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REVIEW PAPER

Regional conservation genomics: insights and opportunities from northern Australia

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Abstract
Biodiversity conservation in northern Australia is characterised by high endemism, data deficiency, and high Indigenous land tenure and population. The Northern Australia Conservation Genomics Forum brought together experts to explore current genetic research with particular emphasis on integration of genomics within conservation practices. We discuss the regional biodiversity of northern Australia, highlighting the unique biogeographic patterns, known and unknown species diversity, and ongoing threats such as habitat degradation, altered fire regimes, invasive species, and climate change. This article synthesises key themes from the forum, including the current application of genomics in conservation, gaps and areas of need and opportunity to advance species conservation in this sparsely populated, yet iconic region of Australia. We highlight the need to expand collaborative research partnerships across land tenures with Indigenous organisations, pastoralists, government and non-government organisations, which is crucial for the effective study and conservation of the region's biodiversity. The paper identifies the challenges and opportunities in applying genomic data to conservation strategies and applied management, including species translocations and habitat management, while acknowledging the limitations and gaps in current research and collections. The insights from this forum emphasise the advantages in using genomics to inform conservation decisions, and the need for continued research and collaboration to protect northern Australia's unique biodiversity.

Keywords Conservation genetics · Northern Australia · Genetic management · Collaborative research partnerships · Wildlife · Biodiversity

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Introduction

Conservation genetics has emerged as a fundamental tool in the pursuit of biodiversity conservation (Kardos 2021). Conservation genetics provides crucial insights into the genetic structure, diversity, and adaptive potential of species and populations within species. Regional conservation genetics assessments across assemblages of species hold value in identifying common and contrasting patterns in shared landscapes (Shaffer et al. 2022). Regional perspectives provide an enhanced understanding of the spatial distribution of genetic diversity, driven by underlying ecological factors, thereby informing effective management strategies and conservation actions. Here, we focus on the current state of conservation genetic information and use in northern Australia, a biodiversity-rich region that faces complex conservation challenges.

Northern Australia (Fig. 1) is home to a diverse array of species, many of which are endemic (Woinarski et al. 2007). The Top End, Kimberley and Cape York regions (Fig. 1a) are dominated by tropical savannas, intersected with landscape-scale biogeographic features such as the Carpentarian Gap, Arnhem Land Plateau and the Ord River Region (Bowman et al. 2010) as well as large seasonal floodplains and water bodies such as the Arafura Swamp and regionally-restricted habitats such as the black soil (clay-pan) plains. The region is separated from the Pilbara in the west by the Great Sandy Desert. The monsoonal climate and geographic features of the region have influenced the evolution of a diverse vertebrate species community (Finlayson et al. 2006; Oliver et al. 2017; Pepper et al. 2013; Pepper and Keogh 2014). The species diversity and endemism in northern Australia make the region of global importance for biodiversity (Woinarski et al. 2007).

Further elevating the significance of the region, northern Australia has a high proportion of Indigenous-owned and managed land (Fig. 1b). Land tenure in this region varies, including Aboriginal freehold, protected areas, and land under native title. Aboriginal freehold land, established under the Aboriginal Land Rights (NT) Act 1976, is inalienable and held by Aboriginal land trusts. Native title, recognised under the Native Title Act 1993, acknowledges that some Aboriginal peoples have ongoing rights and interests in land and waters based on their traditional laws and customs. These tenure arrangements enable Indigenous communities to engage in land stewardship, integrating traditional knowledge with contemporary conservation practices. Many Indigenous groups in northern Australia maintain strong bio-cultural knowledge systems and have a degree of control over management of their ancestral estates, resulting in tangible biodiversity, economic and socio-cultural benefits (Altman and Kerins 2012; Ens et al. 2016). These strategies sustain the environment and uphold the cultural heritage and socio-economic wellbeing of Indigenous communities.

Northern Australia largely evaded the extensive historical extinctions that impacted other biomes across Australia (Legge et al. 2023; Woinarski et al. 2015) However, the region is not insulated from modern environmental challenges (Woinarski et al. 2007). Alarming declines of mammal populations have been observed in recent decades. These declines have been attributed to a range of threatening processes (Stobo-Wilson et al. 2020) including: (1) habitat degradation due to feral herbivores and pastoralism (Legge et al. 2011; Woinarski and Ash 2002); (2) direct or indirect effects of introduced species (Braithwaite and Griffiths 1994; Radford et al. 2020; von Takach et al. 2022a, b) including increased predation (Fisher et al. 2014; Frank et al. 2014; Stobo-Wilson et al. 2020); (3) altered fire regimes (Lawes et al. 2015; von Takach et al. 2020; Woinarski et al. 2011); and (4) a changing climate (Kutt et al. 2009; Traill et al. 2011; Williams et al. 2003). Escalating pressure to further develop large areas of northern Australia (Brewer

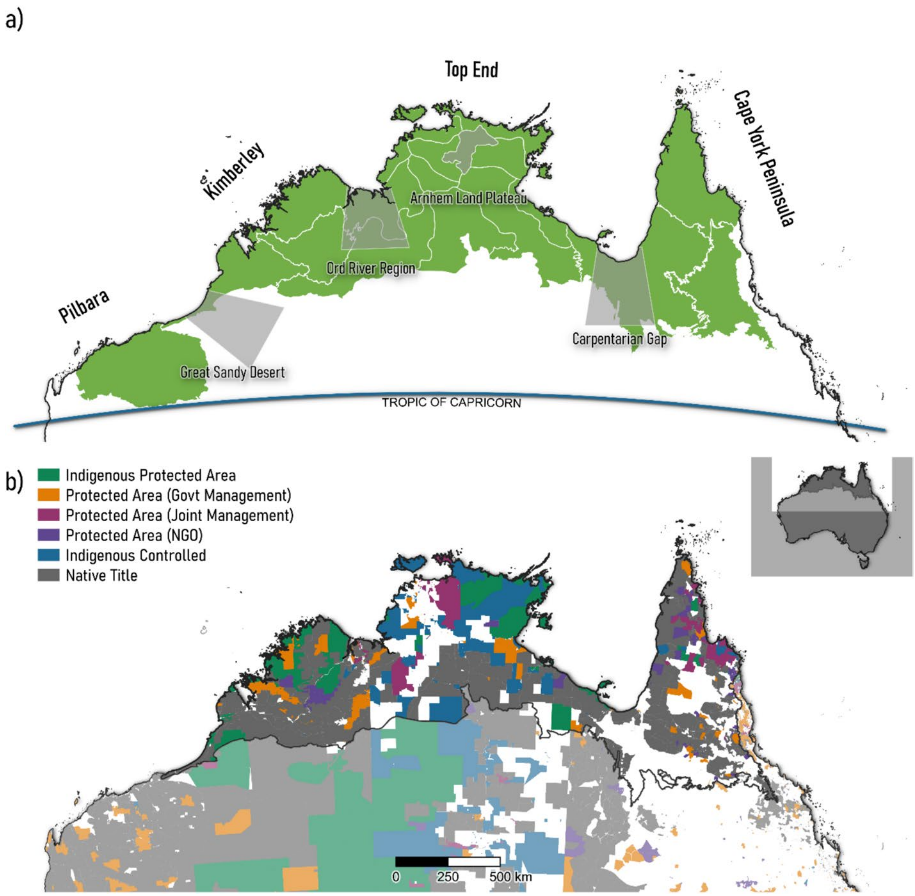

Fig. 1 The northern Australia region **a** region extent in green determined by the relevant Australian Bioregions and showing the major biogeographic barriers shaded in gray (Bowman et al. 2010; Department of Climate Change, Energy, the Environment and Water 2023; Edwards et al. 2017) and **b** land tenure and management classifications (modified from Collaborative Australian Protected Area Database 2022, the National Native Title Register and Australian Land Tenure)

et al. 2021) is likely to affect remnant populations of threatened species that are currently declining, or persisting at low densities, in the region.

While mammals are the most well-studied in terms of their declines in northern Australia, there are indications that the same processes are also responsible for declines in reptile (Geyle et al. 2021; Tingley et al. 2019) and bird populations (Legge et al. 2008; Shoo et al. 2005). Cats impact reptile abundances (Stokeld et al. 2018; Woinarski et al. 2018), as do altered fire regimes, which are hotter and more intense in areas impacted by invasive grass weeds (Rossiter et al. 2003). Furthermore, predation of poisonous cane toads by susceptible reptile species, particularly top predators (e.g. monitors), has led to their widespread decline and local extirpation with broader implications for trophic systems as cane toads spread westward across the north (Doody et al. 2009; Radford et al. 2020). With the exception of direct impacts from cane toads, similar processes have contributed to the decline and extinction of Australian birds (Franklin et al. 2005), with additional pressure from habitat conversion through mining and agricultural development (Gould 2011; Woinarski et al. 2024). Mining and agriculture are likely to impact reptiles also, but there has in general been more limited study of the processes leading to reptile declines as reptiles are vastly more diverse that other vertebrate clades, have much higher levels of unknown and undescribed diversity, and have received relatively little research attention. Because of a high incidence of data deficiency in reptiles it is likely that extinctions and population declines are vastly underreported in this clade.

Conservation genetics is a crucial tool in understanding and addressing the challenges facing biodiversity in northern Australia, by informing decisions about conservation management actions (Supple and Shapiro 2018). Such decisions include identifying which populations are candidates for genetic intervention, quantifying the importance of remnant and insurance/translocated populations for conserving genetic diversity, or characterising putative evolutionarily significant units (ESUs) (Frankham et al. 2017; Ralls et al. 2018; von Takach et al. 2021; von Takach et al. 2022a, b). Understanding taxa from across the continuum of population, phylogeographic and phylogenetic scales further adds value to conservation genomics studies, enabling the designation of ESUs, and potentially new species; as species cannot be effectively conserved unless they are properly delineated and described.

To explore the current state of conservation genetics across northern Australia, and to identify opportunities to harness new molecular tools to preserve this region's rich biodiversity, the Northern Australia Conservation Genomics Forum (NACGF) convened conservation genetics researchers from across Australia. The major themes that emerged during the forum were integral to understanding the genetics of northern Australian wildlife, and encompassed the application of conservation genetics/genomics, as well as how to include Indigenous land-owning groups in genetic research, and enhance preservation of genetic material. The six dominant themes were as follows:

Theme 1: State of population genomic research in northern Australia.
Theme 2: Speciation and evolution.
Theme 3: Tools and metrics for conservation.
Theme 4: Genetic applications in conservation management.
Theme 5: Conservation genomics research partnerships in northern Australia.
Theme 6: Tissue collections and sampling into the future.

This review synthesises NACGF discussions on these major themes and contextualises them within the literature on conservation genetics/omics to explore advances, gaps and opportunities for wildlife conservation in northern Australia. While our focus is conservation genomic research across northern Australia, the case studies provided throughout largely focus on mammals, reflecting the extensive research on their alarming declines in the region. These declines provide insights into broader threats affecting less-studied and data-deficient taxa.

Theme 1: State of population genomic research in northern Australia.

Recent advances in DNA sequencing technology have revolutionised the accessibility and power of data to understand genetic diversity, population structure, and adaptation potential of species. High-throughput sequencing technologies, such as next-generation sequencing (NGS), have significantly reduced the cost and time required for large-scale genomic studies and unleashed the ability to access information from historical museum specimens (e.g. Card et al. 2021; Roycroft et al. 2022). The forum discussed the use of genomics across broad research and management areas in northern Australia, and its value in conservation. In the below section, we summarise recent population and conservation genomic advances across northern Australia, from single species studies, to regional patterns of diversity in species communities.

The northern quoll (*Dasyurus hallucatus*), a well-studied marsupial species in northern Australia, is of particular interest due to the significant population declines it has experienced, largely driven by the invasion of cane toads (*Rhinella marina*). Despite extensive research on northern quolls, there remain gaps in the understanding of its biogeographic variation, particularly in relation to genomic diversity and population structure. Analysis of the patterns of genomic diversity across different northern quoll populations and how the introduction of invasive cane toads has influenced genetic structure bridges these gaps (von Takach et al. 2022a, b). The study identified a clear hierarchical structure of three to five population clusters of northern quolls, a distribution generally consistent with recognised biogeographic barriers in the region, notably the Carpentarian Gap, the Ord River Region, and the Great Sandy Desert (Fig. 1a.; von Takach et al. 2022a, b). Regional populations exhibited a level of internal genetic structure, with island populations typically representing a subset of the diversity found in nearby mainland populations, a pattern seen in many island populations of Australian mammals (Eldridge et al. 2004; Harradine et al. 2015). This observed phylogeographic structure in northern quolls broadly resembles patterns seen in other species such as the brush-tailed rabbit rat (von Takach et al. 2021), the black-footed tree rat (von Takach et al. 2022a, b) as well as delicate mice (although these divergences are species level, rather than ESUs; (Roycroft et al. 2024)). As for some other native predators across northern Australia, the northern quoll has been substantially impacted by the invasion of the toxic cane toad. The genetic consequences of this threat were explored by von Takach et al. (2022b), with a decline in genetic diversity in populations with long exposure to cane toads. While this poses a significant concern for the adaptive capacity of native predator populations, the presented evidence suggests that the loss of genetic diversity may unfold over several decades (i.e. dozens of generations) following the invasion of cane toads, raising the potential for management intervention even in toad-exposed populations/areas.

Genomic data can provide insight into the connectivity of populations, which can be crucial information for conservation management e.g. to inform translocations, and the potential need for genetic rescue. Contrasting patterns of connectivity can indicate different conservation needs. For example, research on the population genomics of two northern Australian tree-rats of the genus *Mesembriomys*, compared population structure of the golden-backed tree-rat (*M. macrurus*) and the black-footed tree-rat (*M. gouldii*) (Nicholl 2022). High connectivity between Kimberley subpopulations of golden-backed tree-rats is reflected by overall low levels of genomic differentiation. In contrast, the more broadly distributed black-footed tree-rats showed substantial levels of genomic differentiation between the offshore Melville Island and the mainland Queensland (Weipa) population, suggesting prolonged isolation and conforming to subspecies boundaries based on morphological differences between regions (Nicholl 2022). Population structure in the extant distribution of the golden-backed tree-rat is best described with $K=1$ or $K=2$ (where K refers to the number of populations), although further research may highlight island populations that are strongly differentiated. Notably, 97% of prioritisation iterations identified Bachsten Creek as the optimal site to conserve allelic diversity, given its central location among survey sites. The Mitchell Plateau and Yampi Sound populations were more frequently selected together for allelic representation when conserving two sites, considering their positions on opposite ends of the survey range (Nicholl 2022). Concerning inbreeding coefficients were identified in some golden-backed tree-rat populations, warranting further exploration and the need for larger sample sizes.

While single-species studies provide crucial, in-depth insights for conservation, studies investigating multiple species across shared landscapes provide the opportunity to understand regional genetic patterns, and to inform conservation of whole species assemblages. This is particularly relevant in the Pilbara region, known for its unique and highly variable landscape and a host of diverse and endemic fauna and flora (Pepper et al. 2013). The region faces the dual challenges of conserving this rich biodiversity while accommodating ongoing economic development due to mining activities. The region's biodiversity is threatened by changes in land use, altered fire, invasive pests and weeds, and climate change, in addition to the threat posed by resource exploitation (Booth et al. 2021). To address this challenge, there is a growing recognition of the potential role of genetics in understanding how animals utilise different elements of the landscape. By identifying core habitat and areas vital for population connectivity, recent and ongoing research aims to enhance the resilience of the mammal community by preserving or increasing genetic diversity. Species distribution models were used to map core habitat for 19 small-medium sized mammal species, with genomic data obtained for ten species (including rodents, marsupials and bats). The analysis revealed a weak population genetic structure, widespread admixture and large genetic neighbourhoods across the Pilbara, suggesting the occurrence of long-distance dispersal events. Notably, *Sminthopsis youngsoni* exhibited strong population genetic structure between Cape Range and the rest of the Pilbara, suggesting that the presence of clay acts as a barrier to dispersal for this species. Contrasting patterns of connectivity across species suggest that dispersal is facilitated by different elements of the landscape, emphasising the need for species-specific considerations in conservation planning (Skey et al. 2023). Overall, the integration of genetic data into conservation strategies holds promise for navigating the complex interplay between biodiversity preservation and economic development in the Pilbara region (Shaw et al. 2023; Skey et al. 2023; Umbrello et al. 2022).

Recent research on native rodents provides a perspective on the associations between genomic diversity and both historical and contemporary species extinctions and declines, and highlights the value of including historical museum specimens in genomic research. Given the overrepresentation of rodents in current mammal declines, a genome-scale examination of the timing of decline and genetic diversity of extinct rodents was explored. Notably, no genetic erosion was observed in extinct species at the time of the last specimen collection, emphasising the dramatic decline of Australian rodents post-European colonisation (Roycroft et al. 2021). Without genetic erosion as a leading cause, factors like body size and biome, alongside various ecological threats, help account for the varying rates of decline in native Australian rodents. Comparatively, when examining current estimates of genetic diversity in extant species, Roycroft et al. (2021) demonstrated a clear relationship between genetic diversity and geographic restriction. Geographically restricted species like the critically endangered central rock rat (Z*yzomys pedunculatus*) and the last remaining population of the Shark Bay mouse (*Pseudomys gouldii)* had the lowest genetic diversity of all Australian rodents, highlighting the potential genetic risk present in small populations (Roycroft et al. 2021).

The forum emphasised the presence of greater genomic diversity at the species and ESU level than previously thought. Many species exhibited significant genetic diversity and cryptic lineages, further highlighting the need for comprehensive genomic studies to accurately understand and conserve species. The various applications of genomics in wildlife conservation explored during the forum demonstrated its importance in the ongoing efforts to conserve biodiversity in northern Australia. The findings and insights generated from this research can help to inform conservation management strategies and facilitate the long-term survival of these unique and important species.

Theme 2: Speciation and evolution

Despite being widely recognised as a hotspot for endemism and biodiversity, northern Australia's fauna remains understudied. Advances in molecular technology have dramatically increased our understanding of the diversity and phylogeography of species in northern Australia over the past decade (Stobo-Wilson and Cremona 2023). Understanding speciation and revealing cryptic diversity is critical in the context of northern Australia, where terrestrial fauna face a severe threat of decline. The region's complex geological history, climatic variability, and geographical isolation have given rise to a remarkable array of species with distinct evolutionary histories, however the difficulties in accessing many of these areas and presumptions of similarity to their southern counterparts have hindered taxonomic investigation in northern Australia. This lack of work has especially impacted our understanding of diversity and decline in northern Australian reptiles, with current estimates sitting at between 50–100 undescribed species just in the Northern Territory. These species predominately occur in the northern part of the territory in habitats at-risk from climate change on low-lying offshore islands, and from increasing development pressure, like the disjunct black soil regions (Dan Edwards, pers. Comm.), in addition to known diversity hotspots like rock escarpments.

Across the region, studies across multiple species have revealed some general patterns of genetic diversity and endemism. Similar to global trends, genetic diversity on islands is typically low, with some islands demonstrating particularly low genetic differentiation. For example the northern quoll population on Marchinbar Island had a particularly low observed heterozygosity (von Takach et al. 2024). Additionally, comparatively low genetic diversity of delicate mice (*Pseudomys delicatulus*) on islands of the Edward Pellew Group, Bonaparte Archipelago and on Niiwalarra, compared to mainland populations. But in contrast, Melville Island and Groote Eylandt maintain diversity similar to mainland populations, highlighting the relationship between genetic diversity and island size (Roycroft et al. 2024). Landscape biogeographic barriers, such as the Carpentarian Gap and the Great Sandy Desert, have given rise to areas of high endemicity in the Gulf of Carpentaria and the Pilbara. Distinct life history and ecology of some fauna has resulted in particularly high levels of genetic divergence (See Box 1).

Recent taxa discoveries in the northern Australia region have predominantly been new endemics and include the reinstated Eastern short-eared rock-wallaby *Petrogale wilkinsi* as well as the description of an additional subspecies *Petrogale brachyotis victoriae* (Potter et al. 2014; and see Box 1). Despite being considered synonymous with the widespread sugar glider *Petaurus breviceps*, mtDNA and morphology differences resulted in the elevation to species of the savanna glider *Petaurus ariel* (Cremona et al. 2021). This investigation revealed further phylogenetic structure potentially representing additional taxa in the Central Kimberley and on the Cape York Peninsula. The family Dasyuridae is a diverse group of carnivorous marsupials ranging in size from 2 g to 14 kg and over 30 species currently occur in northern Australia. However, this is thought to be an underestimate of the true diversity in the group, which is characterised by cryptic species and diverse lineages. One example includes the planigales, Australia's smallest marsupials, where two new species were recently described from the Pilbara region with the help of molecular evidence; *Planigale kendricki* and *P. tealei*

(Umbrello et al. 2023). Molecular studies have revealed high genetic diversity and structure in other Dasyurid species including *Antechinomys laniger* (Westerman et al. 2023), *Sminthopsis macroura* and *S. virginiae* (Blacket et al. 2001; Umbrello et al. 2024) and *Pseudantechinus* (Umbrello et al. 2017). Similarly, a recent study uncovered two new species of murine rodents in northern Australia (Roycroft et al. 2024)), that had previously been included within *Pseudomys delicatulus.* Through the description of western delicate mouse (*P. pilbarensis*) and the reinstatement of the eastern delicate mouse (*P. mimulus*), the northern delicate mouse *P. delicatulus* sensu stricto now has a much smaller geographic range than previously understood. Cases such as these, where species ranges were previously mischaracterised due to incomplete taxonomy, may result in species being assigned inappropriately low conservation priority, and highlights the potential for cryptic diversity in other widespread species across northern Australia.

Box 1: Rock-Wallaby Case study

The Australian marsupial genus *Petrogale* (rock-wallabies) has undergone recent and rapid speciation (Potter et al. 2012). Rock-wallabies are a small (1 – 12 kg) macropod with an Australia-wide distribution. A taxonomic investigation into the brachyotis group; comprised of *Petrogale brachyotis*, *P. burbidgei* and *P. concinna*, revealed a fourth species, *P. wilkinsi* and a subspecies of *P. brachyotis* (*P. b. victoriae*) (Potter et al. 2014). An integrative approach combining both mitochondrial and nuclear DNA with morphology was used to investigate this diversity. Recently, further investigation that incorporated genomic data from historical museum specimens using targeted capture found evidence of greater diversity in the brachyotis group and a complex evolutionary history (Potter et al. 2024). The increase in genomic and geographic coverage of this group enabled evaluation of mitonuclear discordance previously identified (Potter et al. 2012). Approximate Bayesian Computational analyses supported evidence of recent gene flow between species, as well as introgression during speciation which caused this mitonuclear discordance. This was a surprising find given the substantial body size differences between the species involved and chromosomal variation. Sampling from museum skins also supported additional diversity within *P. wilkinsi* from Groote Eylandt and the Gulf of Carpentaria region. The complex evolutionary history in this group has been linked to the dynamic climatic history across the monsoonal tropics.

Extensive chromosomal rearrangements are found amongst lineages and species of rock-wallabies (Fig. 2). Fixation of chromosomal rearrangements has been linked to their small population sizes, likely a consequence of their restriction to patchily distributed 'islands' of rocky habitat throughout their distribution. Further research is needed to understand the role of genetic drift versus selection in driving such genomic reorganisation. Only through cytogenetics and more recently the incorporation of genomic data have we increased our understanding of the intricacies of speciation in this system (Deakin et al. 2019). It highlights the role of structural variation in driving adaptation and speciation and a need to better understand genome organisation in conservation genetics and speciation (Fig. 2).

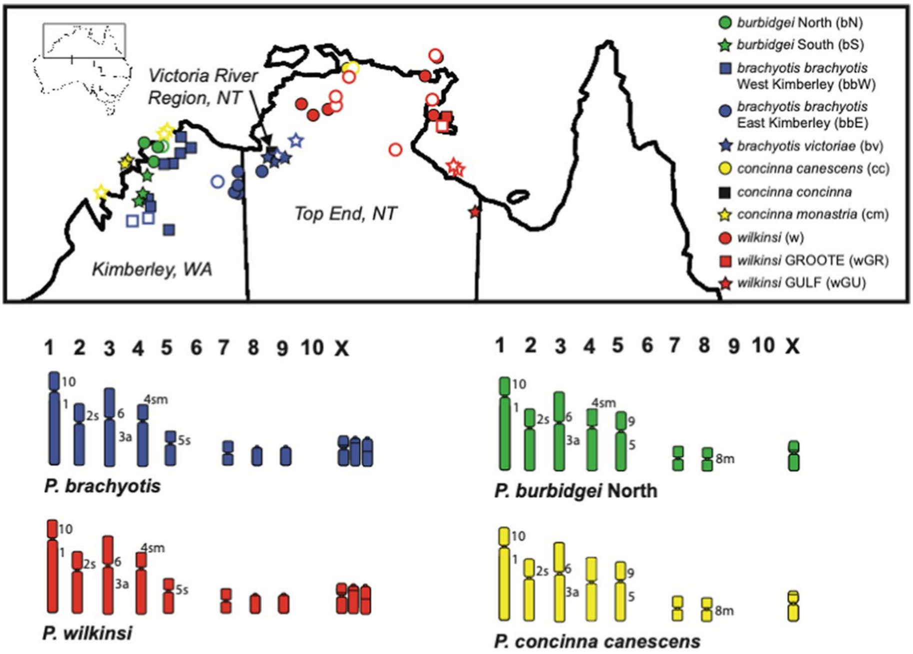

Fig. 2 Sampling locations and chromosomal rearrangements of the marsupial genus *Petrogale* in northern Australia

Theme 3: Tools and Metrics for Conservation

There was a strong consensus among participants regarding the integration of genetic data into conservation strategies, aligning closely with international directives such as recent target updates to the Convention on Biological Diversity (CBD) framework and the Kunming-Montreal Global Biodiversity Framework. Meeting these targets will require appropriate indicators for reporting, such as the proportion of populations with an effective population size above 500 (Hoban et al. 2020), and how these indicators can be calculated when sufficient genetic data is not available. The potential for more extensive genetic reporting, including calculations of Essential Biodiversity Variables (Hoban et al. 2022; Pereira et al. 2013) and genetic proxies like the genetic scorecard approach (Hollingsworth et al. 2020) were highlighted as being an important area of development for conserving genetic diversity in northern Australia.

An example of such a tool, the Victorian Genetic Risk Index, plays a pivotal role in the conservation efforts of the Victorian State Government, particularly in addressing challenges posed by widespread habitat fragmentation (Kriesner et al. 2020). The genetic risk index is calculated from a combination of genetic and life history parameters. The methodology combines data from various sources, including the Atlas of Living Australia and other repositories, integrates demographic, habitat, and genetic information when available. It further involves the creation of resistance maps, both general and species-specific, to identify population clusters. This approach enables the calculation of risk at both population and species levels, enriched by species-specific insights, ultimately aiding in the incorporation of genetic information in conservation management. While in-house metrics like the Victorian

Genetic Risk Index can be useful, moving towards national standards and open-source metrics should be a future goal.

Additionally, the forum included insights and perspectives from the Australian Wildlife Conservancy, a prominent environmental non-governmental organization (NGO) in the region. The emphasis in this context was on genetic monitoring and management, focusing on the overarching goals of maximizing fitness, adaptive potential, and the preservation of remaining diversity. Challenges unique to the Australian context were emphasised, including scenarios involving translocated populations with genetic admixture, temporal inconsistencies in genetic marker panels, and the imperative of addressing genetic adaptation in the context of climate change, ensuring that genetic data seamlessly integrates with practical management. There is an increasing emphasis on utilising genetic tools to manage and protect in situ populations within large-scale landscapes, especially in sanctuaries across northern Australia. Northern quolls are a prime example of this approach, with von Takach et al. (2024) demonstrating how these tools can effectively prioritise wild populations to most efficiently preserve genetic diversity. The need for such genetic prioritisation tools is critical for the sustained and detailed monitoring and management of the diversity and connectivity among priority populations.

The forum explored the priorities and objectives of the Western Australian (WA) government concerning genetic diversity within the conservation landscape. WA has played a key role in translocations for conservation over the past 50 years (Morris et al. 2015). Key genetic objectives associated with these activities included the maximization of connectivity and evolutionary potential, which were closely tied to an in-depth understanding of spatiotemporal patterns in genetic diversity. The use of Population Viability Analyses (PVA) was identified as useful tool to model the genetic outcomes of translocation scenarios that incorporated various combinations of founder source populations. In particular, the value of admixing founder populations was shown to maximise genetic diversity in the translocated population, while minimising harvesting pressure on source populations (Onley et al. 2023). The forum also provided insights into genetic priorities and planning strategies within the Northern Territory government. These encompassed a range of applications, from species identification and the detection of species via environmental DNA (eDNA) to tracking the historical trajectory of communities through DNA barcoding. Additionally, the discussion covered the quantification of the risk of species loss and the identification of critical tipping points. Collaborative engagement with geneticists was underscored as instrumental in comprehending the contemporary patterns underpinning conservation efforts in the NT.

Theme 4: Genetic Applications in Conservation Management

Globally, the speed of developments in the study of genomics has not been matched by integration of these data in conservation planning. For example, species recovery plans from across Europe, the US and Australia rarely include population viability and fitness related parameters with ~ 10% referencing N_e, a fundamental parameter for assessing population viability and ~ 7% mentioned inbreeding and inbreeding depression (Pierson et al. 2016). Historically, there has been a disconnect between the science of conservation genetics and its application in conservation policy and management. However, the increased global focus on maintaining genetic diversity (Hoban et al. 2021), developing relevant metrics for measuring genetic diversity (Hoban et al. 2022) and the collaborative management presented at the forum highlights that we are bridging the gap between genomic research and on-ground management and monitoring. Furthermore, the Australian government is now listing the maintenance or increase of genetic diversity as key components in the new Threatened Species Action Plan 2022–2032 (Department of Climate Change, Energy, the Environment and Water 2022). For instance, by 2023, a stocktake of threatened species susceptible to invasive predators will be undertaken to ensure sufficient genetic diversity can be supported in potential safe haven populations. From 2022 to 2027, the plan aims to strategically enhance or grow the safe havens network by undertaking targeted translocations to improve genetic diversity and address the underrepresentation of predator-susceptible species. Despite earlier gaps, recent initiatives show a clear advancement in embedding genetic considerations into conservation planning.

Translocations have become a valuable tool for conservation management (Batson et al. 2015). Research presented at the forum emphasised the importance of recognising existing patterns of genetic variation when contemplating translocation efforts. Failure to consider these patterns can lead to genetic homogenisation, diminishing the species' resilience and adaptability. Recent research also highlights the Indigenous cultural influence on genetic variation as species were moved for cultural purposes, or deliberately not moved, hence creating genetic cultural heritage signatures (Fahey et al. 2024). Furthermore, the significance of monitoring genetic diversity after translocation was emphasised, highlighting a clear connection between genetic research and on-ground management and monitoring.

The Australian Wildlife Conservancy (AWC) is a key player in conservation management in northern Australia both through landscape scale threat management (Kutt et al. 2012; Legge et al. 2019) and an important focus of the conservation strategy being reintroductions and translocations to restore biodiversity and conserve threatened species nationally (Anson 2018; Kanowski et al. 2018). Demonstrating clear integration of genetic data and management, AWC includes genetic diversity in their primary objectives of translocation plans with the key aim to maintain the long-term adaptive potential of threatened mammals (J Pierson et al. 2023). Drawing on research outside of the region, AWC demonstrated the genetic approach that is taken in planning, implementing and monitoring translocations, exploring the red-tailed phascogale *Phascogale calura* as a case-study (Pierson et al. 2023). The red-tailed phascogale is a threatened mammal occupying < 1% of its former range in small, fragmented populations with limited genetic data. To achieve suitable numbers for translocation, without compromising the source populations, a captive breeding program was established at the Alice Springs Desert Park. Through genetic assessment of source populations, and strategic breeding, captive offspring demonstrated significantly lower inbreeding coefficients and relatedness than source populations (Pierson et al. 2023). By using founders from a combination of source populations distinct to those used in the initial captive breeding program, a second, genetically distinct captive population has been established in collaboration with Adelaide Zoo. The establishment of two genetically distinct captive populations reduces the reliance on remnant source populations for future translocations and population supplementation. AWC also places emphasis on post-translocation monitoring (Anderson et al. 2024) and have demonstrated that translocated populations are breeding successfully in the wild and genetic indicators for inbreeding and relatedness have been maintained (Sinclair et al. 2024). AWC provided a clear framework for adaptive genetic management for reintroductions.

The Northern Territory (NT) government has demonstrated alternative strategies to incorporate genetics into conservation, particularly when in-house genetic expertise is lacking. The NT government, in partnership with the AWC, recently performed a successful translocation of the critically endangered central rock rat (*Zyzomys pedunculatus*). Extinct from ~ 95% of its presumed historical range, and with the lowest recorded species-level heterozygosity of any native rodent species on mainland Australia (Roycroft et al. 2021), the central rock rat only survives in the West MacDonnell Ranges of the Northern Territory, with unstable population numbers. Capitalising on a population irruption, 58 rock rats were translocated to AWC's Newhaven Sanctuary predator free fenced area in 2022 (P McDonald, personal communication, 2023). Additionally, 16 were transferred to the Alice Springs Desert Park to initiate a captive breeding programme. Including translocated individuals, tissue samples were collected from 81 individuals to investigate the population genetics of this isolated species. Instead of relying on in-house resources, the NT government and AWC engaged external specialists for the extraction, sequencing, and subsequent genomic data analysis. Such services are increasingly commercially available in Australia (e.g. Diversity Arrays Technology, or genomics core facilities), or as collaborations with genomics experts facilitated through national consortia (e.g. OMG, AusARG). This approach underscores the potential for bridging the gap between genetics and conservation through external collaboration.

The golden bandicoot *Isoodon auratus*, once widely distributed across Australia, now exists in the northwest Kimberley and offshore islands in Western Australia and the Northern Territory. These significant range contractions have led to the classification of golden bandicoots as vulnerable species. Consequently, various translocation initiatives have been undertaken, relocating individuals to two islands in the Northern Territory, two islands in Western Australia, and three mainland locations within Western Australia (Blythman et al. 2020; Rick et al. 2023). Research incorporating remnant and translocated populations revealed four distinct genetic regions within the golden bandicoot species. Notably, the Kimberley mainland populations exhibited the highest levels of genetic diversity, while the island populations in the Northern Territory displayed the lowest genetic diversity. Genomic data was used to monitor genetic diversity and showed that the translocated populations maintained genetic diversity levels comparable to their source populations. To safeguard at least 90% of the genetic diversity inherent in golden bandicoots, the preservation of three mainland populations and the Augustus Island population was deemed necessary. Importantly, the study underscored the overall limited genetic diversity observed within the species, raising the prospect of potential genetic augmentation strategies. The need for a balanced approach to conserve genetic diversity without compromising genetic adaptation was emphasised, highlighting the complexities inherent in managing these vulnerable marsupials (Rick et al. 2023).

As conservation actions increasingly incorporate translocations, it is crucial to address the unintended consequences of these interventions, particularly when they are implemented on poorly studied islands. For instance, the translocation of the golden bandicoot onto the Wessel Islands in the late 2000s occurred despite limited research on the existing diversity and potential ecological ramifications. The only amphibian-focused survey in the region was conducted in 1993, prior to the inter-island translocation of golden bandicoots, and no follow-up surveys have been undertaken (Catullo and Keogh 2021). Given that bandicoots are omnivores known to consume frogs and reptiles, concerns have been raised about their potential impact on endemic herpetofauna, including the recently described *Uperoleia gurrumuli* (Catullo and Keogh 2021). The introduction of golden bandicoots to Guluwurru and Rarrakala Islands highlights the need for further research to assess their effects on the unique evolutionary diversity of the Wessel Islands. These concerns underscore the importance of conducting thorough pre-translocation studies and ongoing post-translocation monitoring to ensure that conservation efforts do not inadvertently threaten the biodiversity they aim to protect.

The integration of genetic research into practical conservation management is key to the success of conservation actions, as evident from the various case studies and initiatives discussed. Despite the ongoing challenge of adequately incorporating rapidly evolving genetic data into conservation strategies, there are encouraging examples like those of AWC and the NT government that exhibit promising practices. Historical insights from extinct species further amplify the importance of understanding genetic components to address species declines. New techniques are also on the horizon for enhancement of conservation management, approaches using genomic data, like temporal genomic reconstruction (Clark et al. 2023; Jensen and Leigh 2022). These approaches may allow land managers to more effectively track declines and improvements in species' demographic trajectories. As conservationists navigate the intricate landscape of preserving threatened species, the synthesis of genetic knowledge and its application remains a pivotal component in shaping the future of conservation. Continual collaboration between geneticists and conservationists, bridging the existing gaps, especially on Indigenous owned and managed lands, will be essential for informed and adaptable strategies for our northern Australia's biodiversity.

Theme 5: Indigenous conservation genomics research partnerships in northern Australia

The majority of northern Australia is managed and/or owned by First Nations peoples under Aboriginal Reserves, Land Rights and Native Title Acts, and Indigenous Protected Areas (Fig. 1b). Northern Australia is vast (2,773,000 km2, 36% of Australia's land mass; Babacan and Gopalkrishnan 2021) and has low a population (1.2 million, 6% of Australia; Babacan and Gopalkrishnan 2021), concentrated in the main towns. Much of the region is considered remote and is inaccessible, with poor infrastructure and service delivery. These factors have led to a paucity of species records (e.g. Ens et al. 2016; Russell et al. 2023) and even more so, genetic data on the region's biodiversity (Fig. 4). These gaps in data offer great opportunity for biodiversity recording, using not only Western scientific techniques but also Indigenous knowledge due to the strong Indigenous connection and access to Country in this region (Ens et al. 2016; Moritz et al. 2013; Russell et al. 2023).

Much of the environmental management and monitoring of land, coastal and marine environments across northern Australia is conducted by Indigenous ranger groups associated with organisations representing Traditional Owners. The expertise, access and logistical capability of these groups means that in this region, the capacity for Indigenous-led monitoring and management is far greater than in many other parts of Australia. Mutually beneficial research partnerships between Western scientists, ranger groups and communities provide opportunity for new scientific discovery (e.g. Gurrumul's toadlet, Catullo and Keogh 2021) and collaborative biodiversity monitoring programs (Box 2) (Ens et al. 2016; Moritz et al. 2013; Russell et al. 2023). Genetic research increasingly features in such partnerships (Shaw et al. 2024).

Many Indigenous Ranger groups across northern Australia have, and continue to, collaborate on genetic projects with direct conservation/land management applications, e.g. detecting threatened species, informing hunting guidelines and sustainable harvest (Shaw et al. 2024) and investigating species richness and population connectivity of cryptic and morphologically similar species (Campbell et al. in prep).

As the dominant cultural force in the conservation space, it is important for Western scientists to be conscious of methods that foster ethical and equitable research partnerships (Ens and Turpin 2022). To be more inclusive of Indigenous people, knowledge and methods, traditional Western scientific values and practice must be devolved, and co-design methodologies and Indigenous leadership must be prioritised to deliver mutual benefits that safeguard not only biological, but cultural, or 'biocultural' diversity (see Box 2). National and international guidelines for ethical Indigenous research collaborations are a useful starting point for researchers in this regard, (e.g. official guidelines: UNDRIP, AIATSIS Ethical Research Guidelines, and CBD Nagoya Protocol); however, are not without criticism (See Mc Cartney et al. 2023), and ultimately local guidelines, governance structures and leadership should take precedence (Cooke et al. 2022). Knowledge co-production principles have recently emerged as best practice for collaborative research with Indigenous communities, from project conception, method development, data collection, analysis and communication (Hill et al. 2020). Researchers can also learn from previous collaborations (Ens and Turpin 2022; Shaw et al. 2024) and should invest time in discussing local priorities in the context of concepts like the 'FAIR' and 'CARE' data principles, and clearly define sample/data ownership and storage, intellectual property and access and benefit sharing of project outputs (Mc Cartney et al. 2022; Shaw et al. 2024). Innovations like the Local Context Hub's 'biocultural notices,' have been created to guide researchers to maintain Indigenous data sovereignty by ensuring Indigenous rights and interests remain connected to data after projects are finalised (Liggins et al. 2021). Experimenting with communication outputs, such as with the translocation of the golden bandicoot, in picture book form (Lucas and Campbell 2012), supports equitable knowledge transfer, and trust. Indigenous leadership, reciprocity and building time and adequate financial remuneration to initiate and maintain collaborations are also practical ways to foster strong collaborations (Austin et al. 2018; Ens et al. 2012).

Box 2: Warrakan-puy djäma (Animal-related work) cross-cultural fauna survey method

The information presented below is based on research conducted by Bridget Campbell as part of her PhD, in collaboration with the Yirralka Rangers and partner institutions.

Many Yolŋu have expressed concerns about declining fauna, especially those that have cultural significance, and the impact of invasive species such as cats and cane toads. To address these concerns, the 'Warrakan-puy djäma' ('animal-related work') project was established as a collaboration between the Yirralka Rangers and researchers from Macquarie University, the Australian National University, Charles Darwin University and The Nature Conservancy (TNC) (funded by TNC and an ARC Linkage Grant 2021–2024). The project aimed to collaboratively build fauna data and knowledge in the Laynhapuy Indigenous Protected Area (IPA), northeast Arnhem Land, to inform Yolŋu decision-making about animals of concern. Collaborative planning, collaborative cross-cultural methods and analysis, and co-production of diverse communication outputs are key features of this research, and are briefly outlined below.

Collaborative planning: Rangers invited researchers to partipate in local Head Ranger and ward-based governance meetings, where the focus, frequency and location of fauna surveys (trapping and camera arrays) were discussed and planned. Through

Fig. 3 Wäŋa wat̲aŋu from Gurka'wuy and researcher Shaina Russell mapping priority places for the camera trap array (Left). Brendan Banygada Wunuŋmurra and PhD student Bridget Campbell measuring and collecting a tissue sample from a gunydjul̲u (skinks) on a survey camp (Centre). Ŋal̲apal̲mi (Elders) Clancy Marrkula, and Linda Bandawuŋu being interviewed by Thomas Marrkula (Yirralka Ranger) and Bridget Campbell (Right; Photo credit: Yirralka Rangers)

these meetings and further consultations with wäŋa wat̲aŋu (Traditional Owners) and djuŋgayarr (caretakers) a set of priority species, places and practices were identified. Key to this project was the involvement of key Elders and youth (especially from the 'Learning on Country' program). A memorandum of understanding (MOU) was developed at the outset to solidify each parties expectations of project methods and outcomes.

Cross-cultural fauna survey methods: To record species occurrence we agreed to: conduct on-Country field surveys (modified NTG design); a motion sensor camera trap network; and importantly, record Yolŋu knowledge of species sightings, habitat, behaviour, threats and cultural significance. During the on-Country field surveys (trapping and 'hunting'), genetic samples were collected of cryptic common lizards to aid identification and conduct landscape scale genetic analyses (Fig. 3).

Prior to the field surveys, wäŋa wataŋu were consulted about the location, species they expected the team to find, and desired cultural practices to be performed by participants. This consultation was audio-visually recorded by the researchers and rangers, following written prior informed consent as per Macquarie University Human Research Ethics Approval. Wäŋa wat̲aŋu were encouraged to attend the fauna survey camps and pass on local Indigenous knowledge to participating rangers and youth including 'Learning on Country' school groups.

Participating wäŋa wat̲aŋu and rangers directed where the traps were set up at survey sites. Wäŋa wat̲aŋu taught the school students, rangers and researchers about the survey location, e.g. history and location of prohibited areas, and led cultural activities, e.g. hunting, and collecting/cooking bush foods. Local knowledge on animal tracks and habitat use guided placement of cage, Elliott, pitfall and camera traps. Trap deployment was demonstated by rangers and researchers. The animals found in traps and through participant hunting and searching were recorded by the rangers, youth and researchers using user-friendly electronic data recording applications (on a tablet). Researchers demonstated how to collect and record tissue samples from species caught in traps.

After the surveys, researchers and rangers visited the consulting wäŋa wataŋu and handed the field survey information back in a 'community report' booklet and recorded their feedback on the species caught and cultural practices performed, as well as what they would like to the team to do next time. This was recorded as part of the improved cross-cultural survey method. Wäŋa wataŋu were paid for their time including consultations, interviews and participation on surveys.

Data analysis: Wäŋa waṯaŋu consultations were transcribed by the rangers and researchers and analysed using NVivo text analysis software to detect common themes: fauna of interest, concern and known threats and cultural significance. The fauna records were added to the Yirralka Ranger's species database and will be uploaded to the Atlas of Living Australia. DNA from tissue samples of three hard to identify speciose genera (Carlia, Ctenotus and Diporiphora) were extracted, sequenced (SNPs) and analysed by the researchers to help correctly identify species using reference datasets. Species were further analysed to show regional relatedness between populations of species, connectivity and areas of potential endemism.

Communicating results and listening to feedback: Community reports and videos of the survey camps and consultations were created in English and Yolŋu matha so the results could be fed back and accessible to the broader community. Results from analyses conducted by researchers were presented and discussed at Head Ranger meetings. Yolŋu research partners were consulted on how to communicate the results of the genetics research in an accessible and meaningful way. Scientific journal articles were written with the Yirralka Rangers as co-authors and a cross-cultural fauna field guide is being produced. Cross-cultural methods and results are being presented at national conferences by rangers and researchers.

Theme 6: Tissue collections and sampling into the future

Natural history collections have allowed much of the genetic research undertaken in northern Australia (Cremona et al. 2021; Roycroft et al. 2021; von Takach et al. 2024, 2021). Voucher specimens and tissue collections offer a timeline of biodiversity, crucial for documenting changes and informing future scientific endeavours. Museums play a crucial role by providing the infrastructure, resources and expertise necessary to preserve these vouchers and tissue collections. Currently, there is significant global effort to transform the access and use of natural history collections greatly enhancing their value to diverse scientific fields (Johnson et al. 2023). Despite the value of these collections, the current rates of voucher and tissue deposition do not match the rapid pace of scientific research (Salvador and Cunha 2020). If this trend continues, future researchers will look back to a void in an otherwise continuous series of specimens to study, compromising the potential of these collections.

This is significant challenge for implementing the same strategies used to understand conservation in northern Australian mammals in other taxa, especially declining birds and reptiles. The availability of publicly accessible tissue samples for conservation work in northern Australia is inconsistent among animal groups. A significant number of tissue samples collected in northern Australia are not housed in public museum collections, limiting accessibility for future research. This is also an equity concern as Traditional Owners take on more responsibility for land management now and into the future. Without publicly accessible collections holding intellectual property rights to genomic resources as a public resource, Traditional Owners do not necessarily have access to material or the rights to intellectual property for tissue samples collected on their lands into the future to utilise these management tools and be trained in their use. This poses challenges to implementing principles for access to genomic resources guided by Nagoya, and is thus a significant future equity concern. In addition to these concerns a lack of baseline information for birds and reptiles inhibits the use of temporal genomic approaches (Clark et al. 2023; Jensen and Leigh 2022) to track declines without using expensive approaches used to obtain DNA from formalin-fixed specimens that are increasingly being refined, but are still unable to be deployed at a large scale due to high costs (Hahn et al. 2024, 2022, 2020).

As we move forward, it is crucial that museums not only act as public repositories but also as active participants in leading the ethical collection, acknowledgements and approvals as well as sharing of specimens. This means working closely with Indigenous communities and other stakeholders to ensure that the collection processes respect local customs, ecological knowledge, and social justice principles (Carroll et al. 2020). Examples in northern Australia of these partnerships have included work undertaken by all three Natural Science Curators at the Museum and Art Gallery of the Northern Territory – who through partnerships with Traditional Owners and ranger groups have led to the collection of material from Indigenous Protected Areas and the description of extinct and extant vertebrate species in Traditional languages from central and northern Australia. The historical acquisition of much of the physical material present in our national collections and collected by researchers at universities has likely been collected and used without the knowledge or consent of the Traditional Owners. This includes collections with permissions, but without adequate cross-cultural explanation of the work being undertaken. Complex research topics may get lost in cross-cultural communication between Traditional Owners and researchers, leading to a lack of complete understanding of what is being collected and how it will be used. To address these past injustices, there has been a recent push to enable Indigenous communities to provide their own definitions and aspirations for access and benefit-sharing in research publications. First Nations Land Councils now play a formal role in ensuring compliance with appropriate research protocols through facilitating approvals, consent and issuing permits for research on Indigenous lands. Globally, platforms such as the Local Contexts Hub aim to address the challenges associated with the ethical handling, sharing, and management of Indigenous knowledge and data, including genetic samples and specimens collected from Indigenous territories (Liggins et al. 2021). It provides a labelling system to support Indigenous communities in asserting their rights and interests over their cultural heritage and biological resources. Similar acknowledgement systems have recently to be included in terrestrial vertebrate tissue and specimen collections to facilitate recognition and permissions for use at the Museum and Art Gallery of the Northern Territory (Dan Edwards, pers. Comm.), for specimens from culturally significant species and places. Once these approaches are more widely adopted, museums will continue to support a wide array of knowledge systems and scientific research while navigating the ethical landscape of specimen collection in a way that respects the origins and the rights of communities associated with biological samples.

The Oz Mammals Genomics (OMG) initiative (BioPlatforms Australia) helped to facilitate the production of genomic datasets for Australian rodents, bats and marsupials at a continental scale (Eldridge et al. 2020). OMG has enabled researchers to investigate a range of questions surrounding the ongoing population declines of small mammals, including identifying important sources of genetic diversity. Similarly, the Australian Amphibian and Reptile Genomics Initiative (AusARG) has been established to facilitate genomics research to better understand the evolution and conservation of Australia's amphibians and reptiles. National initiatives will continue to play an important role in the exploration and conservation of Australia's biodiversity and addressing the gaps in the current sampling distribution.

The northern Australian region is vast, remote and largely inaccessible. Similar geographic patterns of sampling, related to accessibility (Fig. 4) are noted in much of the current genomic research for northern Australian fauna. The issue of underrepresentation of remote areas has long been recognised and led to the creation of the Bush Blitz program, a continent-scale nature discovery project that aims to fill gaps in the biodiversity knowledge of Australia (Preece et al. 2015). To date there have been seven Bush Blitz expeditions in areas of conservation significance in northern Australia. While Bush Blitz and similar initiatives such as WA government Pilbara Biological Surveys and Kimberley Island Surveys have made a significant contribution to our understanding of biodiversity in the region, when we examine the current genomic research there are still significant geographic gaps in remote sampling. Furthermore, examination of biogeographic patterns across multiple species suggests the potential for undiscovered diversity and areas of evolutionary importance that remain to be fully explored (Fig. 4).

Similarly, a bias is evident in the representation of species within research and zoological collections. The northern quoll, for instance, has been subjected to intensive genomic sampling and analysis, resulting in an abundance of data pertaining to its genetic diversity and structure. Conversely, there exists a substantial number of taxa that are markedly underrepresented in both empirical research and institutional collections (Johnson et al. 2023). This imbalance is attributable to an array of determinants, including the differential observability of species, disparities in their perceived conservation priorities, and the historical allocation of research funding that tend to focus on threatened or iconic species.

Species such as the northern quoll, which are often highlighted due to their conservation imperilment and the charismatic nature that engenders public and scientific interest, receive a disproportionate share of research resources. The large amount of data, tissue collections, and baseline knowledge has enabled the development of new genomic approaches to guide conservation in wild, threatened species. On the other hand, species that may not immediately present as conservation concerns (based on Western scientific

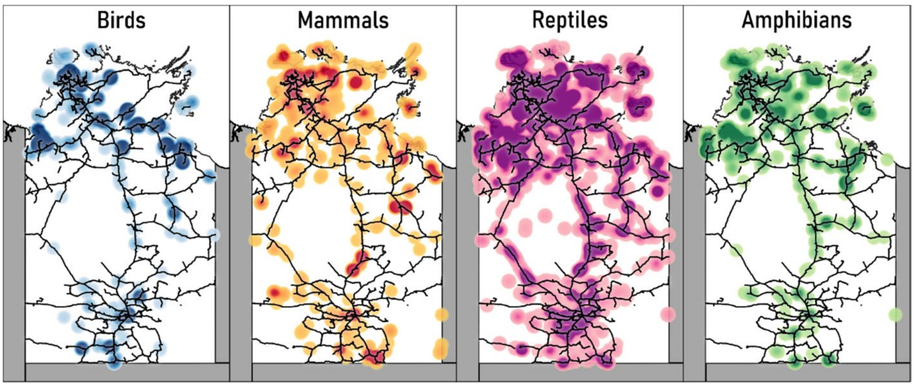

Fig. 4 Spatial distribution of specimens and samples for birds, mammals, reptiles and amphibians in relation to the government serviced road network of the Northern Territory. The maps reveal patterns of specimen collection in relation to accessibility, providing insights into potential biases in sampling efforts and highlighting areas that may be under-sampled. Specimen records from the Atlas of Living Australia (2024)

principles), or those that are less detectable in their natural habitats, tend to be neglected in genomic studies, even though their genetic data could be pivotal in elucidating the broader ecological and evolutionary patterns of the region (e.g. Fenker et al. 2023, 2021). This skewed emphasis in scientific exploration reflects a need for a recalibration towards a more equitable research paradigm—one that recognises the inherent value of a more inclusive array of species, including culturally significant species of importance to Indigenous communities (Goolmeer et al. 2022). Such an approach would facilitate a holistic understanding of the region's biodiversity and contribute to a more comprehensive and inclusive conservation strategy that safeguards the genetic integrity and evolutionary potential of native fauna.

Emerging technologies in cell culture promise a significant leap in maintaining "living" collections, which are critical for ongoing genetic studies and conservation efforts. Techniques such as cultivating cell lines from minimal tissue samples, like ear biopsies, facilitate the creation of perpetual cell repositories. These living cell collections offer unprecedented opportunities for characterising, cataloguing, and conserving biological diversity while maintaining adaptive potential (Ryder and Onuma 2018). Such technologies should be an important consideration for the future-proofing of biodiversity collections.

Non-invasive research methodologies such as environmental DNA (eDNA) are transforming biodiversity monitoring and species detection (Sahu et al. 2023). By extracting DNA from environmental samples such as soil, water, or air, researchers can detect species presence and abundance without direct or disruptive interaction with the wildlife. This technique is invaluable in inaccessible or sensitive habitats, allowing for a broad-scale and efficient assessment of biodiversity, which is particularly useful in the remote regions of northern Australia. To support the deployment of eDNA surveillance in northern Australia, the establishment of reference sequence banks is required. eDNA surveillance is likely to be a key future monitoring method useful for detecting changes in biodiversity as well as identifying rare or evasive species.

The advancement of tissue collections and sampling technologies marks a shift towards more sustainable and ethical research practices in northern Australia. Emerging technologies not only broaden the capacity to capture and analyse genetic diversity but also enable approaches that are less invasive and aligned with the ethical considerations of working on Indigenous lands. With continued collaboration among Traditional Owners, museums, research institutions and conservation practitioners, scientific endeavours can be enhanced while respecting the cultural and ecological significance of the region. The ongoing development and application of tissue collections will be crucial in securing a comprehensive and accessible repository of biological data for future generations.

Conclusion

This review synthesised six key themes from the Northern Australia Conservation Genomics Forum, including detailed case studies on speciation, evolution, and the practical application of genomics in conservation management. The research presented at the forum reinforced northern Australia's status as a global biodiversity and endemism hotspot while identifying critical knowledge gaps, particularly in understudied areas such as the Gulf of Carpentaria and within various taxa. A central theme emerging from the forum was the importance of collaborative research partnerships—particularly with Indigenous groups—to ensure ethical, effective, and regionally relevant conservation efforts. Given that much of northern Australia is Indigenous-owned or managed, strengthening these partnerships is crucial for aligning genomic research with Traditional Ecological Knowledge and local conservation priorities. The application of conservation genomics at a regional scale provides a powerful tool for biodiversity conservation, offering insights into genetic diversity, species structure, and evolutionary processes. These insights are instrumental in formulating targeted conservation strategies, including species translocations, habitat management, and mitigating threats posed by climate change, invasive species, and land-use changes. Moreover, genetic research and tissue sample repositories serve as vital resources that reduce dependence on extensive field studies, which are often costly, time-consuming, and logistically challenging in remote areas. Ultimately, the integration of genomics with Traditional Knowledge, rigorous conservation planning, and interdisciplinary collaboration will be key to protecting the unique biodiversity of northern Australia for future generations.

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Declarations

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References

Altman, J, & Kerins, S. (2012) People on country: vital landscapes Indigenous futures. Federation Press.

Anderson, GE, Volck, G, Dickins, P et al (2024) Remote camera monitoring and arboreal trapping methods used to evaluate the outcomes of a reintroduction of red-tailed phascogales (*Phascogale calura*) in Western Australia. Australian Mammalogy, 46(3), -. https://doi.org/10.1071/AM23040

Anson JR (2018) Predator proofing for conservation: an AWC perspective. Australian Zoologist 39(2):352–358. https://doi.org/10.7882/az.2016.004

Atlas of Living Australia. (2024, 07/03/2024) Occurrence download. https://doi.org/10.26197/ala.ce944181-c47a-48b8-9ffe-25ae27844bd1

Austin BJ, Robinson CJ, Fitzsimons JA et al (2018) Integrated measures of Indigenous land and sea management effectiveness - challenges and opportunities for improved conservation partnerships in Australia. Conserv Soc 16(3):372–384. https://doi.org/10.4103/cs.cs_16_123
Babacan, H, & Gopalkrishnan, N. (2021) Investing in the future: human and social service development in Northern Australia. In Leading from the North (pp. 45). https://doi.org/10.2307/j.ctv1zcm2r5.9
Batson WG, Gordon IJ, Fletcher DB et al (2015) Review: Translocation tactics: a framework to support the IUCN Guidelines for wildlife translocations and improve the quality of applied methods. J Appl Ecol 52(6):1598–1607. https://doi.org/10.1111/1365-2664.12498
Blacket, MJ, Adams, M, Cooper, SJB et al (2001) Systematics and evolution of the dasyurid marsupial genus *Sminthopsis*: I. The macroura species group. Journal of Mammalian Evolution, 8(2), 149–170. https://doi.org/10.1023/a:1011322031747
Blythman, M, Lohr, C, Sims, C et al (2020) Translocation of Golden Bandicoots, *Isoodon auratus barrowensis*, from a fenced enclosure to unfenced managed land on Matuwa (formally Lorna Glen) September 2015: Final Report. Department of Biodiversity Conservation and Attractions, Perth Western Australia.
Booth, C, Adams, V, Kruse, B et al (2021) The Enduring Pilbara: A conservation vision for a land rich in nature, culture and resources. Centre for Conservation Geography and University of Tasmania.
Bowman DM, Brown G, Braby M et al (2010) Biogeography of the Australian monsoon tropics. J Biogeogr 37(2):201–216. https://doi.org/10.1111/j.1365-2699.2009.02210.x
Braithwaite RW, Griffiths AD (1994) Demographic variation and range contraction in the northern quoll, *Dasyurus hallucatus* (Marsupialia : Dasyuridae). Wildl Res 21:203–217. https://doi.org/10.1071/WR9940203
Brewer, T, Dale, A, Gerritsen, R et al (2021) Leading from the north: rethinking northern Australia development. ANU press.
Card DC, Shapiro B, Giribet G et al (2021) Museum Genomics. Ann Rev Genet 55:633–659. https://doi.org/10.1146/annurev-genet-071719-020506
Carroll SR, Garba I, Figueroa-Rodríguez OL et al (2020) The CARE principles for Indigenous data governance. Data Science Journal 19:43–43. https://doi.org/10.5334/dsj-2020-043
Catullo RA, Keogh JS (2021) Seen only once: an evolutionarily distinct species of Toadlet (Uperoleia: Myobatrachidae) from the Wessel Islands of northern Australia. Zootaxa 5057(1):52–68. https://doi.org/10.11646/zootaxa.5057.1.3
Clark RD, Catalano KA, Fitz KS et al (2023) The practice and promise of temporal genomics for measuring evolutionary responses to global change. Mol Ecol Resour. https://doi.org/10.1111/1755-0998.13789
Cooke P, Fahey M, Ens EJ et al (2022) Applying biocultural research protocols in ecology: Insider and outsider experiences from Australia. Ecol Manage Restor 23(S1): 64-74. https://doi.org/10.1111/emr.12545
Cremona T, Baker AM, Cooper SJB et al (2021) Integrative taxonomic investigation of *Petaurus breviceps* (Marsupialia: Petauridae) reveals three distinct species. Zool J Linn Soc 191(2):503–527. https://doi.org/10.1093/zoolinnean/zlaa060
Deakin JE, Potter S, O'Neill R et al (2019) Chromosomics: Bridging the gap between genomes and chromosomes. Genes 10(8):627. https://doi.org/10.3390/genes10080627
Department of Climate Change, Energy, the Environment and Water. (2022) Threatened Species Strategy Action Plan 2022–2032. Canberra
Department of Climate Change, Energy, the Environment and Water. (2023) Interim Biogeographic Regionalisation for Australia (IBRA), Version 7. Canberra: Australian Government Retrieved from https://www.dcceew.gov.au/environment/land/nrs/science/ibra
Doody JS, Green B, Rhind D et al (2009) Population-level declines in Australian predators caused by an invasive species. Anim Conserv 12(1):46–53. https://doi.org/10.1111/j.1469-1795.2008.00219.x
Edwards RD, Crisp MD, Cook DH et al (2017) Congruent biogeographical disjunctions at a continent-wide scale: Quantifying and clarifying the role of biogeographic barriers in the Australian tropics. PLoS ONE 12(4):e0174812. https://doi.org/10.1371/journal.pone.0174812
Eldridge MDB, Kinnear JE, Zenger KR et al (2004) Genetic diversity in remnant mainland and "pristine" island populations of three endemic Australian Macropodids (Marsupialia): *Macropus eugenii*, *Lagorchestes hirsutus* and *Petrogale lateralis*. Conserv Genet 5(3):325–338. https://doi.org/10.1023/b:coge.0000031148.59923.aa
Eldridge MDB, Deakin JE, MacDonald AJ et al (2020) The Oz Mammals Genomics (OMG) initiative: developing genomic resources for mammal conservation at a continental scale. Australian Zoologist 40(3):505–509. https://doi.org/10.7882/AZ.2020.003

Ens EJ, Turpin G (2022) Synthesis of Australian cross-cultural ecology featuring a decade of annual Indigenous ecological knowledge symposia at the Ecological Society of Australia conferences. Ecol Manag Restor 23(S1):3–16. https://doi.org/10.1111/emr.12539

Ens EJ, Finlayson M, Preuss K et al (2012) Australian approaches for managing 'Country' using Indigenous and non-Indigenous knowledge. Ecol Manag Restor 13(1):100–107. https://doi.org/10.1111/j.1442-8903.2011.00634.x

Ens E, Scott ML, Rangers YM et al (2016) Putting Indigenous conservation policy into practice delivers biodiversity and cultural benefits. Biodivers Conserv 25(14):2889–2906. https://doi.org/10.1007/s10531-016-1207-6

Fahey M, Rossetto M, Ens E et al (2024) *Araucaria bidwillii* genomics suggest Indigenous Peoples broadened translocation practices in response to settler colonialism. People and Nature. https://doi.org/10.1002/pan3.10576

Fenker J, Tedeschi LG, Melville J et al (2021) Predictors of phylogeographic structure among codistributed taxa across the complex Australian monsoonal tropics. Mol Ecol 30(17):4276–4291. https://doi.org/10.1111/mec.16057

Fenker J, Melville J, Moritz C (2023) Dragons in the tropics – Phylogeography and speciation in diporiphora Lizards and common geographic breaks in co-distributed taxa. SSRN. https://doi.org/10.2139/ssrn.4481765

Finlayson CM, Lowry J, Bellio MG et al (2006) Biodiversity of the wetlands of the Kakadu Region, northern Australia. Aquat Sci 68(3):374–399. https://doi.org/10.1007/s00027-006-0852-3

Fisher DO, Johnson CN, Lawes MJ et al (2014) The current decline of tropical marsupials in Australia: is history repeating? Glob Ecol Biogeogr 23(2):181–190. https://doi.org/10.1111/geb.12088

Frank ASK, Johnson CN, Potts JM et al (2014) Experimental evidence that feral cats cause local extirpation of small mammals in Australia's tropical savannas. J Appl Ecol 51(6):1486–1493. https://doi.org/10.1111/1365-2664.12323

Frankham R, Ballou JD, Ralls K et al (2017) Genetic management of fragmented animal and plant populations. Oxford University Press. https://doi.org/10.1093/oso/9780198783398.001.0001

Franklin DC, Whitehead PJ, Pardon G et al (2005) Geographic patterns and correlates of the decline of granivorous birds in northern Australia. Wildl Res 32(5):399. https://doi.org/10.1071/wr05052

Geyle HM, Tingley R, Amey AP et al (2021) Reptiles on the brink: identifying the Australian terrestrial snake and lizard species most at risk of extinction. Pac Conserv Biol 27(1):3. https://doi.org/10.1071/pc20033

Goolmeer T, Skroblin A, Grant C et al (2022) Recognizing culturally significant species and Indigenous-led management is key to meeting international biodiversity obligations. Conserv Lett 15(6):e12899. https://doi.org/10.1111/conl.12899

Gould SF (2011) Does post-mining rehabilitation restore habitat equivalent to that removed by mining? A case study from the monsoonal tropics of northern Australia. Wildl Res 38(6):482. https://doi.org/10.1071/wr11019

Hahn EE, Grealy A, Alexander M et al (2020) Museum epigenomics: Charting the future by unlocking the past. Trends Ecol Evol 35(4):295–300. https://doi.org/10.1016/j.tree.2019.12.005

Hahn EE, Alexander MR, Grealy A et al (2022) Unlocking inaccessible historical genomes preserved in formalin. Mol Ecol Resour 22(6):2130–2147. https://doi.org/10.1111/1755-0998.13505

Hahn EE, Alexander M, Stiller J et al (2024) Hot alkaline lysis gDNA extraction from formalin-fixed archival tissues. PLoS ONE 19(1):e0296491. https://doi.org/10.1371/journal.pone.0296491

Harradine E, How RA, Schmitt LH et al (2015) Island size and remoteness have major conservation significance for how spatial diversity is partitioned in skinks. Biodivers Conserv 24(8):2011–2029. https://doi.org/10.1007/s10531-015-0923-7

Hill R, Walsh FJ, Davies J et al (2020) Knowledge co-production for Indigenous adaptation pathways: Transform post-colonial articulation complexes to empower local decision-making. Glob Environ Chang 65:102161. https://doi.org/10.1016/j.gloenvcha.2020.102161

Hoban S, Bruford M, D'Urban Jackson J et al (2020) Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. Biol Cons 248:108654. https://doi.org/10.1016/j.biocon.2020.108654

Hoban S, Bruford MW, Funk WC et al (2021) Global commitments to conserving and monitoring genetic diversity are now necessary and feasible. Bioscience 71(9):964–976. https://doi.org/10.1093/biosci/biab054

Hoban S, Archer FI, Bertola LD et al (2022) Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. Biol Rev 97(4):1511–1538. https://doi.org/10.1111/brv.12852

Hollingsworth, P, O'Brien, D, Ennos, R et al (2020) Scotland's biodiversity progress to 2020 Aichi targets: conserving genetic diversity–development of a national approach for addressing Aichi Biodiversity Target 13 that includes wild species. Scottish Natural Heritage.
Jensen EL, Leigh DM (2022) Using temporal genomics to understand contemporary climate change responses in wildlife. Ecol Evol. https://doi.org/10.1002/ece3.9340
Johnson, KR, Owens, IFP, & Group, tGC (2023) A global approach for natural history museum collections. Science 379(6638):1192–1194. https://doi.org/10.1126/science.adf6434
Kanowski, J, Roshier, D, Smith, M et al (2018) Effective conservation of critical weight range mammals: reintroduction projects of the Australian Wildlife Conservancy. In s. garnett, P. Latch, D. Lindenmayer, & J. Woinarski (Eds.), Recovering Australian Threatened Species: a Book of Hope (pp. 269–280). CSIRO.
Kardos M (2021) Conservation genetics. Curr Biol 31(19):R1185–R1190. https://doi.org/10.1016/j.cub.2021.08.047
Kriesner, P, Weeks, A, Razeng, E et al (2020) Assessing genetic risks to Victorian flora and fauna. Department of Environment, Land, Water and Planning.
Kutt AS, Vanderduys EP, Perry JJ et al (2012) Signals of change in tropical savanna woodland vertebrate fauna 5 years after cessation of livestock grazing. Wildl Res 39(5):386–396. https://doi.org/10.1071/WR11137
Kutt, A, Felderhof, L, VanDerWal, J et al (2009) Northern Australia Land and Water Science Review. Department of Infrastructure, Transport, Regional Development and Local Government, 1–42.
Lawes MJ, Murphy BP, Fisher A et al (2015) Small mammals decline with increasing fire extent in northern Australia: evidence from long-term monitoring in Kakadu National Park. Int J Wildland Fire 24(5):712–722. https://doi.org/10.1071/WF14163
Legge S, Murphy S, Heathcote J et al (2008) The short-term effects of an extensive and high-intensity fire on vertebrates in the tropical savannas of the central Kimberley, northern Australia. Wildl Res 35(1):33–43. https://doi.org/10.1071/WR07016
Legge S, Kennedy MS, Lloyd RAY et al (2011) Rapid recovery of mammal fauna in the central Kimberley, northern Australia, following the removal of introduced herbivores. Austral Ecol. https://doi.org/10.1111/j.1442-9993.2010.02218.x
Legge S, Smith JG, James A et al (2019) Interactions among threats affect conservation management outcomes: Livestock grazing removes the benefits of fire management for small mammals in Australian tropical savannas. Conservation Science and Practice 1(7):e52. https://doi.org/10.1111/csp2.52
Legge S, Rumpff L, Garnett ST et al (2023) Loss of terrestrial biodiversity in Australia: magnitude, causation, and response. Science 381(6658):622–631. https://doi.org/10.1126/science.adg7870
Liggins L, Hudson M, Anderson J (2021) Creating space for Indigenous perspectives on access and benefit-sharing: Encouraging researcher use of the Local Contexts Notices. Mol Ecol 30(11):2477–2482. https://doi.org/10.1111/mec.15918
Lucas, D, & Campbell, C. (2012) Wan'kurra the golden bandicoot, . Waterlily Publishing.
Mc Cartney AM, Anderson J, Liggins L et al (2022) Balancing openness with Indigenous data sovereignty: An opportunity to leave no one behind in the journey to sequence all of life. Proc Natl Acad Sci 119(4):e2115860119. https://doi.org/10.1073/pnas.2115860119
Mc Cartney, AM, Head, MA, Tsosie, KS et al (2023) Indigenous peoples and local communities as partners in the sequencing of global eukaryotic biodiversity. npj Biodiversity, 2(1), 8. https://doi.org/10.1038/s44185-023-00013-7
Moritz C, Ens EJ, Potter S et al (2013) The Australian monsoonal tropics: An opportunity to protect unique biodiversity and secure benefits for Aboriginal communities. Pac Conserv Biol 19(4):343–355. https://doi.org/10.1071/PC130343
Morris, K, Page, M, Kay, R et al (2015) Forty years of fauna translocations in Western Australia: lessons learned. In Advances in reintroduction biology of Australian and New Zealand fauna (Vol. 217).
Nicholl, E. (2022) Population genomics and conservation management of the Mesembriomys genus Charles Darwin University]. Darwin, NT.
Oliver PM, Laver RJ, De Mello Martins F et al (2017) A novel hotspot of vertebrate endemism and an evolutionary refugium in tropical Australia. Divers Distrib 23(1):53–66. https://doi.org/10.1111/ddi.12506
Onley IR, White LC, Moseby KE et al (2023) Disproportionate admixture improves reintroduction outcomes despite the use of low-diversity source populations: population viability analysis for a translocation of the greater stick-nest rat. Anim Conserv 26(2):216–227. https://doi.org/10.1111/acv.12812

Pepper M, Keogh JS (2014) Biogeography of the Kimberley, Western Australia: a review of landscape evolution and biotic response in an ancient refugium. J Biogeogr 41(8):1443–1455. https://doi.org/10.1111/jbi.12324

Pepper M, Doughty P, Keogh JS (2013) Geodiversity and endemism in the iconic Australian Pilbara region: a review of landscape evolution and biotic response in an ancient refugium. J Biogeogr 40(7):1225–1239. https://doi.org/10.1111/jbi.12080

Pereira HM, Ferrier S, Walters M et al (2013) Essential Biodiversity Variables. Science 339(6117):277–278. https://doi.org/10.1126/science.1229931

Pierson JC, Coates DJ, Oostermeijer JGB et al (2016) Genetic factors in threatened species recovery plans on three continents. Front Ecol Environ 14(8):433–440. https://doi.org/10.1002/fee.1323

Pierson JC, Berry L, Alexander L et al (2023) Adaptive genetic management of a reintroduction program from captive breeding to metapopulation management of an arboreal marsupial. Diversity 15(7):848. https://doi.org/10.3390/d15070848

Potter S, Eldridge MDB, Taggart DA et al (2012) Multiple biogeographical barriers identified across the monsoon tropics of northern Australia: phylogeographic analysis of the *brachyotis* group of rock-wallabies. Mol Ecol 21(9):2254–2269. https://doi.org/10.1111/j.1365-294x.2012.05523.x

Potter S, Moritz C, Piggott MP et al (2024) Museum skins enable identification of introgression associated with cytonuclear discordance. Syst Biol. https://doi.org/10.1093/sysbio/syae016

Potter, S, Close, RL, Taggart, DA et al (2014) Taxonomy of rock-wallabies, *Petrogale* (Marsupialia: Macropodidae). IV. Multifaceted study of the *brachyotis* group identifies additional taxa. Australian Journal of Zoology, 62(5), 401–414. https://doi.org/10.1071/ZO13095

Preece M, Harding J, West JG (2015) Bush Blitz: journeys of discovery in the Australian outback. Aust Syst Bot 27(6):325–332. https://doi.org/10.1071/SB15009

Radford IJ, Woolley L-A, Dickman CR et al (2020) Invasive anuran driven trophic cascade: An alternative hypothesis for recent critical weight range mammal collapses across northern Australia. Biol Invasions 22(6):1967–1982. https://doi.org/10.1007/s10530-020-02226-4

Ralls K, Ballou JD, Dudash MR et al (2018) Call for a paradigm shift in the genetic management of fragmented populations. Conserv Lett 11(2):e12412. https://doi.org/10.1111/conl.12412

Rick K, Byrne M, Cameron S et al (2023) Population genomic diversity and structure in the golden bandicoot: a history of isolation, extirpation, and conservation. Heredity 131(5):374–386. https://doi.org/10.1038/s41437-023-00653-2

Rossiter NA, Setterfield SA, Douglas MM et al (2003) Testing the grass-fire cycle: alien grass invasion in the tropical savannas of northern Australia. Divers Distrib 9(3):169–176. https://doi.org/10.1046/j.1472-4642.2003.00020.x

Roycroft E, Macdonald AJ, Moritz C et al (2021) Museum genomics reveals the rapid decline and extinction of Australian rodents since European settlement. Proc Natl Acad Sci 118(27):e2021390118. https://doi.org/10.1073/pnas.2021390118

Roycroft E, Moritz C, Rowe KC et al (2022) Sequence capture from historical museum specimens: maximizing value for population and phylogenomic studies. Front Ecol Evol. https://doi.org/10.3389/fevo.2022.931644

Roycroft E, Ford F, Ramm T et al (2024) Speciation across biomes: Rapid diversification with reproductive isolation in the Australian delicate mice. Mol Ecol 33(7):e17301. https://doi.org/10.1111/mec.17301

Russell SR, Sultana R, Rangers NY et al (2023) Mepimbat tedul proujek: Indigenous knowledge of culturally significant freshwater turtles addresses species knowledge gaps in Northern Australia. Austral Ecol 48(7):1306–1327. https://doi.org/10.1111/aec.13353

Ryder OA, Onuma M (2018) Viable cell culture banking for biodiversity characterization and conservation. Ann Rev Animal Biosci. https://doi.org/10.1146/annurev-animal-030117-014556

Sahu A, Kumar N, Pal Singh C et al (2023) Environmental DNA (eDNA): Powerful technique for biodiversity conservation. J Nat Conserv 71:126325. https://doi.org/10.1016/j.jnc.2022.126325

Salvador RB, Cunha CM (2020) Natural history collections and the future legacy of ecological research. Oecologia 192(3):641–646. https://doi.org/10.1007/s00442-020-04620-0

Shaffer HB, Toffelmier E, Corbett-Detig RB et al (2022) Landscape Genomics to Enable Conservation Actions: The California Conservation Genomics Project. J Hered 113(6):577–588. https://doi.org/10.1093/jhered/esac020

Shaw RE, Spencer PB, Gibson LA et al (2023) Linking life history to landscape for threatened species conservation in a multiuse region. Conserv Biol 37(1):e13989. https://doi.org/10.1111/cobi.13989

Shaw RE, Brockett B, Pierson JC et al (2024) Building meaningful collaboration in conservation genetics and genomics. Conserv Genet. https://doi.org/10.1007/s10592-024-01636-4

Shoo LP, Williams SE, Hero J-M (2005) Climate warming and the rainforest birds of the Australian Wet Tropics: Using abundance data as a sensitive predictor of change in total population size. Biol Cons 125(3):335–343. https://doi.org/10.1016/j.biocon.2005.04.003

Sinclair, R, Anderson, G, Callander, S et al (2024) Mt Gibson Wildlife Sanctuary Ecohealth Report for 2023. A. W. Conservancy.

Skey ED, Ottewell KM, Spencer PB et al (2023) Empirical landscape genetic comparison of single nucleotide polymorphisms and microsatellites in three arid-zone mammals with high dispersal capacity. Ecol Evol 13(5):e10037. https://doi.org/10.1002/ece3.10037

Stobo-Wilson A, Stokeld D, Einoder L et al (2020) Bottom-up and top-down processes influence contemporary patterns of mammal species richness in Australia's monsoonal tropics. Biol Cons 247:108638. https://doi.org/10.1016/j.biocon.2020.108638

Stobo-Wilson, AM, & Cremona, T. (2023) Diversity and endemism of the marsupials of Australia's Top End and Kimberley. In N. C. Cáceres & C. R. Dickman (Eds.), American and Australasian Marsupials: An Evolutionary, Biogeographical, and Ecological Approach (pp. 1–23). Springer International Publishing. https://doi.org/10.1007/978-3-030-88800-8_36-1

Stokeld D, Fisher A, Gentles T et al (2018) Rapid increase of Australian tropical savanna reptile abundance following exclusion of feral cats. Biol Cons 225:213–221. https://doi.org/10.1016/j.biocon.2018.06.025

Supple MA, Shapiro B (2018) Conservation of biodiversity in the genomics era. Genome Biol 19:1–12. https://doi.org/10.1186/s13059-018-1520-3

Tingley R, Macdonald SL, Mitchell NJ et al (2019) Geographic and taxonomic patterns of extinction risk in Australian squamates. Biol Cons 238:108203. https://doi.org/10.1016/j.biocon.2019.108203

Traill LW, Perhans K, Lovelock CE et al (2011) Managing for change: wetland transitions under sea-level rise and outcomes for threatened species. Divers Distrib 17(6):1225–1233. https://doi.org/10.1111/j.1472-4642.2011.00807.x

Umbrello LS, Woolley PA, Westerman M (2017) Species relationships in the dasyurid marsupial genus *Pseudantechinus* (Marsupialia : Dasyuridae): a re-examination of the taxonomic status of *Pseudantechinus roryi*. Aust J Zool 65(4):240. https://doi.org/10.1071/zo17059

Umbrello L, Bullen R, Shaw R et al (2022) Extensive gene flow in a threatened bat (Rhinonicteris aurantia) in an arid landscape. Global Ecol Conserv 37:e02154. https://doi.org/10.1016/j.gecco.2022.e02154

Umbrello LS, Cooper NK, Adams M et al (2023) Hiding in plain sight: two new species of diminutive marsupial (Dasyuridae: Planigale) from the Pilbara. Australia. Zootaxa 5330(1):1–46. https://doi.org/10.11646/zootaxa.5330.1.1

Umbrello LS, Newton H, Baker AM et al (2024) Vicariant speciation resulting from biogeographic barriers in 90the Australian tropics: The case of the red-cheeked dunnart (Sminthopsis virginiae). Ecol Evol. https://doi.org/10.1002/ece3.70215

von Takach B, Scheele BC, Moore H et al (2020) Patterns of niche contraction identify vital refuge areas for declining mammals. Divers Distrib 26(11):1467–1482. https://doi.org/10.1111/ddi.13145

von Takach B, Penton CE, Murphy BP et al (2021) Population genomics and conservation management of a declining tropical rodent. Heredity 126(5):763–775. https://doi.org/10.1038/s41437-021-00418-9

von Takach B, Jolly CJ, Dixon KM et al (2022a) Long-unburnt habitat is critical for the conservation of threatened vertebrates across Australia. Landscape Ecol 37(6):1469–1482. https://doi.org/10.1007/s10980-022-01427-7

von Takach B, Ranjard L, Burridge CP et al (2022b) Population genomics of a predatory mammal reveals patterns of decline and impacts of exposure to toxic toads. Mol Ecol 31(21):5468–5486. https://doi.org/10.1111/mec.16680

von Takach B, Cameron SF, Cremona T et al (2024) Conservation prioritisation of genomic diversity to inform management of a declining mammal species. Biol Cons 291:110467. https://doi.org/10.1016/j.biocon.2024.110467

Westerman M, Umbrello L, Woolley PA (2023) On the composition of *Antechinomys* (Marsupialia: Dasyuridae): how many species? Aust J Zool 70(3):95–103. https://doi.org/10.1071/ZO22041

Williams, SE, Bolitho, EE, & Fox, S. (2003) Climate change in Australian tropical rainforests: an impending environmental catastrophe. Proceedings of the Royal Society of London. Series B: Biological Sciences, 270(1527): 1887–1892. https://doi.org/10.1098/rspb.2003.2464

Woinarski JCZ, Ash AJ (2002) Responses of vertebrates to pastoralism, military land use and landscape position in an Australian tropical savanna. Austral Ecol 27(3):311–323. https://doi.org/10.1046/j.1442-9993.2002.01182.x

Woinarski J, Mackey B, Nix H et al (2007) The Nature of Northern Australia: its natural values, ecological processes and future prospects. ANU E Press. https://doi.org/10.26530/oapen_459382

Woinarski JCZ, Legge S, Fitzsimons JA et al (2011) The disappearing mammal fauna of northern Australia: context, cause, and response. Conserv Lett 4(3):192–201. https://doi.org/10.1111/j.1755-263X.2011.00164.x

Woinarski JCZ, Burbidge AA, Harrison PL (2015) Ongoing unraveling of a continental fauna: Decline and extinction of Australian mammals since European settlement. Proc Natl Acad Sci 112(15):4531–4540. https://doi.org/10.1073/pnas.1417301112

Woinarski JCZ, Murphy BP, Palmer R et al (2018) How many reptiles are killed by cats in Australia? Wildl Res 45(3):247. https://doi.org/10.1071/wr17160

Woinarski JCZ, Legge SM, Garnett ST (2024) Extinct Australian birds: numbers, characteristics, lessons and prospects. Emu - Austral Ornithol 124(1):8–20. https://doi.org/10.1080/01584197.2023.2240345

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