. and *Melia yakimaensis* Pigg, DeVore, Benedict & Creekmore. This clade characterised by a drupaceous fruit morphology. The author suggests that the close relationship of *Manchestercarpa* with *Melia* indicates that the fossil represents a crown member of the tribe Melieae. Given the rigor of the analysis, I accept the assignment of *Manchestercarpa* and use it to calibrate the crown of the Melieae tribe of Meliaceae.

Calibration no.	C24
Family	Rutaceae
Full taxon name	†*Rutaspermum biornatum* Knobloch & Mai
Reference (first description)	Knobloch & Mai (1986)
Reference (latest description)	
Organs	Seed
Specimens	Holotype: MMG (9231)
Locality	Walbeck, graue Tone
Formation	
Country	Germany
Reference (age)	Magallón *et al*. (2015)
Oldest stratum	Maastrichtian
Age quality	Unrevised (old source < 2000)
Age justification	Stratigraphy.
Reference (fossil relationships)	Magallón *et al.* (2015)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	66
Calibration	crown Rutaceae
Node justification	The seeds of *Rutaspermum biornatum* are thought to be the oldest reliable representatives of Rutaceae (Gregor 1988). *Rutaspermum* is closely related to the subfamily Zanthoxyleae (=Amyridoideae), particularly *Zanthoxylum* and *Fagara* (Magallón *et al.,* 2015). However, traditional sub-classifications of Rutaceae are not

retrieved in our analysis as monophyletic, and therefore this fossil is used to constrain the crown node of Rutaceae.

Calibration no.	C25
Family	Rutaceae
Full taxon name	†*Clausena* sp.
Reference (first description)	Pan (2010)
Reference (latest description)	
Organs	Leaf
Specimens	CH41-70, CH41-67, CH41-73, CH41-81
Locality	Sublocality CH41, Gondar, Amhara District
Formation	Guang River flora
Country	Ethiopia
Reference (age)	Pan (2010)
Oldest stratum	Late Oligocene
Age quality	Revised (radioisotropic)
Age justification	The age of the Guang River flora is well constrained based on K/Ar radiometric dating methods, 40Ar/39Ar radiometric dating, paleomagnetic reversal stratigraphy and 206Pb/238U analysis. As such the age of 27.23± 0.1 Ma is applied to the flora.
Reference (fossil relationships)	Pan (2010)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	27.23
Calibration	stem *Clausena* + *Glycosmis*
Node justification	The the crenate margins of the fossil leaflets and presence “rutoid” teeth are thought to be consistent with the family Rutaceae (Pan, 2010). The multicellular uniseriate hairs suggest an affinity with the genus *Clausena* (Pan, 2010). I use this fossil conservatively to constrain the minumum age of *Clausena* + *Glycosmis* to 27.23 Mya.

Calibration no.	C26
Family	Rutaceae
Full taxon name	†*Citrus linczangensis* Xie et al.
Reference (first description)	Xie *et al*. (2013)

Reference (latest description)	
Organs	Leaf
Specimens	Holotype: LUMCD090206-022A&B, Institute of Paleontology and Stratigraphy, Lanzhou University, China
Locality	Bangmai Village, Lincang City, Yunnan Province
Formation	Bangmai Formation
Country	China
Reference (age)	Xie *et al*. (2013)
Oldest stratum	Late Miocene
Age quality	Revised (stratigraphic)
Age justification	The Bangmai Formation is considered to be of late Miocene age (no later than 11.6 Ma), on the basis of floristic and stratigraphic correlations.
Reference (fossil relationships)	
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	11.6
Calibration	stem *Citrus*
Node justification	Together, the articulated and broadly winged petiole, well-developed intramarginal venation in the lower part of the lamina and the entire margin place this fossil in *Citrus* (Xie *et al*., 2013). This is considered to be the oldest reliable fossil of *Citrus*, and I assign it to the stem of the genus.
Calibration no.	C27
Family	Rutaceae
Full taxon name	†*Ptelea paliuruoides* (Brown) Manchester & O'Leary
Reference (first description)	Manchester & O'Leary (2010)
Reference (latest description)	
Organs	Fruit, seed
Specimens	Holotype: "Brown, 1934, Roan Creek, Colorado"
Locality	Colorado and Utah
Formation	Green River Formation
Country	USA
Reference (age)	Manchester & O'Leary (2010)
Oldest stratum	Middle Eocene

Age quality	Revised (radioisotropic)
Age justification	The Green River Formation is thought to encompass a ~5 My period between ca. 53.5 and 48.5 Ma, based on the global marine O isotope record.
Reference (fossil relationships)	Manchester & O'Leary (2010)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	48.5
Calibration	stem *Ptelea* + *Peltostigma* + *Plethadenia* + *Decazyx* clade
Node justification	Evidence of pellucid dots on this fossil are an important feature in common with Rutaceae; along with the locule structure, thin pedicel and hypogynous perianth, this fossil is though to be most closely aligned with *Ptelea* (Manchester & O'Leary, 2010). I take a conservative approach with this fossil and use it to calibrate the stem node of the clade including *Ptelea* + *Peltostigma* + *Plethadenia* + *Decazyx*.

Calibration no.	C28
Family	Rutaceae
Full taxon name	†*Zanthoxylum* sp.
Reference (first description)	Chandler (1961)
Reference (latest description)	
Organs	Seed
Specimens	Holotype: V.29693
Locality	Oldhaven Beds, Bishopstone, Herne Bay, Kent
Formation	London Clay Flora
Country	UK
Reference (age)	Chandler (1961)
Oldest stratum	Ypresian
Age quality	Unrevised (old source < 2000)
Age justification	Chandler (1961) places the London Clay Flora in the Ypresian, an age that has apparently not been challenged since.
Reference (fossil relationships)	Chandler (1961)
Node assignment method	Intuitive or unspecified (trusted source)

Reconciliation method	Pre-molecular era (before 1990)
Min. age (Mya)	47.8
Calibration	stem *Zanthoxylum*
Node justification	Seed has morphological affinities with *Zanthoxylum*. Although there are no extant species in Europe, *Zanthoxylum* has a rich and reliable fossil record, and the oldest fossils are from Early Eocene sediments in England (Chandler 1961; Gregor 1989). I therefore accept the assignment of this fossil to *Zanthoxylum* and use it to calibrate the minimum age of the stem node of the genus.

Calibration no.	C29
Family	Rutaceae
Full taxon name	*†Euodia costata* (Chandler) Tiffney
Reference (first description)	Tiffney (1981)
Reference (latest description)	
Organs	Seed
Specimens	Holotype: V 20062, British Museum (Natural History)
Locality	Central and south London and north Kent
Formation	Reading Formation
Country	UK
Reference (age)	Aldiss (2014)
Oldest stratum	Latest Paleocene (Thanetian)
Age quality	Revised (radioisotropic)
Age justification	The Reading Formation is placed in the Early Eocene (earliest Ypresian), possibly including the latest Paleocene (Thanetian), by reference to magnetostratigraphy and stable isotope stratigraphy.
Reference (fossil relationships)	Tiffney (1981)
Node assignment method	Intuitive or unspecified (trusted source)
Reconciliation method	Molecular tree only
Min. age (Mya)	56
Calibration	crown Rutoideae clade
Node justification	This fossil was originally described as *Phellodendron costatum* Chandler and was later transferred to *Euodia* by Tiffney (1981). Since then, many extant species have been transferred to *Tetradium* and *Melicope*, and the species most similar to the fossil *Euodia costata* was transferred to *Tetradium*. Pending revision of the fossil in light of modern

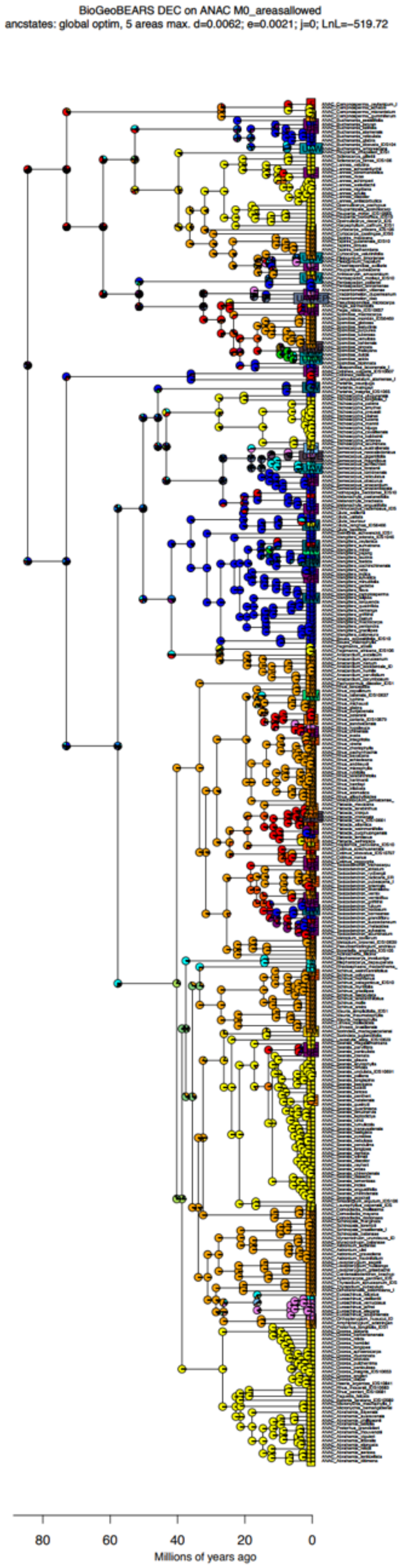
	taxonomy, I take a conservative approach with this fossil and assign it to calibrate the crown node of the Rutoideae clade, which contains *Euodia, Tetradium* and *Phellodendron*.

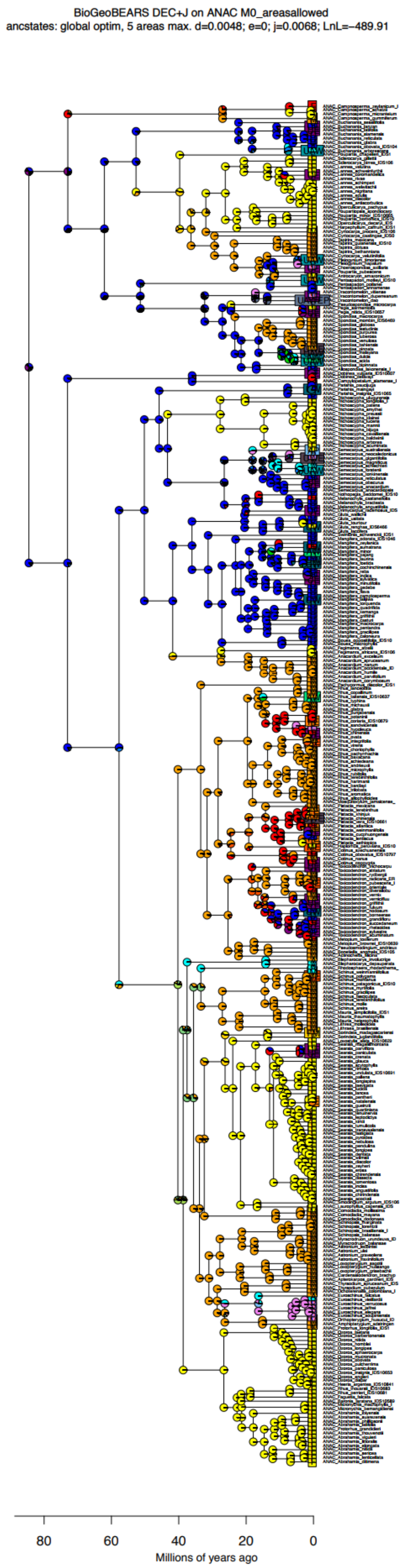
Calibration no.	C30
Family	Rutaceae
Full taxon name	†*Vepris* sp.
Reference (first description)	Pan (2010)
Reference (latest description)	
Organs	Leaf
Specimens	CH41-78 and CH41-99
Locality	Sublocality CH41, Gondar, Amhara District
Formation	Guang River flora
Country	Ethiopia
Reference (age)	Pan (2010)
Oldest stratum	Late Oligocene
Age quality	Revised (radioisotropic)
Age justification	The age of the Guang River flora is well constrained based on K/Ar radiometric dating methods, 40Ar/39Ar radiometric dating, paleomagnetic reversal stratigraphy and 206Pb/238U analysis. As such the age of 27.23± 0.1 Ma is applied to the flora.
Reference (fossil relationships)	Pan (2010)
Node assignment method	Apomorphy-based (apomorphies unlisted or tested)
Reconciliation method	Molecular tree only
Min. age (Mya)	27.23
Calibration	stem *Vepris*
Node justification	This fossil was assigned to the genus *Vepris* based on leaflet morphology and venation, stomatal structure, petiolule length, epidermis indumentum and cell wall structure (Pan, 2010). I accept this assignment and use this fossil to calibrate the minimum age for the stem of *Vepris*.

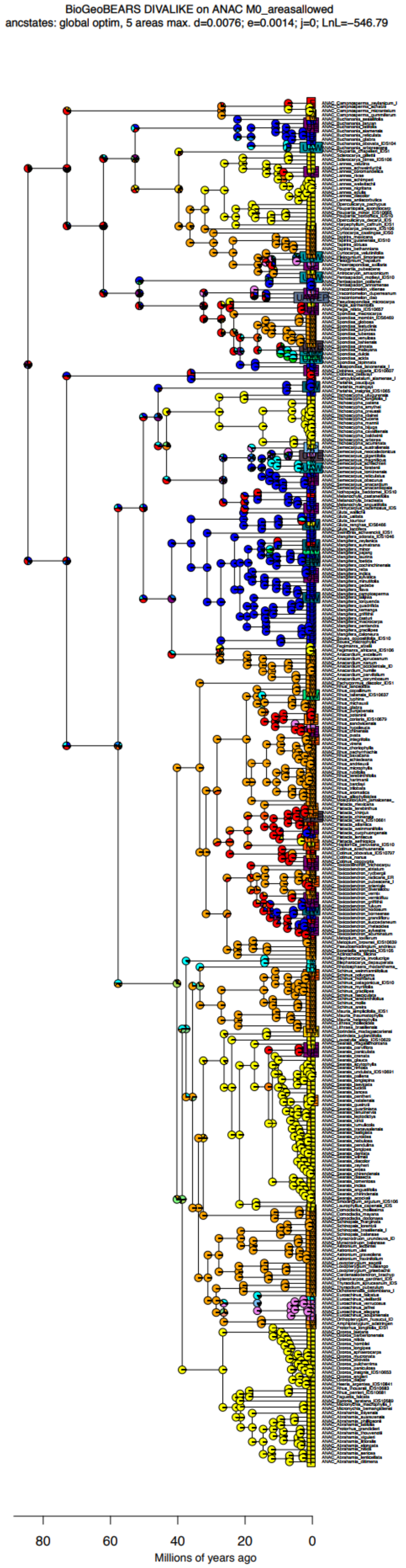
Appendix C3 AIC test of model fit in the ancestral area reconstruction of the species-level Anacardiaceae tree in BioGeoBEARS.

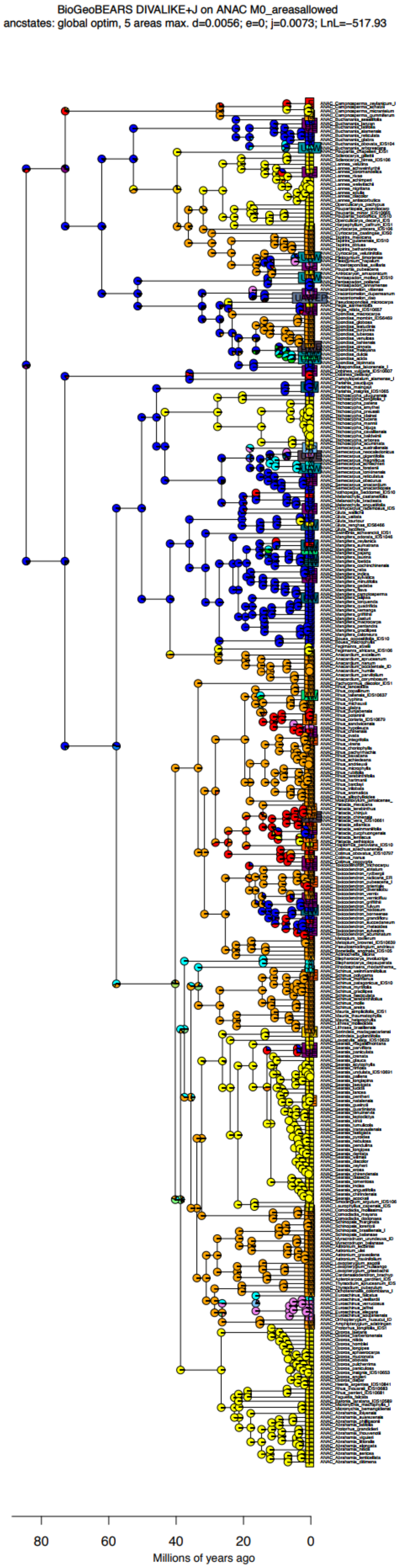
	LnL	numparams	d	e	j	AIC	AIC_wt
DEC	-567.8	2	0.0039	1.00E-12	0	1140	0.097
DEC+J	-564.6	3	0.0036	1.00E-12	0.0036	1135	0.9
DIVALIKE	-600.2	2	0.0049	1.00E-12	0	1204	8.40E-16
DIVALIKE+J	-596.8	3	0.0043	1.00E-12	0.0045	1200	9.40E-15
BAYAREALIKE	-718.7	2	0.01	0.01	0	1441	2.90E-67
BAYAREALIKE+J	-601.4	3	0.0024	0.0052	0.012	1209	9.30E-17

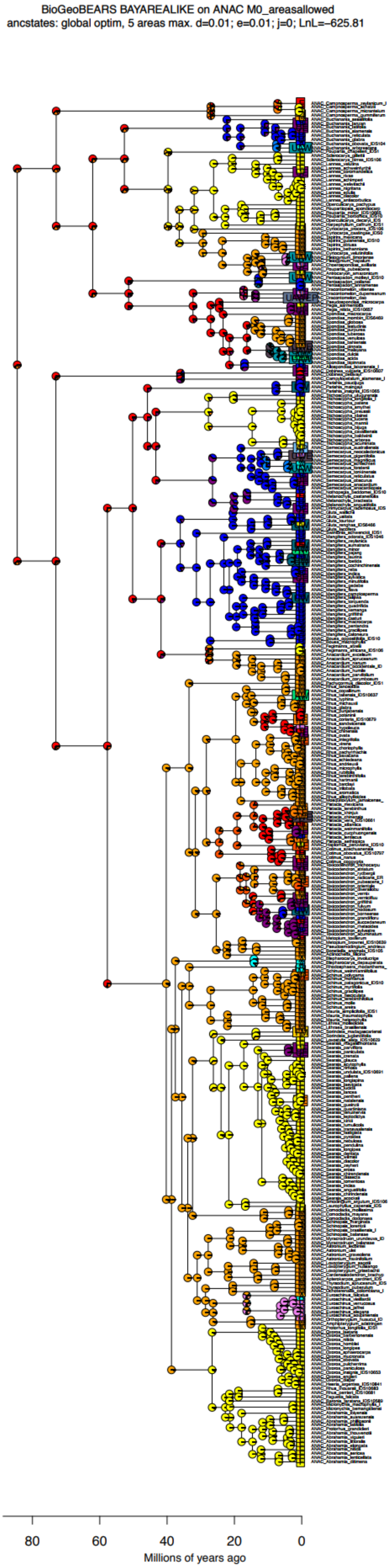
Appendix C4 Output of ancestral area reconstruction under a DEC (+J), DIVALIKE (+J) and BAYAREALIKE (+J) biogeographic model as generated in BioGeoBEARS. Colours of areas are as per Figure 5.4.

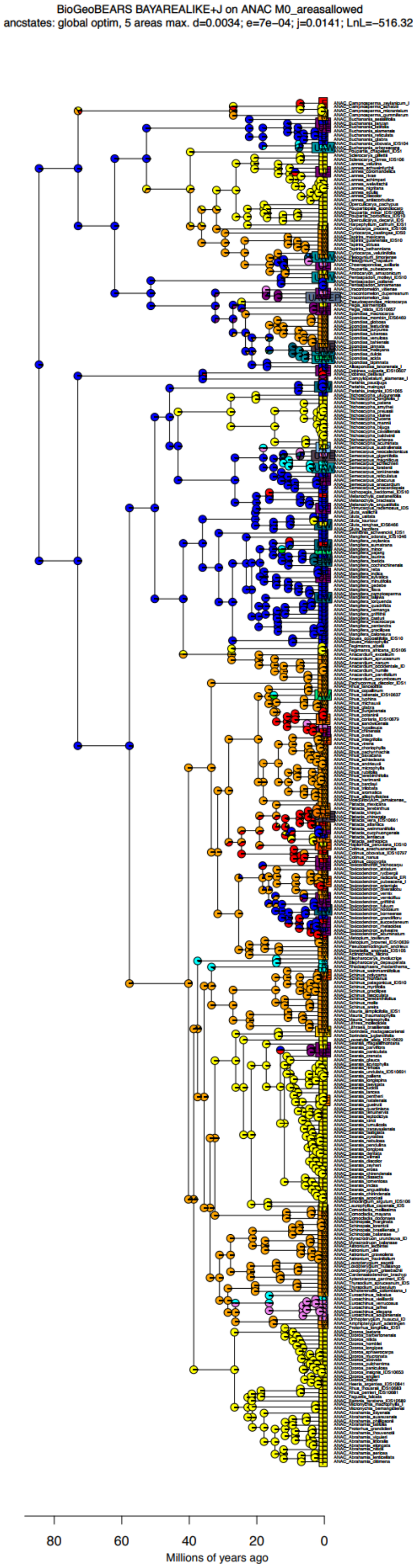



BioGeoBEARS DEC+J on ANAC M0_areasallowed
ancstates: global optim, 5 areas max. d=0.0048; e=0; j=0.0068; LnL=-489.91
80
60
40
20
0
Millions of years ago

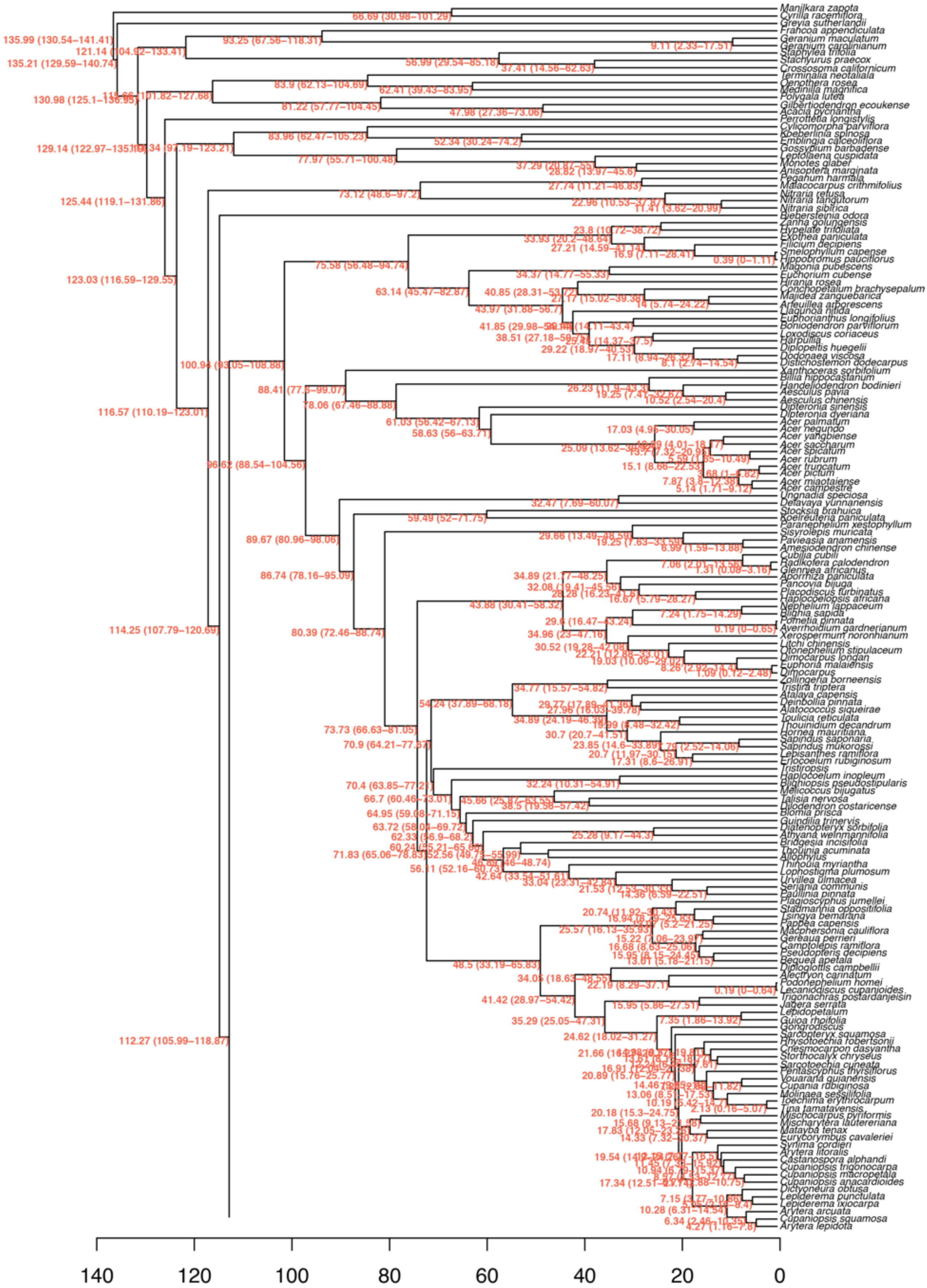

BioGeoBEARS DIVALIKE on ANAC M0_areasallowed
ancstates: global optim, 5 areas max. d=0.0076; e=0.0014; j=0; LnL=-546.79
80
60
40
20
0
Millions of years ago

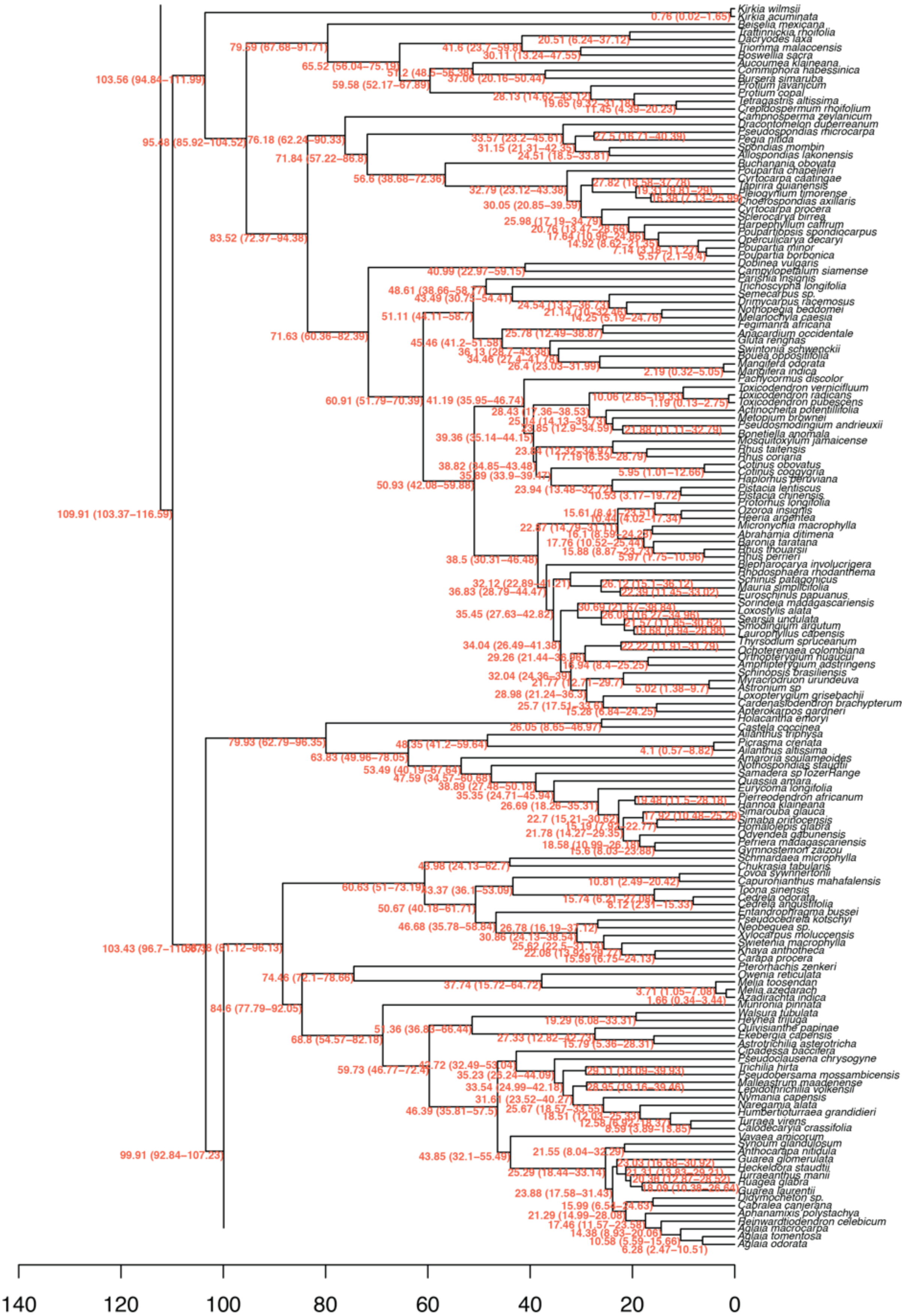

BioGeoBEARS DIVALIKE+J on ANAC M0_areasallowed
ancstates: global optim, 5 areas max. d=0.0056; e=0; j=0.0073; LnL=-517.93
80
60
40
20
0
Millions of years ago

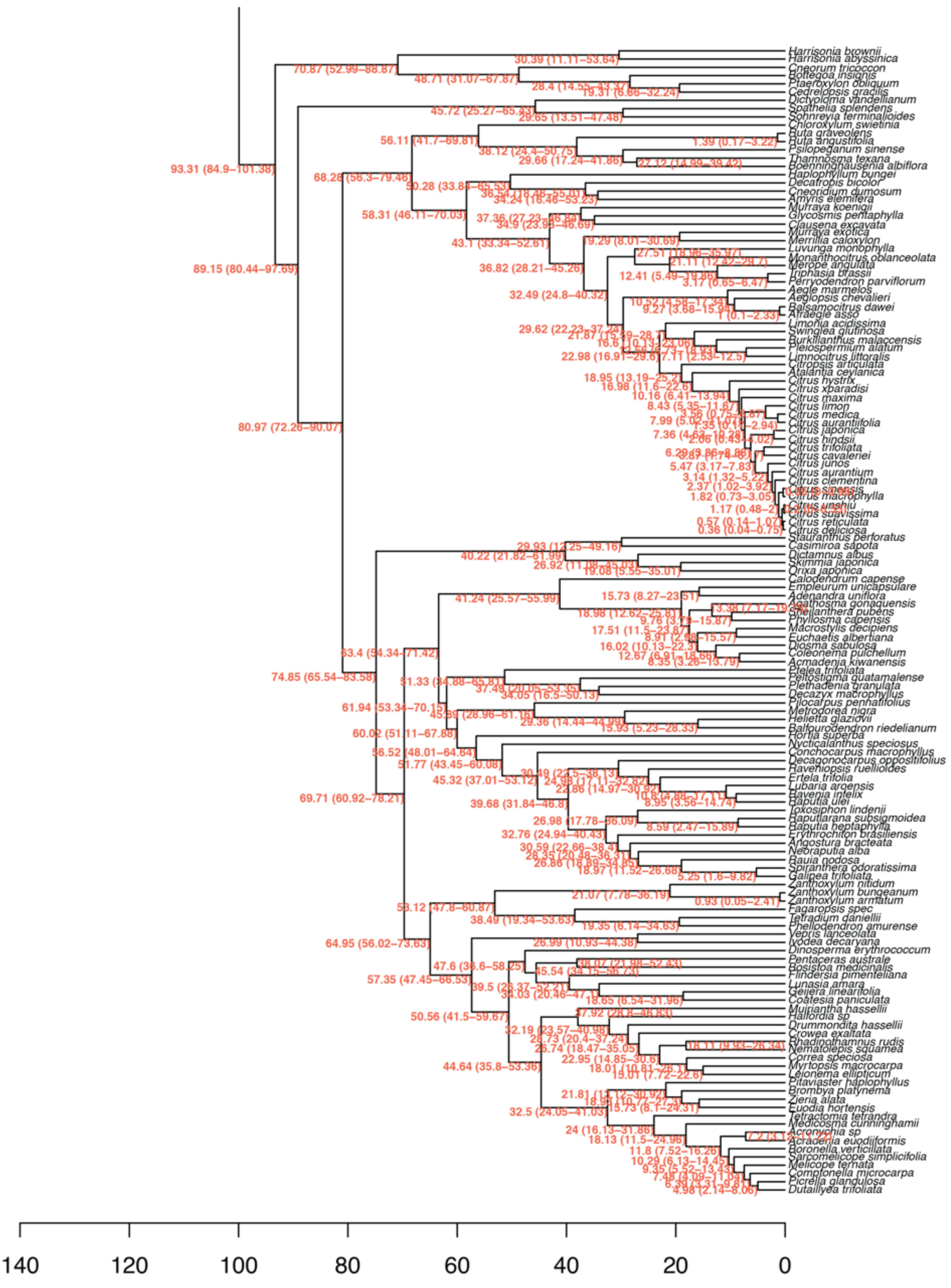

BioGeoBEARS BAYAREALIKE on ANAC M0_areasallowed
ancstates: global optim, 5 areas max. d=0.01; e=0.01; j=0; LnL=-625.81
80
60
40
20
0
Millions of years ago


BioGeoBEARS BAYAREALIKE+J on ANAC M0_areasallowed
ancstates: global optim, 5 areas max. d=0.0034; e=7e−04; j=0.0141; LnL=−516.32
80
60
40
20
0
Millions of years ago

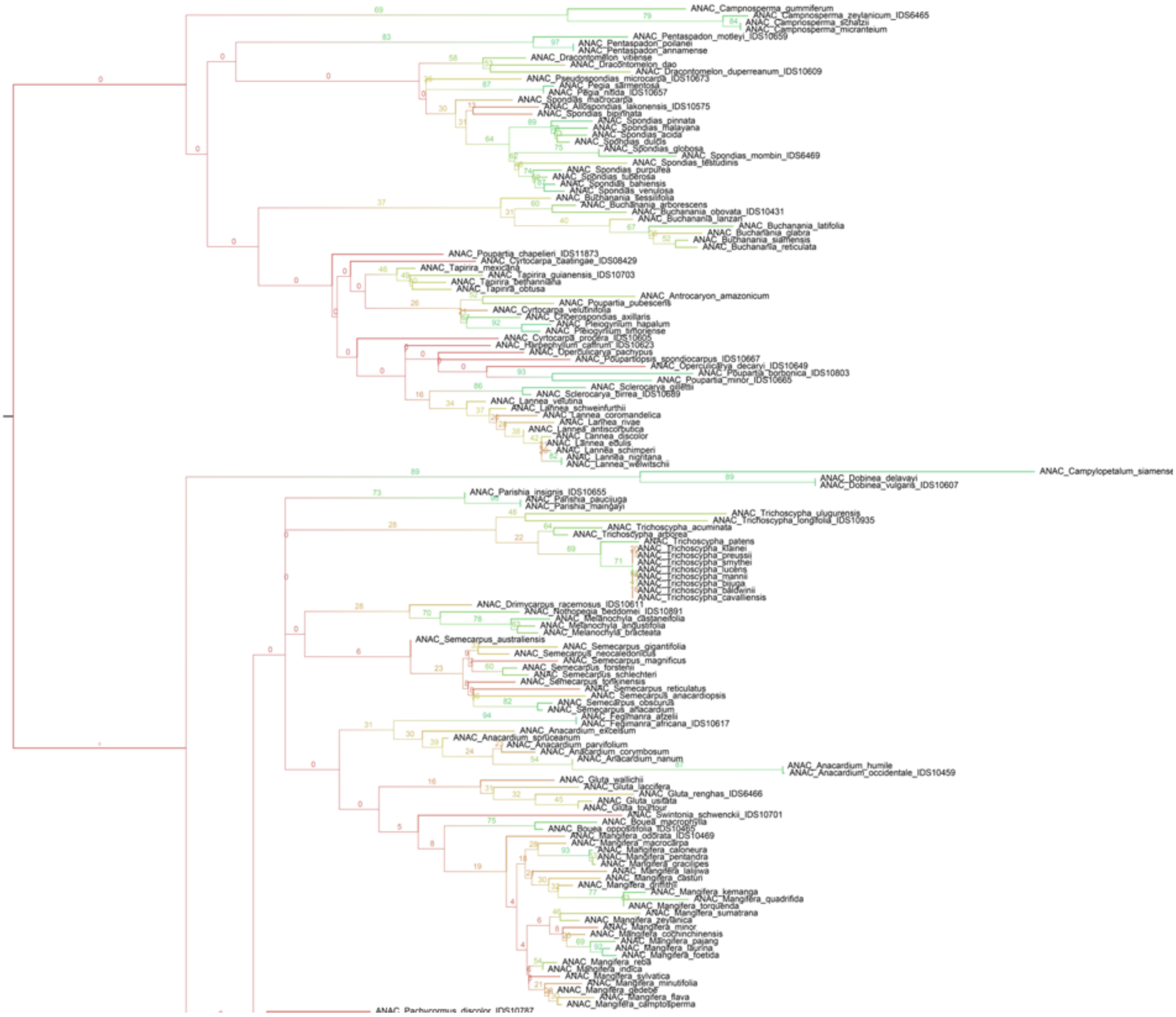
Appendix C5 Genus-level Sapindales tree including node ages with 95% HPD confidence interval shown in parentheses.

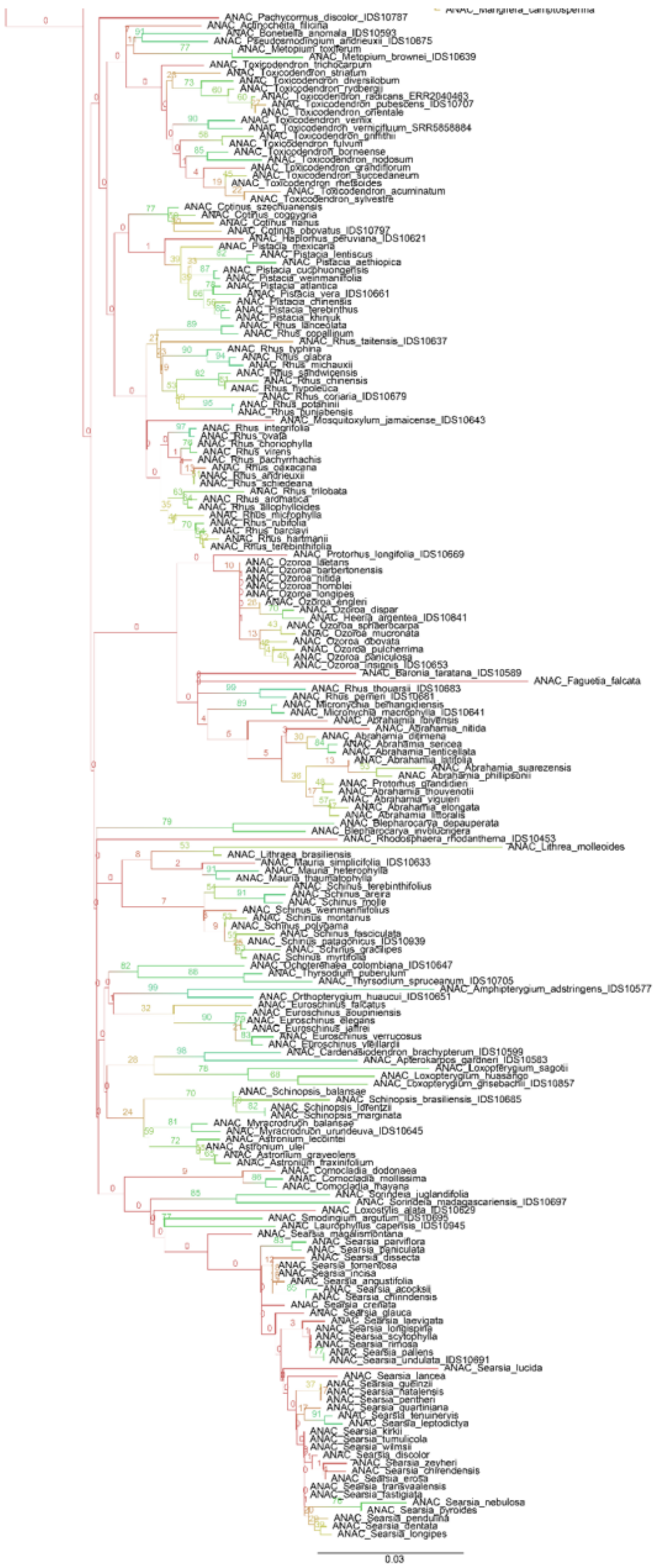



Kirkia wilmsii
Kirkia acuminata
Beiselia mexicana
Trattinnickia rhoifolia
Dacryodes laxa
Triomma malaccensis
Boswellia sacra
Aucoumea klaineana
Commiphora habessinica
Bursera simaruba
Protium javanicum
Protium copal
Tetragastris altissima
Crepidospermum rhoifolium
Campnosperma zeylanicum
Dracontomelon duperreanum
Pseudospondias microcarpa
Pegia nitida
Spondias mombin
Allospondias lakonensis
Buchanania obovata
Poupartia chapelieri
Cyrtocarpa caatingae
Tapirira guianensis
Pleiogynium timorense
Choerospondias axillaris
Cyrtocarpa procera
Sclerocarya birrea
Harpephyllum caffrum
Poupartiopsis spondiocarpus
Operculicarya decaryi
Poupartia minor
Poupartia borbonica
Dobinea vulgaris
Campylopetalum siamense
Parishia insignis
Trichoscypha longifolia
Semecarpus sp.
Drimycarpus racemosus
Nothopegia beddomei
Melanochyla caesia
Fegimanra africana
Anacardium occidentale
Gluta renghas
Swintonia schwenckii
Bouea oppositifolia
Mangifera odorata
Mangifera indica
Pachycormus discolor
Toxicodendron vernicifluum
Toxicodendron radicans
Toxicodendron pubescens
Actinocheita potentillifolia
Metopium brownei
Pseudosmodingium andrieuxii
Bonetiella anomala
Mosquitoxylum jamaicense
Rhus taitensis
Rhus coriaria
Cotinus obovatus
Cotinus coggygria
Haplorhus peruviana
Pistacia lentiscus
Pistacia chinensis
Protorhus longifolia
Ozoroa insignis
Heeria argentea
Micronychia macrophylla
Abrahamia ditimena
Baronia taratana
Rhus thouarsii
Rhus perrieri
Blepharocarya involucrigera
Rhodosphaera rhodanthema
Schinus patagonicus
Mauria simplicifolia
Euroschinus papuanus
Sorindeia madagascariensis
Loxostylis alata
Searsia undulata
Smodingium argutum
Laurophyllus capensis
Thyrsodium spruceanum
Ochoterenaea colombiana
Orthopterygium huaucui
Amphipterygium adstringens
Schinopsis brasiliensis
Myracrodruon urundeuva
Astronium sp
Loxopterygium grisebachii
Cardenasiodendron brachypterum
Apterokarpos gardneri
Holacantha emoryi
Castela coccinea
Ailanthus triphysa
Picrasma crenata
Ailanthus altissima
Amaroria soulameoides
Nothospondias staudtii
Samadera spTozerRange
Quassia amara
Eurycoma longifolia
Pierreodendron africanum
Hannoa klaineana
Simarouba glauca
Simaba orinocensis
Homalolepis glabra
Odyendea gabunensis
Perriera madagascariensis
Gymnostemon zaizou
Schmardaea microphylla
Chukrasia tabularis
Lovoa swynnertonii
Capuronianthus mahafalensis
Toona sinensis
Cedrela odorata
Cedrela angustifolia
Entandrophragma bussei
Pseudocedrela kotschyi
Neobeguea sp.
Xylocarpus moluccensis
Swietenia macrophylla
Khaya anthotheca
Carapa procera
Pterorhachis zenkeri
Owenia reticulata
Melia toosendan
Melia azedarach
Azadirachta indica
Munronia pinnata
Walsura tubulata
Heynea trijuga
Quivisianthe papinae
Ekebergia capensis
Astrotrichilia asterotricha
Cipadessa baccifera
Pseudoclausena chrysogyne
Trichilia hirta
Pseudobersama mossambicensis
Malleastrum maadenense
Lepidotrichilia volkensii
Nymania capensis
Naregamia alata
Humbertioturraea grandidieri
Turraea virens
Calodecaryia crassifolia
Vavaea amicorum
Synoum glandulosum
Anthocarapa nitidula
Guarea glomerulata
Heckeldora staudtii
Turraeanthus manii
Huagea glabra
Guarea laurentii
Didymocheton sp.
Cabralea canjerana
Aphanamixis polystachya
Reinwardtiodendron celebicum
Aglaia macrocarpa
Aglaia tomentosa
Aglaia odorata
140
120
100
80
60
40
20
0

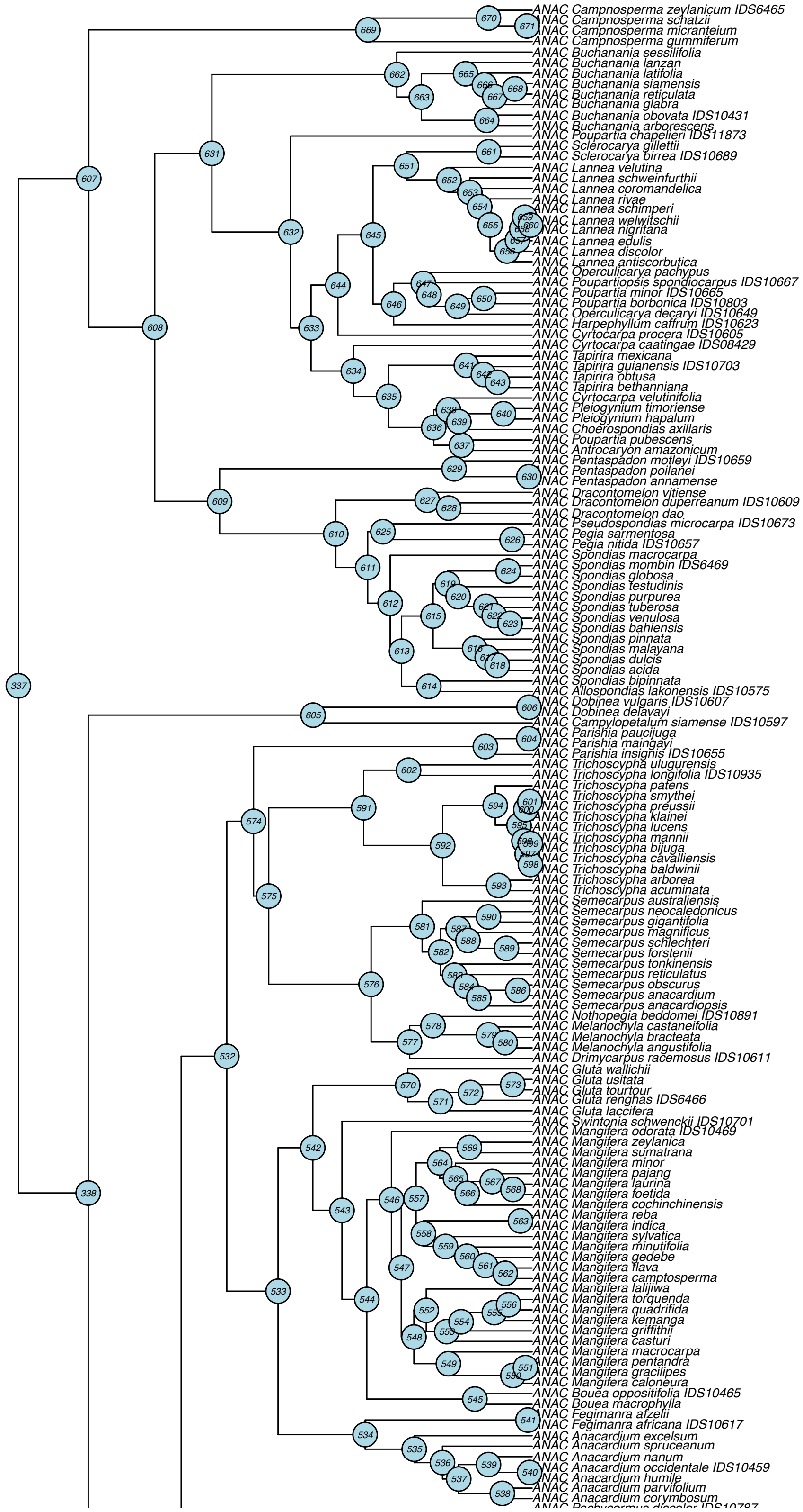


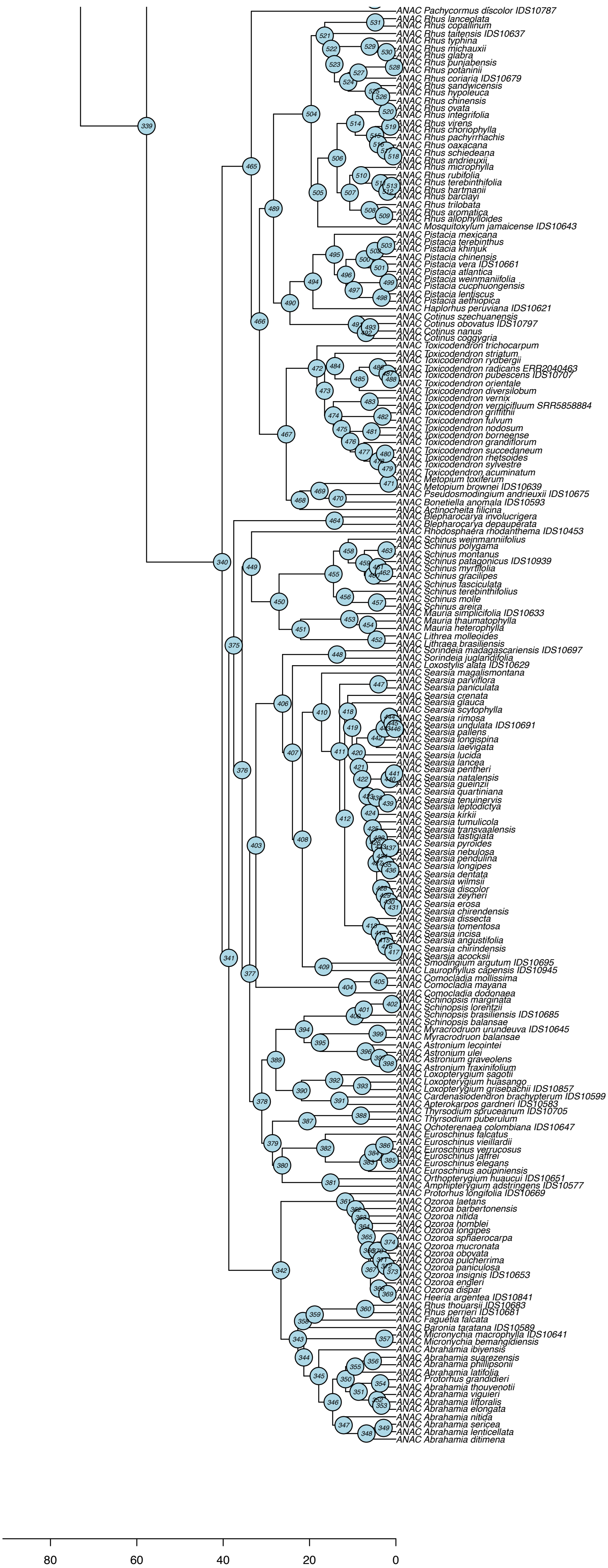
Appendix C6 RAxML species-level Sanger phylogeny of Anacardiaceae generated with a fixed topology from the Angiosperms353 genus-level Sapindales phylogeny. Bootstrap support indicated on each branch and coloured accordingly.





Appendix C7 Anacardiaceae species-level chronogram with node labels for reference in Appendix C8.




ANAC Pachycormus discolor IDS10787
ANAC Rhus lanceolata
ANAC Rhus copallinum
ANAC Rhus taitensis IDS10637
ANAC Rhus typhina
ANAC Rhus michauxii
ANAC Rhus glabra
ANAC Rhus punjabensis
ANAC Rhus potaninii
ANAC Rhus coriaria IDS10679
ANAC Rhus sandwicensis
ANAC Rhus hypoleuca
ANAC Rhus chinensis
ANAC Rhus ovata
ANAC Rhus integrifolia
ANAC Rhus virens
ANAC Rhus choriophylla
ANAC Rhus pachyrrhachis
ANAC Rhus oaxacana
ANAC Rhus schiedeana
ANAC Rhus andrieuxii
ANAC Rhus microphylla
ANAC Rhus rubifolia
ANAC Rhus terebinthifolia
ANAC Rhus hartmanii
ANAC Rhus barclayi
ANAC Rhus trilobata
ANAC Rhus aromatica
ANAC Rhus allophylloides
ANAC Mosquitoxylum jamaicense IDS10643
ANAC Pistacia mexicana
ANAC Pistacia terebinthus
ANAC Pistacia khinjuk
ANAC Pistacia chinensis
ANAC Pistacia vera IDS10661
ANAC Pistacia atlantica
ANAC Pistacia weinmaniifolia
ANAC Pistacia cucphuongensis
ANAC Pistacia lentiscus
ANAC Pistacia aethiopica
ANAC Haplorhus peruviana IDS10621
ANAC Cotinus szechuanensis
ANAC Cotinus obovatus IDS10797
ANAC Cotinus nanus
ANAC Cotinus coggygria
ANAC Toxicodendron trichocarpum
ANAC Toxicodendron striatum
ANAC Toxicodendron rydbergii
ANAC Toxicodendron radicans ERR2040463
ANAC Toxicodendron pubescens IDS10707
ANAC Toxicodendron orientale
ANAC Toxicodendron diversilobum
ANAC Toxicodendron vernix
ANAC Toxicodendron vernicifluum SRR5858884
ANAC Toxicodendron griffithii
ANAC Toxicodendron fulvum
ANAC Toxicodendron nodosum
ANAC Toxicodendron borneense
ANAC Toxicodendron grandiflorum
ANAC Toxicodendron succedaneum
ANAC Toxicodendron rhetsoides
ANAC Toxicodendron sylvestre
ANAC Toxicodendron acuminatum
ANAC Metopium toxiferum
ANAC Metopium brownei IDS10639
ANAC Pseudosmodingium andrieuxii IDS10675
ANAC Bonetiella anomala IDS10593
ANAC Actinocheita filicina
ANAC Blepharocarya involucrigera
ANAC Blepharocarya depauperata
ANAC Rhodosphaera rhodanthema IDS10453
ANAC Schinus weinmanniifolius
ANAC Schinus polygama
ANAC Schinus montanus
ANAC Schinus patagonicus IDS10939
ANAC Schinus myrtifolia
ANAC Schinus gracilipes
ANAC Schinus fasciculata
ANAC Schinus terebinthifolius
ANAC Schinus molle
ANAC Schinus areira
ANAC Mauria simplicifolia IDS10633
ANAC Mauria thaumatophylla
ANAC Mauria heterophylla
ANAC Lithrea molleoides
ANAC Lithraea brasiliensis
ANAC Sorindeia madagascariensis IDS10697
ANAC Sorindeia juglandifolia
ANAC Loxostylis alata IDS10629
ANAC Searsia magalismontana
ANAC Searsia parviflora
ANAC Searsia paniculata
ANAC Searsia crenata
ANAC Searsia glauca
ANAC Searsia scytophylla
ANAC Searsia rimosa
ANAC Searsia undulata IDS10691
ANAC Searsia pallens
ANAC Searsia longispina
ANAC Searsia laevigata
ANAC Searsia lucida
ANAC Searsia lancea
ANAC Searsia pentheri
ANAC Searsia natalensis
ANAC Searsia gueinzii
ANAC Searsia quartiniana
ANAC Searsia tenuinervis
ANAC Searsia leptodictya
ANAC Searsia kirkii
ANAC Searsia tumulicola
ANAC Searsia transvaalensis
ANAC Searsia fastigiata
ANAC Searsia pyroides
ANAC Searsia nebulosa
ANAC Searsia pendulina
ANAC Searsia longipes
ANAC Searsia dentata
ANAC Searsia wilmsii
ANAC Searsia discolor
ANAC Searsia zeyheri
ANAC Searsia erosa
ANAC Searsia chirendensis
ANAC Searsia dissecta
ANAC Searsia tomentosa
ANAC Searsia incisa
ANAC Searsia angustifolia
ANAC Searsia chirindensis
ANAC Searsia acocksii
ANAC Smodingium argutum IDS10695
ANAC Laurophyllus capensis IDS10945
ANAC Comocladia mollissima
ANAC Comocladia mayana
ANAC Comocladia dodonaea
ANAC Schinopsis marginata
ANAC Schinopsis lorentzii
ANAC Schinopsis brasiliensis IDS10685
ANAC Schinopsis balansae
ANAC Myracrodruon urundeuva IDS10645
ANAC Myracrodruon balansae
ANAC Astronium lecointei
ANAC Astronium ulei
ANAC Astronium graveolens
ANAC Astronium fraxinifolium
ANAC Loxopterygium sagotii
ANAC Loxopterygium huasango
ANAC Loxopterygium grisebachii IDS10857
ANAC Cardenasiodendron brachypterum IDS10599
ANAC Apterokarpos gardneri IDS10583
ANAC Thyrsodium spruceanum IDS10705
ANAC Thyrsodium puberulum
ANAC Ochoterenaea colombiana IDS10647
ANAC Euroschinus falcatus
ANAC Euroschinus vieillardii
ANAC Euroschinus verrucosus
ANAC Euroschinus jaffrei
ANAC Euroschinus elegans
ANAC Euroschinus aoupiniensis
ANAC Orthopterygium huaucui IDS10651
ANAC Amphipterygium adstringens IDS10577
ANAC Protorhus longifolia IDS10669
ANAC Ozoroa laetans
ANAC Ozoroa barbertonensis
ANAC Ozoroa nitida
ANAC Ozoroa homblei
ANAC Ozoroa longipes
ANAC Ozoroa sphaerocarpa
ANAC Ozoroa mucronata
ANAC Ozoroa obovata
ANAC Ozoroa pulcherrima
ANAC Ozoroa paniculosa
ANAC Ozoroa insignis IDS10653
ANAC Ozoroa engleri
ANAC Ozoroa dispar
ANAC Heeria argentea IDS10841
ANAC Rhus thouarsii IDS10683
ANAC Rhus perrieri IDS10681
ANAC Faguetia falcata
ANAC Baronia taratana IDS10589
ANAC Micronychia macrophylla IDS10641
ANAC Micronychia bemangidiensis
ANAC Abrahamia ibityensis
ANAC Abrahamia suarezensis
ANAC Abrahamia phillipsonii
ANAC Abrahamia latifolia
ANAC Protorhus grandidieri
ANAC Abrahamia thouvenotii
ANAC Abrahamia viguieri
ANAC Abrahamia littoralis
ANAC Abrahamia elongata
ANAC Abrahamia nitida
ANAC Abrahamia sericea
ANAC Abrahamia lenticellata
ANAC Abrahamia ditimena
80
60
40
20
0

Appendix C8 Probabilities (%) of each area being the ancestral area at each node in the biogeographic ancestral area analysis of Anacardiaceae under a DEC+J model in BioGeoBEARS, as shown in Figure 5.4 of Chapter 5. For node numbers, refer to Appendix C7. Area codes are as follows: U = Sunda; A = Sahul; W = Wallacea; F = Africa; M = the Americas; E = Eurasia; P = the Pacific.

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
1	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
4	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
6	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
7	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
9	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
12	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
13	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
14	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
15	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
16	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
17	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
18	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
19	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
20	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
21	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
22	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
23	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
24	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
25	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
26	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
27	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
28	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
29	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
30	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
31	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
32	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
33	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
34	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
35	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
36	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
37	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
38	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
39	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
40	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
41	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
42	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
43	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
44	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
45	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
46	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
47	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
48	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
49	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
50	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
51	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
52	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
53	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
54	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
55	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
56	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
57	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
58	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
59	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
60	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
61	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
62	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
63	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
64	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
65	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
66	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
67	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
68	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
69	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
70	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
71	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
72	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
73	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
74	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
75	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
76	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
77	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
78	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
79	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
80	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
81	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
82	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
83	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
84	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
85	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
86	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
87	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
88	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
89	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00
91	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
92	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
93	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
94	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
95	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
96	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
97	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
98	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
99	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
102	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
103	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
104	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
105	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
106	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
107	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00
108	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
109	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
110	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
111	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
112	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
113	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
114	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
115	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
116	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
117	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
118	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
119	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
120	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
121	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00
122	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
123	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
124	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
125	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
126	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
127	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
128	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
129	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
130	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
131	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
132	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
133	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
134	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
135	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
136	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
137	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
138	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
139	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
140	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
141	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
142	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
143	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
144	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00
145	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
146	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
147	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
148	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
149	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
150	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
151	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
152	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
153	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00
154	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
155	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00
156	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
157	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
158	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00
159	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
160	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
161	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00
162	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00
163	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
164	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
165	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
166	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
167	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
168	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
169	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
170	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
171	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
172	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
173	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
174	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
175	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
176	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
177	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
178	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
179	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00
180	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
181	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
182	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
183	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
184	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00
185	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
186	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
187	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
188	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
189	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
190	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
191	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
192	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
193	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
194	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
195	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
196	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
197	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
198	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
199	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
200	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
201	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
202	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
203	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
204	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
205	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
206	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
207	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
208	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
209	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
210	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
211	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
212	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
213	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
214	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
215	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
216	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
217	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
218	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
219	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
220	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
221	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
222	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
223	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
224	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
225	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
226	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
227	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
228	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
229	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
230	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
231	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
232	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
233	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
234	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
235	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
237	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
238	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
239	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
240	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
241	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
242	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
243	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
245	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
246	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
247	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
248	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
249	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
250	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
251	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
252	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
253	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
254	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
255	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
256	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
257	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
258	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
259	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
260	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
261	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
262	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
263	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
264	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
265	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
266	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
267	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
268	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
269	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
270	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
271	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
272	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
273	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
274	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
275	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
276	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
277	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
278	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
279	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
280	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
281	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
282	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
283	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
284	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
285	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
286	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
287	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
288	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
289	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
290	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
291	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
292	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
293	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
294	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
295	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
296	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
297	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
298	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
299	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
300	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
301	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
302	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
303	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
304	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
305	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
306	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
307	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
308	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
309	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
310	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
311	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
312	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
313	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
314	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
315	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
316	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
317	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
318	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
319	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
320	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
321	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
322	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
323	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
324	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
325	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
326	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
327	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
328	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
329	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
331	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
332	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
333	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
334	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
335	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
336	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
337	30.20	0.17	0.01	0.43	0.29	0.54	0.01	5.59	0.98	34.60	0.65	0.04	0.43	0.33	0.02	0.04	0.00	0.27	0.55	0.39	0.01	0.03
338	81.30	0.30	0.01	0.52	0.39	0.41	0.00	11.40	0.13	2.72	0.05	0.00	0.02	0.02	0.00	0.00	0.00	0.05	0.49	0.36	0.00	0.00
339	58.54	0.78	0.01	1.19	0.92	0.04	0.00	34.63	0.09	0.36	0.03	0.04	0.40	0.25	0.01	0.00	0.00	0.74	0.05	0.04	0.01	0.00
340	0.00	1.03	0.00	0.44	11.44	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.48	16.01	0.00	0.00	0.00	12.34	0.05	0.30	0.00	0.00
341	0.00	3.28	0.00	2.40	7.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.81	6.87	0.00	0.00	0.00	8.69	0.00	0.00	0.00	0.00
342	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
343	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
344	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
345	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
346	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
347	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
348	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
349	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
350	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
351	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
352	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
353	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
354	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
355	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
356	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
357	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
358	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
359	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
360	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
361	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
362	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
363	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
364	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
365	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
366	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
367	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
368	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
369	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
370	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
371	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
372	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
373	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
374	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
375	0.00	11.43	0.00	0.13	9.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.34	73.61	0.00	0.00	0.00	0.33	0.00	0.00	0.00	0.00
376	0.00	1.71	0.00	0.02	26.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	66.41	0.00	0.00	0.00	3.37	0.00	0.00	0.03	0.00
377	0.00	0.01	0.00	0.07	92.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.59	0.00	0.00	0.00	6.94	0.00	0.00	0.11	0.00
378	0.00	0.00	0.00	0.00	98.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10	0.00	0.00	0.00	0.00	0.00	0.00	0.61	0.00
379	0.00	0.00	0.00	0.00	93.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.30	0.00	0.00	0.00	0.00	0.00	0.00	2.91	0.00
380	0.00	0.35	0.00	0.00	71.54	0.00	0.34	0.00	0.00	0.00	0.00	0.00	0.00	12.97	0.02	0.00	0.00	0.00	0.00	0.00	12.74	0.00
381	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
382	0.00	22.56	0.00	0.00	0.00	0.00	22.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	54.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00
383	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
384	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
385	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
386	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
387	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
388	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
389	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
390	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
391	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
392	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
393	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
394	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
395	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
396	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
397	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
398	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
399	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
400	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
401	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
402	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
403	0.00	0.00	0.00	0.46	85.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.27	0.00	0.00	0.00	0.00
404	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
405	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
406	0.00	0.00	0.00	39.29	3.97	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	56.70	0.03	0.00	0.00	0.00
407	0.00	0.00	0.00	99.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.00	0.00
408	0.00	0.00	0.00	99.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.00	0.00	0.00
409	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
410	0.00	0.00	0.00	95.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.56	0.00	0.00	0.00
411	0.26	0.00	0.00	75.09	0.00	0.40	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	24.22	0.00	0.00	0.00
412	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
413	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
414	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
415	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
416	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
417	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
418	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
419	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
420	0.00	0.00	0.00	99.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
421	0.00	0.00	0.00	99.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
422	0.00	0.00	0.00	99.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00
423	0.00	0.00	0.00	98.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12	0.00	0.00	0.00
424	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
425	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
426	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
427	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
428	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
429	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
430	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
431	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
432	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
433	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
434	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
435	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
436	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
437	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
438	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
439	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
440	0.00	0.00	0.00	77.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22.68	0.00	0.00	0.00
441	0.00	0.00	0.00	53.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	46.26	0.00	0.00	0.00
442	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
443	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
444	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
445	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
446	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
447	15.49	0.00	0.00	0.00	0.00	24.11	0.00	0.00	0.00	60.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
448	0.00	0.00	0.00	33.75	0.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	65.98	0.00	0.00	0.00	0.00
449	0.00	5.39	0.00	0.00	23.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	71.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
450	0.00	0.00	0.00	0.00	99.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00
451	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
452	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
453	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
454	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
455	0.00	0.00	0.00	0.00	99.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.47	0.00	0.00
456	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
457	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
458	0.00	0.00	0.00	0.00	98.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10	0.00	0.00
459	0.00	0.00	0.00	0.00	95.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.91	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
460	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
461	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
462	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
463	0.00	0.00	0.00	0.00	66.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	33.75	0.00	0.00
464	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
465	0.00	0.00	0.00	0.00	98.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.01	0.00	1.64	0.00	0.00
466	0.00	0.00	0.00	0.00	96.69	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.02	0.00	3.18	0.00	0.00
467	0.02	0.00	0.00	0.00	88.01	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11.91	0.00	0.00
468	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
469	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
470	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
471	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
472	3.19	0.00	0.00	0.00	26.53	2.48	0.00	0.00	0.00	0.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	66.87	0.00	0.00
473	3.70	0.00	0.00	0.00	39.38	1.62	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	55.17	0.00	0.00
474	12.51	0.00	0.00	0.00	23.42	20.12	0.00	0.00	0.01	3.76	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	40.17	0.00	0.00
475	37.45	0.00	0.00	0.00	0.00	37.16	0.00	0.00	0.11	25.05	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00
476	41.90	0.00	0.02	0.00	0.00	16.19	0.00	0.00	0.51	40.23	0.00	0.00	0.00	0.00	0.00	0.59	0.00	0.00	0.00	0.00	0.00	0.00
477	3.84	0.00	0.00	0.00	0.00	25.57	0.00	0.00	0.00	70.59	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
478	4.43	0.00	0.00	0.00	0.00	13.56	0.00	0.00	0.00	82.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
479	0.36	0.00	0.00	0.00	0.00	41.70	0.00	0.00	0.00	57.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
480	41.24	0.00	0.00	0.00	0.00	0.97	0.00	0.00	0.00	57.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
481	83.69	0.00	0.12	0.00	0.00	0.00	0.00	0.00	16.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
482	32.85	0.00	0.00	0.00	0.00	0.51	0.00	0.00	0.00	66.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
483	10.65	0.00	0.00	0.00	18.20	9.45	0.00	0.00	0.00	5.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	55.99	0.00	0.00
484	0.00	0.00	0.00	0.00	96.06	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.90	0.00	0.00
485	0.00	0.00	0.00	0.00	93.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.29	0.00	0.00
486	0.00	0.00	0.00	0.00	83.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.26	0.00	0.00
487	0.00	0.00	0.00	0.00	55.49	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	44.46	0.00	0.00
488	0.00	0.00	0.00	0.00	3.11	4.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	92.36	0.00	0.00
489	0.00	0.00	0.00	0.00	90.06	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.05	0.00	9.40	0.01	0.00
490	0.00	0.00	0.00	0.00	53.74	8.97	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.02	36.91	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
491	0.00	0.00	0.00	0.00	0.32	41.10	0.00	0.00	0.00	3.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	55.56	0.00	0.00
492	0.01	0.00	0.00	0.00	0.25	37.39	0.00	0.00	0.00	5.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	57.30	0.00	0.00
493	0.00	0.00	0.00	0.00	2.57	37.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	59.76	0.00	0.00
494	0.00	0.00	0.00	0.00	47.51	9.06	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.31	0.06	42.12	0.00	0.00
495	0.01	0.00	0.00	0.02	34.40	10.75	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.82	0.10	50.51	0.00	0.00
496	0.13	0.00	0.01	0.60	0.00	90.25	0.00	0.00	0.00	1.76	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	6.78	0.00	0.00	0.00
497	0.17	0.00	0.00	0.59	0.00	84.69	0.00	0.00	0.00	4.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.66	0.00	0.00	0.00
498	0.00	0.00	0.00	2.93	0.00	1.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	95.51	0.00	0.00	0.00
499	1.32	0.00	0.00	0.00	0.00	0.77	0.00	0.00	0.00	97.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
500	0.00	0.00	0.00	0.18	0.00	85.31	0.00	0.00	0.00	2.83	0.00	0.00	0.00	0.00	0.00	2.87	0.00	0.00	8.18	0.00	0.00	0.00
501	0.00	0.00	0.00	0.03	0.00	80.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19.32	0.00	0.00	0.00
502	0.01	0.00	0.01	0.12	0.00	69.70	0.00	0.00	0.00	8.53	0.00	0.00	0.00	0.00	0.00	8.79	0.00	0.00	9.38	0.00	0.00	0.00
503	0.00	0.00	0.00	0.56	0.00	49.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	50.20	0.00	0.00	0.00
504	0.00	0.00	0.00	0.00	96.49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.90	0.00	0.00	0.00	0.02	0.00	1.24	0.08	0.00
505	0.00	0.00	0.00	0.00	99.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.00
506	0.00	0.00	0.00	0.00	99.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.94	0.00	0.00
507	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
508	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
509	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
510	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
511	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
512	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
513	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
514	0.00	0.00	0.00	0.00	94.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.01	0.00	0.00
515	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
516	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
517	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
518	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
519	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
520	0.00	0.00	0.00	0.00	55.49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	44.51	0.00	0.00
521	0.00	0.01	0.00	0.00	91.85	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.93	0.00	0.00	0.00	0.04	0.00	2.22	0.17	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
522	0.01	0.85	0.56	0.01	79.65	0.91	0.05	0.00	0.00	0.00	0.00	0.03	0.00	11.52	0.01	0.14	0.01	0.06	0.00	4.08	0.23	0.00
523	0.02	0.00	0.00	0.02	85.28	1.56	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.00	11.60	0.81	0.01
524	0.11	0.00	0.00	0.08	0.00	85.50	0.67	0.00	0.00	2.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.00	0.00	8.50
525	0.07	0.00	0.00	0.00	0.00	43.68	0.95	0.00	0.00	2.56	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	39.14
526	0.02	0.00	0.00	0.00	0.00	76.99	0.00	0.00	0.00	23.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
527	0.00	0.00	0.00	0.02	0.00	92.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.59	0.00	0.00	0.00
528	0.00	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
529	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
530	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
531	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
532	93.94	0.01	0.02	1.70	0.55	0.01	0.00	1.17	0.85	0.38	0.22	0.00	0.05	0.01	0.00	0.00	0.00	0.08	0.04	0.02	0.01	0.00
533	96.58	0.00	0.00	2.15	0.98	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.27	0.00	0.00	0.00	0.00
534	0.00	0.00	0.00	18.76	17.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	64.11	0.00	0.00	0.00	0.00
535	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
536	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
537	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
538	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
539	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
540	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
541	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
542	99.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
543	99.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
544	99.95	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.03	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
545	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
546	99.74	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.14	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
547	99.27	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.41	0.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
548	99.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
549	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
550	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
551	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
552	97.55	0.00	0.01	0.00	0.00	0.00	0.00	0.00	2.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
553	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
554	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
555	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
556	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
557	95.92	0.00	0.01	0.00	0.00	0.01	0.00	0.45	2.03	1.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
558	98.20	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	1.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
559	95.09	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	4.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
560	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
561	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
562	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
563	41.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	58.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
564	73.94	0.01	0.68	0.00	0.00	0.03	0.00	2.93	13.69	5.58	0.00	0.02	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00
565	55.51	0.36	3.25	0.00	0.00	0.00	0.00	11.43	25.16	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
566	86.73	0.00	0.15	0.00	0.00	0.00	0.00	0.00	13.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
567	79.42	0.00	0.03	0.00	0.00	0.00	0.00	0.00	20.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
568	45.31	0.00	0.77	0.00	0.00	0.00	0.00	0.00	53.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
569	41.42	0.00	3.32	0.00	0.00	1.04	0.00	0.00	4.38	28.85	0.00	0.00	0.00	0.00	0.00	2.53	0.00	0.00	0.00	0.00	0.00	0.00
570	99.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
571	97.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
572	90.14	0.00	0.02	0.01	0.00	0.00	0.00	0.00	9.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
573	99.29	0.00	0.00	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
574	93.09	0.03	0.18	1.25	0.00	0.03	0.01	1.36	1.63	0.67	0.43	0.04	0.03	0.00	0.00	0.02	0.01	0.00	0.05	0.00	0.00	0.00
575	90.54	0.53	0.38	2.29	0.00	0.41	0.29	1.47	0.45	0.96	0.76	0.02	0.34	0.00	0.02	0.02	0.01	0.00	0.29	0.00	0.00	0.02
576	44.49	0.04	0.00	0.00	0.00	0.18	0.01	10.58	1.97	9.02	6.92	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.09
577	63.27	0.00	0.00	0.00	0.00	10.03	0.00	0.00	0.00	26.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
578	46.03	0.00	0.00	0.00	0.00	10.41	0.00	0.00	0.00	43.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
579	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
580	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
581	6.64	1.04	0.01	0.00	0.00	0.02	0.50	23.30	0.11	0.10	12.45	0.10	0.00	0.00	0.50	0.00	0.07	0.00	0.00	0.00	0.00	0.12
582	16.99	0.16	0.01	0.00	0.00	0.01	0.07	17.21	1.12	0.97	5.97	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01
583	98.64	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	1.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
584	95.10	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	4.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
585	97.37	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	2.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
586	66.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	33.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
587	10.29	1.04	0.17	0.00	0.00	0.09	0.43	14.07	1.21	0.57	2.82	0.76	0.00	0.00	0.99	0.04	0.16	0.00	0.00	0.00	0.00	0.06
588	1.52	69.30	0.28	0.00	0.00	0.00	0.00	20.88	0.05	0.00	0.00	3.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
589	0.03	40.22	0.01	0.00	0.00	0.00	0.00	23.36	0.01	0.00	0.00	12.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
590	8.40	0.00	0.92	0.00	0.00	0.37	1.81	0.00	1.50	1.57	8.96	0.00	0.00	0.00	0.00	0.17	1.33	0.00	0.00	0.00	0.00	0.65
591	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
592	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
593	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
594	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
595	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
596	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
597	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
598	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
599	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
600	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
601	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
602	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
603	62.89	0.00	0.01	0.00	0.00	0.00	0.00	0.00	37.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
604	19.51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	80.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
605	81.98	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	17.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
606	0.05	0.00	0.00	0.00	0.00	0.30	0.00	0.00	0.00	99.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
607	23.63	0.30	0.13	1.03	0.71	4.42	0.05	0.24	0.19	40.78	0.11	0.02	0.58	0.47	0.01	0.73	0.01	0.38	0.77	0.56	0.07	0.34
608	60.32	0.55	0.25	0.93	0.41	0.67	0.03	4.33	3.00	5.48	1.67	0.13	0.64	0.34	0.04	0.15	0.03	0.04	0.28	0.13	0.04	0.04
609	55.12	0.97	0.60	0.02	0.02	0.11	0.03	5.54	4.71	4.85	2.83	0.31	0.02	0.02	0.15	0.27	0.13	0.00	0.00	0.00	0.00	0.01
610	32.99	0.02	0.02	0.01	0.01	0.19	0.03	3.46	3.13	5.78	8.48	0.00	0.01	0.01	0.01	0.07	0.01	0.00	0.04	0.07	0.02	0.11
611	92.04	0.02	0.03	0.09	0.16	2.81	0.00	0.04	0.13	2.05	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.13	0.29	1.34	0.00	0.00
612	91.09	0.02	0.08	0.00	7.14	0.36	0.00	0.10	0.36	0.19	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.57	0.00	0.00
613	91.48	0.03	0.07	0.00	5.57	0.36	0.00	0.30	1.06	0.60	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.37	0.00	0.00
614	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
615	78.29	0.22	1.79	0.00	7.12	0.51	0.00	1.62	5.67	1.81	0.00	0.04	0.00	0.50	0.00	0.10	0.00	0.00	0.00	1.13	0.00	0.00
616	28.95	0.12	3.85	0.00	0.00	0.13	0.00	6.89	33.70	4.44	0.00	1.05	0.00	0.00	0.00	1.84	0.00	0.00	0.00	0.00	0.00	0.00
617	14.97	3.35	25.52	0.00	0.00	0.00	0.00	15.36	21.90	0.00	0.00	6.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
618	1.69	16.10	37.12	0.00	0.00	0.00	0.00	10.63	13.25	0.00	0.00	12.66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
619	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
620	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
621	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
622	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
623	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
624	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
625	88.93	0.00	0.00	1.47	0.00	4.45	0.00	0.00	0.00	2.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.74	0.00	0.00	0.00
626	17.74	0.00	0.00	0.00	0.00	1.48	0.00	0.00	0.00	80.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
627	1.22	0.00	0.00	0.00	0.00	0.04	0.45	0.07	0.07	0.17	12.04	0.00	0.00	0.00	0.09	0.00	0.15	0.00	0.00	0.00	0.00	0.67
628	2.92	0.00	0.00	0.00	0.00	0.13	0.03	0.75	0.74	2.60	5.65	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.36
629	30.47	0.04	0.04	0.00	0.00	0.00	0.00	17.82	17.73	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
630	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
631	84.63	1.99	1.30	1.88	0.84	0.80	0.00	0.80	0.42	0.40	0.00	0.06	2.17	0.97	0.00	0.02	0.00	0.27	0.80	0.34	0.00	0.00
632	0.00	0.00	0.00	40.91	3.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	54.97	0.04	0.00	0.00	0.00
633	0.00	0.00	0.00	6.10	20.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	73.03	0.01	0.02	0.00	0.00
634	0.00	0.00	0.00	0.07	96.54	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	3.21	0.00	0.05	0.04	0.00
635	0.00	0.00	0.00	0.01	94.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.00	0.00	4.62	0.00	0.16	0.17	0.00
636	0.01	0.00	0.00	0.03	83.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.60	0.00	0.00	0.00	13.92	0.00	0.80	0.89	0.00
637	0.00	0.00	0.00	0.99	54.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	44.94	0.00	0.00	0.00	0.00
638	0.54	0.06	0.02	0.00	92.75	0.09	0.06	0.01	0.01	0.01	0.01	0.00	0.00	1.38	0.00	0.00	0.00	0.00	0.00	2.03	2.08	0.00
639	70.82	1.30	0.90	0.00	0.00	3.02	2.05	4.10	3.31	4.48	5.84	0.07	0.00	0.00	0.12	0.24	0.07	0.00	0.00	0.00	0.00	0.67
640	9.59	0.35	0.33	0.00	0.00	0.00	1.22	2.85	2.80	0.00	9.76	0.18	0.00	0.00	0.69	0.00	0.70	0.00	0.00	0.00	0.00	0.00
641	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
642	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
643	0.00	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
644	0.00	0.00	0.00	6.93	13.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	79.47	0.00	0.01	0.00	0.00
645	0.00	0.00	0.00	99.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00

Node	U	A	W	F	M	E	P	UA	UW	UE	UP	AW	AF	AM	AP	WE	WP	FM	FE	ME	MP	EP
646	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
647	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
648	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
649	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
650	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
651	0.00	0.00	0.00	99.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.38	0.00	0.00	0.00
652	0.00	0.00	0.00	98.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.70	0.00	0.00	0.00
653	0.00	0.00	0.00	94.78	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.21	0.00	0.00	0.00
654	0.29	0.00	0.00	85.39	0.00	0.47	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13.82	0.00	0.00	0.00
655	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
656	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
657	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
658	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
659	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
660	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
661	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
662	74.71	0.04	0.01	0.00	0.00	0.01	0.00	11.67	3.84	3.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
663	66.49	0.10	0.02	0.00	0.00	0.04	0.00	15.33	5.08	3.78	0.00	0.02	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
664	1.07	3.43	0.02	0.00	0.00	0.00	0.00	46.96	0.30	0.00	0.00	2.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
665	79.65	0.00	0.00	0.00	0.00	0.41	0.00	0.00	0.00	19.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
666	86.83	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00	13.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
667	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
668	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
669	0.00	0.00	0.00	0.56	0.81	2.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.55	1.56	19.83	0.00	0.00
670	0.00	0.00	0.00	1.80	0.00	5.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	92.33	0.00	0.00	0.00
671	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Appendix C8 continued

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
7	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
54	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
58	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
59	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
61	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
83	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
95	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
97	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
100	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
102	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
103	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
104	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
105	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
106	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
107	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
108	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
111	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
112	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
113	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
114	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
115	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
116	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
117	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
118	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
119	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
120	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
121	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
122	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
123	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
124	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
125	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
126	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
127	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
128	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
129	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
130	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
131	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
132	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
133	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
134	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
135	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
136	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
137	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
138	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
139	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
140	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
141	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
142	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
143	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
144	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
145	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
146	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
147	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
148	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
149	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
150	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
151	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
152	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
153	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
154	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
155	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
156	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
157	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
158	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
159	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
160	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
161	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
162	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
163	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
164	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
165	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
166	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
167	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
168	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
169	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
170	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
171	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
172	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
173	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
174	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
175	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
176	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
177	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
178	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
179	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
180	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
181	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
182	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
183	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
184	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
185	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
186	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
187	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
188	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
189	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
190	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
191	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
192	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
193	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
194	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
195	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
196	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
197	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
198	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
199	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
200	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
201	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
202	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
203	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
204	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
205	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
206	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
207	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
208	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
209	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
210	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
211	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
212	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
213	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
214	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
215	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
216	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
217	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
218	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
219	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
220	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
221	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
222	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
223	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
224	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
225	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
226	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
227	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
228	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
229	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
230	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
231	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
232	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
233	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
234	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
235	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
237	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
238	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
240	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
241	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
242	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
243	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
245	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
246	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
247	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
248	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
249	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
250	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
251	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
252	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
253	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
254	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
255	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
256	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
257	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
258	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
259	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
260	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
261	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
262	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
263	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
264	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
265	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
266	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
267	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
269	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
270	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
271	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
273	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
274	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
275	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
276	0.00	0.00	0.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
277	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
278	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
279	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
280	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
281	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
282	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
283	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
284	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
285	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
286	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
287	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
288	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	100.00	0.00
289	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
290	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
291	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
293	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
294	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
295	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
296	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
297	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
298	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
299	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
300	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
301	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
302	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
303	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
304	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
305	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
307	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
308	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
309	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
310	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
311	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
312	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
313	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
314	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
315	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
316	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
317	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
318	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
319	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
320	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
321	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
322	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
323	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
325	100.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
326	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
327	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
328	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
329	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
331	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
332	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
333	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
334	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
335	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
336	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
337	0.86	7.67	0.55	3.53	0.35	2.46	0.10	0.08	0.01	0.38	0.04	0.04	0.01	0.61	0.03	2.33	0.42	1.87	1.61	0.10	0.03	0.02	0.04	1.28	0.02
338	0.24	0.84	0.09	0.02	0.01	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.35	0.00	0.05	0.07	0.03	0.01	0.00	0.00	0.00	0.00	0.03	0.00
339	0.50	0.27	0.19	0.01	0.00	0.00	0.05	0.03	0.01	0.36	0.01	0.01	0.00	0.05	0.00	0.08	0.07	0.05	0.00	0.03	0.03	0.01	0.01	0.06	0.02
340	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	57.58	0.00	0.01	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00
341	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	63.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00
342	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
343	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
344	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
345	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
346	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
347	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
348	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
349	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
350	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
351	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
352	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
353	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
354	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
355	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
356	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
357	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
358	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
359	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
360	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
361	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
362	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
363	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
364	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
365	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
366	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
367	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
368	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
369	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
370	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
371	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
372	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
373	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
374	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
375	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.34	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
376	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.82	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
377	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
378	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
379	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
380	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
381	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
382	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
383	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
384	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
385	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
386	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
387	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
388	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
389	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
390	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
391	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
392	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
393	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
394	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
395	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
396	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
397	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
398	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
399	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
400	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
401	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
402	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
403	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
404	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
405	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
406	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
407	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
408	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
409	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
410	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
411	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
412	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
413	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
414	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
415	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
417	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
418	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
419	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
420	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
421	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
422	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
423	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
424	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
425	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
426	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
427	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
428	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
429	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
430	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
431	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
432	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
433	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
434	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
435	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
436	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
437	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
438	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
439	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
440	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
441	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
442	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
443	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
444	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
445	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
446	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
447	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
448	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
449	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
450	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
451	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
452	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
453	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
454	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
455	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
456	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
457	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
458	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
459	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
460	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
461	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
462	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
463	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
464	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
465	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
466	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
467	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
468	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
469	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
470	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
471	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
472	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
473	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
474	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
475	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
476	0.00	0.00	0.00	0.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
477	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
478	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
479	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
480	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
481	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
482	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
483	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
484	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
485	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
486	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
487	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
488	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
489	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
490	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
491	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
492	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
493	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
494	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
495	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
496	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
497	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
498	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
499	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
500	0.00	0.00	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
501	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
502	0.00	0.00	0.00	3.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
503	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
504	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.00	0.01	0.00	0.03	0.00	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
505	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
506	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
508	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
509	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
510	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
511	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
512	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
513	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
514	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
515	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
516	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
517	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
518	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
519	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
520	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
521	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.58	0.00	0.02	0.00	0.09	0.00	0.01	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
522	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.41	0.00	0.06	0.00	0.25	0.00	0.03	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
523	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09	0.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
524	0.00	0.00	0.00	0.00	0.00	0.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
525	0.00	0.00	0.00	0.00	0.00	13.47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
526	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
527	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
528	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
529	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
530	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
531	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
532	0.15	0.10	0.08	0.06	0.05	0.03	0.08	0.01	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.05	0.07	0.04	0.04	0.02	0.05	0.01	0.00	0.05	0.02
533	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
534	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
535	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
536	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
537	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
538	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
540	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
541	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
542	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
543	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
544	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
545	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
546	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
547	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
549	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
550	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
551	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
552	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
553	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
554	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
555	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
556	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
557	0.04	0.01	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
558	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
559	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
560	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
561	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
562	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
563	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
564	0.91	0.19	0.00	1.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
565	4.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
566	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
567	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
568	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
569	0.00	0.00	0.00	18.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
570	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
571	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
572	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

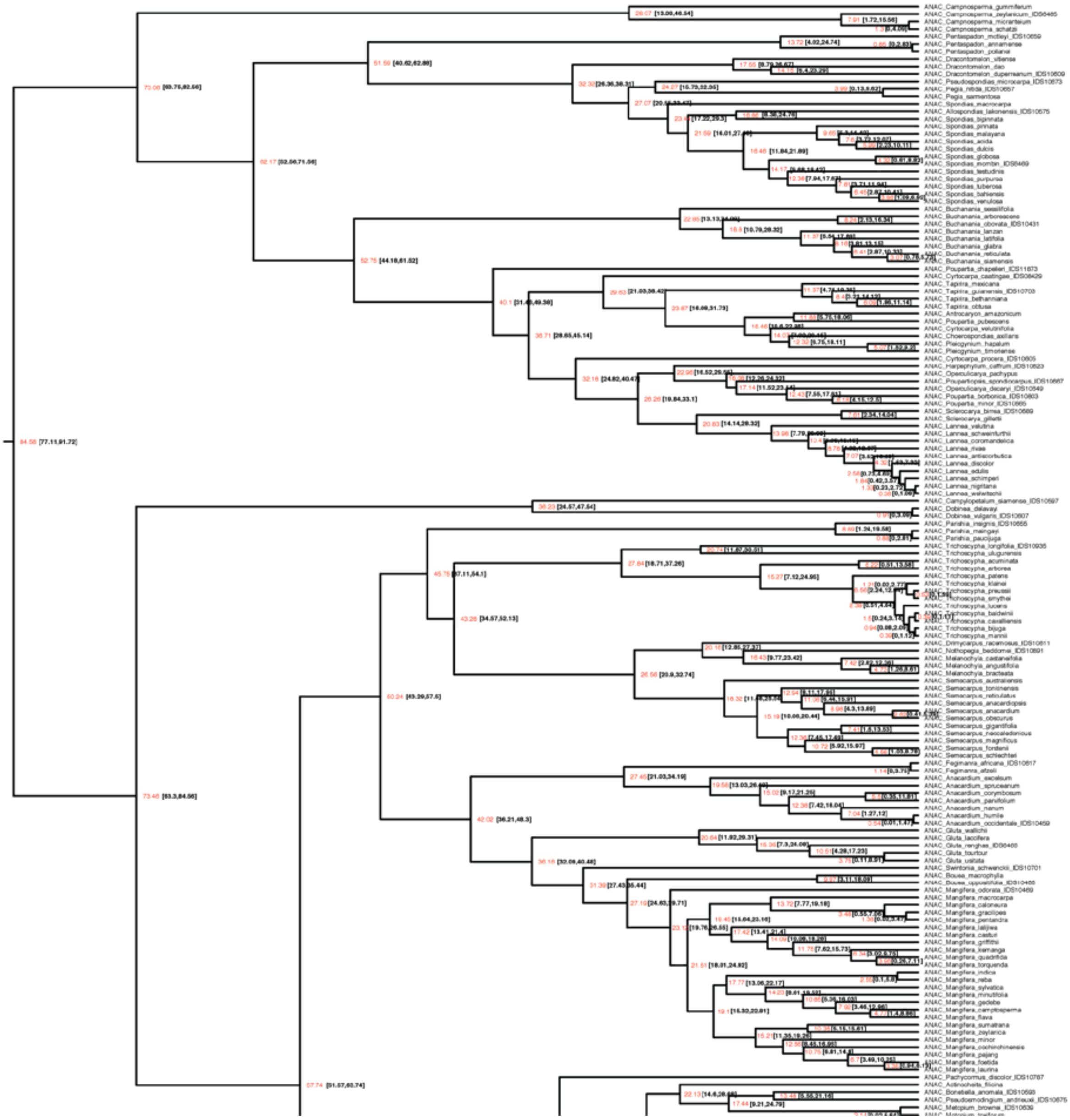
Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
573	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
574	0.16	0.13	0.11	0.08	0.06	0.05	0.16	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.06	0.05	0.04	0.00	0.12	0.00	0.00	0.07	0.00
575	0.09	0.21	0.11	0.05	0.04	0.07	0.13	0.00	0.01	0.00	0.10	0.00	0.01	0.00	0.00	0.06	0.04	0.08	0.03	0.00	0.11	0.00	0.00	0.07	0.00
576	1.71	5.04	3.56	1.23	1.28	3.17	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	1.88	1.50	3.54	1.40	0.00	0.00	0.00	0.00	2.26	0.00
577	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
578	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
579	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
580	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
581	4.04	5.12	12.26	0.02	2.43	2.70	0.00	0.00	0.14	0.00	0.00	0.00	0.06	0.00	0.00	3.01	5.97	8.76	1.89	0.00	0.00	0.00	0.00	8.64	0.00
582	4.77	4.95	8.46	0.53	2.15	2.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.05	6.88	9.57	2.24	0.00	0.00	0.00	0.00	11.71	0.00
583	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
584	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
585	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
586	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
587	5.07	4.07	8.27	0.33	1.54	1.04	0.00	0.00	1.05	0.00	0.00	0.00	0.16	0.00	0.00	4.23	8.41	12.00	1.57	0.00	0.00	0.00	0.00	19.56	0.00
588	4.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
589	24.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
590	0.00	0.00	0.00	1.20	13.33	15.44	0.00	0.00	0.00	0.00	0.00	0.00	1.33	0.00	0.00	0.00	0.00	0.00	43.02	0.00	0.00	0.00	0.00	0.00	0.00
591	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
592	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
593	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
594	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
595	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
596	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
597	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
598	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
599	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
600	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
601	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
602	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
603	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
604	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
605	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
606	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
607	0.05	5.50	0.03	3.57	0.03	2.42	0.25	0.20	0.00	0.38	0.10	0.07	0.31	0.47	0.11	3.19	0.03	2.51	2.00	0.16	0.09	0.08	0.06	2.83	0.03
608	2.07	2.10	1.25	1.58	1.02	1.29	0.29	0.15	0.05	0.26	0.09	0.05	0.06	0.07	0.04	1.89	1.82	1.73	1.55	0.14	0.09	0.05	0.05	2.83	0.00
609	2.23	2.14	1.43	1.86	1.33	1.74	0.01	0.01	0.22	0.01	0.00	0.01	0.20	0.00	0.00	2.17	2.06	2.16	2.24	0.00	0.01	0.01	0.00	4.44	0.00
610	1.48	2.71	3.19	2.40	2.98	5.35	0.01	0.01	0.00	0.02	0.01	0.02	0.12	0.09	0.06	2.58	3.19	5.51	5.52	0.00	0.02	0.03	0.00	10.25	0.00
611	0.00	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.79	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
612	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
613	0.03	0.01	0.00	0.04	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
614	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
615	0.31	0.10	0.00	0.50	0.00	0.00	0.00	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
616	6.53	1.06	0.00	10.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
617	12.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
618	8.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
619	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
620	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
621	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
622	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
623	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
624	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
625	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
627	0.03	0.07	5.26	0.05	5.09	10.27	0.00	0.00	0.12	0.00	0.00	0.00	0.76	0.00	0.00	0.08	6.47	13.82	11.70	0.00	0.00	0.00	0.00	31.30	0.00
628	0.97	2.64	3.23	2.17	3.26	7.02	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.00	0.00	7.82	4.79	11.91	10.47	0.00	0.00	0.00	0.00	32.01	0.00
629	33.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
630	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
631	0.09	0.06	0.00	0.02	0.00	0.00	0.43	0.19	0.00	1.19	0.00	0.00	0.00	0.32	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
632	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
633	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
634	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
635	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.00	0.02	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01	0.00	0.01
636	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.07	0.00	0.13	0.00	0.10	0.11	0.00	0.00	0.00	0.00	0.01	0.00	0.04	0.02	0.00	0.02
637	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
638	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.33	0.00	0.00	0.31	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00
639	0.57	0.08	0.98	0.09	0.64	0.21	0.00	0.00	0.02	0.00	0.00	0.00	0.10	0.00	0.00	0.01	0.28	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00
640	2.47	0.00	16.95	0.00	16.58	0.00	0.00	0.00	1.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	33.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
641	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
642	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
643	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
644	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
645	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
646	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
647	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Node	UAW	UAE	UAP	UWE	UWP	UEP	AWF	AWM	AWP	AFM	AFP	AMP	WEP	FME	MEP	UAWE	UAWP	UAEP	UWEP	AWFM	AWFP	AWMP	AFMP	UAWEP	AWFMP
648	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
649	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
650	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
651	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
652	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
653	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
654	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
655	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
656	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
657	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
658	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
659	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
660	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
661	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
662	4.60	1.20	0.00	0.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
663	6.46	1.73	0.00	0.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
664	46.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
665	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
666	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
667	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
668	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
669	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	68.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
670	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
671	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Appendix C9 Ages of species-level Anacardiaceae tree with 95% HPD confidence interval shown in parentheses.



Appendix D

Additional work published during my candidature

CSIRO PUBLISHING

Australian Systematic Botany, 2018, **31**, 504–522
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Evolution of *Geosiris* (Iridaceae): historical biogeography and plastid-genome evolution in a genus of non-photosynthetic tropical rainforest herbs disjunct across the Indian Ocean

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Abstract. Mycoheterotrophs, i.e. plants that acquire carbon from root-associated soil fungi, often have highly degraded plastomes, reflecting relaxed selective constraints on plastid genes following the loss of photosynthesis. *Geosiris* Baill. is the only mycoheterotrophic genus in Iridaceae and comprises two species in Madagascar and nearby islands, and a third recently discovered species in north-eastern Australia. Here, we characterise the plastomes of the Australian and one Madagascan species to compare patterns of plastome degradation in relation to autotrophic and other mycoheterotrophic taxa and investigate the evolutionary and biogeographical history of the genus in Iridaceae. Both examined species have lost approximately half their plastid-encoded genes and a small but significant reduction in purifying selection in retained non-photosynthetic genes was observed. *Geosiris* is confirmed as monophyletic, with initial divergence of the genus occurring *c.* 53 million years ago, and subsequent diversification occurring *c.* 30 million years ago. Africa (including Madagascar) is reconstructed as the most likely ancestral area of the genus, implying a major range-expansion event of one lineage to Australia after its divergence in the Oligocene. Our study has highlighted the dynamic evolutionary history of *Geosiris*, contributed to the characterisation of mycoheterotrophic plastomes, and furthered our understanding of plastome structure and function.

Additional keywords: degradation, heterotrophic, monocot, mycoheterotroph, plastome.

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ANNUAL REVIEWS

Annual Review of Ecology, Evolution, and Systematics

Origins and Assembly of Malesian Rainforests

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Keywords

great Asiatic floristic interchange, GAFI, India, Malesia, rainforest assembly, paleobotany, Sunda–Sahul

Abstract

Unraveling the origins of Malesia's once vast, hyperdiverse rainforests is a perennial challenge. Major contributions to rainforest assembly came from floristic elements carried on the Indian Plate and montane elements from the Australian Plate (Sahul). The Sahul component is now understood to include substantial two-way exchanges with Sunda inclusive of lowland taxa. Evidence for the relative contributions of the great Asiatic floristic interchanges (GAFIs) with India and Sahul, respectively, to the flora of Malesia comes from contemporary lineage distributions, the fossil record, time-calibrated phylogenies, functional traits, and the spatial structure of genetic diversity. Functional-trait and biome conservatism are noted features of montane austral lineages from Sahul (e.g., diverse Podocarpaceae), whereas the abundance and diversity of lowland lineages, including *Syzygium* (Myrtaceae) and the Asian dipterocarps (Dipterocarpoideae), reflect a less well understood combination of dispersal, ecology, and adaptive radiations. Thus, Malesian rainforest assembly has been shaped by sharply contrasting evolutionary origins and biogeographic histories.

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Applications in Plant Sciences

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APPLICATION ARTICLE

INVITED SPECIAL ARTICLE

For the Special Issue: Exploring Angiosperms353: a Universal Toolkit for Flowering Plant Phylogenomics

HybPhaser: A workflow for the detection and phasing of hybrids in target capture data sets

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PREMISE: Hybrids contain divergent alleles that can confound phylogenetic analyses but can provide insights into reticulated evolution when identified and phased. We developed a workflow to detect hybrids in target capture data sets and phase reads into parental lineages using a similarity and phylogenetic framework.

METHODS: We used Angiosperms353 target capture data for *Nepenthes*, including known hybrids to test the novel workflow. Reference mapping was used to assess heterozygous sites across the data set and to detect hybrid accessions and paralogous genes. Hybrid samples were phased by mapping reads to multiple references and sorting reads according to similarity. Phased accessions were included in the phylogenetic framework.

RESULTS: All known *Nepenthes* hybrids and nine additional samples had high levels of heterozygous sites, had reads associated with multiple divergent clades, and were phased into accessions resembling divergent haplotypes. Phylogenetic analysis including phased accessions increased clade support and confirmed parental lineages of hybrids.

DISCUSSION: HybPhaser provides a novel approach to detect and phase hybrids in target capture data sets, which can provide insights into reticulations by revealing origins of hybrids and reduce conflicting signal, leading to more robust phylogenetic analyses.

KEY WORDS alleles; Angiosperm353; HybPiper; introgression; *Nepenthes*; paralogs; polyploidy; reticulation.

Reticulation events caused by hybridization are common and important sources of novelty in angiosperm evolution (Wood et al., 2009; Palfalvi et al., 2020). The detection, investigation, and representation of hybridization remains a challenge in phylogenomics (Kellogg, 2016; Mallet et al., 2016; Spooner et al., 2020). The combination of divergent genomes in hybrids (herein used for any organism that contains divergent genomes due to a hybridization event, e.g., many polyploids) introduces conflicting phylogenetic signal and can lead to topologically incorrect or poorly resolved phylogenetic trees (McDade, 1992; Soltis et al., 2008). However, the advancement of target capture data and universal probe kits such as Angiosperms353 (Johnson et al., 2018) provides an opportunity to gain insight into historical reticulations in angiosperm evolution and reduce phylogenetic conflict, if ortholog (or homeolog in polyploids) gene variants can be identified and separated (phased).

Previously, inclusion of phased gene variants in phylogenetic studies has been used to confirm hybrid status of organisms (Sang and Zhang, 1999), determine the origin of polyploids (Popp and Oxelman, 2001), reveal parental lineages (Triplett et al., 2012; Estep et al., 2014), enable reconstruction of past reticulations (Estep et al., 2014; Brassac and Blattner, 2015), and date ancient hybridization events (Marcussen et al., 2015). Using Sanger sequencing, single-gene studies generated sequences for each variant separately using cloning (Sang and Zhang, 1999; Popp and Oxelman, 2001), and multi-gene studies linked these gene variants using their phylogenetic association in single-gene phylogenies (Triplett et al., 2012; Estep et al., 2014; Marcussen et al., 2015). However, linking phased gene variants was limited by the resolution of single-locus phylogenies to detect parental clades and the low numbers of nuclear genes available using Sanger sequencing to generate robust data sets. Universal target capture sequencing bait kits such as Angiosperms353 (Johnson et al., 2018) have revolutionized the study of angiosperm evolution by enabling the recovery of sequence reads from all variants of hundreds of nuclear genes across broad phylogenetic groups. Two challenges remain: assembling reads into phased sequences from each gene variant and linking genes according to their origin to investigate phased accessions.

De novo assembly, as implemented in common pipelines such as PHYLUCE (Faircloth, 2016), HybPiper (Johnson et al., 2016), and SECAPR (Andermann et al., 2018), can only recover complete phased gene variants when all polymorphic sites are frequent enough to connect all sequence reads across the whole gene locus (Fig. 1A). If this is not the case, sequences from different gene variants (including paralogs) can be unwittingly combined to generate chimeric contigs (Kates et al., 2018). Some approaches utilize paired-end reads to increase the connectivity of polymorphisms across reads (Andermann et al., 2019); however, phased blocks do not always span across all gene loci (Kates et al., 2018). Even if all gene variants are perfectly phased, the problem of linking phased sequences across gene loci and unconnected exons to generate phased haplotypes persists.

An alternative method for sequence assembly is reference mapping, where reads are mapped to a single reference (as implemented in pipelines such as HybPhyloMaker [Fér and Schmickl, 2018]). Reads from all gene variants are mapped, and the presence of heterozygous sites generated by multiple haplotypes can be handled in two ways (Fig. 1A): (1) the nucleotide is called using a majority rule (as in HybPhyloMaker) or (2) an International Union of Pure and Applied Chemistry (IUPAC) ambiguity code is used to accommodate divergent nucleotides and prevent the creation of chimeric sequences (Uribe-Convers et al., 2016; Kates et al., 2018). However, phasing of hybrid accessions is not possible.

Here we present HybPhaser, a bioinformatic workflow that can phase hybrid accessions by simultaneously mapping sequence reads to references from the parental clades and sorting reads accordingly to generate accessions that approximate phased haplotypes. This approach performs the phasing before the assembly and thus avoids difficulties with linking of heterozygous sites and gene loci but requires a phylogenetic framework and method to select suitable references.

HybPhaser is built as an extension to the de novo assembly of HybPiper and consists of three parts (Fig. 1B, Table 1): (1) assessment of heterozygous sites in assembled sequences to detect putative hybrid accessions; (2) creation of a read-to-clade association framework; and (3) the phasing of read files based on the clade association framework. It extends the HybPiper pipeline further by enabling the modulation of paralog detection based on the heterozygosity of the data set, facilitating the optimization of the data set by cleaning samples and loci with poor recovery, and enabling the collation of consensus sequences (with ambiguity codes) as well as de novo contigs into sequence lists for subsequent analyses.

Herein we detail the HybPhaser (version 1.0) workflow and demonstrate its utility for detecting hybrids and identifying parental lineages using Angiosperms353 data from the carnivorous plant genus *Nepenthes* L. (Nepenthaceae).

METHODS

Preparation of the data set and assembly

Study group—*Nepenthes* is a paleotropical genus of ca. 160 species known to hybridize readily in horticulture and nature (Clarke et al., 2018). Molecular phylogenetic studies of the genus based on Sanger-sequenced loci have resulted in poorly resolved and supported trees due to limited resolution of the markers, incongruence between plastid and nuclear phylogenies, and the possible inclusion of ITS paralogs (Meimberg and Heubl, 2006; Alamsyah and Ito, 2013). Recently, phylogenomic approaches including genome skimming (Nauheimer et al., 2019) and Angiosperms353 target capture (Murphy et al., 2020) have provided great advances in resolving the *Nepenthes* phylogeny but were unable to clarify past reticulations evident in the data sets. In a study that sampled almost all recognized species in the genus, Murphy et al. (2020) included two known hybrids and inferred one putative hybrid accession from conflict between supermatrix and gene tree analyses. Given the availability of suitable data with good species coverage and presence of known natural and cultivated hybrids, *Nepenthes* is a suitable model group for demonstrating hybrid detection and phasing using HybPhaser (version 1.0) and the Angiosperms353 probe set.

Input data—We generated Angiosperms353 target capture data for 125 samples of 68 *Nepenthes* species, including 15 samples of 12 different horticultural hybrids. In addition, we downloaded the Murphy et al. (2020) *Nepenthes* raw read files from the National Center for Biotechnology Information (NCBI) Sequence Read Archive (BioProject PRJEB35235, 185 accessions including one known and one suspected hybrid) and added them to the data set to increase species coverage across the genus. In total, 310 accessions representing 157 *Nepenthes* taxa including 17 accessions of 14 known hybrid taxa were analyzed (Appendix S1).

DNA extraction, library enrichment, and sequencing—Total genomic DNA was isolated from leaf material stored in silica gel for 125 *Nepenthes* samples. DNA was extracted using the cetyltrimethylammonium bromide (CTAB) method (Doyle and Doyle, 1987), and DNA extracts were further processed at the Australian Genomic Research Facility (AGRF; Melbourne, Australia) for library preparation (using the NEBNext Ultra II DNA Kit protocol [New England BioLabs, Ipswich, Massachusetts, USA] per the manufacturer's

FIGURE 1. (A) Illustration of the linkage of heterozygous sites in the assembly of hybrid accessions that contain reads from two divergent haplotypes (blue = TAG, yellow = ACT). The two SNPs on the left can be linked (continuous line), but they cannot be linked to the third SNP on the right (dotted line). Reference mapping can result in consensus sequence coding SNPs as ambiguities (WMK) or represent the most common nucleotide (AAG) generating a chimeric sequence. De novo assembly can either connect phased blocks correctly into phased alleles (TAG/ATC) or generate chimeric sequences (ACG/TAT). (B) Illustration of major parts and concepts of the workflow: (1) assembly in HybPiper; (2) SNPs assessment in HybPhaser; (3) phylogenetic analysis; (4) clade association; and (5) phasing.

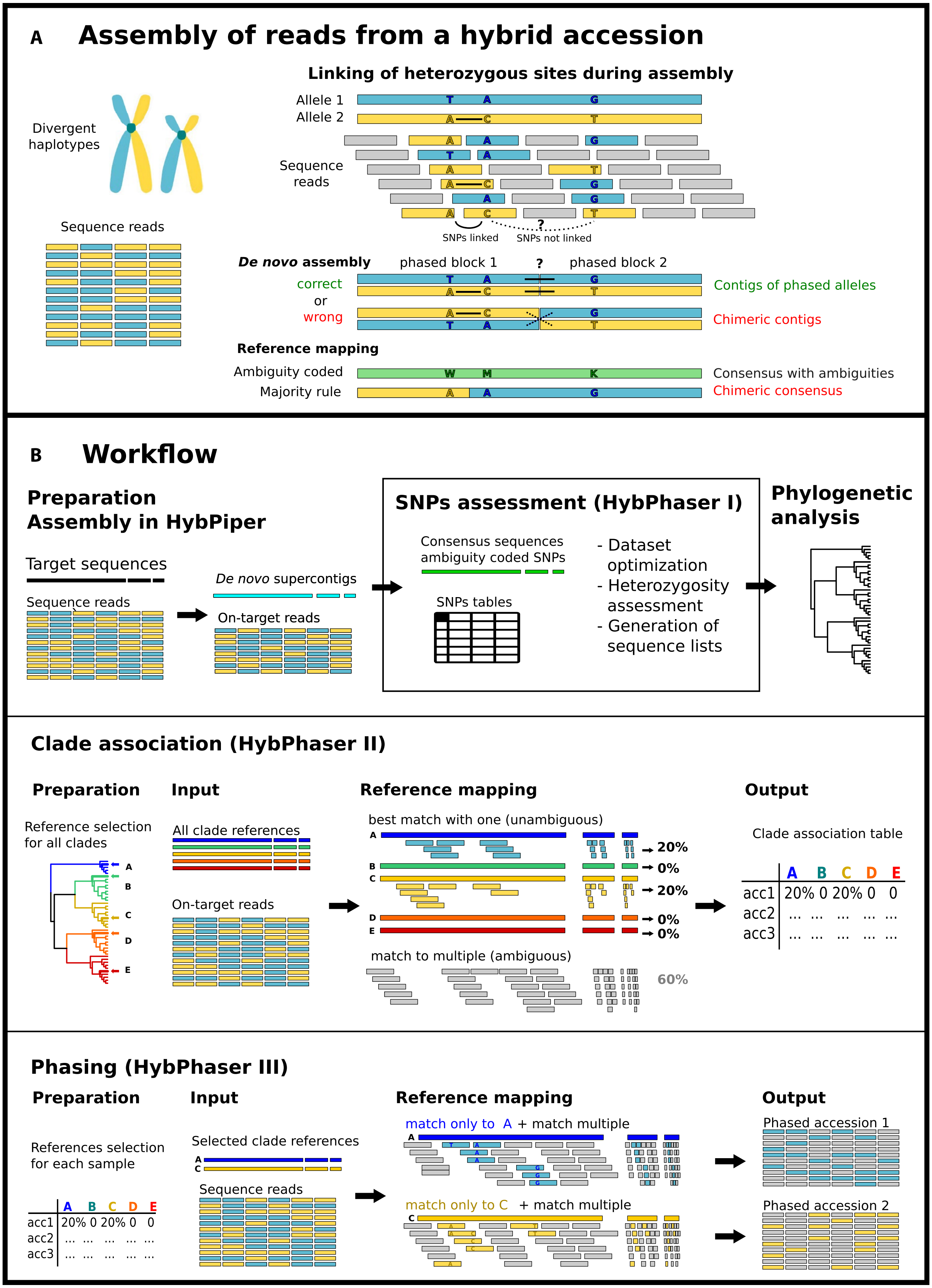
A Assembly of reads from a hybrid accession
Linking of heterozygous sites during assembly
Allele 1
Allele 2
Divergent haplotypes
Sequence reads
SNPs linked
SNPs not linked
Sequence reads
De novo assembly
phased block 1
?
phased block 2
correct
or
wrong
Contigs of phased alleles
Chimeric contigs
Reference mapping
Ambiguity coded
Majority rule
Consensus with ambiguities
Chimeric consensus
B Workflow
Preparation
Assembly in HybPiper
Target sequences
Sequence reads
De novo supercontigs
On-target reads
SNPs assessment (HybPhaser I)
Consensus sequences ambiguity coded SNPs
SNPs tables
- Dataset optimization
- Heterozygosity assessment
- Generation of sequence lists
Phylogenetic analysis
Clade association (HybPhaser II)
Preparation
Input
Reference mapping
Output
Reference selection for all clades
All clade references
On-target reads
best match with one (unambiguous)
20%
0%
20%
0%
0%
match to multiple (ambiguous)
60%
Clade association table
A B C D E
acc1 20% 0 20% 0 0
acc2 ... ...
acc3 ... ...
Phasing (HybPhaser III)
Preparation
Input
Reference mapping
Output
References selection for each sample
A B C D E
acc1 20% 0 20% 0 0
acc2 ... ...
acc3 ... ...
Selected clade references
Sequence reads
match only to A + match multiple
match only to C + match multiple
Phased accession 1
Phased accession 2

TABLE 1. HybPhaser workflow overview containing all steps with a short description, the script/software used, required input, and generated output for each step.

Part/Step	Description	Script/ software	Input	Output
1. Assessment of SNPs				
Consensus sequence generation	Reads are mapped to the de novo–assembled contigs to generate consensus sequences with SNPs where reads differ.	Bash 1 (BWA, bcftools)	de novo contigs (HybPiper), reads mapped to each locus (HybPiper)	Consensus sequences
Consensus sequence assessment	Proportion of SNPs and length of consensus sequences for each locus are collected.	R1a	Consensus sequences	Tables with SNPs/locus and sequence length
Data set optimization	Missing data can be reduced and putative paralogs removed.	R1b	Tables with SNPs/locus and sequence length	Lists with samples and loci to be removed
Assessment of heterozygosity and allele divergence	Summary tables are generated.	R1c	Tables with SNPs/locus and sequence length (cleaned)	Summary table and graphs for the assessment of heterozygosity and the detection of hybrids
Sequence lists generation	Sequences from HybPiper and HybPhaser folders are collated into sequence lists.	R1d	Contigs and consensus sequences and list with samples/loci to be removed	Sequence lists for loci or samples with contigs or consensus sequences, raw or cleaned (optimized)
2. Clade association				
Phylogenetic analysis	Alignments and phylogenetic analysis	e.g., MAFFT*, IQ-TREE*	Sequence lists	Phylogenetic tree
Selection of clade references	Taxa that represent major clades are selected by the user.		Information from phylogeny and summary table	Table (csv) with names of clade references
Extraction of mapped reads	Generation of read files that contain only reads that mapped on the target sequences	Bash 2 (samtools)	Bam file from HybPiper	Read files (mapped only)
BBSplit script preparation/ execution	Generate and run BBSplit script to match reads (mapped only) to clade references	R2a	Table (csv) with names of clade references	BBSplit stats files with proportions of reads mapped to each reference
Collation of BBSplit results	Generation of summary table for clade association	R2b	BBSplit stats files, summary table	Clade association summary table
3. Phasing				
Selection of accessions for phasing			Clade association summary table	Table (csv) with names of accessions to phase with respective references
BBSplit phasing script preparation and execution	Generate and run BBSplit script to map and phase read files	R3a	Table (csv) with names of accessions to phase with respective references, sequence read files	Read files of phased accessions, BBSplit stats files
Collation of BBSplit phasing results	Generation of summary table for phasing	R3b	BBSplit stats files	Summary table for phasing stats
4. Data set merging				
Assembly of phased accessions	Phased accessions are assembled using HybPiper and HybPhaser (part 1)	HybPiper, HybPhaser	Read files of phased accessions, target sequence list	Sequence lists of phased accessions
Merging of data sets	Sequences of phased accessions are merged with sequences of non-phased accessions	R4	Sequence lists of phased and non-phased accessions	Merged sequence lists of phased and non-phased accessions
Phylogenetic analysis	Alignments and phylogenetic analysis	e.g., MAFFT*, IQ-TREE*	Merged sequence lists	Phylogenetic tree including phased and non-phased accessions

*Software marked with an asterisk are not part of the workflow.

instructions) and sequencing. Target sequence capture was carried out using the 'Angiosperms353 v1' universal probe set (catalog no. 308196; Arbor Biosciences, Ann Arbor, Michigan, USA) following Johnson et al. (2018). Sequencing was performed on an Illumina HiSeq 2500 sequencer (Illumina, San Diego, California, USA) producing 150-bp paired-end reads.

Read trimming—The sequence reads were trimmed using Trimmomatic (v.0.39; Bolger et al., 2014) to remove sequencing adapters and poor-quality bases (illuminaclip 2:30:10, leading 20, trailing 20, sliding window 4:20). Final reads of less than 30 nucleotides were excluded.

HybPiper sequence assembly—De novo sequence assembly was performed with HybPiper (version 1.3.1) using the Angiosperms353 target file (https://github.com/mossmatters/Angiosperms353) in order to efficiently generate gene sequences consisting of concatenated exons and extract reads matching each gene. HybPiper performs reference mapping to pre-select reads matching each gene for an efficient de novo assembly of relevant reads only. If genes consist of multiple exons, assembled contigs are mapped onto the target gene and concatenated to generate a complete gene sequence. We used the nucleotide format and BWA (Li and Durbin, 2009) for mapping, but the workflow can also handle amino acid sequences and BLASTX mapping. The script 'intronerate.py' was run to retrieve gene sequences that included intron regions. Summary statistics were generated using the script 'hybpiper_stats.py' (Appendix S2).

HybPhaser part I: SNPs assessment

Reference mapping of reads from divergent gene variants leads to heterozygous sites or single-nucleotide polymorphisms (SNPs) where gene variants diverge (Fig. 1A). Assessing the distribution of SNPs across samples and loci can provide insights into the occurrence of hybrid accessions and paralogous genes, both of which are expected to have considerable divergence between gene versions. HybPhaser generates consensus sequences through reference mapping and codes SNPs as IUPAC ambiguity characters, which can be recorded and quantified using custom scripts in R (R Core Team, 2014) and assessed in generated graphs and tables.

Generation of consensus sequences—HybPhaser relies on the output of HybPiper assembly for remapping and consensus sequence generation using the Bash script 'Generate_consensus_sequences.sh'. For each sample and gene, the HybPiper de novo contig was used as reference to which the pre-selected on-target reads were mapped using BWA, generating a BAM file. Consensus sequence files containing ambiguity codes at SNP sites were generated using bcftools (v1.9, http://samtools.github.io/bcftools/bcftools.html). To prevent sequencing artifacts being coded as SNPs, variants are only called as SNPs if the read depth is ≥10, the alternative nucleotide count is ≥4, and the proportion of alternative nucleotides is ≥0.15. The script 'Rscript_1a_count_snps_in_consensus_seqs.R' was then used to collate information on the proportions of SNPs and length of sequences from all samples and loci (Appendix S3).

Reducing proportions of missing data—Missing data can have negative consequences for downstream analyses (e.g., for gene tree summary analyses; Mirarab et al., 2014), and low sequence recovery can indicate poor assembly quality. The HybPhaser script 'R1b_optimize_dataset.R' can be used to explore loci and sample quality, and to exclude loci with poor sequence recovery. Thresholds for minimum proportions of loci recovered per sample and samples recovered per locus, as well as minimum proportions of target sequence length, can be adjusted in the configuration script 'Configure_1_SNPs_assessment.R'. An initial run without data set optimization resulted in phylogenies with poorly placed low-quality samples. To improve the quality of the data set while keeping important samples, we set thresholds to remove all loci that had sequences recovered for less than 20% of samples or less than 25% of the target sequence length recovered and all samples that had less than 20% of loci or less than 45% of the target sequence length recovered.

Removal of putative paralogous genes—Genes that had been subject to gene or genome duplications can be retained as paralogs, leading to the sequencing of multiple gene variants that are potentially assembled into chimeric gene sequences (Morales-Briones et al., 2018) or to high proportions of SNPs in reference mapping (Andermann et al., 2020).

The assessment of heterozygosity in HybPhaser provides a method to detect putative paralogous genes because they are expected to have higher values compared to non-paralogous genes. HybPhaser flags genes as putative paralogs that have an unusually high proportion of SNPs compared to other genes, first as averaged across all samples to detect paralogs shared across many samples, and second in each sample individually to detect paralogs that might not be shared with other samples. HybPhaser generates a graph and boxplot to visualize SNP distribution, and manually sets a threshold for removing these putative paralogs for all samples. Alternatively, one can choose to automatically remove samples and loci with SNP frequencies that are statistical outliers (here defined as more than 1.5× the interquartile range above the third quartile). Here we used the statistical outlier method to flag loci with a frequency of SNPs greater than 1.5× the interquartile range as paralogs (Appendix S4). This was done across the whole *Nepenthes* data set to identify and flag loci that are paralogous in all *Nepenthes* samples, as well as within each sample, so that paralogous loci unique to each sample could also be identified.

Assessment of locus heterozygosity and allele divergence—Hybrids inherit divergent alleles from their parental species; therefore, hybrid samples are expected to have a high proportion of loci that contain SNPs (here called locus heterozygosity or LH) and a high proportion of SNPs across all loci (here called allele divergence or AD), which should correlate to the divergence of the parental lineages. Using the script 'Rscript_1c_summary_table.R', we generated tables and figures that summarized the LH and AD of each sample to identify putative hybrid *Nepenthes* samples (Fig. 2A, Appendix S5). Finally, the script 'Rscript_1d_generate_sequence_lists.R' was used to collate sequence lists for downstream analyses. The script collates all loci for each sample or all samples for each loci, either HybPiper de novo contigs or HybPhaser consensus sequences, and either with data set optimization (paralogs and poor-quality data removed) or without.

Framework phylogeny—The sequence lists produced by HybPhaser can be used for alignment and further phylogenetic analyses. Here, we first inferred phylogenetic relationships in *Nepenthes* based on unphased accessions to act as a framework for phasing later in the HybPhaser workflow. To do this, we used the consensus sequences for each locus after reducing missing data and removing putative paralogs. We preferred to use consensus sequences over contigs, as they mask heterozygous sites with ambiguity codes and therefore reduce conflicting phylogenetic signal from any hybrids. We aligned the consensus sequences using MAFFT (version 7.467; Katoh and Standley, 2013) and removed columns with more than 50% gaps using TrimAl (version 1.4.rev22; Capella-Gutierrez et al., 2009). Phylogenetic analyses were performed using maximum likelihood in the IQ-TREE2 package (version 2.0.5; Minh et al., 2020b). A supermatrix phylogeny was created by concatenating all locus alignments and using the 'edge proportional' partition model with single loci as partitions. Phylogenetic clade support was estimated using ultrafast bootstrap with 1000 replicates (Hoang et al., 2018) as well as gene and site concordance factors (gCF, sCF; Minh et al., 2020a), which indicate the concordance of single gene trees and of 1000 randomly chosen parsimony informative sites with the phylogeny of the concatenated data set. To determine gCF, single-gene phylogenies were generated using IQ-TREE2 applying the best-fit model for each locus selected by ModelFinder (Kalyaanamoorthy et al., 2017). In addition to the supermatrix phylogeny, we summarized the gene trees using ASTRAL-III (version 5.6.3; Zhang et al., 2018) to generate a phylogeny that is consistent under the multi-species coalescence model (Degnan and Rosenberg, 2009). While this model is only consistent when incomplete lineage

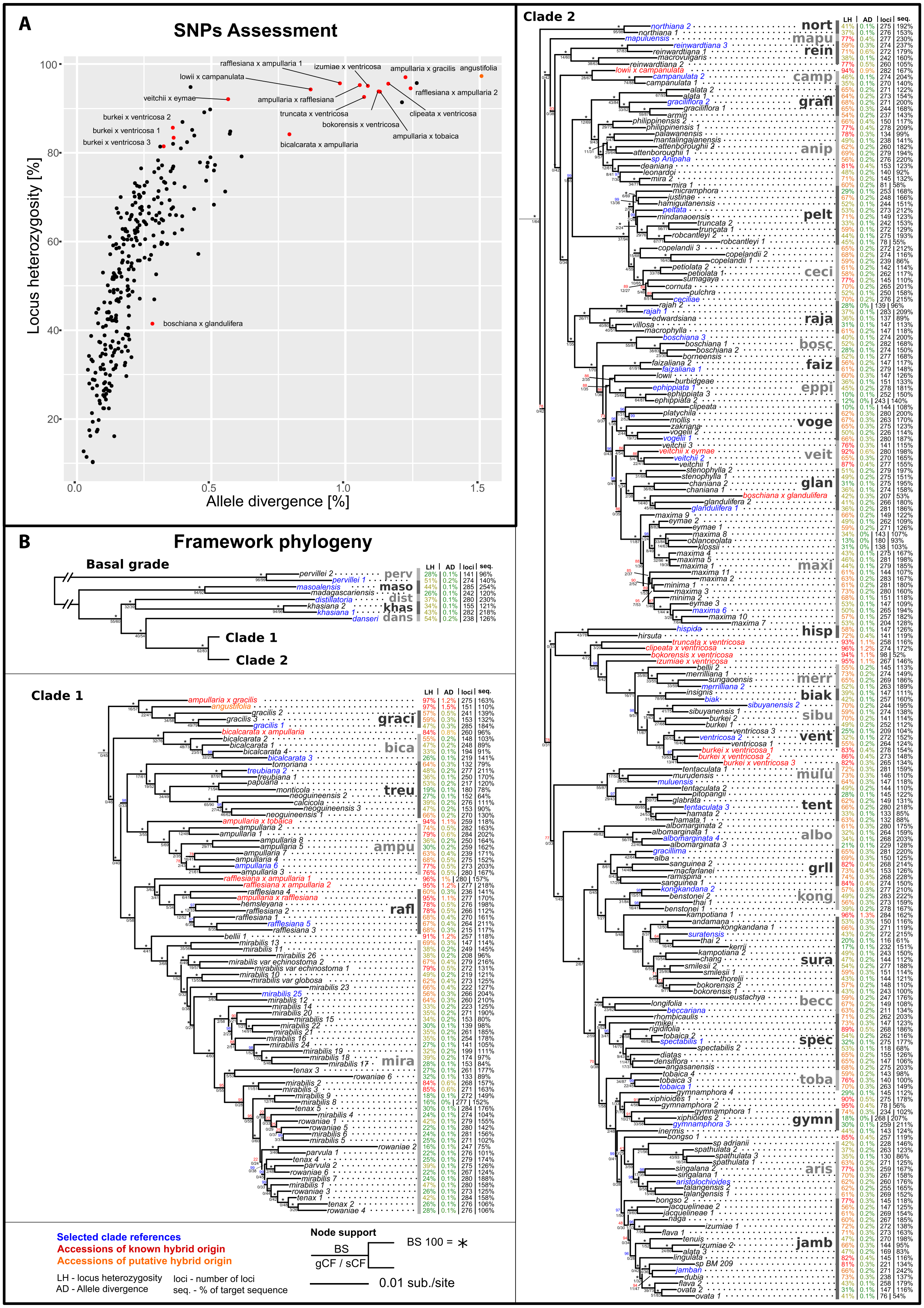
A
SNPs Assessment
Locus heterozygosity [%]
Allele divergence [%]
B
Framework phylogeny
Basal grade
Clade 1
Clade 2
Selected clade references
Accessions of known hybrid origin
Accessions of putative hybrid origin
LH - locus heterozygosity
AD - Allele divergence
loci - number of loci
seq. - % of target sequence
Node support
BS
gCF / sCF
BS 100 = *
0.01 sub./site

FIGURE 2. (A) Scatterplot displaying the locus heterozygosity and allele divergence of samples. Known hybrids (red dots) and putative hybrid (orange dot) are labeled. (B) Phylogenetic tree of the consensus supermatrix displayed in three parts: the basal grade with two diverging clades, clade 1 below, and clade 2 on the right. Summary statistics for each accession are given: locus heterozygosity (LH), allele divergence (AD), number of loci (loci), and proportion of target sequence recovered (seq.). Clades selected for clade association are shown in gray with bars. Clade references are displayed in blue, known hybrids in red, and the putative hybrid in orange. Node support is shown above the node in bootstrap (BS) (*=BS100), and below the node in gene and site concordance factors (gCF/sCF).

sorting is the only source for gene tree discordance, the comparison with the supermatrix analysis can provide valuable insights and corroborate supported clades. The resulting phylogenies were rooted using *Nepenthes pervillei* Blume, the sister species to all other *Nepenthes* species (Murphy et al., 2020).

HybPhaser part II: Clade association

To select suitable references for phasing, the association of sequence reads with divergent clades must be established. Hybrid accessions contain reads from divergent parental clades, which can be detected by mapping sequence reads to multiple references simultaneously. If the references are chosen carefully, reads from hybrid accessions will associate with parental clades. In HybPhaser part II, the software BBSplit (BBMap v38.47; B. Bushnell, https://sourceforge.net/projects/bbmap/) is used to map reads simultaneously to multiple references and record the proportion of reads matching to references from clades across the phylogeny (Fig. 1B). The reads of samples with non-hybrid origin are expected to only map to one clade reference, whereas the reads of hybrid samples are expected to map to two clades, reflecting the divergent origins of their alleles. Reads of higher-level polyploids may map to more than two references. This establishes the read-to-clade association required for the phasing in part III.

Reference selection—The selection of clade references from the framework phylogeny is critical to the efficacy of the clade association step and should be carefully considered. Clade references should be evenly distributed across the phylogeny and have low LH as well as low AD but high coverage of target sequences. References that are too closely related will result in many ambiguous matches, while references that are too distantly related can lead to reads not matching either reference. The optimal distance between clade references depends on the divergence between samples and the AD of putative hybrids, as well as factors like the allele diversity and the extent of incomplete lineage sorting or introgression in the study group. Determining a suitable number of clade references might require multiple iterations of clade association. Here, we selected a relatively high number of clade references (44) from the framework phylogeny (Fig. 2A). This enables the capture of putative hybrids with low AD (e.g., >0.4 in *N. burkei* × *ventricosa*) but also increases the chance for multiple clade associations of non-hybrids.

Clade association—Sequence read files varied in the proportion of reads that matched to the target sequences. To only take into account on-target reads, we extracted those reads from the BAM file generated by HybPiper using the Bash script 'extract_mapped_reads.sh'. The software BBSplit (BBMap v38.47) was then used to map each on-target read file simultaneously to all 44 selected clade references, recording the proportions of reads that mapped to either reference unambiguously. The script 'Rscript_2a_prepare_BBSplit_script.R' was used to generate a BBSplit commands file with the selected clade reference names and abbreviations. The mapping results were summarized using the script 'Rscript_2b_collate_BBSplit_results.R' (Appendix S6).

HybPhaser part III: Phasing

Phasing of sequence reads—Once hybrid samples have been detected and their parental clades identified, the putative hybrid accessions can be phased by simultaneously mapping the sequence reads to the relevant references and separating the reads accordingly into new read files that represent phased haplotype accessions. In this step, BBSplit is used to distribute reads that match unambiguously to one clade reference into the respective read file and then write read files that match similarly well onto multiple references into all read files for that sample (Fig. 1B). Therefore, the resulting phased accessions differ only in the reads that contain sites in which the references diverge. Ideally, hybrids containing one haplotype from each parent will be phased into two accessions representing both haplotypes. Similarly, polyploids containing multiple haplotypes can be phased into multiple accessions, in which case the proportions of reads can indicate the proportions of haplotypes.

For phasing, we considered samples with multiple clade associations as well as a high LH (>80%). Although there are samples with multiple clade associations that have low LH, they are unlikely to be hybrids that can be unambiguously phased. However, we make one exception, the known hybrid *Nepenthes boschiana* Korth. × *glandulifera* Chi. C. Lee, which had low LH (41.6%) likely due to low sequence recovery impacting variant calling. In total, we selected 26 samples for phasing, which included all 17 accessions of known hybrids and nine additional samples that had not previously been identified as hybrids.

The R script 'Rscript_3a_prepare_phasing_script.R' was used to generate a Bash script to run all 26 BBSplit commands that mapped the original sequence read files to the selected references for each chosen sample. Finally, the script 'Rscript_3b_collate_phasing_stats.R' was used to collate phasing statistics and generate a table with the proportions of reads mapped to either reference, which can give insights into the proportions of haplotypes and ploidy levels (Appendix S7).

Processing of phased accessions in HybPiper and HybPhaser part I—The newly generated read files of the phased accessions were passed through the HybPiper and HybPhaser part I pipelines using the R scripts 'Configure_1_SNPs_assessment.R' and 'Rscript_1a_count_snps_in_consensus_sequences.R' to 'Rscript_1d_generate_sequence_lists.R' with the same settings as for the non-phased samples. For the data set optimization step, we removed the same 24 loci flagged as putative paralogs for the non-phased accessions and performed the paralog removal step for each sample, individually flagging and removing statistical outliers using the scripts (Appendix S8).

Combined data set of phased and non-phased accessions—In order to analyze the phased accessions in the context of the whole genus, we generated a data set that combined the phased accessions with all non-phased accessions using the R scripts 'Configure_4_Combining_sequence_lists.R' and 'Rscript_4a_combine_phased_with_normal_sequence_lists.R'. Alignments and phylogenetic analyses were then performed with the same methodology as was used for the framework phylogeny using the consensus sequences.

HybPhaser is compatible with Linux and consists of a collection of Bash and R scripts (Table 1) that are protected under the terms of a free GNU General Public License; the scripts, along with the manual, are available online on GitHub (https://github.com/LarsNauheimer/HybPhaser). Sequence data generated for this study are available at the NCBI Sequence Read Archive (PRJNA706038).

RESULTS

HybPiper sequence assembly

The HybPiper assembly was performed successfully for 307 of the 310 samples (Appendix S2). Paralog warnings were issued for 38 samples and between one and five genes per sample (average 0.16 paralogous genes per sample).

Reducing proportions of missing data

A total of 20 samples and 41 loci were excluded from the data set (Appendix S4) due to poor sequence recovery. Ten of the excluded samples had less than 20% of loci recovered, and all 20 had a total sequence length of less than 45% of the target sequence length recovered. Thirty-nine loci had sequences recovered for less than 20% of the samples, and five loci had on average across all samples less than 50% of the target sequence length of the gene recovered. The remaining data set comprised 290 samples and 312 loci.

Removal of paralogous genes

Twenty-four loci were flagged as putative paralogous genes across all samples, with an average proportion of SNPs of 0.0062 or greater (Appendix S4). On average, 7.5 loci per sample were flagged as putative paralogs by comparing the SNPs between all genes in each sample individually.

Assessment of locus heterozygosity and allele divergence

The sampled known hybrids displayed considerably higher values of LH and AD compared to other samples, although the distinction between hybrids and non-hybrids was not clear cut. Across all samples, LH varied gradually between 10.3% and 97.4% and AD varied between 0.03% and 1.51%. Known and suspected hybrids had an average of 89.4% LH and 0.86% AD, while all other samples had an average of 52.3% LH and 0.21% AD (Fig. 2A, Appendix S5). All included hybrids except one had an LH of more than 80%. The hybrid accession *Nepenthes boschiana* × *glandulifera*, which had poor sequence recovery (50.5% of target sequence length before optimization), had very low values of LH (41.6%) and AD (0.28%) compared to the other hybrids.

Framework phylogeny alignment generation

The supermatrix data set consisted of 285 genes and 290 taxa, with an aligned sequence length of 423,105 bp and 30.4% missing data. Overall, clades in the framework phylogeny were well supported, and largely corresponded to the clades retrieved by Murphy et al. (2020) (Fig. 2B). Many clades obtained maximum bootstrap support, although the gCF values were often low. Some of the backbone nodes received very low support. Most hybrid accessions fell within the clade containing one of the parental taxa where the hybrid was often found in a basally diverging position within the clade (e.g., *N. ampullaria* Jack × *gracilis* Korth.; Fig. 2B). The gene tree summary phylogeny (Appendix S9) is largely congruent with the supermatrix phylogeny, with the only exception being the position of the 'albo' clade, which groups with moderate support in a different clade in each phylogeny. Hybrid accessions group either basal in one of the parental clades or between parental clades.

Clade association

Interpretation of clade association must be done for each sample individually, taking into consideration the phylogenetic distance between that sample and the clade references, the phylogenetic distance between clade references, and the sequence length of the clade reference sequences. Most samples had a single clade association with a higher proportion of reads matching unambiguously to one clade reference compared to the others (Fig. 3, Appendix S6). In contrast, all known hybrids showed associations with multiple, often divergent clades. In most cases, the association with both clades is strong (e.g., *N. ampullaria* × *gracilis*), whereas in others the association with one clade is weak (e.g., *N. truncata* Macfarl. × *ventricosa* Blanco) or very weak (e.g., *N. clipeata* Danser × *ventricosa*). Even *N. boschiana* × *glandulifera*, which had low values of LH and AD, showed an association to both parental clades. Nine non-hybrid accessions with high LH (>80%) showed associations with two clades (e.g., *N. kampotiana*-1 Lecomte, *N. bellii*-1 K. Kondo, *N. xiphioides*-1 B. R. Salmon & Maulder). Samples with lower LH values generally showed either a single clade association or multiple associations of closely related references.

The highest proportions of matching reads were found in phylogenetically distinct, basally diverging lineages (e.g., >60% in *N. khasiana* Hook. f.), while multiple clade associations were often found in taxa with low LH and AD when they were not closely related to one or were in between two clade references (e.g., *N. petiolata* Danser, *N. clipeata*). Few samples had reads associated with multiple divergent clades but had medium to low values for LH and AD (e.g., *N. talangensis* Nerz & Wistuba or *N.* sp 'adrianii').

Phasing of sequence reads

In mapping onto the selected references, an average of 4.9% (1.1–13.9%) of original sequence reads mapped unambiguously to a single reference. Thirteen phased accessions had approximately equal proportions of unambiguous mapped reads, six accessions had a proportion of approximately 3 : 2, nine accessions had a proportion of approximately 2 : 1, and four accessions had a proportion of roughly 1 : 3 (Appendix S7).

Processing of phased accessions

Most phased accessions had considerably lower LH and AD compared to the non-phased accessions before phasing (Appendix S8).

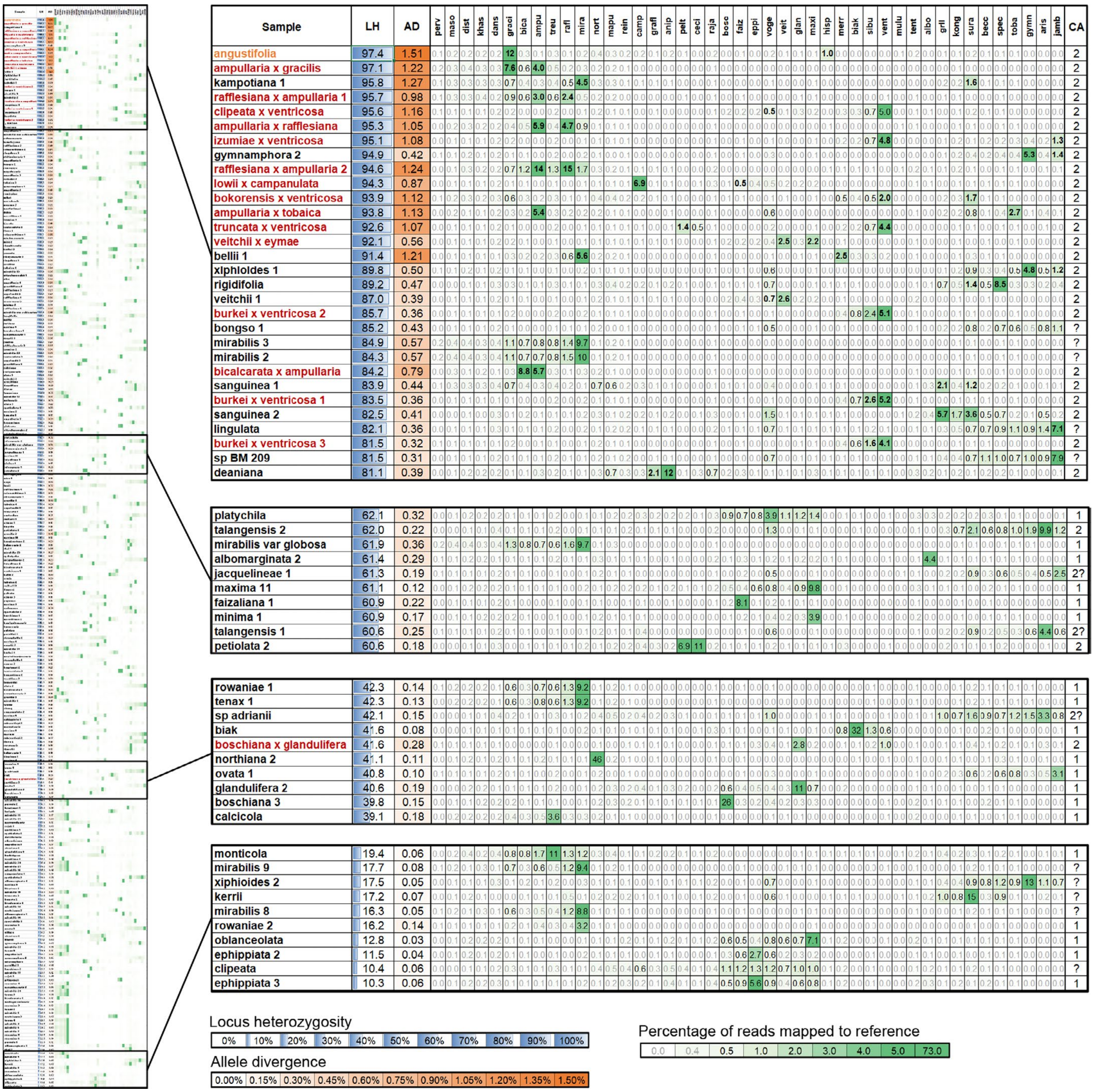

FIGURE 3. Clade association table and heatmap displaying the percentage of reads matching to each of the 44 clade references. The complete table is on the left, with extracts of example rows shown on the right. The table includes locus heterozygosity (LH) and allele divergence (AD), percentages of reads matching to each reference, and the number of clade associations (CA). Known hybrids are in red, and the putative hybrid is in orange.

Both phased accessions of *N. boschiana* × *glandulifera* had very low sequence recovery (35.5% and 10.5%) and were removed from the data set. The paralog detection for each sample individually resulted in flagging of on average 6.8 genes per sample as putative paralogs that were removed from the data set.

Combined data set of phased and non-phased accessions

The combined data set consisted of 285 genes and 315 taxa, with an aligned sequence length of 400,685 bp and 32.6% missing data. The topology of the supermatrix phylogeny based on the combined data set including phased accessions is congruent with the framework

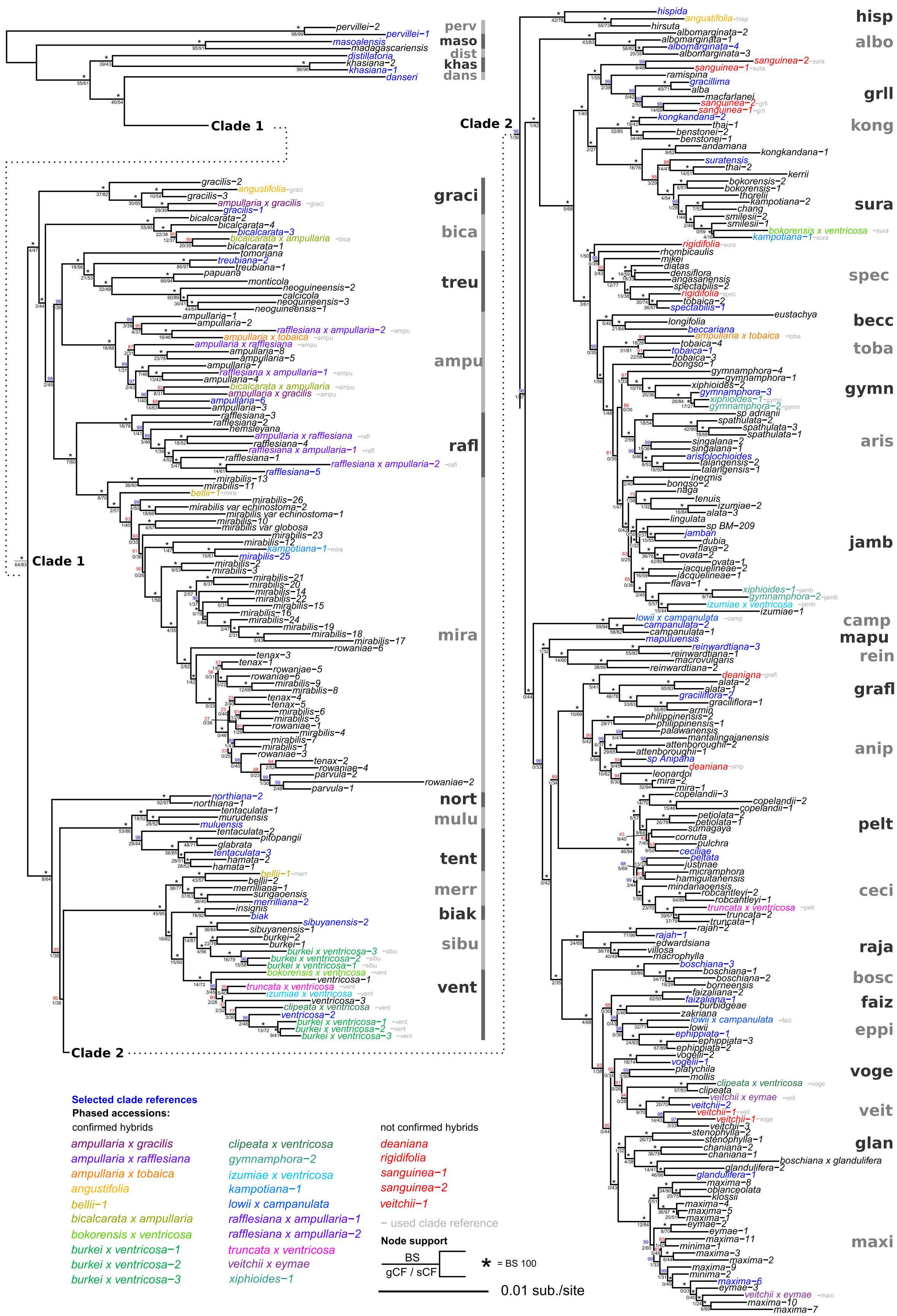
Clade 1
Clade 2
perv
maso
dist
khas
dans
graci
bica
treu
ampu
rafl
mira
nort
mulu
tent
merr
biak
sibu
vent
hisp
albo
grll
kong
sura
spec
becc
toba
gymn
aris
jamb
camp
mapu
rein
grafl
anip
pelt
ceci
raja
bosc
faiz
eppi
voge
veit
glan
maxi
Selected clade references
Phased accessions:
confirmed hybrids
ampullaria x gracilis
ampullaria x rafflesiana
ampullaria x tobaica
angustifolia
bellii−1
bicalcarata x ampullaria
bokorensis x ventricosa
burkei x ventricosa−1
burkei x ventricosa−2
burkei x ventricosa−3
clipeata x ventricosa
gymnamphora−2
izumiae x ventricosa
kampotiana−1
lowii x campanulata
rafflesiana x ampullaria−1
rafflesiana x ampullaria−2
truncata x ventricosa
veitchii x eymae
xiphioides−1
not confirmed hybrids
deaniana
rigidifolia
sanguinea−1
sanguinea−2
veitchii−1
− used clade reference
Node support
BS
gCF / sCF
* = BS 100
0.01 sub./site

FIGURE 4. Phylogenetic tree of the consensus supermatrix including phased haplotype accessions. Phased accessions are displayed in different colors. Clade references are displayed in blue. Node support is shown above the node in bootstrap (BS) (*=BS100) and below the node in gene and site concordance factors (gCF/sCF).

phylogeny in all nodes, but displays stronger support (Fig. 4). The support for the backbone nodes and for the clades that contained hybrids increased compared to the framework phylogeny with non-phased accessions due to the reduction of conflicting phylogenetic signal. This was especially prominent regarding gene concordance factors showing that phasing hybrids reduced conflicting information and increased concordance in the data set.

The phased haplotype accessions from all 16 known hybrids grouped in the clade of their respective parental species, mostly as sister to the parental species, e.g., *N. ampullaria* × *gracilis* grouped with *N. gracilis*-1 in the graci clade and *N. ampullaria* × *gracilis* grouped with *N. ampullaria*-6 and *N. ampullaria*-3 in the ampu clade. The phased accessions of the putative hybrid *N. angustifolia* grouped in divergent clades with *N. gracilis*-3 and *N. hirsuta* Hook. f. Of the nine accessions previously considered to be non-hybrids but with high LH and multiple clade associations, five had phased accessions grouping in divergent clades; three of these groupings were with putative parent taxa: *N. kampotiana*-1 with *N. mirabilis*-25 and *N. smilesii*-1 Hemsl., *N. bellii*-1 with *N. mirabilis*-12 and *N. bellii*-2, and both *N. gymnamphora*-2 Reinw. ex Nees as well as *N. xiphioides*-1 with *N. gymnamphora*-3, and *N. izumiae*-1. The phased accessions of *N. deaniana* Macfarl. grouped more ambiguously with one clade containing *N.* sp-Anipaha and *N. leonardoi* and another clade of *N. alata*-1,2 and *N. graciflora*-1,2. The phased haplotypes of four more accessions, *N. rigidifolia*, *N. sanguinea*-1,2, and *N. veitchii*-1 did not separate into divergent clades. The summary gene tree phylogeny (Appendix S10) is largely concordant with the supermatrix tree (Fig. 4), but with considerably lower support for many nodes. Supported topological differences are found in the positions of the phased accessions within the graci clade, as well as *N. boschiana* × *glandulifera*, which had low sequence recovery, and the phased accessions of *N. veitchii*-1, which had not been phased successfully.

DISCUSSION

Read phasing with HybPhaser

With the *Nepenthes* data set, we have shown that phasing reads prior to sequence assembly through HybPhaser is an effective way to detect and characterize haplotypes in hybrid accessions. Previous approaches perform phasing during or after the sequence assembly (Kates et al., 2018; Andermann et al., 2019); however, linking reads using de novo assembly requires frequent heterozygous sites to connect reads across the loci (Fig. 1A), which can be difficult to achieve even with read-backed phasing methods using paired-end reads assembly (Kates et al., 2018). Linking phased genes to generate a concatenated multi-gene data set can be performed by assigning genes to clades based on single-locus phylogenies, which requires sufficient phylogenetic signal in each locus for successful clade assignment (Triplett et al., 2012; Estep et al., 2014; Marcussen et al., 2015). In HybPhaser, sequence reads are phased by mapping to multiple reference sequences representing parental clades prior to their assembly, thereby avoiding these issues.

Although this pre-assembly phasing approach of HybPhaser is advantageous, it must be emphasized that the phased haplotypes only represent an approximation of the parental haplotypes. BBSplit, as used in the HybPhaser workflow, assigns reads to a single phased accession that matches unambiguously to its reference, while all other reads are assigned to all phased accessions. Therefore, the differences between the references determine the phasing. Theoretically, haplotypes of hybrids will phase perfectly (100% unambiguous matches) if the references are the actual parents of the hybrid sample and no random mutations or cross-over events occurred. However, if the selected references diverge from the actual parental lineages, are heterozygous, or differ in the sequence length or locus coverage, haplotypes will not be phased perfectly and will only approximate the parental haplotypes.

Furthermore, the efficacy of the HybPhaser phasing approach is sensitive to the selection of appropriate reference sequences. First, successful phasing will be dependent on the phylogenetic divergence between references; when references are closely related, more reads will be ambiguous and the number of successfully matched reads will be low. Second, the divergence between the clade reference and the parental lineage of the hybrid has an influence on clade association; with increasing divergence from the clade reference, fewer reads will match unambiguously. We therefore recommend that selected references represent samples that are evenly distributed across the phylogeny, have high loci coverage, and contain little allele divergence. In *Nepenthes*, we chose 44 clade references based on a phylogenetic framework and the assessment of heterozygosity across the data set. This included relatively closely related references in order to resolve known hybrids with closely related parents (*N. burkei* × *ventricosa* and *N. veitchii* × *eymae*), as well as putative hybrids with similarly high LH but low AD (e.g., *N. sanguinea*, *N. gymnamphora*-2, or *N. xiphioides*-1). Choosing suitable reference sequences was crucial for successfully phasing *Nepenthes* hybrids with parents of differing relatedness using HybPhaser.

Hybrid detection with HybPhaser

In this study, we have shown the utility of HybPhaser not only in characterizing the parentage of known hybrids, but also in detecting previously unknown, putative hybrids. Almost all known hybrid accessions of *Nepenthes* had high LH (>80%) and an AD that reflected the divergence of the parental lineages (most had >0.6%). This contrasts with most samples, which had LH between 20% and 70% and an AD of 0.1% and 0.3%, reflecting the occurrence of allelic variation in species. Several samples had an AD between 0.3% and 0.6% or low to medium LH and multiple clade associations; both of these might indicate the occurrence of introgression through backcrossing of hybrids into one parental population. Evolution is dynamic, and a variety of processes (e.g., introgression, polyploidization and diploidization, gene duplications and losses, as well as incomplete lineage sorting) or a combination of these can impact LH and AD values as well as the clade association analysis (Mallet et al., 2016; Soltis et al., 2016). In addition, low coverage of sequence reads can lead to low LH and AD values due to the method of variance calling. Here, the hybrid *N. boschiana* × *glandulifera* had by far the lowest

LH (41.6%) and AD (0.42%) of all included hybrids. This might be an underestimate due to low sequence coverage, which is indicated by the low sequence recovery of the original accession (50.5% of the target sequence length) and the very low sequence recovery of the phased accessions (10.6% and 35.5%). Although *N. bokorensis* Mey × *ventricosa* and *N. gymnamphora*-2 had similarly low sequence recovery in the original mapping, they had normal values of LH and AD and a sequence recovery of phased accessions similar to the normal accessions.

The assessment of heterozygous sites and thus the conflict between the gene variants or divergent haplotypes in the data set provides a simple way to gain insights into the reticulation of samples. *Nepenthes* is known for including a variety of horticultural and natural hybrids (Clarke et al., 2018). We found a gradient of LH and AD across the genus, with many samples having intermediate values between known hybrids and most other samples, which indicates introgression and the presence of unknown hybrid accessions. Fourteen samples had LH (>80%) and AD (>0.3%) similar to the closely related hybrids, of which nine had reads associated with multiple clades and were phased. After phasing and inclusion of phased accession into the phylogenetic analyses, four samples had phased accessions clearly grouping in divergent clades with specific taxa confirming their hybrid status and revealing parental lineages: *N. bellii*-1 (*bellii* × *mirabilis*), *N. kampotiana*-1 (*smilesii* × *mirabilis*), *N. gymnamphora*-2 (*gymnamphora* × *izumiae*), and *N. xiphioides*-1 (*gymnamphora* × *izumiae*). Furthermore, the AD of phased accessions combined from each of the samples was lower than the AD of the non-phased accessions. Four samples were not confirmed as hybrids based on the phasing, because the phased accessions did not group in divergent clades (*N. rigidifolia*, *N. sanguinea*-1,2, and *N. veitchii*-1). One sample was more ambiguous; *N. deaniana* had phased accessions grouping in divergent clades but not clearly associated with other samples, thus reducing the phylogenetic support of the affected clades. Furthermore, the AD of the phased accessions combined (0.36% + 0.21%) was much higher than the AD of the non-phased accessions (0.39%). Therefore, it is unlikely that *N. deaniana* is a hybrid between species of these clades.

Paralog detection with HybPhaser

Our results suggest that the paralog detection of HybPhaser greatly improves on existing methods. In approaches such as the paralog investigator of HybPiper, a paralog warning is only issued when multiple de novo contigs are recovered with comparable size, i.e., when multiple contigs have at least 75% of the whole target sequence length (Johnson et al., 2016). To successfully detect a paralogous gene, heterozygous sites must occur frequently enough to connect reads of all versions across most of the locus and, because the target length is used as a reference, the gene must not consist of multiple exons shorter than 75% of the gene. The paralog detection provided in HybPhaser is based on the idea that paralogous genes have higher rates of heterozygous sites than normal genes, and therefore can detect paralogs independent of exon size or distribution of heterozygous sites across the gene.

In *Nepenthes*, HybPiper issued warnings for only 0.16 of genes per sample, while the approach taken by HybPhaser flagged 31.5 genes per sample (ca. 10% of the genes). This large difference is due not only to the methodology, but also to the chosen conservative approach to remove more rather than fewer genes. First, flagging genes that have unusually high proportions of SNPs across all samples (here 24 genes) will lead to removing those genes for samples without multiple variants. This might be desired, however, as gene loss can lead to leaving only one version active, which is not guaranteed to be the ortholog. Second, this method flags genes that have unusually high rates of SNPs as a result of reasons other than paralog variants (e.g., sequencing or assembly artifacts, indels, or non-paralogous but similar sequences from other genes). HybPhaser provides graphs and tables to assess the distribution of SNPs in each locus either averaged across all samples or for each sample individually. It further provides methods to remove putative paralogous loci from the data set. The assessment of individual BAM files can give more insights into the cause of the dubious loci.

Reconciling phylogenetic conflict with HybPhaser

In this study, we have demonstrated how HybPhaser can be used to handle phylogenetic conflict in target capture data sets and to more accurately estimate phylogenies using supermatrix and gene tree summary approaches. Hybrids introduce phylogenetic conflict in the data set, leading to poorly resolved clades or incorrect topology (McDade, 1992; Soltis et al., 2008). The effect will differ depending on the method of sequence generation and handling heterozygous sites. Hybrids might group together with one parent, basal to one parent, or in between multiple parental clades. Here, we used ambiguity codes in the non-phased data set, and most hybrids were in a basal position in the clade of one parent with a shorter total branch length. Phasing of hybrid accessions reduced the conflicting signal and improved the clade support of affected clades, especially in gene and site concordance factors. To further decrease the conflicting signal in the data set, one might consider removing all samples with high LH or AD values. This can be especially useful as a means to increase clade support for the framework phylogeny for clade association.

Concluding remarks

HybPhaser provides a novel workflow to detect and phase hybrid accessions in target capture data sets. In this study, we have used HybPhaser to untangle the reticulate evolutionary history of *Nepenthes* and demonstrated its utility for phasing reads into parental haplotypes, revealing and characterizing hybrids, detecting putative paralogous genes, and resolving phylogenetic conflict.

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AUTHOR CONTRIBUTIONS

L.N. developed the workflow, performed analyses, and wrote the manuscript. N.W. contributed to data curation and analysis. C.C. provided sample collections and plant identifications. E.J. tested the

workflow and contributed to manuscript preparation. D.C. and K.N. contributed to project administration, supervision, and manuscript preparation. C.C., D.C., and K.N. acquired funding for the project. All authors read and approved the final manuscript.

DATA AVAILABILITY STATEMENT

All workflow scripts are available through the HybPhaser repository on GitHub (https://github.com/LarsNauheimer/HybPhaser; Nauheimer, 2021). Sequence data are available through the National Center for Biotechnology Information (NCBI) (BioProjects: PRJNA706038 [this study] and PRJEB35235 [Murphy et al., 2020]).

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

APPENDIX S1. List of accessions included in this study with DNA or SRA number, short name used in this paper, voucher information, geographic origin, and whether the sample was used in Murphy et al. (2020) or was generated for this study.

APPENDIX S2. Statistics retrieved from HybPiper script 'hybpiper_stats.py' for the normal contigs (not those including intron regions).

APPENDIX S3. Tables with recovered sequence length and proportion of SNPs for each sample and locus, before and after data set optimization.

APPENDIX S4. Graphs and tables generated in the data set optimization step.

APPENDIX S5. Summary table from heterozygosity assessment.

APPENDIX S6. Table from clade association analysis.

APPENDIX S7. Input table and summary statistics from phasing analysis.

APPENDIX S8. Graphs and tables from data set optimization and heterozygosity assessment of phased accessions.

APPENDIX S9. Gene tree summary phylogeny from normal data set (framework phylogeny).

APPENDIX S10. Gene tree summary phylogeny from data set including phased accessions.

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Applications in Plant Sciences

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APPLICATION ARTICLE

INVITED SPECIAL ARTICLE

For the Special Issue: Exploring Angiosperms353: a Universal Toolkit for Flowering Plant Phylogenomics

New targets acquired: Improving locus recovery from the Angiosperms353 probe set

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PREMISE: Universal target enrichment kits maximize utility across wide evolutionary breadth while minimizing the number of baits required to create a cost-efficient kit. The Angiosperms353 kit has been successfully used to capture loci throughout the angiosperms, but the default target reference file includes sequence information from only 6–18 taxa per locus. Consequently, reads sequenced from on-target DNA molecules may fail to map to references, resulting in fewer on-target reads for assembly, and reducing locus recovery.

METHODS: We expanded the Angiosperms353 target file, incorporating sequences from 566 transcriptomes to produce a 'mega353' target file, with each locus represented by 17–373 taxa. This mega353 file is a drop-in replacement for the original Angiosperms353 file in HybPiper analyses. We provide tools to subsample the file based on user-selected taxon groups, and to incorporate other transcriptome or protein-coding gene data sets.

RESULTS: Compared to the default Angiosperms353 file, the mega353 file increased the percentage of on-target reads by an average of 32%, increased locus recovery at 75% length by 49%, and increased the total length of the concatenated loci by 29%.

DISCUSSION: Increasing the phylogenetic density of the target reference file results in improved recovery of target capture loci. The mega353 file and associated scripts are available at: https://github.com/chrisjackson-pellicle/NewTargets.

KEY WORDS Angiosperms353; HybPiper; locus recovery; target capture; target file.

Target enrichment (also known as target capture, exon capture, or Hyb-Seq) has become the leading high-throughput sequencing methodology for phylogenomics, offering reliable retrieval of hundreds or thousands of loci at a reasonable price per base pair (Cronn et al., 2012; Grover et al., 2012; Barrett et al., 2016; Bragg et al., 2016; Dodsworth et al., 2019). The method has proven useful for resolving relationships at all taxonomic ranks, including higher-level phylogenetic relationships among orders or families, as well as lower-level relationships among genera or species, and for species delimitation (Bi et al., 2013; Nicholls et al., 2015; Song et al., 2017; Choi et al., 2019; Breinholt et al., 2021). Target enrichment uses available genome sequence information in the form of genomes, transcriptomes, or genome skimming data to identify a set of target loci (e.g., genes, exons, or ultra-conserved elements [UCEs]), which are typically low- or single-copy (Faircloth, 2017; McKain et al., 2018). From the target loci set, short 80–120 bp RNA baits (also called probes) are designed, to create a "bait kit." These short RNA baits are used in a hybridization reaction to bind to DNA fragments matching the target loci, which are then captured and PCR-amplified for sequencing. The increasing availability of genomic resources held in public repositories, combined with the use of pipelines to identify low- or single-copy genes based on these resources, has enabled bait kit design for a wide range of plant groups (Kadlec et al., 2017; Campana, 2018; Chafin et al., 2018; Vatanparast et al., 2018).

Universal bait kits, such as the Angiosperms353 bait kit, aim to capture the same set of loci from samples representing significant phylogenetic breadth and evolutionary timescales (Bossert and Danforth, 2018; Breinholt et al., 2021; Johnson et al., 2019). Such kits typically require a larger number of baits to encompass the sequence diversity potentially found among samples at each locus. Larger kits are more costly (Hutter et al., 2019; Couvreur et al., 2019), and therefore to keep costs manageable universal bait kits balance the number of baits synthesized, and hence bait sequence diversity for each locus, against the total number of RNA baits strictly required to fully capture diversity at each locus. Incomplete representation of sample sequence diversity in the synthesized baits is in part compensated for by the high affinity of the biochemical interaction in the hybridization reaction binding the RNA bait to the DNA target. This high affinity enables successful capture reactions between the RNA baits and the target DNA even in cases where bait and target sequences differ by ~20% (although Johnson et al., 2019 extended this to 30% when designing the Angiosperms353 kit, based on the findings of Liu et al., 2019), and provides a constraint around the minimal sequence diversity required to capture loci across the desired phylogenetic breadth (Mayer et al., 2016; Branstetter et al., 2017; Faircloth, 2017; Couvreur et al., 2019). This is demonstrated by the wide range of flowering plant groups that have successfully utilized the Angiosperms353 kit (Johnson et al., 2019; Van Andel et al., 2019; Larridon et al., 2020; Shee et al., 2020), as well as many other universal bait kits (e.g., flagellate plants [GoFlag; Breinholt et al., 2021], ferns [Wolf et al., 2018], arachnids [Starrett et al., 2017], Cnidaria [Quattrini et al., 2018], and Gastropoda [Teasdale et al., 2016]).

The assembly of raw sequence reads into the desired locus typically follows one of two strategies: (1) de novo assembly of reads and subsequent matching of contigs to target loci, or (2) mapping reads to each locus, followed by de novo assembly of the mapped reads for each locus. Various pipelines are available to perform locus assembly, such as HybPiper (read-mapping; Johnson et al., 2016), PHYLUCE (de novo assembly; Faircloth, 2016), and SECAPR (both de novo assembly and read-mapping; Andermann et al., 2018). For any strategy, a file containing the target loci sequences (i.e., the target file) is required. This is typically the same file that was used to design the baits. For universal-scale kits, this means that closely related reference sequences might not be present in the target file for a given data set. This raises a question: what if the biochemistry of hybrid enrichment enables the successful capture of target loci DNA in vitro, but subsequent bioinformatic processing of raw or assembled data to reconstruct the target locus is inefficient or fails because there is no suitable reference in silico? A mismatch between biochemical locus capture and bioinformatic locus recovery is expected to have a larger impact in broader-scale universal kits, or groups where suitable reference sequences are lacking, and could influence locus recovery at any phylogenetic level. To investigate the impact of target file sequence diversity on locus recovery, we developed tools to expand the Angiosperms353 target file and compared locus recovery across a range of phylogenetic depths against the default Angiosperms353 file, using HybPiper for locus assembly.

METHODS

Generating the mega353 target file

The target file for the Angiosperms353 kit was downloaded from https://github.com/mossmatters/Angiosperms353/blob/master/Angiosperms353_targetSequences.fasta (referred to here as the 'default353' target file). To obtain a phylogenetically diverse set of angiosperm sequences from which to recover the Angiosperms353 loci, transcriptomes were downloaded from the 1KP portal (http://www.onekp.com/public_data.html; Carpenter et al., 2019). A maximum of two samples per genus were added, with samples with the largest number of sequences preferentially included. The resulting set included 566 transcriptomes (see https://github.com/chrisjackson-pellicle/NewTargets/blob/master/filtering_options.csv).

To create the mega353 target file, the following process was carried out (summarized in Fig. 1). For each locus in the default353 target file, a single locus alignment was produced using MAFFT (Katoh and Standley, 2013), and a corresponding hidden Markov model (HMM) profile was generated using HMMER (Eddy, 2011). HMM profiles were used to search the 1KP transcriptomes using hmmsearch with an *E*-value cut-off of 1e-50, and the top hit (if present) was recovered. Transcriptome hits were added to the corresponding locus alignment, and the 5′ and 3′ termini were trimmed to the longest original target file sequence from either *Arabidopsis thaliana* (L.) Heynh. (Brassicaceae), *Amborella trichopoda* Baill. (Amborellaceae), or *Oryza sativa* L. (Poaceae), as at least one of these three species was included for each locus in the default353 target file. In cases where a transcriptome hit sequence was shorter than the longest original target file sequence for a given locus, the transcriptome hit sequence was extended by grafting with the 5′ and/or 3′ termini of the closest related original sequence. If the resulting grafted sequence was still shorter than the longest original target file sequence, it was grafted again with the longest original sequence. In such cases, the resulting target file sequence was therefore a chimeric construct, and these cases are flagged in the sequence name. This grafting process was necessary as HybPiper translates a single chosen target file sequence for each locus and sample, and the resulting protein sequence is used as a query in Exonerate (Slater and Birney, 2005) to search against assembled nucleotide contigs, using the protein2genome model. Consequently, short protein queries recover truncated nucleotide loci sequences, even if longer contigs have been successfully assembled.

As recovery of target loci using HybPiper requires correct translation of the chosen target file sequences in the first reading frame, any frameshifts observed in trimmed and/or grafted transcriptome hit sequences were corrected or compensated for (see https://github.com/chrisjackson-pellicle/NewTargets for further details). In cases where a frameshift could not be corrected, the corresponding transcriptome hit sequence was removed for that locus/sample. Finally, sequences were extracted from each locus alignment, gap positions were removed, and all sequences were concatenated to create a new target file.

Filtering the mega353 target file

To tailor the large mega353 target file to investigation-specific taxon sampling, we include the script filter_megatarget.py. This script can be used to create a filtered target file based on user-selected taxa or taxon groups, defined by unique 1KP transcriptome codes, families, orders, or clades (see https://github.com/chrisjackson-pellicle/NewTargets for full options). In addition to the chosen samples, all sequences from the default353 target file are retained.

Adding sequences from any transcriptome to any existing target file

As an additional resource, we provide the script BYO_transcriptome.py, which allows sequences from any transcriptome (e.g., from

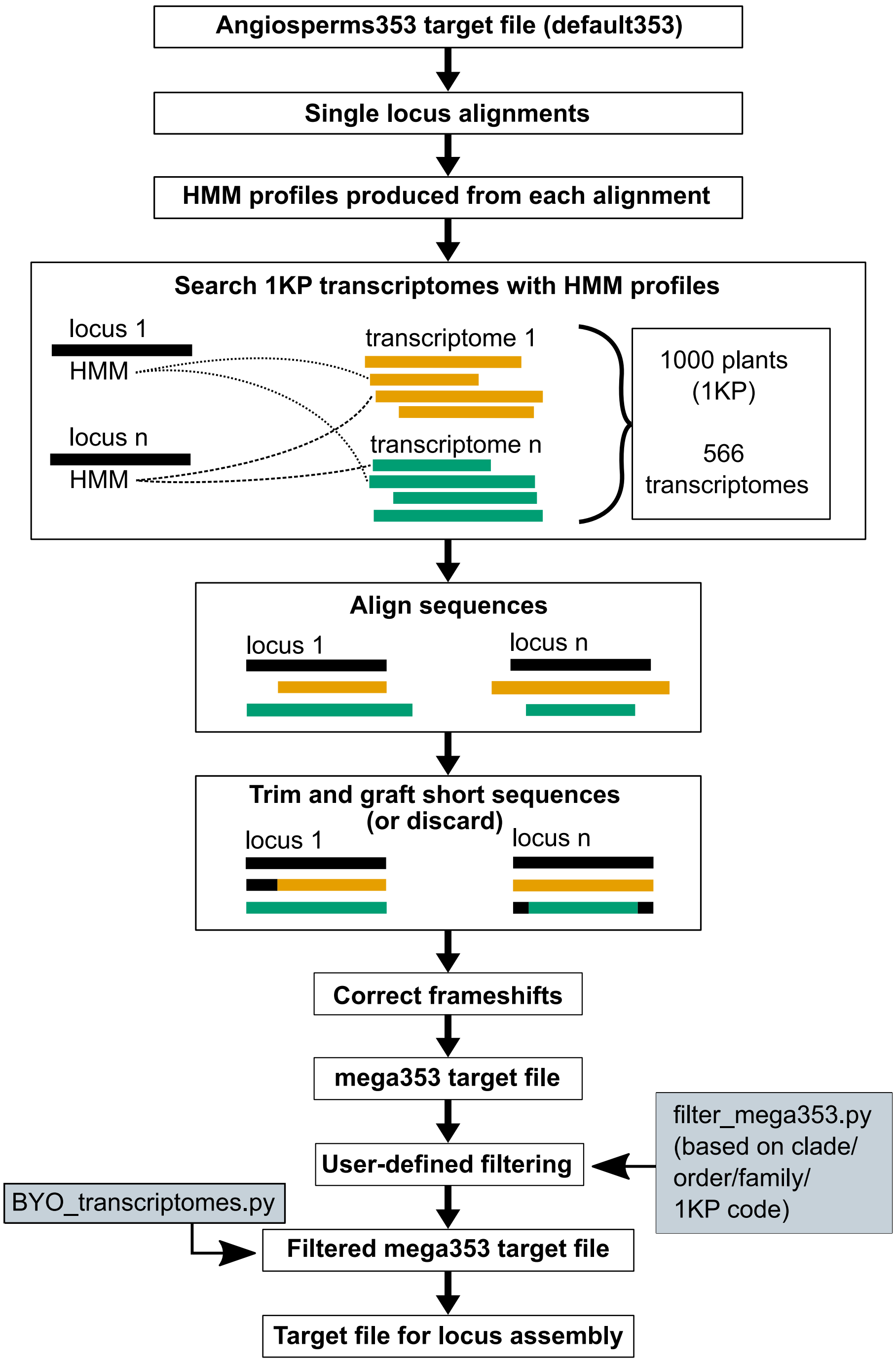

FIGURE 1. Overview of the steps involved in creating the mega353 target file. First, loci in the default353 file are aligned and hidden Markov model (HMM) profiles are created for each locus. The HMM profiles are used to identify these loci in the 1KP transcriptomes, and transcript hits are added to the alignment. The alignment of each locus is then trimmed, grafted if necessary, a frameshift correction is performed, and all loci are combined in the mega353 target file. The gray boxes indicate steps the user can take to modify the mega353 target file. The mega353 target file can be filtered (based on sample identifiers in the filtering_options.csv file) to select samples included in the target file. The BYO_transcriptome.py script can be used to add GenBank or personal transcriptomes to the filtered mega353 target file.

GenBank or personal data) to be added to an existing target file. A target file and a directory of transcriptomes are the only inputs required. For Angiosperms353 analyses, this script can be run using a filtered mega353 target file to expand phylogenetic coverage of target file sequences in a custom manner. The default BYO_transcriptome.py pipeline is the same as that described above for creation of the mega353 target file. Optionally, a flag can be specified to discard short transcriptome hits rather than grafting them, and this option can be applied with a user-specified length threshold. This allows recovery of non-chimeric homologous sequences from transcriptomes that can be used in downstream phylogenetic analyses. For additional options, see https://github.com/chrisjackson-pellicle/NewTargets/wiki.

Comparing locus recovery between the default353 target file and the expanded mega353 target file

To compare locus recovery between the default353 versus the expanded mega353 target file, we used several data sets, encompassing orders (Asparagales, Sapindales), families (Ericaceae), and genera (*Azorella* Lam., Apiaceae; *Nepenthes* L., Nepenthaceae; *Cyperus* L., Cyperaceae [Larridon et al., 2020]; *Bulbophyllum* Thouars, Orchidaceae), as well as the data set used to test the bait kit in the original Angiosperms353 publication (i.e., the exemplar Angiosperms353 data set; Johnson et al., 2019) (Table 1). A target file corresponding to each data set was produced by filtering the mega353 target file to include sequences for the respective family and/or order, depending on the data set. Because the exemplar Angiosperms353 data set included a phylogenetically diverse set of angiosperms, the full mega353 target file was used without filtering. The filtered Orchidaceae target file was expanded using a set of *Bulbophyllum* transcriptomes and the BYO_transcriptome.py script to create a third, more specific target file for the *Bulbophyllum* data set, in addition to the family and default target files. Trimmomatic (Bolger et al., 2014) was used to trim low-quality bases and remove Illumina sequencing adapters and primers, with default settings. HybPiper was used to assemble and extract loci, using a nucleotide target file and the flag to call BWA (Li and Durbin, 2009) for each data set, first using the default353 target file as the reference and then the corresponding filtered mega353 target file. For each sample, 16 CPUs and 16 GB of RAM were allocated.

TABLE 1. Summary of recovery statistics produced by HybPiper comparing the default353 target set to the mega353 target set (filtered by family or order). Values represent averages of each data set for each target file.

Data set (no. of samples)	Target file	% reads on target (average)	No. of loci with sequences (average)	No. of loci at 75% of target length (average)	Length of concatenated loci (bp, average)
Angiosperms353 exemplar data (41)	default353	22.3%	275.5	117.7	144,283.5
	mega353	32.3%	287.9	132.2	165,867.4
	mega353 vs. default353 % improvement	44.9%	4.5%	12.3%	15%
Asparagales (8)	default353	1.2%	146.9	22.9	55,484.3
	Order (Asparagales)	1.7%	159.5	27.8	65,637.4
	Order vs. default353 % improvement	37.1%	8.6%	21.3%	18.3%
Azorella (5)	default353	15.7%	292.8	89	131,292.6
	Family (Apiaceae)	16.3%	299.2	107.6	144,951
	Order (Apiales)	19.4%	309	119.8	158,014.8
	Family vs. default353 % improvement	3.7%	2.2%	20.9%	10.4%
	Order vs. default353 % improvement	23.1%	5.5%	34.6%	20.4%
Bulbophyllum (12)	default353	12.30%	238.8	46	93,043
	Family (Orchidaceae)	14.6%	268.2	75.5	122,451.8
	Family + genus (Orchidaceae+*Bulbophyllum*)	15%	273.1	83.8	131,549.8
	Family vs. default353 % improvement	19%	12.3%	64.1%	31.6%
	Family+genus vs. default353 % improvement	22.2%	14.3%	82.2%	41.4%
Cyperaceae (6)	default353	9.4%	201.1667	68	91,865.5
	Family (Cyperaceae)	11.1%	249	103.8333	129,220
	Order (Poales)	12.1%	251.3333	100.3333	131,571
	Family vs. default353 % improvement	18.1%	23.8%	52.7%	40.7%
	Order vs. default353 % improvement	28.3%	24.9%	47.5%	43.2%
Ericaceae (12)	default353	7.5%	307	97.2	145,031.8
	Family (Ericaceae)	11.9%	335.8	185.6	198,784.3
	Order (Ericales)	12.9%	338.6	189.2	205,629
	Family vs. default353 % improvement	60%	9.4%	91%	37.1%
	Order vs. default353 % improvement	73.3%	10.3%	94.7%	41.8%
Nepenthes (8)	default353	8.8%	306.6	105.5	145,598.6
	Order (Caryophyllales)	12%	322.9	147.5	182,845.1
	Order vs. default353 % improvement	36%	5.3%	39.78%	25.6%
Sapindales (6)	default353	26.6%	335.6	188.6	193,205.6
	Order (Sapindales)	31.3%	341.4	248.7	229,415.1
	Order vs. default353 % improvement	17.4%	1.7%	31.9%	18.7%
Average percentage improvement		31.9%	10.2%	49.4%	28.7%
Minimum percentage improvement		3.7%	1.7%	12.3%	10.4%
Maximum percentage improvement		73.3%	24.9%	94.7%	43.2%

Expanding the phylogenetic density of target files for custom bait kits with BYO_transcriptome.py

The input required for the script BYO_transcriptome.py is a target file and a directory of transcriptomes and/or nucleotide sequences corresponding to protein-coding genes, and it can therefore be used to expand target files from other bait kits. To test this functionality, BYO_transcriptome.py was used to expand target files for an Asteraceae-specific bait kit (Mandel et al., 2014) and a Hibisceae-specific bait kit (McLay et al., in prep.).

The Asteraceae bait kit was designed using *Helianthus annuus* L. (Asteroideae), *Lactuca sativa* L. (Cichorioideae), and *Carthamus tinctorius* L. (Carduoideae). The Asteraceae target file (comprising only the *H. annuus* and *L. sativa* target sequences) was expanded using 1KP transcriptomes of taxa closely related to Asteraceae tribe Gnaphalieae (Appendix S1). The Hibisceae-specific bait kit was designed using three Hibisceae transcriptomes, *Abelmoschus esculentus* (L.) Moench, *Hibiscus cannabinus* L., and *Hibiscus syriacus* L. The Hibisceae target file was expanded using available sequence data from the other Malvaceae subfamily Malvoideae tribes, Malveae and Gossypieae (Appendix S2).

RESULTS

Sequence number and phylogenetic density in the default353 target file compared to the mega353 target file

In the default353 file, there are 4780 target reference sequences, and each locus is represented on average by 13.5 reference sequences (range 6–18). In the mega353 target file, there are 98,994 target reference sequences, and each locus is represented on average by 280 reference sequences (range 17–373). In terms of improvement in phylogenetic density, the default353 target file has an average of 13.5 orders and 13.5 families per locus, whereas the mega353 target file has an average of 49.8 orders and 170 families per locus (see Fig. 2 for order comparisons and Appendix S3 for family comparisons, Appendix S4).

Comparing locus recovery between the default353 target file and the mega353 target file

To compare locus recovery between the default353 and filtered mega353 target files, results were evaluated using statistics provided by the HybPiper scripts hybpiper_stats.py and get_seq_lengths.py, averaged across all samples for each data set (Table 1). Four statistics were considered: (1) the percentage of reads on target, i.e., the number of reads for a sample that map to the loci in the target file, (2) the number of loci with sequences, or the total number of loci that are in the final locus set for each sample, (3) the number of loci ≥75% of the target length, i.e., of those loci in the final data set, the number that are ≥75% of the length of the target sequence for that loci, and (4) the concatenated length (in base pairs) of the final loci set for each sample.

For each data set, the mega353 target file improved each of these measures (Table 1, Fig. 3). The average percentage of reads on target improved by 31.9% across all data sets (between 3.7% and 73.3%). This had the downstream impact of increasing the number of loci with sequences by an average of 10.2% (24 loci) across all data sets (between 1.7% or six loci, and 24.9% or 50 loci). A greater increase was found in the number of loci at ≥75% of the target length, with an average increase of 49.4% (41 loci) across all data sets (between 12.3% or five loci, and 94.7% or 92 loci). The total length of the concatenated loci increased by an average of 28.7% (from an average of 125 kbp to an average of 155 kbp). This increase in sequence length was an accumulation of length improvements across many loci, rather than large improvements in a small number of loci (Fig. 4). Rarely, locus length decreased for some samples and genes when using the mega353 target file instead of the default353 target file (see Fig. 4 and Appendices S5–S16, red boxes). This most often occurred when many reads mapped to a particular mega353 target sequence reference at some positions, causing HybPiper to select the reference for filtering of assembled contigs via Exonerate. However, this mega353 reference was overall less similar to the sample being assembled than the target reference selected from the default target file. In these instances, HybPiper filtering of assembled contigs via Exonerate returned shorter contig matches (see https://github.com/chrisjackson-pellicle/NewTargets/wiki for further information). Nonetheless, the overall length of concatenated sequences was still higher when using the mega353-derived target files compared to the default files.

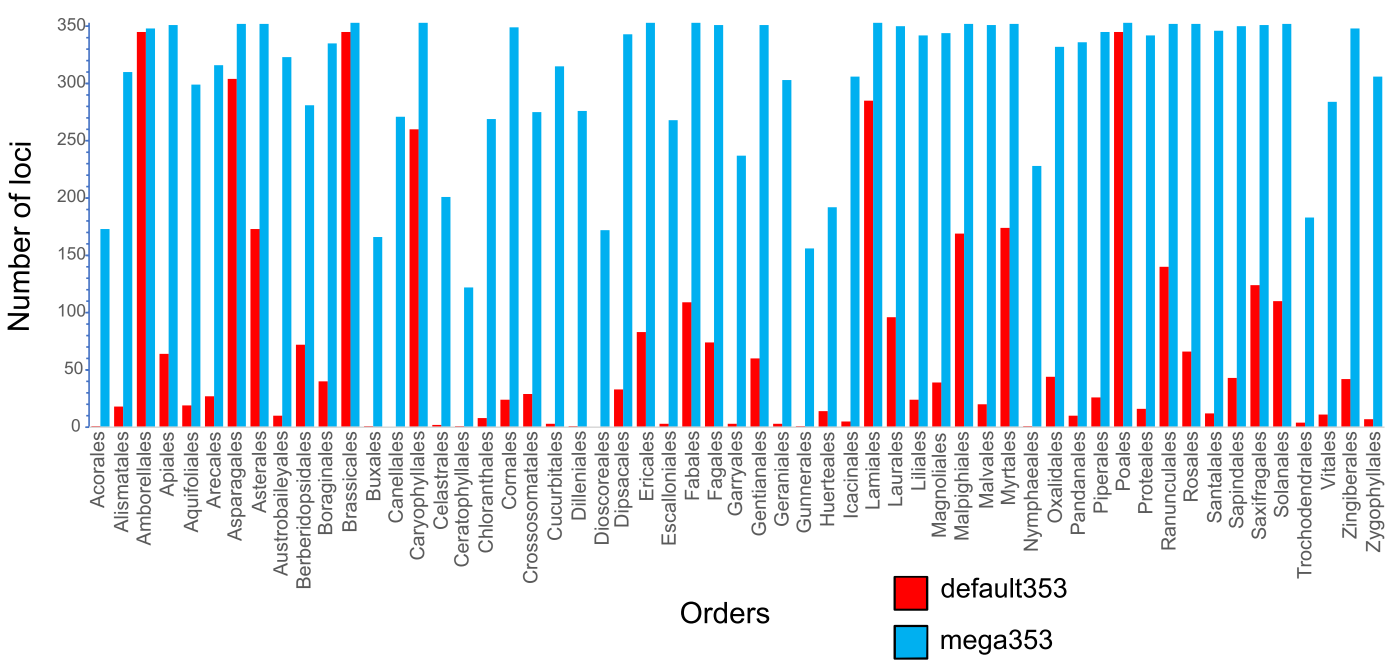

FIGURE 2. The number of loci represented for each order in the default353 (red) compared to the mega353 (blue) target files.

For the *Bulbophyllum* data set, analyses using the target file with sequences from 12 additional *Bulbophyllum* transcriptomes showed improvements over the filtered Orchidaceae target file, with a 2.5% increase in mapped reads, an 11% increase in loci over 75%, and a 7% increase in concatenated loci length (Table 1).

Impact of the mega353 target file on HybPiper paralog detection

HybPiper includes a method to detect paralogs as part of its main pipeline, and it alerts the user if at least one paralog is detected for a given sample and locus, in addition to the "primary" contig output. For most of the smaller Angiosperms353 data sets, analyses with the expanded target files resulted in slightly more paralog warnings, with a total increase of only one or two warnings for each data set (Appendix S17). However, for the Sapindales data set, there were an additional 27 paralog warnings. For the custom Asteraceae kit, the expanded target file reduced the total number of paralog warnings by 50.4% (from 698 to 346). For the Hibisceae custom kit, the expanded target file increased the number of paralog warnings by 8.94% (from 705 to 768).

Impact of the mega353 target file on HybPiper computation time

The first script in the HybPiper pipeline is reads_first.py, which includes mapping of sequence reads to target references and subsequent assembly, and is the most computationally time-consuming step of the pipeline. For most data sets, using a filtered mega353 target file resulted in a small increase in the number of CPU hours taken by each HybPiper run, because as more reference targets are added the time taken for reads_first.py increases (Appendix S2). However, the CPU hours used by HybPiper to run the Angiosperms353 exemplar

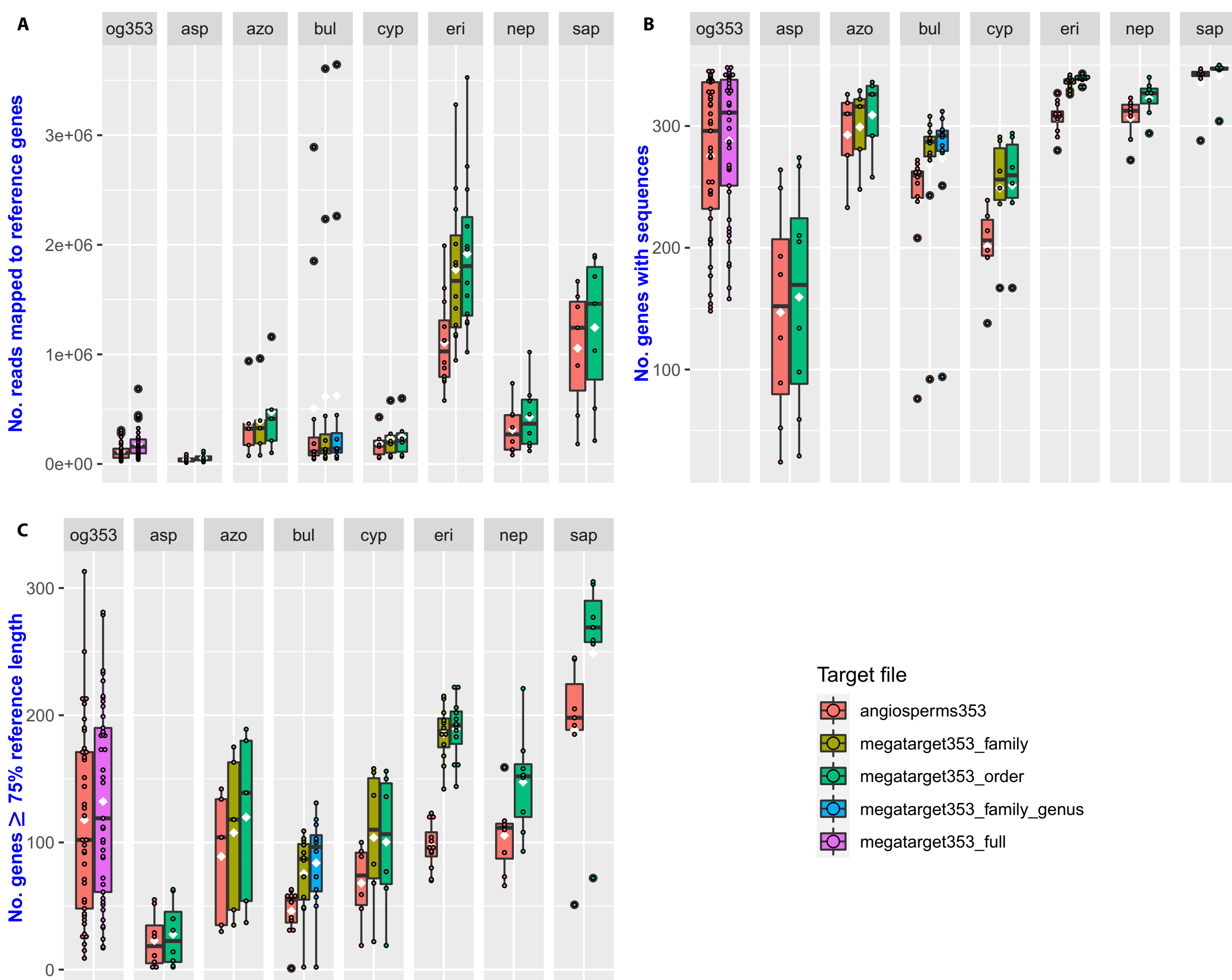

FIGURE 3. Summary of recovery statistics produced by HybPiper comparing the default353 target set to the mega353 target set (filtered by family or order), for (A) the number of reads mapped to reference sequences, (B) the number of loci with sequences, and (C) the number of loci recovered at ≥75% of reference length. Data set abbreviations for boxplot headings: og353 (Angiosperms353 exemplar), asp (Asparagales), azo (*Azorella*), bul (*Bulbophyllum*), cyp (Cyperaceae), eri (Ericaceae), nep (*Nepenthes*), sap (Sapindales).

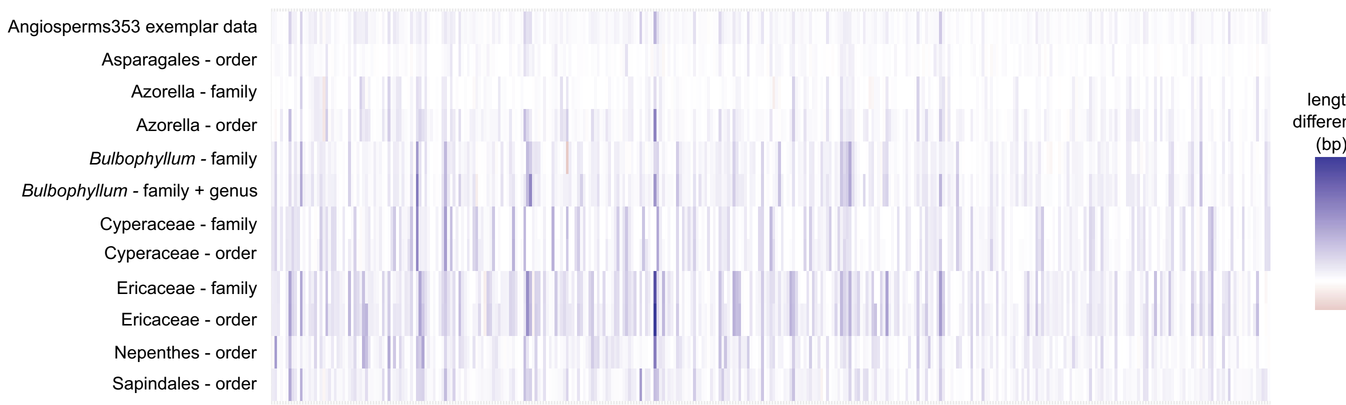

FIGURE 4. Heatmap of locus length changes for each locus, averaged across all samples for each data set, where the default353 locus lengths are subtracted from the mega353 locus lengths. Increases in length are shown in blue, decreases in length are shown in red.

data set increased by 40% with the mega353 target file compared to the default353 target file, and by more than 60% for the Ericaceae data set using the order-filtered mega353 target file.

Comparing locus recovery for custom bait kits using target files expanded with BYO_transcriptome

Each new target file was compared to its default target file using HybPiper with the approach described above. Seven representative samples from Asteraceae tribe Gnaphalieae, captured using the Asteraceae bait kit (Mandel et al., 2014), were used to compare the default Asteraceae target file (two targets per locus) to the expanded Asteraceae target file (average of 3.88 targets per locus). Five representative taxa from Malvaceae tribes Malveae and Gossypieae, captured using the Hibisceae bait kit, were used to compare the default Hibisceae target file (average of 2.5 targets per locus) to the expanded Malvoideae target file (average 4.34 targets per locus). Locus recovery was improved using the expanded target file for both data sets. This improvement was more pronounced with the expanded Asteraceae target file, with a 31% increase in the number of loci at ≥75% of the target length, and a 22% increase in concatenated loci length (Appendix S18).

DISCUSSION

We have demonstrated that sequence recovery for a universal sequence capture bait kit can be substantially improved by appropriate tailoring of target files to the group under study. To enable the best possible locus recovery from Angiosperms353 capture data, we have developed an expanded target file using 1KP transcriptomes. As the Angiosperms353 bait kit is becoming increasingly widely used, tools such as those developed here will allow researchers to optimize use of their target enrichment sequence data by assembling more and longer loci, thereby creating larger and more complete data sets for phylogenetic analyses, increasing cost efficiency, and improving data set combinability.

The use of the mega353 target file does increase the computation time for HybPiper. For this reason, we recommend strategically selecting the phylogenetic rank used to filter the target file (i.e., clade, order, or family should be preferred where possible), rather than using the complete mega353 target file. Filtering can be applied using multiple phylogenetic ranks or sample identifiers (see https://github.com/chrisjackson-pellicle/NewTargets/blob/master/filtering_options.csv). For example, a filtered mega353 target file for Malvales could comprise the target sequences from the order, in addition to selected outgroup sequences (e.g., Brassicaceae), and a specific 1KP sample name (e.g., UPZX, *Cleome gynandra* L., Cleomaceae). Filtering of the mega353 target file allows the user to develop a data set–appropriate target file and ensures a more efficient trade-off between increased locus recovery and computational time.

We have demonstrated these improvements using the bioinformatic tool HybPiper. However, it is likely that any pipeline that involves read-mapping to reference files as a first step will see similar improvements when provided with a more phylogenetically dense target file (e.g., tools such as HybPhyloMaker [Fér and Schmickl, 2018]). It is less clear whether expanded target files would improve locus recovery using tools that perform a de novo assembly first, and then map contigs to a reference sequence (such as SECAPR [Andermann et al., 2018] or PHYLUCE [Faircloth, 2016]). Regardless, HybPiper is currently the most widely used tool to assemble target enrichment data sets in plants, and researchers using HybPiper can obtain improved locus recovery using expanded target files.

Finally, our BYO_transcriptome.py script can be used to incorporate additional target sequences from any available transcriptome, and we have shown that this tool can be used with target files from custom bait kits to improve locus recovery. With the growing number of transcriptomes and whole genome data becoming available in public repositories, the approach developed here will prove to be an increasingly valuable resource for efficient recovery of target enrichment data.

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AUTHOR CONTRIBUTIONS

T.G.B.M. and C.J.J. conceived and developed the bioinformatic workflow and drafted the manuscript; T.G.B.M., C.J.J., A.N.S.L., and L.S. performed data analyses; and all authors contributed data and approved the final manuscript.

DATA AVAILABILITY

NewTargets is an open source software that is freely available on GitHub (https://github.com/chrisjackson-pellicle/NewTargets) for Linux or OSX under the GNU General Public License v3. NewTargets is written in Python and requires Python 3.7 or higher. Documentation for the software can be found on GitHub (https://github.com/chrisjackson-pellicle/NewTargets/wiki).

Sources of the publicly available data sets used in this study include the 1KP project (http://www.onekp.com/samples/list.php), the original Angiosperms353 sequence reads (National Center for Biotechnology Information Sequence Read Archive [SRA]: SRP151601), the Cyperaceae data set (SRA BioProject PRJNA553989), the *Nepenthes* data set (SRA BioProject PRJEB35235), and the Sapindales data set (European Nucleotide Archive project PRJEB35285, from the Plant and Fungal Trees of Life [PAFTOL] project).

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

APPENDIX S1. Samples used to expand the custom bait kit target files using 'BYO_transcriptomes.py'.

APPENDIX S2. CPU hours used by the HybPiper pipeline to complete for each data set and each target file. HybPiper was allocated 16 CPUs and 16 GB of RAM for each data set.

APPENDIX S3. The number of loci represented for each family in the default353 (red) compared to the mega353 (blue) target files.

APPENDIX S4. The number of target sequences in the default353 target file compared to the mega353 target file, including the average number of targets per locus, and the average number of orders and families for each locus.

APPENDIX S5. Heatmap of locus lengths for each sample for each locus for the Angiosperms353 exemplar data set, where the default353 locus lengths are subtracted from the mega353 locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S6. Heatmap of locus lengths for each sample for each locus for the Asparagales data set, where the default353 locus lengths are subtracted from the mega353 (order filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S7. Heatmap of locus lengths for each sample for each locus for the *Azorella* data set, where the default353 locus lengths are subtracted from the mega353 (family filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S8. Heatmap of locus lengths for each sample for each locus for the *Azorella* data set, where the default353 locus lengths are subtracted from the mega353 (order filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S9. Heatmap of locus lengths for each sample for each locus for the *Bulbophyllum* data set, where the default353 locus lengths are subtracted from the mega353 (family filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S10. Heatmap of locus lengths for each sample for each locus for the *Bulbophyllum* data set, where the default353 locus lengths are subtracted from the mega353 (family + genus filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S11. Heatmap of locus lengths for each sample for each locus for the Cyperaceae data set, where the default353 locus lengths are subtracted from the mega353 (family filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S12. Heatmap of locus lengths for each sample for each locus for the Cyperaceae data set, where the default353 locus lengths are subtracted from the mega353 (order filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S13. Heatmap of locus lengths for each sample for each locus for the Ericaceae data set, where the default353 locus lengths are subtracted from the mega353 (family filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S14. Heatmap of locus lengths for each sample for each locus for the Ericaceae data set, where the default353 locus lengths are subtracted from the mega353 (order filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S15. Heatmap of locus lengths for each sample for each locus for the *Nepenthes* data set, where the default353 locus lengths are subtracted from the mega353 (order filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S16. Heatmap of locus lengths for each sample for each locus for the Sapindales data set, where the default353 locus lengths are subtracted from the mega353 (order filtered) locus lengths. Increases in length are shown in blue; decreases in length are shown in red.

APPENDIX S17. Summary of paralog warnings produced by HybPiper for the default353 and mega353 target files.

APPENDIX S18. Comparing custom bait kit target files (Asteraceae/Hibisceae) that were expanded using BYO_transcriptomes.py. Values represent averages of each data set for each target file.

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