


## RESEARCH ARTICLE OPEN ACCESS

# Local Adaptation Drives Leaf Thermoregulation in Tropical Rainforest Trees

Kali B. Middleby<sup>1,2</sup>  | Rebecca Jordan<sup>3</sup>  | Alexander W. Cheesman<sup>1,4</sup>  | Maurizio Rossetto<sup>5</sup>  | Martin F. Breed<sup>6</sup>  | Darren M. Crayn<sup>7,8</sup>  | Lucas A. Cernusak<sup>1</sup> 

<sup>1</sup>College of Science and Engineering and Centre for Tropical Environmental and Sustainability Science, James Cook University, Cairns, Queensland, Australia | <sup>2</sup>AMAP, University of Montpellier, CIRAD, CNRS, INRAE, IRD, Montpellier, France | <sup>3</sup>CSIRO Environment, Sandy Bay, Tasmania, Australia | <sup>4</sup>College of Life and Environmental Science, University of Exeter, Exeter, UK | <sup>5</sup>Research Centre for Ecosystem Resilience, Australian Institute of Botanic Science, Royal Botanic Garden Sydney, Sydney, New South Wales, Australia | <sup>6</sup>College of Science and Engineering, Flinders University, Bedford Park, South Australia, Australia | <sup>7</sup>Australian Tropical Herbarium, James Cook University, Cairns, Queensland, Australia | <sup>8</sup>ARC Centre of Excellence for Indigenous and Environmental Histories and Futures, James Cook University, Cairns, Queensland, Australia

**Correspondence:** Kali B. Middleby ([kalimiddleby@gmail.com](mailto:kalimiddleby@gmail.com))

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## ABSTRACT

Tropical forests play a critical role in biodiversity, carbon sequestration, and climate regulation, but are increasingly affected by heatwaves and droughts. Vulnerability to warming may vary within and between species because of phenotypic divergence. Leaf trait variation can affect leaf operating temperatures—a phenomenon termed ‘limited homeothermy’ when it helps avoid heat damage in warmer conditions. However, evidence for this capacity and the relative roles of acclimation or adaptation remain limited. We measured photosynthetic heat tolerance and leaf thermal traits of three co-occurring rainforest tree species across a thermal gradient in the Australian Wet Tropics. Using a leaf energy balance model parameterised with field-measured traits, we predicted variation in leaf-to-air temperature differences ( $\Delta T_{\text{trait}}$ ) and resulting thermal safety margins. We combined this with individual-based genome-wide data to detect signals of adaptive divergence and validated findings in a glasshouse trial with provenances grown under contrasting temperature and humidity conditions. Intraspecific trait variation reduced  $\Delta T_{\text{trait}}$  and increased heat tolerance in warmer sites for *Darlingia darlingiana* and *Elaeocarpus grandis*, but not *Cardwellia sublimis*. As a result, thermal safety margins declined less steeply with increasing growth temperature in species capable of increased heat tolerance and avoidance, indicating these strategies can effectively buffer warming. All species showed genomic signals of selection, with associations to temperature and moisture variables. In *E. grandis*, glasshouse results confirmed a negative cline in  $\Delta T_{\text{trait}}$  with temperature of origin. Although contrasting growth temperature and humidity lead to acclimation of individual traits, their coordination maintained  $\Delta T_{\text{trait}}$  across the conditions imposed. Our findings provide evidence of limited homeothermy and suggest climate gradients have selected for trait combinations that reduce leaf temperatures at warmer sites in some but not all species. Given the rapid pace of climate change, those species with limited capacity to adjust their thermal safety margins through acclimation or adaptation may be at greater risk of local extinction.

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## 1 | Introduction

Global warming is rapidly increasing temperatures, raising concerns about the ability of species to persist (IPCC 2022). Tropical forest trees, vital for biodiversity, carbon sequestration and water cycling (Mitchard 2018), may be particularly vulnerable because of their evolution under relatively stable thermal environments (Trew and Maclean 2021). However, populations across climate gradients may respond differently to environmental change because of plasticity and/or local adaptation (Barton et al. 2020; Halbritter et al. 2018; Leites and Garzón 2023). Although local adaptation can enhance fitness under stable conditions, it may inhibit future persistence if climate change creates a mismatch between the historic conditions a population is adapted to and the new environment (Jordan et al. 2024). Therefore, understanding how tropical trees have adapted to temperature is crucial for evaluating their resilience to global warming and informing effective management strategies.

Plants have evolved various mechanisms to cope with heat stress and maintain physiological function, such as altering leaf-level biochemistry to increase their photosynthetic heat tolerance (Geange et al. 2021; Middleby, Cheesman, and Cernusak 2024). Such adjustments help prevent leaf damage and maintain carbon uptake during heatwaves (Drake et al. 2018). However, recent studies indicate that this may be insufficient to preserve thermal safety margins—the difference between a leaf's thermal tolerance threshold and the temperatures it experiences—in warmer environments (Kitudom et al. 2022; Perez and Feeley 2020). As such, species or populations near their thermal limits, such as those in lowland tropical forests, may be particularly vulnerable to even small temperature increases in the coming decades (Araujo et al. 2021; Dougherty et al. 2023; Pau et al. 2018).

Plants can also cope with thermal stress by avoiding high temperatures through morphological and physiological trait variations that influence leaf energy balance (Michaletz et al. 2015). Traits like leaf width, absorptance, leaf angle and stomatal conductance to water vapour ( $g_s$ ) interact with the canopy microclimate to influence the fluxes of sensible and latent heat and the interception of radiation (Campbell and Norman 1998; Jones 2013). This leads to significant differences between leaf and air temperatures ( $\Delta T = T_{\text{leaf}} - T_{\text{air}}$ ), because of differences in water use (Fauset et al. 2018), leaf morphology (Leigh et al. 2017) and canopy architecture (Leuzinger and Korner 2007; Woods et al. 2018). Given the importance of maintaining  $T_{\text{leaf}}$  within safe operating limits, it is hypothesized that traits influencing  $\Delta T$  may undergo selection (Mahan and Upchurch 1988; Michaletz et al. 2015). Although such thermoregulation has been noted across different ecosystems (Guo et al. 2023; Kitudom et al. 2022), studies within species are limited (Kullberg et al. 2023; Kullberg and Feeley 2022), and few have explored the relative roles of phenotypic plasticity and ecotypic variation (Middleby, Cheesman, and Cernusak 2024; Posch et al. 2024).

Understanding whether intraspecific variation in leaf traits affecting  $\Delta T$  results from plasticity or genetic differentiation is essential for predicting future vulnerability and for guiding revegetation efforts to match provenance with future site conditions (Breed et al. 2013; Jordan et al. 2024). Although common garden and reciprocal transplant experiments are ideal

for studying local adaptation, they are resource-intensive (Sork et al. 2013), especially in remote areas. Population and ecological genomic methods, such as genotype–environment (GEA) and genotype–phenotype associations (GPA), offer complementary insights into adaptive potential without extensive field trials (Arab et al. 2020; Breed et al. 2019; Shryock et al. 2021).

To assess whether tropical trees have the capacity to cope with future climate change, we examined the patterns and drivers of intraspecific variation in leaf traits affecting thermoregulation. We define leaf thermoregulation as coordinated trait variation that alters the difference between leaf and air temperature ( $\Delta T_{\text{trait}}$ ) across a thermal gradient. Since leaves are typically warmer than air during the day because of solar radiation,  $\Delta T$  values are generally positive. We use  $\Delta T_{\text{trait}}$  to represent the component of  $\Delta T$  attributable to trait variation and interpret limited homeothermy as a negative slope of  $\Delta T_{\text{trait}}$  versus maximum temperature of the warmest month (MTWM) or MTWM of origin—indicating that leaves heat up less in warmer environments because of trait adjustments. A flat slope would indicate no thermoregulatory adjustment, whereas a positive slope would suggest increased leaf warming at warmer sites. By isolating the effects of trait variation and focusing on the slope of  $\Delta T_{\text{trait}}$ , this approach avoids confounding by environmental influences on  $T_{\text{leaf}}$  and circumvents the flawed assumption that limited homeothermy requires  $T_{\text{leaf}}$  to fall below  $T_{\text{air}}$ .

We hypothesized that traits associated with leaf cooling are under selection, specifically:

1. Within species, individuals from warmer climates of origin show coordination of leaf thermal traits that enhance leaf cooling relative to individuals from cooler climates.
2. Adaptive genetic variation associated with leaf traits is positively correlated with temperature gradients across species distributions.
3. Both plasticity and ecotypic differentiation will affect the observed patterns of leaf thermoregulation in *E. grandis*, grown under controlled thermal environments.

To test these predictions, we measured photosynthetic heat tolerance and leaf traits in populations of three tree species across a thermal gradient and predicted leaf temperatures with a leaf energy balance model. We also examined genome-wide single nucleotide polymorphisms (SNP), using GEA and GPA analyses to explore genome-wide signals of selection and identify the environmental drivers of adaptive variation in thermoregulation using generalized dissimilarity modeling. Finally, this approach was validated in *E. grandis* using a climate-controlled glasshouse trial with seedlings collected across a thermal gradient.

## 2 | Methods

### 2.1 | Study System: Rainforest Tree Species in the Wet Tropics of Queensland, Australia

The Wet Tropics of Queensland World Heritage Area comprises 8,945 km<sup>2</sup> of mostly rainforest vegetation in northeastern Queensland, Australia. Its mountainous terrain creates

geographic and spatial variation in climatic conditions across elevation over small distances. This presents an ideal opportunity for exploring patterns of intraspecific trait variation and local adaptation. The Wet Tropics of Queensland experiences warm temperatures year-round, with high but seasonal rainfall and periodic cyclone disturbance (UNESCO World Heritage Centre 1988). We selected three tropical rainforest species—*Elaeocarpus grandis* F. Muell. (Elaeocarpaceae), *Cardwellia sublimis* F. Muell. (Proteaceae) and *Darlingia darlingiana* F. Muell. L.A.S. Johnson (Proteaceae)—that are relatively abundant, upper canopy species occurring across a wide elevational range (0–1300 m). Both *C. sublimis* and *D. darlingiana* are endemic to the Wet Tropics of Queensland and have wind-dispersed seeds, whereas *E. grandis* has a wider distribution extending into Southeast Asia and the Australian subtropics and has large fleshy fruits dispersed primarily by birds.

## 2.2 | Field Sampling

During October 2021 to May 2022, we sampled trees from 16 mature remnant forest sites from across the Wet Tropics of Queensland, spanning an elevation range of 1299 m a.s.l (5 to 1304 m a.s.l), a mean annual temperature range of 7.1°C (18.6°C to 25.8°C) and a mean annual precipitation range of 2940 mm (1355 to 4295 mm). At each site, 3–10 individuals per population (median 6), spaced > 100 m apart, were selected, with the intention to avoid sampling closely related individuals. Sun-exposed

branches from the upper canopy were sampled using a pole pruner or big shot, placed in large opaque, water-sprayed bags, and kept shaded during transport to the field lab (up to 4 h). At the lab, branches were recut underwater and rehydrated in the dark for trait measurements (c. 3 h for functional traits and 12 h for chlorophyll fluorescence). Leaf samples for genomic analysis were dried on silica beads. In total, we measured leaf traits on 105 *C. sublimis*, 96 *D. darlingiana*, and 104 *E. grandis* individuals, and generated genomic data for 98 *C. sublimis*, 96 *D. darlingiana*, and 89 *E. grandis* individuals (Table 1). Additionally, seeds were collected from 11 *E. grandis* individuals from six sites for the glasshouse experiment (Figures 1 and S1, Table 1).

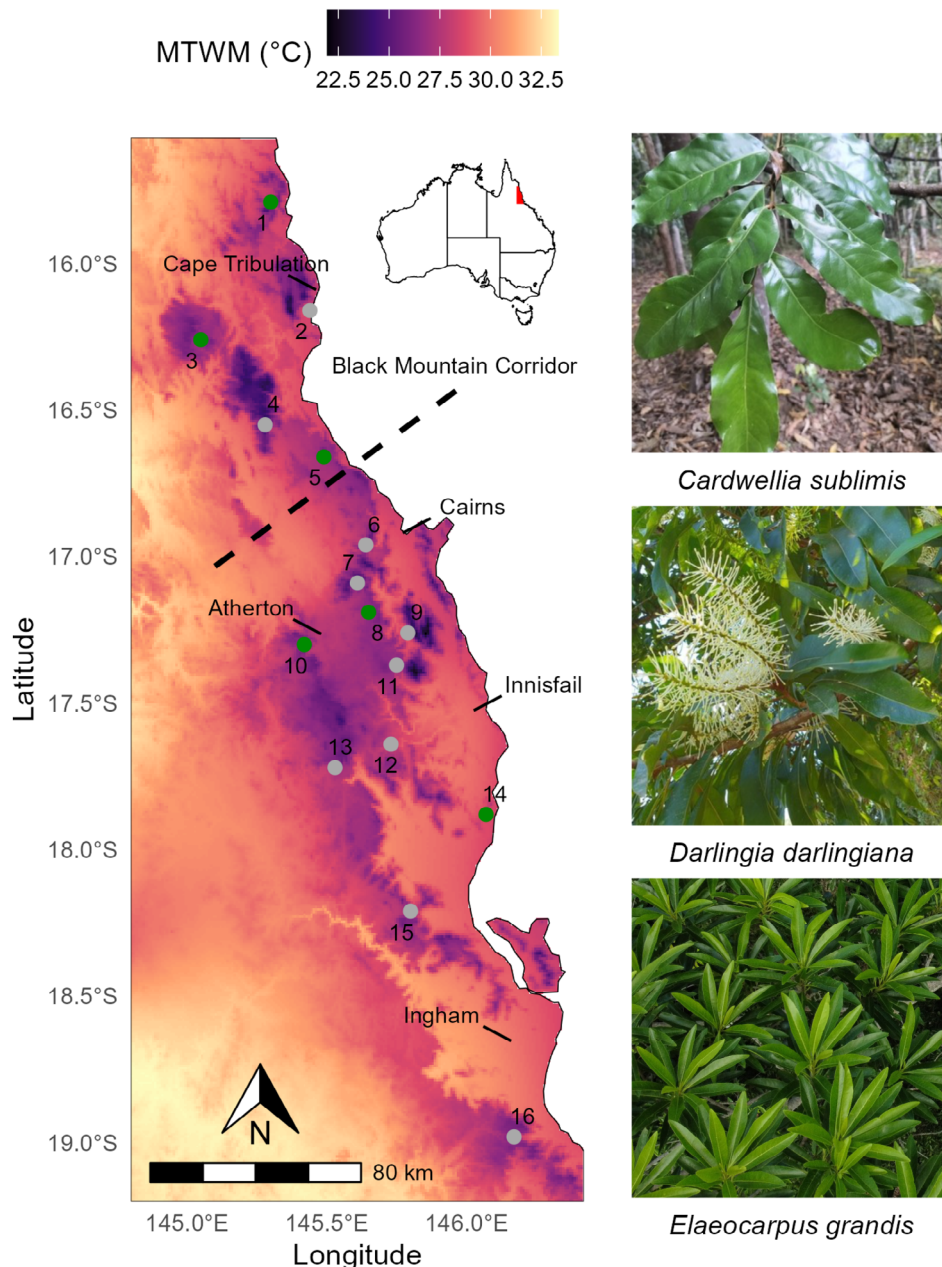
## 2.3 | Leaf Traits

We measured leaf traits known to reflect trade-offs between resource acquisition and conservation strategies (Wright et al. 2004) and those impacting leaf energy balance. These included leaf mass per area (LMA,  $\text{g m}^{-2}$ ), leaf dry matter content (LDMC,  $\text{mg g}^{-1}$ ), leaf thickness ( $\mu\text{m}$ ), effective leaf width (cm), leaf reflectance spectra including absorptance (Abs, %) and reflectance (Ref, %) to shortwave radiation, leaf carbon isotope composition ( $\delta^{13}\text{C}$ ), leaf nitrogen ( $N_{\text{mass}}$ , %), and the mass ratio of carbon to nitrogen. We also measured stomatal density (stoma  $\text{mm}^{-2}$ ) and size ( $\mu\text{m}^2$ ) to calculate theoretical maximum conductance ( $g_{\text{max}}$ ,  $\text{mol m}^{-2}\text{s}^{-1}$ ). Leaf traits were measured according to standard techniques on fully expanded sun-exposed

**TABLE 1** | Site coordinates and means for environmental variables. Sites are ordered by decreasing latitude, and numbers correspond to those in Figure 1. Sample size per population is given for trait measurements, and, where this differs, for the genetic dataset in brackets.

Population	Lat.	Long.	Elev	MTWM	PDM	Sample size per population		
	(°)	(°)	(m)	(°C)	(mm)	CS	DD	EG
1. Cedar Bay*	−15.79	145.3	172	28.0	35	6	6	6
2. Daintree	−16.16	145.44	43	28.1	69	6 (5)	6	6 (5)
3. Mt. Windsor*	−16.26	145.05	1098	26.1	17	6	6	6 (5)
4. Mt. Lewis	−16.55	145.28	1028	25.1	28	9 (8)	6	6
5. Kuranda*	−16.66	145.49	450	26.8	31	6	6	6
6. Dinden	−16.96	145.64	493	27.4	31	6	4	6
7. Mt. Edith	−17.09	145.62	977	25.7	39	6	6	3
8. School for field studies*	−17.19	145.65	770	26.5	61	10 (8)	9	10 (6)
9. Goldsborough	−17.26	145.79	149	28.8	87	0	6	6
10. Mt. Baldy*	−17.30	145.42	1162	25.8	30	7	6	5 (4)
11. Topaz	−17.37	145.75	743	26.4	111	6	0	6
12. South Johnstone	−17.64	145.73	540	27.9	109	8 (7)	8	8 (6)
13. Koombaloomba	−17.72	145.53	870	26.9	59	6	6	6
14. Mission Beach*	−17.88	146.07	28	28.7	90	10 (7)	7	10 (6)
15. Kirrama	−18.21	145.8	677	27.1	51	6	6	6
16. Paluma Range	−18.98	146.17	832	26.4	34	8	8	8 (6)

Note: Lat = latitude, Long = longitude, Elev = elevation (m a.s.l), MTWM = max temperature of the warmest month (Bio5, °C), PDM = precipitation of the driest month (Bio14, mm). CS = *Cardwellia sublimis*, DD = *Darlingia darlingiana*, and EG = *Elaeocarpus grandis*. Sites with an \* had *E. grandis* seedlings included in the glasshouse trial.



**FIGURE 1** | Map of study region. Map color shows the max temperature of the warmest month from 1981 to 2010 retrieved from the CHELSA database at 1 km resolution (Karger et al. 2017). The dashed black line indicates position of the Black Mountain Corridor, a putative geographic barrier during glacial maxima (Schneider et al. 1998). Grey points labeled with numbers indicate the populations where genetic and trait samples were collected for each of the three species shown to the right (see Table 1 for further information on populations). Green points highlight populations where *E. grandis* seedlings were collected from in the subsequent glasshouse experiment. Map lines delineate study areas and do not necessarily depict accepted national boundaries. Photos of *D. darlingiana* were provided by David Tng, *C. sublimis* by Mathew Borella, and *E. grandis* by Alexander Cheesman.

leaves from each tree (Perez-Harguindeguy et al. 2013), with 10 leaf replicates for leaf functional traits and three for absorptance and stomatal traits (for detailed measurement protocols, see Supporting Information, Methods S1).

## 2.4 | Leaf Temperature ( $T_{\text{leaf}}$ ) Modelling

We tested how covariation of leaf traits affects predicted leaf-to-air temperature differences ( $\Delta T$ ) across a thermal gradient and

whether this helps maintain  $T_{\text{leaf}}$  within safe margins.  $T_{\text{leaf}}$  was predicted using a steady-state leaf energy balance model based on the Penman-Monteith equation (Jones 2013; Monteith and Unsworth 2013), requiring plant trait-based inputs (leaf width, absorptance to shortwave radiation, stomatal ratio, and conductance), and microclimate inputs (air temperature, vapour pressure deficit, radiation, and wind speed).

Microclimate inputs were parameterized using the *micro\_global* function in 'NicheMapr' v.3.2.0 (Kearney and



Porter 2020) which uses the New et al. (2002) global monthly climate database at a  $10 \times 10$  km grid centered on 1960 to 1990. Hourly estimates of  $T_{\text{air}}$ , VPD, and solar radiation (converted to photosynthetic photon flux density, PPFD) were obtained for the 15th of each month, using tree coordinates and elevation, with solar radiation adjusted for terrain using the ‘microclima’ setting (Maclean et al. 2019). From this typical monthly, diel data, daytime means (09:00 to 15:00) were calculated for each individual tree as well as an overall mean across all individuals and species.

To separate changes in  $\Delta T$  due to microclimate from those due to leaf trait covariation, we used two microclimate parameterisations when running the leaf energy balance model. For  $\Delta T$  based solely on leaf traits (hereafter  $\Delta T_{\text{trait}}$ ), microclimate inputs were set to the overall daytime means described above, with  $T_{\text{air}} = 24.8^\circ\text{C}$ ,  $\text{VPD} = 1.4$  kPa,  $\text{PPFD} = 1403 \mu\text{mol m}^{-2} \text{s}^{-1}$ , and assuming calm conditions with a wind speed of  $0.5 \text{ m s}^{-1}$ . For  $\Delta T$  based on both traits and climate ( $\Delta T_{\text{clim}}$ ), we used the tree-level daytime mean modelled microclimate described above.

We implemented the leaf energy balance model using the *PhotosynEB* function in ‘plantecophys’ v.1.4–6 (Duursma 2015), which couples an energy balance model to the Farquhar, von Caemmerer, and Berry photosynthesis model (Farquhar et al. 1980) and the optimality-based unified  $g_s$  (USO) model (Medlyn et al. 2011), with  $T_{\text{leaf}}$  solved iteratively. The leaf traits that were ultimately involved in  $\Delta T$  parameterization include effective leaf width, absorptance to shortwave radiation,  $N_{\text{mass}}$ , and  $\delta^{13}\text{C}$ . For methodological comparison, we also calculated  $g_{\text{max}}$  from stomatal anatomy (Supporting Information, Methods S1), this was not used for downstream genetic analysis. To convert estimated  $T_{\text{leaf}}$  to  $\Delta T$ , we used the same  $T_{\text{air}}$  values used as inputs for each respective model (i.e., a common  $T_{\text{air}} = 24.8^\circ\text{C}$  for  $\Delta T_{\text{trait}}$  and a tree-level  $T_{\text{air}}$  for  $\Delta T_{\text{clim}}$ ).

## 2.5 | Stomatal Conductance Modelling

An assumption of the USO model used to predict  $g_s$  is that plants maximize carbon gain while minimizing water loss. To obtain  $g_s$ , traits that impact gas exchange are required, such as the maximum rate of carboxylation ( $V_{\text{cmax25}}$ ) and light-saturated rate of electron transport ( $J_{\text{max25}}$ ), as well as the slope parameter ( $g_1$ ) that describes the relationship between photosynthesis and stomatal conductance and responses to changes in VPD (Medlyn et al. 2011). Since characterizing  $V_{\text{cmax25}}$ ,  $J_{\text{max25}}$  and  $g_1$  in the field for each tree was not feasible, we varied these according to observed linear relationships with leaf  $N_{\text{mass}}$  ( $V_{\text{cmax25}}$ ) determined during the glasshouse experiment (Figure S9), and as a ratio of  $V_{\text{cmax25}}$  to  $J_{\text{max25}}$  and used thermal sensitivity of  $V_{\text{cmax}}$  and  $J_{\text{max}}$  parameters determined in Australian tropical trees (Kelly 2014). The parameter  $g_1$  was calculated using the following equation (Medlyn et al. 2011):

$$g_1 = \frac{\left(\frac{C_i}{C_a} \sqrt{\text{VPD}}\right)}{\left(1 - \frac{C_i}{C_a}\right)}$$

where VPD is the tree-level mean daytime vapour pressure deficit (kPa), and  $C_i/C_a$  is the ratio of intercellular to ambient  $\text{CO}_2$  concentrations, estimated from leaf  $\delta^{13}\text{C}$  using the ‘isocalcr’ package in R (Mathias and Hudiburg 2022).

This model effectively captures dynamic gas exchange and produces realistic leaf temperature estimations under non-stressful conditions (Guo et al. 2022; Kearney and Leigh 2024). However, evidence suggests that at higher temperatures,  $g_s$  and photosynthesis decouple, with  $g_s$  maintained or even increasing (De Kauwe et al. 2019; Diao et al. 2024; Drake et al. 2018; Marchin et al. 2023; Urban et al. 2017). This decoupling may reflect a strategy to enhance transpirational cooling rather than optimizing carbon gain, especially under heat stress. Relying solely on the USO model could thus overlook plant responses aimed at maintaining  $T_{\text{leaf}}$  within a viable range. In addition, our parameterisation relies on a within-species correlation between  $V_{\text{cmax25}}$  and leaf  $N_{\text{mass}}$  that was only determined in *E. grandis*. To address these assumptions, we also calculated  $\Delta T_{\text{trait}}$  and  $\Delta T_{\text{clim}}$  using theoretical  $g_{\text{max}}$  determined from stomatal anatomy via the *findTleaf* function, which estimates  $T_{\text{leaf}}$  independently of photosynthesis. These are referred to as anatomical  $\Delta T_{\text{trait}}$  and anatomical  $\Delta T_{\text{clim}}$  throughout the manuscript. By incorporating  $g_{\text{max}}$ , we aim to account for the upper limits of stomatal conductance that plants may employ in response to heat stress.

## 2.6 | Photosynthetic Heat Tolerance

Photosynthetic heat tolerance was assessed by examining the decline in maximum photosynthetic efficiency of photosystem II with increasing incubation temperature. To do so, the ratio of variable fluorescence ( $F_v$ ) to maximum fluorescence ( $F_m$ ) was measured following an established protocol (Leon-Garcia and Lasso 2019) modified from Krause et al. (2013). For each tree, 15 to 20 rehydrated leaves were sampled, and six 9 mm leaf discs per leaf were pooled and randomly assigned to heat treatments. Discs were incubated for 30 min in water baths at  $36^\circ\text{C}$ ,  $40^\circ\text{C}$ ,  $42^\circ\text{C}$ ,  $44^\circ\text{C}$ ,  $46^\circ\text{C}$ ,  $48^\circ\text{C}$ ,  $50^\circ\text{C}$ ,  $52^\circ\text{C}$ ,  $54^\circ\text{C}$ , and  $58^\circ\text{C}$ , with an untreated control at  $\sim 24^\circ\text{C}$ , then placed in petri dishes at  $24^\circ\text{C}$  for 24 h. Chlorophyll fluorescence was then measured on leaves that had been dark adapted for 30 min using a chlorophyll fluorometer (PAM-2000, Heinz Walz GmbH, Effeltrich, Germany). Five sites (and six for *E. grandis*) at varying elevations were measured during October–November 2021. Individuals showing photoinhibition (control  $F_v/F_m < 0.6$ ) were excluded from analysis. A 4-parameter log-logistic curve was fitted using ‘drc’ v.3.0–1 (Ritz et al. 2015), with the lower asymptote set to 0. The thermal tolerance metric  $T_{50}$  ( $T_{\text{leaf}}$  at 50% decline in  $F_v/F_m$ ) was obtained from the curves.

## 2.7 | Thermal Safety Margins

To determine how intraspecific trait variation may influence thermal safety margins (TSM) across species distributions, TSMs were calculated as the difference between thermal tolerance ( $T_{50}$ ) and modeled  $T_{\text{leaf}}$  ( $\Delta T + T_{\text{air}}$ ) as described above. We calculated TSMs using both  $\Delta T_{\text{trait}}$  and  $\Delta T_{\text{clim}}$ , where  $\Delta T_{\text{trait}}$

assesses the contribution of trait variation to TSMs, and  $\Delta T_{\text{clim}}$  assesses whether this variation offsets differences in local climate conditions across the species' range. Additionally, we calculated anatomical TSMs using anatomical  $\Delta T$  calculated from stomatal anatomical traits.

We were interested in assessing relative changes in TSM across a species distribution, as such our TSM estimates were calculated using daytime average (09:00 to 15:00) conditions and are likely higher than studies assessing instantaneous point measurements of  $T_{\text{leaf}}$  or those that use  $T_{\text{crit}}$  (the temperature at which photosystem II function first begins to decline) as the upper threshold instead of  $T_{50}$ . Canopy leaves of tropical forests already surpass  $T_{\text{crit}}$  (Doughty et al. 2023), and although some photosynthetic function can recover after a single exposure, recovery is less likely after  $T_{50}$  exposure (Cook et al. 2024; Javad et al. 2025; Tarvainen et al. 2022) but see Javad et al. (2025). It is also important to note that heat tolerance itself can be dynamic and influenced by recent thermal exposure (Drake et al. 2018), which may introduce variability into TSM estimates.

## 2.8 | Climate and Environmental Variables

To explore environmental drivers of trait and genomic variation, we retrieved gridded maps of bioclimatic variables, as well as wind speed and relative humidity for the Wet Tropics of Queensland from the CHELSA database at 1 km resolution, averaged for 1981–2010 (Brun et al. 2022; Karger et al. 2017). Gridded soil data products at 5–15 cm depth, 30 m resolution, for the period 1950–2013 were obtained from the Soil and Landscape Grid of Australia and resampled to 1 km resolution using 'raster' v.3.6–11 (Hijmans 2022) to match the bioclimatic data. To avoid multicollinearity and ensure interpretability, we selected uncorrelated variables ( $r < 0.7$ , calculated using values for the sampled sites) relevant to tropical tree functioning: maximum temperature of the warmest month (Bio5, °C), precipitation of the driest month (Bio14, mm), minimum relative humidity ( $\text{RH}_{\text{min}}$ , %), mean wind speed ( $\text{Wind}_{\text{mean}}$ ,  $\text{ms}^{-1}$ ), soil pH (pH), and total soil phosphorus (P).

## 2.9 | Genotyping

Dried leaf tissue samples were sent to Diversity Arrays Technology Australia Pty Ltd., Canberra, Australia for DNA extraction and genotyped using DArTseq, a reduced representation sequencing method (Sansaloni et al. 2010). Data quality and SNP filtering were performed using 'RRtools' v.0.1 (Bragg et al. 2020; Rossetto et al. 2019). SNPs with a reproducibility score below 0.96, over 20% missing data, or redundant loci were excluded. Individuals with 80% missing loci were also removed, and a minor allele frequency threshold of 0.05 was applied. The cleaned dataset comprised 8884 SNPs across 98 individuals from 15 populations for *C. sublimis* (6.48% missing data), 8009 SNPs across 96 individuals from 15 populations for *D. darlingiana* (8.15% missing data), and 4935 SNPs across 89 individuals from 16 populations for *E. grandis* (6.65% missing data).

## 2.10 | Population Genetic Diversity and Structure

We assessed population genetic diversity by estimating allelic richness, expected heterozygosity ( $H_e$ ), observed heterozygosity ( $H_o$ ) and the inbreeding coefficient ( $F_{\text{IS}}$ ) using 'diveRsity' v1.9.90 (Keenan et al. 2013), with 1000 bootstrap replicates for confidence intervals. Genetic similarity was evaluated through Principal Component Analysis (PCA) using 'ade4' v2.1.8 (Jombart 2008). Overall  $F_{\text{ST}}$ , a measure of genetic differentiation based on allele frequency variation at neutral loci, was estimated for each species using analysis of molecular variance on all SNPs with the 'poppr' package and converted into a  $\chi^2$  distribution. Ancestry coefficients were estimated via discriminant analysis of principal components (DAPC) and sparse non-negative matrix factorization (sNMF). For both methods, we tested 1 to 16 genetic clusters ( $K$ ). DAPC was performed with  $K$ -means clustering on PCA-transformed genotypes, selecting the optimal  $K$  via the Bayesian information criterion and retaining 10 principal component axes using cross-validation. For sNMF, 'LEA' v.3.8.0 (Frichot and François 2015) was used, selecting the optimal  $K$  based on the stabilization of cross-entropy values and choosing the best replicate with the lowest cross-entropy.

## 2.11 | Signals of Selection

To detect potentially adaptive loci, we used  $F_{\text{ST}}$  outlier analysis, GEA, and GPA. Association analyses were performed using latent factor mixed modeling (LFMM) and partial redundancy analysis (pRDA). This approach combined univariate and multivariate methods to detect both single-locus and multilocus signatures of selection with high power and low false-positive rates (Forester et al. 2018). For GPA, we tested two trait sets: (1)  $\Delta T_{\text{trait}}$  as an integrative trait, and (2) a suite of leaf traits (LMA, thickness, width, Absorptance,  $N_{\text{mass}}$ , and  $g_1$ ) selected for their relevance to leaf energy balance, low intercorrelation ( $r < 0.7$ ), and evidence of population differentiation. For *C. sublimis*,  $g_1$  was included despite population effects being only marginally significant ( $p = 0.0731$ ).

To ensure complete SNP datasets, missing values were imputed with the most common allele across individuals. Given multiple potential  $K$  values identified in prior population structure analyses, we conducted analyses for  $K = 1$ –3, treating all significant SNPs as putatively adaptive.  $F_{\text{ST}}$  outlier analysis was done using 'pcadapt' v.4.3.3 (Luu et al. 2017) using default parameters, with SNPs considered putatively adaptive if the  $q$ -value was  $< 0.05$ . LFMM was run for both GPA and GEA analyses with a lasso penalty using 'lfmm' v.1.1 (Caye et al. 2019) testing multiple latent factors.  $Z$  scores were calibrated for genomic inflation before being converted into  $p$ -values. Candidate SNPs were identified using a false discovery threshold of  $q < 0.1$ . The pRDA analyses in both GPA and GEA were conducted using 'vegan' v.2.6–4 (Oksanen et al. 2022), with two principal components for genetic structure (see previous section) as conditional variables. For GPA, elevation was also included as a conditional variable to account for non-genetic variation in leaf traits. SNPs associated with phenotypes (GPA), or environments (GEA) were identified by extreme loadings, defined as 3 standard deviations along pRDA axes.

## 2.12 | Generalized Dissimilarity Modelling

We employed generalized dissimilarity modeling (GDM) to further investigate nonlinear GEA and GPA and identify potential environmental drivers of variation. In contrast to LFMM and pRDA, this approach assesses multivariate, nonlinear patterns of genomic or trait turnover along environmental gradients, while accounting for isolation by distance (Ferrier et al. 2007; Mokany et al. 2022). GDM is useful for evaluating the relative importance of environmental predictors (via the sum of I-spline coefficients) and for identifying where the steepest gradients of change occur (by observing the change in slope).

For the genomic data, we ran GDMs on three SNP datasets. First, we used the putatively adaptive SNPs identified through trait associations (GPA analysis by both LFMM and pRDA). The second dataset included SNPs identified as genomic outliers ( $F_{ST}$  outlier analysis) and through association with the environment (GEA analysis). We explored both GEA and GPA datasets because GPA was not measured in a common garden; thus, GEA helps determine if the environmental variables linked to trait variation also drive adaptive variation. Although the environmental drivers of genomic variation are already inherently assessed within the GEA analyses, we performed GDM on this SNP set to allow direct comparison of driver relative importance across the different genomic GDMs. The third dataset investigated whole genome variation across environmental space, using the original cleaned SNP set that includes both adaptive and neutral SNPs. For all three analyses, we used a population-level pairwise  $F_{ST}$  distance matrix generated with 'SNPRelate' v.1.30.1 (Zheng et al. 2012) using the relative beta estimator in Weir and Hill (2002).

Additionally, we conducted two trait GDMs to assess the extent to which temperature or other environmental factors explained variation in  $\Delta T_{\text{trait}}$  and leaf trait variation. We calculated population-level means for  $\Delta T_{\text{trait}}$  and other leaf traits (the uncorrelated suite described above). For the leaf trait GDM, we reduced variables to two principal component axes using the *princomp* function. Euclidean distance matrices were computed for each dataset using the *dist* function.

All five GDMs were fit using 'gdm' v.1.5.9–9.1 (Ferrier et al. 2007; Mokany et al. 2022). Predictor significance was tested with matrix permutation ( $n = 50$  permutations) using the *gdm.varImp* function, with predictor significance defined by increases in explained deviance. Variables with the highest sum of I-Spline Coefficients were considered most important. We estimated model sensitivity with bootstrapping ( $n = 1000$  iterations), retaining 90% of populations (Shryock et al. 2015).

## 2.13 | Glasshouse Experiment

Our goal in the glasshouse experiment was to assess how the climate of origin and growth environment influences intraspecific variation in leaf thermoregulation. Specifically, we tested whether plants from warmer climates, or grown under warmer conditions, exhibited lower predicted  $\Delta T_{\text{trait}}$  than those from cooler climates or grown under cooler conditions. To do this, we grew *E. grandis* seedlings collected from multiple mother trees

across a temperature gradient under controlled cool-humid, warm-humid, and warm-dry chamber treatments.

The glasshouse experiment included 59 naturally germinated *E. grandis* seedlings collected from the base of 11 likely mother trees across six sites, and grown in pots at James Cook University's Environmental Research Complex in Cairns (Figures 1, 2, and S1). The number of mother trees per site ranged from one to three. Seedlings originated from sites spanning a mean annual temperature range of 18.8°C to 24.9°C.

To test the effects of climate of origin and growth environment on leaf traits, we allocated seedlings to one of three climate-controlled chambers: a cool-humid chamber (26°C, 1 kPa VPD), a warm-humid chamber (32°C, 1 kPa VPD), and a warm-dry chamber (32°C, 2 kPa VPD). These treatments simulated typical summer conditions in the uplands (cool-humid) and lowlands (warm-dry), with the warm-humid chamber used to isolate the effects of VPD from temperature (Table S1).

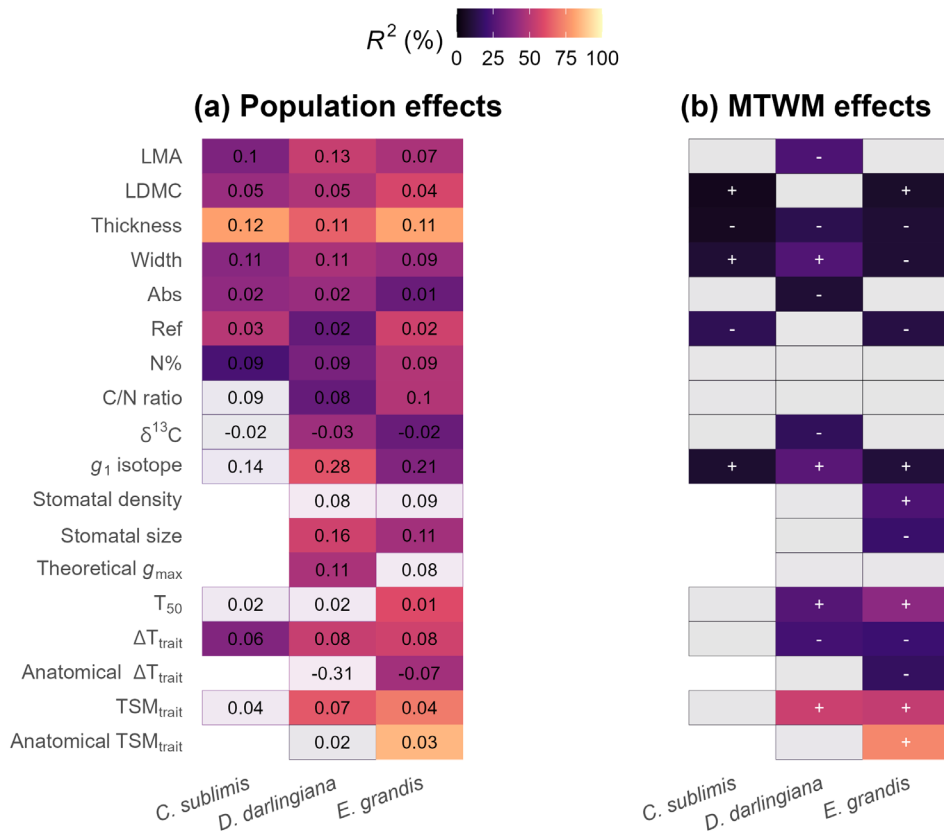
In August 2022, one to two seedlings per mother tree were randomly assigned across the chambers. Two seedlings in the cool-humid treatment died, leaving 57 surviving seedlings while maintaining representation across all mother trees. After 2 months, leaf-level gas exchange and functional traits were measured on new, fully expanded sun leaves. These trait data were used to calculate  $\Delta T_{\text{trait}}$  following the same approach as for field measured traits. Detailed measurement protocols are described in Supporting Information, Methods S2.

## 2.14 | Analysis

Our goal was to assess if coordinated variation in leaf traits across tropical tree distributions reflects adaptation to temperature through increased heat avoidance or tolerance at warmer sites.

We first quantified overall intraspecific variation, population differentiation, and the association of trait variation with thermal gradients. Traits included leaf functional traits (e.g., LMA, LDMC, leaf thickness, and  $\delta^{13}\text{C}$ ) or thermal parameters (e.g.,  $T_{50}$ ,  $\Delta T_{\text{trait}}$ , and TSM). Intraspecific variation was assessed using the quartile coefficient of variation to account for issues with standard CV (Botta-Dukát 2023). Population differentiation in leaf traits was measured using  $P_{ST}$ , the phenotypic analogue of  $F_{ST}$ , which quantifies the proportion of total trait variance attributable to differences among populations. If the 95% confidence intervals for  $P_{ST}$  exceed  $F_{ST}$ , this can indicate trait divergence beyond neutral expectations. We also used  $R^2$  from a linear model with population identity as the predictor to estimate trait differentiation, analogous to  $P_{ST}$  but without assuming trait heritability. Finally, linear regression was used to test for associations between leaf traits and the max temperature of the warmest month (MTWM).

To examine if trait variation across sites was an adaptation to thermal gradients across species distributions, we identified signals of selection using association analysis and compared the relative importance of environmental predictors in genomic versus trait generalized dissimilarity modeling. To complement



**FIGURE 2** | Comparison of regression results for the effect of population or max temperature of the warmest month (MTWM) on trait variation for each species. Tiles are colored by  $R^2$ , with transparent tiles indicating non-significant ( $p > 0.05$ ) results. Values within tiles for panel a) show the quartile coefficient of variation, and symbols in panel b) show the sign of the slope estimate for the linear regression. For more information on model results, see Tables S2 and S3.

association analyses and explicitly test the contribution of genotype and environment to intraspecific variation in leaf traits and  $\Delta T_{\text{trait}}$  for *E. grandis* saplings grown in the glasshouse, we used mixed effects models to test the influence of mean annual temperature of origin (continuous) and treatment (cool-humid, warm-humid, warm-dry) on leaf traits and  $\Delta T_{\text{trait}}$ , including ‘mother tree’ as a random effect nested within ‘site’. We then removed non-significant variables and presented estimated marginal means for the final models.

### 3 | Results

#### 3.1 | Extent of Intraspecific Leaf Trait Variation in Natural Populations

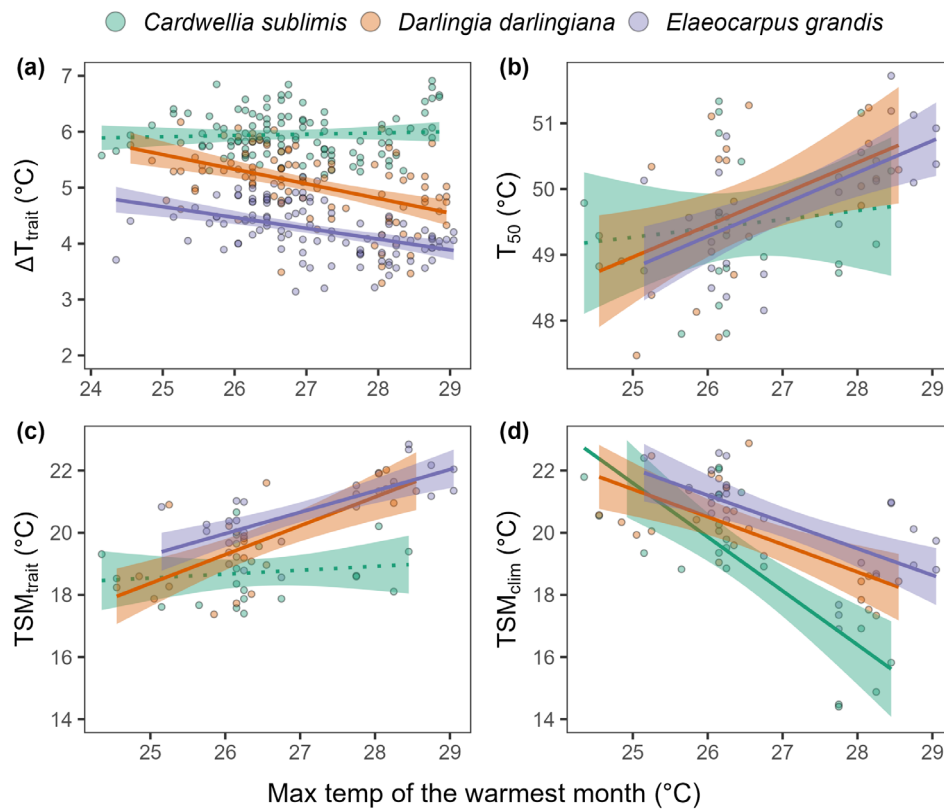
In most cases, intraspecific trait variation (defined as the quartile coefficient of variation, CV) for each trait was similar across the three species (Figure 2a). Traits with the lowest quartile CV ( $< 0.05$ ) included LDMC, Absorptance, Reflectance,  $\delta^{13}\text{C}$ , and  $T_{50}$ . The trait  $g_1$ , which is calculated from  $\delta^{13}\text{C}$  (but accounts for some influence of the environment), had the highest variation and showed the greatest differences in CV across species, with CV = 0.14, 0.28, and 0.21 in *C. sublimis*, *D. darlingiana*, and *E. grandis*, respectively. For most traits, population effects on trait variation were significant ( $p < 0.05$ ), except for leaf C/N ratio,  $\delta^{13}\text{C}$ ,  $g_1$ , and  $T_{50}$  in *C. sublimis*; stomatal density and  $T_{50}$  in *D. darlingiana*; and stomatal density and theoretical  $g_{\text{max}}$  in

*E. grandis* (Figure 2a, Table S2). Where significant population effects on trait variation were observed, population explained between 23% and 85% of trait variation across all species and traits, with the strongest effects observed for leaf thickness (Figure 2a, Table S2). Population differentiation for most traits was stronger than expected because of genetic drift ( $P_{\text{ST}} > F_{\text{ST}}$ ), except for leaf elemental concentrations or  $T_{50}$  in *C. sublimis* (Figure S2).

#### 3.2 | Relationship Between Leaf Traits and Maximum Temperature of the Warmest Month

We observed differences in the relationship between traits and max temperature of the warmest month (MTWM) across the three target species, although the explained variance was relatively low for many of these traits (Figures 2b and S3, Table S3). Across all species,  $g_1$  increased with MTWM, suggesting a decline in intrinsic water use efficiency potentially driven by higher stomatal conductance at warmer growth temperatures. Leaf thickness also consistently decreased with increasing MTWM across all species, indicating the development of thinner leaves in warmer climates. In *C. sublimis*, LDMC and leaf width increased with MTWM, and reflectance decreased (Figures 2b and S3, Table S3). For *D. darlingiana*, as MTWM increased, LMA, Absorptance, and  $\delta^{13}\text{C}$  all decreased, whereas leaf width increased (Figures 2b and S3, Table S3). In *E. grandis*, as MTWM increased, width, reflectance, and stomatal size decreased, whereas LDMC and stomatal





**FIGURE 3** | Variation in daytime mean leaf-to-air temperature differences ( $\Delta T_{\text{trait}}$ , a), thermal tolerance metrics ( $T_{50}$ , b), and thermal safety margins (TSM; c, d) with max temperature of the warmest month across the distribution of three tropical tree species. Note in a and c  $\Delta T$  is only based on leaf trait variation, with the same microclimate inputs for all trees, whereas in d, both traits and microclimate inputs vary with each individual tree ( $\text{TSM}_{\text{clim}}$ ). Microclimate inputs are derived from NicheMapR and not from max temp of the warmest month. Each point represents an individual-tree level average. Significant correlations with max temperature of the warmest month are denoted by solid regression lines, whereas non-significant correlations are dotted. The shaded region represents standard errors.

density increased (Figures 2b and S3, Table S3). For *D. darlingiana* and *E. grandis*, the covariation between stomatal density and size resulted in no significant change in theoretical  $g_{\text{max}}$  with MTWM (Figures 2b and S3, Table S3).

### 3.3 | Implications of Intraspecific Trait Variation on Leaf Thermoregulation

The consequences of intraspecific trait trade-offs for leaf thermoregulation were investigated through the prediction of trait-based leaf-to-air temperature differences ( $\Delta T_{\text{trait}}$ ) and how these vary with MTWM. Note that  $\Delta T_{\text{trait}}$  is calculated using a single set of microclimate parameters and thus represents the influence of traits only. Mean  $\Delta T_{\text{trait}}$  was 6.0°C, 5.1°C, and 4.2°C in *C. sublimis*, *D. darlingiana*, and *E. grandis*, respectively (Table S2). Intraspecific variation in  $\Delta T_{\text{trait}}$  was similar across the three species, with quartile CV = 0.06 to 0.08 (Figure 2a). Population was a significant predictor of  $\Delta T_{\text{trait}}$  for all species, although the proportion explained was slightly higher for *D. darlingiana* and *E. grandis* than for *C. sublimis* (Figure 2a and Table S2). We found evidence of leaf thermoregulation for two of the three species, with  $\Delta T_{\text{trait}}$  decreasing with increasing MTWM for *D. darlingiana* ( $R^2 = 0.22$ ,  $p < 0.001$ ) and *E. grandis* ( $R^2 = 0.2$ ,  $p < 0.001$ ) but not for *C. sublimis* (Figures 2b and 3, Table S3). This represented a 0.26°C (95% CI: 0.16–0.36) and a 0.19°C (95% CI: 0.12–0.27) decrease in  $\Delta T_{\text{trait}}$  per 1°C increase in MTWM for *D. darlingiana*

and *E. grandis*, respectively (Table S3). In other words, in these two species, leaf traits varied with climate in such a way that modeled leaf temperatures were closer to air temperatures under common conditions, and populations from warmer sites were predicted to experience less leaf heating relative to air temperature than those from cooler sites.

Unsurprisingly, using theoretical  $g_{\text{max}}$  from stomatal anatomy to calculate trait-based leaf-to-air temperature differences (anatomical  $\Delta T_{\text{trait}}$ ) led to substantially lower values of  $\Delta T_{\text{trait}}$  (Figure S4). Mean anatomical  $\Delta T_{\text{trait}}$  was equal to  $-0.6^\circ\text{C}$  for *D. darlingiana* and  $-1.8^\circ\text{C}$  for *E. grandis* (with negative values indicating  $T_{\text{leaf}}$  cooler than  $T_{\text{air}}$ ). Levels of intraspecific variation for anatomical  $\Delta T_{\text{trait}}$  in *D. darlingiana* and *E. grandis* were different, with a quartile CV =  $-0.31$  for *D. darlingiana* and  $-0.07$  for *E. grandis* (Figure 2a). Population was only a significant predictor of anatomical  $\Delta T_{\text{trait}}$  for *E. grandis*, with  $R^2 = 0.45$ ,  $p = 0.014$  (Figure 2a and Table S2). This time we found evidence of thermoregulation only for *E. grandis* ( $R^2 = 0.17$ ,  $p = 0.00495$ ) where anatomical  $\Delta T_{\text{trait}}$  decreased 0.09°C (95% CI: 0.03–0.15) per 1°C increase in MTWM (Figures 2b and S4, Table S3).

### 3.4 | Intraspecific Variation in Thermal Tolerance

Thermal tolerance metrics were similar for all three species, with species-mean  $T_{50}$  ranging from 49.5°C to 49.8°C (Table S2).

Intraspecific variation was low relative to other traits, and population differences were only significant in *E. grandis* (Figure 2a and Table S2). We observed significant positive relationships between  $T_{50}$  and MTWM for both *D. darlingiana* and *E. grandis*, but not *C. sublimis* (Figures 2b and 3, Table S3).  $T_{50}$  increased by 0.48°C per 1°C rise in MTWM for both *D. darlingiana* ( $R^2 = 0.26$ ,  $p = 0.044$ ) and *E. grandis* ( $R^2 = 0.40$ ,  $p < 0.001$ , Figure 3).

### 3.5 | Isolating Trait-Mediated Effects on Thermal Safety Margins

The combined variation in  $T_{50}$  and  $\Delta T_{\text{trait}}$  was assessed through calculation of trait-based thermal safety margins ( $\text{TSM}_{\text{trait}} = T_{50} - T_{\text{leaf}}^{\circ\text{C}}$ ), using common microclimate inputs across all individuals. Because environmental conditions are held constant, all variation in  $\text{TSM}_{\text{trait}}$  reflects the effects of either  $T_{50}$  or trait-mediated cooling. We observed a significant increase in  $\text{TSM}_{\text{trait}}$  with MTWM for *D. darlingiana* and *E. grandis*, with  $\text{TSM}_{\text{trait}}$  increasing by 0.93°C per 1°C increase in MTWM for *D. darlingiana* (95% CI: 0.53–1.32), and by 0.69°C for *E. grandis* (95% CI: 0.42–0.95). No significant relationship was found for *C. sublimis* (Figures 2b and 3, Table S3). This pattern reflects coordinated variation in both thermal tolerance and trait-mediated leaf cooling, with thermal tolerance contributing approximately twice as much to the increase in thermal safety margins across the temperature gradient. When calculating trait-based thermal safety margins using stomatal anatomical traits (anatomical  $\text{TSM}_{\text{trait}}$ ), we only observed a relationship with MTWM in *E. grandis* ( $R^2 = 0.74$ ,  $p < 0.0001$ ), representing an increase in  $\text{TSM}_{\text{trait}}$  of 0.83°C (95% CI: 0.55–1.11) per 1°C increase in MTWM (Figures 2b and S4, Table S3).

### 3.6 | Variation in Operational Thermal Safety Margins

To demonstrate the effect of this intraspecific variation on operational TSMs, we plot TSM calculated with individual tree-level variation in both traits and modeled microclimate (daytime mean radiation, humidity, wind speed, and air temperature) (Figure 3).  $T_{\text{leaf}}$  is still higher in warmer climates, but for *E. grandis* and *D. darlingiana*, this is to a lesser extent than would have been if they exhibited no trait variation across the thermal gradient. As a result,  $\text{TSM}_{\text{clim}}$  declined significantly more slowly with MTWM in *D. darlingiana* and *E. grandis* (slopes =  $-0.89$  and  $-0.86$ , respectively) than in *C. sublimis* (slope =  $-1.74$ ), indicating a stronger buffering capacity in species that exhibit trait-based thermoregulation and adjustments in heat tolerance.

### 3.7 | Genetic Diversity and Population Structure

Genetic diversity was relatively low in our study species. Expected heterozygosity across all populations was 0.19 ( $\pm 0.012$  SD) in *C. sublimis*, 0.19 ( $\pm 0.011$  SD) in *D. darlingiana*, and 0.23 ( $\pm 0.013$  SD) in *E. grandis* (Table S4). Observed heterozygosity was less than expected heterozygosity for all populations of all species and was 0.15 ( $\pm 0.014$  SD) in *C. sublimis*, 0.12 ( $\pm 0.010$  SD)

in *D. darlingiana*, and 0.18 ( $\pm 0.016$  SD) in *E. grandis* (Table S4). All three species showed strong isolation by distance, with mantel tests showing  $R^2$  of 0.86 ( $p = 0.001$ ) in *C. sublimis* (Figure S5),  $R^2$  of 0.77 ( $p = 0.001$ ) in *D. darlingiana* (Figure S6), and  $R^2$  of 0.51 ( $p = 0.011$ ) in *E. grandis* (Figure S7). Ancestry analysis indicated the presence of 1, 2, or 3 genetic clusters across the sampled range, supported by PCA analysis. The main break for all species corresponds to the Black Mountain Corridor, a biogeographic barrier for multiple taxa coinciding with a break in the Great Dividing Range (Figures S4–S6) (Schneider et al. 1998).

### 3.8 | Genomic Signals of Adaptation

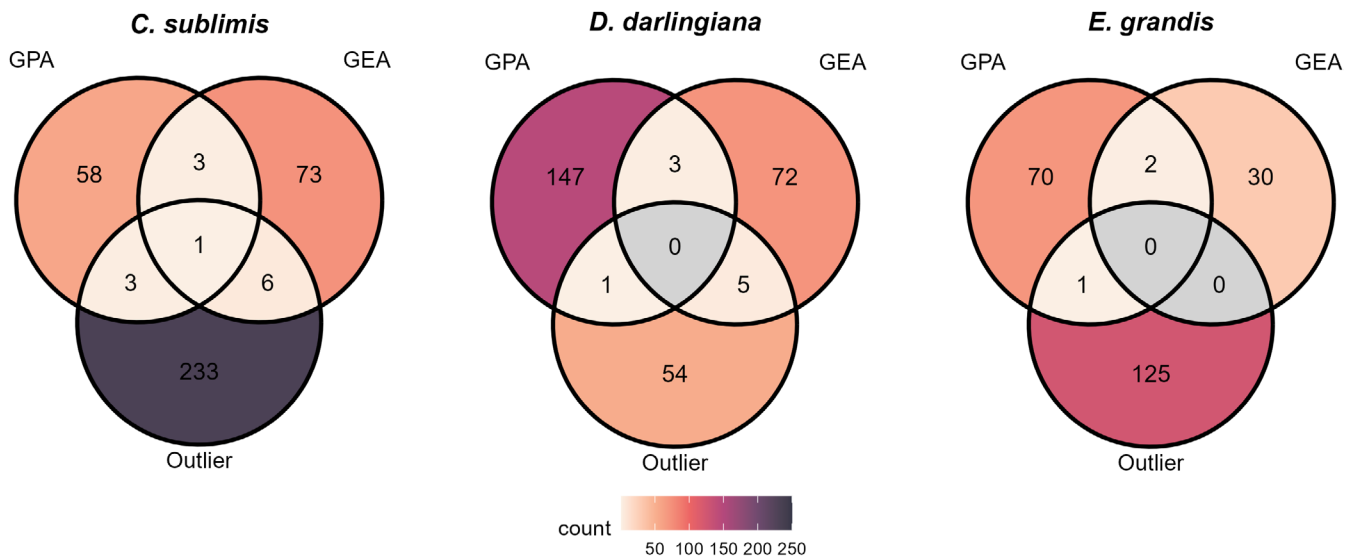
We identified genomic signals of adaptation in all three species using multiple complementary methods (Figure 4). These included  $F_{\text{ST}}$  outlier detection, GPA, and GEA, applied using both univariate (LFMM) and multivariate (pRDA) approaches.

LFMM identified relatively few candidate SNP overall (Table S5), reflecting its conservative detection of strong single-locus signals. *D. darlingiana* exhibited the clearest LFMM signal, particularly with  $N_{\text{mass}}$  (25 SNPs) and  $g_1$  (11 SNPs)—traits tied to photosynthesis and stomatal behavior. In contrast, few or no SNPs were detected in *E. grandis* and *C. sublimis* for  $\Delta T_{\text{trait}}$  or leaf traits. *D. darlingiana* also showed broader environmental associations, particularly with  $\text{RH}_{\text{min}}$ , MTWM, and soil phosphorus.

Multivariate pRDA identified more candidate SNPs than LFMM across all species (Table S6), highlighting its greater sensitivity to polygenic patterns and small-effect loci that may be missed by univariate approaches. Trait-based pRDAs yielded 28 to 69 SNPs per species, and environment-based pRDAs identified between 31 and 74 SNPs. In trait-based pRDA, RDA loadings were most strongly influenced by thickness and LMA (*C. sublimis*), absorbance and  $g_1$  (*D. darlingiana*), and thickness and  $N_{\text{mass}}$  (*E. grandis*) (Figure S8). In environmental pRDAs, Bio14,  $\text{RH}_{\text{min}}$ , and MTWM consistently explained the most variation (Figure S8), aligning with LFMM results. The explanatory power of these pRDAs was low (Adjusted  $R^2$  values all  $< 0.01$ ) but within the expected range for genome scans, where most genetic variation is neutral. Explanatory power was higher for the environment pRDAs (0.0063–0.0177) than for trait pRDAs (0.0019–0.0031), suggesting that some key traits under selection may not have been captured.

PCAdapt identified the largest number of candidate SNPs, especially in *C. sublimis* (243 SNPs), which also exhibited the strongest isolation by distance. Although this may indicate adaptation, it could also reflect underlying neutral structure, as PCAdapt is sensitive to demographic effects.

Despite the large number of SNPs identified, overlap across all three methods within each species was limited (Figure 4), with only one SNP in *C. sublimis* shared across GPA, GEA, and outlier analyses. However, all species showed overlap between at least two methods, including between GPA and GEA, providing stronger evidence that phenotypic variation is shaped by environmental selection. This partial concordance reflects the different selection signals captured by each method and suggests a



**FIGURE 4** | Overlap of candidate SNPs identified using  $F_{ST}$  outlier analysis, and genotype phenotype (GPA) and genotype environment (GEA) association analyses for three tropical tree species. Numbers indicate the total number of overlapping SNPs across analyses. Candidate SNPs identified from GPA and GEA include all SNPs identified using either latent factor mixed modeling (LFMM) or partial redundancy analysis (pRDA). For GPA analyses, candidate SNPs were identified using two different sets of response variables: modeled leaf-to-air temperature differences ( $\Delta T_{\text{trait}}$ ), and the principal component axes derived from a suite of leaf traits (Trait PCA). Intersections are colored by the total number of SNPs, with gray panels indicating no shared SNPs detected.

polygenic basis of adaptation involving many small-effect loci. Together, these findings highlight the value of combining multiple approaches to detect complementary signals of selection in natural populations.

### 3.9 | Genotypic and Trait Turnover Across Environmental Gradients

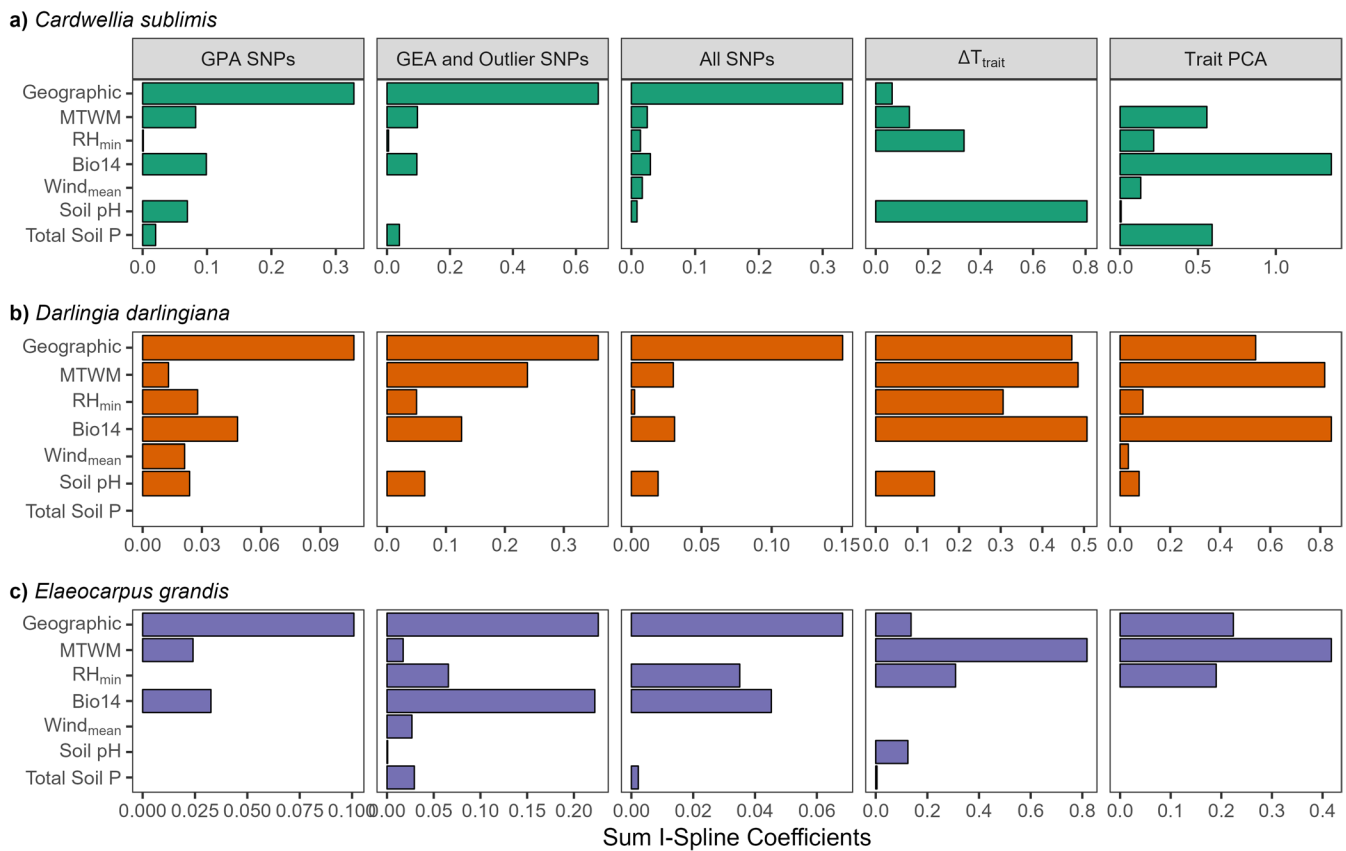
We used generalized dissimilarity modeling to investigate the relative importance of environmental predictors in explaining deviance in the spatial patterns of genetic turnover based on (1) GPA SNPs, (2) GEA and outlier SNPs, and (3) all SNPs, as well as phenotypic turnover in (4)  $\Delta T_{\text{trait}}$ , and (5) leaf functional traits-PCA values. Genetic turnover refers to differences in allele frequencies among populations, whereas phenotypic turnover refers to differences in population-mean trait values across the landscape. Across all three species, the generalized dissimilarity models based on SNP datasets had generally high explained deviance (28.8% to 76.8%) and low intercepts (0 to 0.07), indicating the included predictors had good explanatory power. The generalized dissimilarity models based on  $\Delta T_{\text{trait}}$  or the leaf trait PCA values explained less variance in the response variables (explained deviance 7.2 to 36.3%, intercepts 0.04 to 0.35) (Table S7).

For SNP-based GDMs, geographic distance, maximum temperature of the warmest month, and precipitation of the driest month (Bio14) consistently emerged among the strongest predictors of allele frequency turnover across all three species GDMs, though their relative importance differs (Figure 5 and Table S7). For the two Proteaceae species, *C. sublimis* and *D. darlingiana*, soil pH was also influential, whereas minimum relative humidity ( $RH_{\text{min}}$ ) was influential for *E. grandis*.

Trait-based GDM analyses differed somewhat from SNP-based GDMs, with geographic distance no longer a consistent key predictor of trait variation (Figure 5 and Table S7). Instead, environmental factors were primary drivers, although their relative importance varied among species. Notably, environmental predictors identified by trait-based GDMs strongly overlapped with those identified by SNP-based GDMs for *C. sublimis* and *D. darlingiana* but differed slightly for *E. grandis*. Specifically, for *C. sublimis*, both maximum temperature of the warmest month and moisture-related ( $RH_{\text{min}}$ , or Bio14) and soil-related (soil pH or soil phosphorus) variables were important predictors. In *D. darlingiana*, the maximum temperature of the warmest month and Bio14 were again the dominant predictors of population variation in  $\Delta T_{\text{trait}}$  and trait PCA values. By contrast, in *E. grandis*, the maximum temperature of the warmest month, followed by minimum relative humidity, overwhelmingly explained variation in both  $\Delta T_{\text{trait}}$  and trait PCA analyses, with Bio14, important in SNP-based analyses, playing minimal to no role.

### 3.10 | Effects of Climate of Origin and Growth Environment on Leaf Traits in *E. grandis*

In the climate-controlled glasshouse experiment, *E. grandis* showed trait variation resulting from both plastic responses to treatment conditions and adaptation to mean annual temperature of origin, but not their interaction (Figure 6 and Table S8). Leaf width had a negative correlation with MAT of origin and had significant effects of treatment, exhibiting narrower leaves when grown under warmer conditions. We observed a significant positive correlation between  $g_1$  and MAT of origin, but no effect of treatment. Variation in  $N_{\text{mass}}$  (a proxy for  $V_{\text{cmax25}}$ ) was not associated with MAT of origin, but was influenced by treatment, with plants grown under cool-humid conditions having



**FIGURE 5** | Relative importance of predictors in generalized dissimilarity models (GDM) for three tropical tree species. Relative importance is calculated as the sum of I-Spline coefficients for that predictor in the model. Panels present results for a) *Cardwellia sublimis*, b) *Darlingia darlingiana*, and c) *Elaeocarpus grandis*. For each species, there are five separate analyses presented, with the response variable a population-level pairwise  $F_{ST}$  matrix on SNPs identified by GPA analyses (GPA SNPs), the SNPs identified from GEA or  $F_{ST}$  outlier analyses (GEA and Outlier SNPs), or the entire suite of neutral and non-neutral SNPs (All SNPs). For the last two columns, the response variable was a Euclidean distance matrix based on either population-mean  $\Delta T_{\text{trait}}$  or principal component axes on a suite of leaf traits (Trait PCA). Model performance metrics can be found in Table S7. For the predictor variables, Geographic = geographic distance, MTWM = max temperature of the warmest month,  $RH_{\text{min}}$  = minimum relative humidity, Bio14 = precipitation of the driest month,  $Wind_{\text{mean}}$  = mean wind speed.

a higher  $N_{\text{mass}}$  than plants grown under both warm-humid and warm-dry conditions.

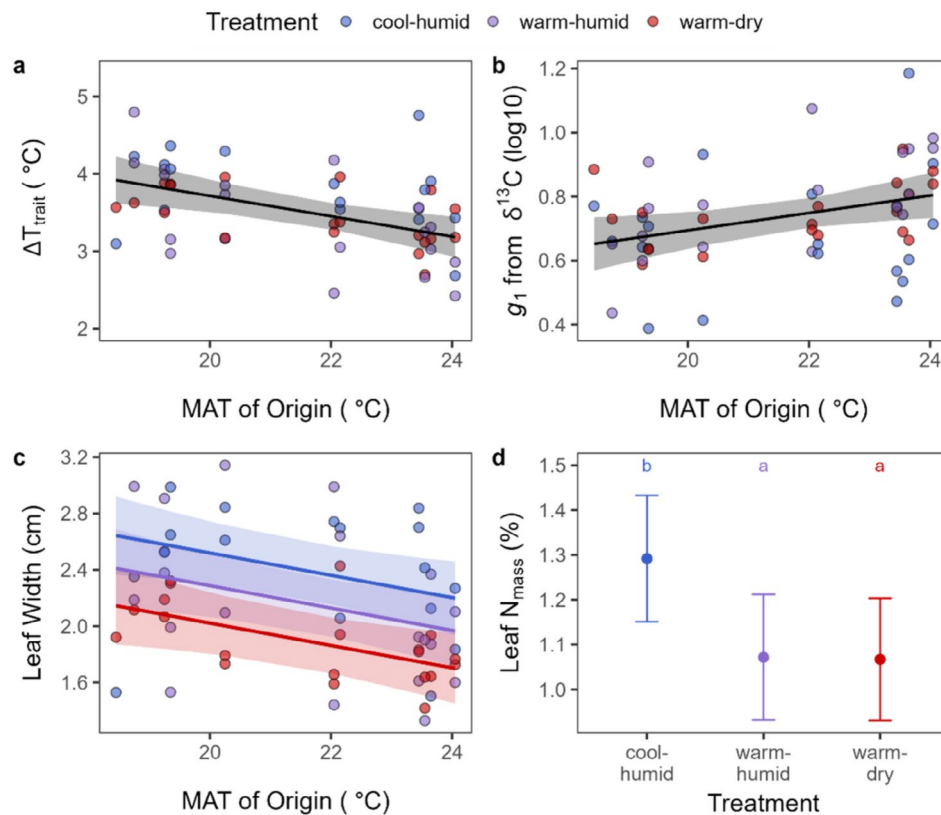
When these traits were input into a leaf energy balance model parameterised with standard microclimate to determine  $\Delta T_{\text{trait}}$ , we found evidence of adaptation to MAT of origin but no apparent effect of treatment (Figure 6 and Table S8). Seedlings from warm-origin provenances exhibited lower  $\Delta T_{\text{trait}}$  than seedlings from cool-origin provenances, meaning that their traits acted to reduce leaf temperatures more effectively under common conditions. This supports the idea that intraspecific variation in leaf traits can offset the effect of higher air temperatures in warmer climates, contributing to enhanced evaporative cooling. These patterns were driven by intraspecific variation in both leaf width and  $g_1$ . The decline in  $\Delta T_{\text{trait}}$  with increasing MAT of origin is likely due to the combined effects of narrower leaves and higher  $g_1$  (indicating lower water use efficiency), both of which reduce  $T_{\text{leaf}}$  under common conditions and thus decrease  $\Delta T_{\text{trait}}$ . The lack of a clear treatment effect on  $\Delta T_{\text{trait}}$  likely arises from opposing responses of individual traits to treatments. Specifically, wider leaves observed in the cool treatment increase the boundary layer resistance, which decreases leaf total conductance compared to narrower leaves in the warm treatment. However,

cool treatment leaves also show increased  $N_{\text{mass}}$ , which the stomatal model translates into higher stomatal conductance (for leaves with common  $g_1$ ). These trait responses effectively cancel each other out, so whereas trait acclimation did affect  $\Delta T_{\text{trait}}$ , the outcome was a maintenance of  $\Delta T_{\text{trait}}$  across treatments.

#### 4 | Discussion

Globally increasing temperatures threaten to push tropical rainforest plants beyond their physiological limits. However, populations adapted to contrasting climates may exhibit phenotypic divergence because of local adaptation in trait means, phenotypic plasticity, or both, that affect their capacity to cope with warming. Intraspecific variation of leaf traits across species distributions can enhance leaf cooling, thereby avoiding lethal temperatures in warmer regions. Yet, evidence of this thermoregulatory ability and the roles of acclimation or adaptation remain limited despite it being key information to assess population resilience. Here we show how leaf energy balance modeling combined with landscape genomics can assess patterns and drivers of variation in thermoregulatory traits in mature tropical rainforest trees. We found





**FIGURE 6** | Results from the glasshouse experiment showing significant effects ( $p < 0.05$ ) of both treatment conditions and mean annual temperature of origin for mother trees in *E. grandis*. Panels show (a) response of predicted leaf-to-air temperature differences based on leaf traits ( $\Delta T_{\text{trait}}$ ), (b)  $g_1$  calculated from leaf  $\delta^{13}\text{C}$  plotted as log10 transformed values, note that  $g_1$  is inversely proportional to intrinsic water use efficiency, (c) effective leaf width, and (d) leaf  $N_{\text{mass}}$  (a proxy for  $V_{\text{cmax}25}$ ). Points represent observed plant-level averages, and lines and shaded regions show the estimated marginal means and 95% confidence intervals. Letters in panel (d) show significant differences.

intraspecific variation of field-measured leaf traits associated with enhanced leaf cooling and partial maintenance of modeled thermal safety margins in warmer sites for two of the three species, providing partial support for our first hypothesis. Signals of selection were detected in all species; however, contrary to our second hypothesis, adaptive genomic variation associated with predicted  $\Delta T_{\text{trait}}$  was best explained by geographic distance and moisture-related variables rather than temperature alone. Finally, our glasshouse trial of *E. grandis* seedlings supported our third hypothesis: clines in  $\Delta T_{\text{trait}}$  with MAT of origin were a result of both phenotypic plasticity and adaptation.

#### 4.1 | Intraspecific Trait Variation Leads to Enhanced Leaf Cooling in Warmer Climates

Our expectation that leaf trait variation would enhance leaf cooling in plants from warmer sites was observed in two of the three species. This is consistent with the limited homeothermy hypothesis (Mahan and Upchurch 1988; Michaletz et al. 2015), which suggests that trait-based regulation of leaf temperatures may help maintain carbon uptake in suboptimal environments. Although evidence for this phenomenon varies across biomes and species (Blonder et al. 2020; Fauset et al. 2018; Guo et al. 2023; Helliker et al. 2018; Liancourt et al. 2020; Still et al. 2022; Zhou et al. 2023), the theory is

debated because of inconsistencies in its definition and testing (Garen et al. 2023; Still et al. 2023). By using a leaf energy balance model parameterized with observed leaf trait variations and common microclimate inputs, we isolate  $\Delta T$  variations resulting from leaf trait covariation, excluding passive changes because of radiation, humidity, wind speed, and air temperature.

We found that traits varied significantly with MTWM in *E. grandis* and *D. darlingiana*, but their responses differed: leaf width increased with MTWM for *D. darlingiana* and decreased for *E. grandis*. Wider leaves have lower boundary layer conductance, leading to higher leaf temperatures (Leigh et al. 2017; Wright et al. 2017). Despite this, both species showed similar declines in  $\Delta T_{\text{trait}}$  with increasing MAT. This suggests that variables associated with stomatal conductance ( $g_s$ ) played crucial roles in offsetting the heating effect of wider leaves in *D. darlingiana*. When comparing predicted  $\Delta T_{\text{trait}}$  using the coupled photosynthesis-stomatal conductance model with predictions based on theoretical maximum conductance, the  $\Delta T_{\text{trait}}$  trends aligned for *E. grandis* but not for *D. darlingiana*. Given the impact of  $g_s$  modeling on our results, it is crucial to develop approaches that accurately account for how  $g_s$  varies with temperature.

We examined whether variation in leaf traits and thermal tolerance helps maintain thermal safety margins across a wide thermal gradient. Thermal tolerance increased with MTWM,

whereas predicted  $\Delta T_{\text{trait}}$  decreased for two of the three species. These adjustments worked together to increase both heat tolerance and avoidance in mature trees at warmer sites. When accounting for observed microclimate, this trait variation was not sufficient to perfectly maintain thermal safety margins but did lead to a shallower decrease in thermal safety margin with MTWM than for *C. sublimis*, which showed no variation in either  $\Delta T_{\text{trait}}$  or thermal tolerance. This supports other studies showing that trait variation (both intra- and inter-specific) increases thermal safety margins in plants grown under warm environments compared to cooler environments (Kitudom et al. 2022; Kullberg et al. 2023; Perez and Feeley 2020). Notably, the species that exhibited thermoregulation were also those that showed increased thermal tolerance with MTWM, suggesting that avoidance and tolerance strategies can co-occur. In contrast, the species that showed no evidence of either trait-based cooling or increased thermal tolerance (*C. sublimis*) may be more vulnerable to climate change or rely on alternative mechanisms, such as leaf shedding, to mitigate heat stress. Failure to consider intraspecific trait variation in trait-based thermal safety margins may bias assessment of species vulnerability to climate change.

## 4.2 | Environmental Drivers of Adaptive Genomic and Phenotypic Divergence

Population differentiation for most traits was stronger than expected because of genetic drift ( $P_{\text{ST}} > F_{\text{ST}}$ ), indicating phenotypic plasticity, divergent selection, or both in natural populations. We detected evidence of selection in all three species, with both GEA and GPA analyses identifying SNPs associated with climate and leaf traits. Moisture-related variables, particularly precipitation of the driest month and relative humidity, were the most consistent selective drivers, though the maximum temperature of the warmest month also contributed. SNPs shared across GEA and GPA approaches in all species suggest that trait variation is shaped by environmental selection. This was further supported by GDM results, which revealed similar environmental predictors of genomic turnover for both traits and climate, highlighting the role of climatic selection in driving adaptive differentiation. Moisture availability and temperature are well-established drivers of mortality (Aleixo et al. 2019; Bauman, Fortunel, Delhay, et al. 2022), growth (Bauman, Fortunel, Cernusak, et al. 2022), regeneration (Comita and Engelbrecht 2017) and thereby species distributions (Gaviria et al. 2017) in tropical trees. Interestingly, the importance of edaphic variables such as soil pH was also reflected in our GDM for the two Proteaceae species. This is likely related to their formation of proteoid roots (Cheesman et al. 2018), an adaptation that enhances phosphorus availability in nutrient-poor and acidic soils (Griebenow et al. 2022; Lamont 2003).

Geographic distance emerged as a stronger driver of genomic variation than any single environmental variable across all species. This correlation highlights the need for caution in interpreting our results, as the adaptive signal may in part reflect neutral population structure. This aligns with evidence that functional genetic variation might be influenced by neutral processes rather than selection alone (Kardos et al. 2021; Mathur et al. 2023). Alternatively, it could indicate that loci under

selection, which contribute to trait clines, may be associated with other environmental variables not explored here that correlate with geographic distance, or they may not form monotonic allele frequency clines in response to environmental gradients (Lotterhos 2023). This does not negate the presence of adaptive signals but highlights the complexity of adaptation, driven by intricate genetic systems. Thus, our findings, while pointing to potential adaptive significance, also reflect the challenges in distinguishing selection and drift in natural populations. To address this, we complemented our field-based analyses with a genotype  $\times$  environment study using climate-controlled glasshouse chambers.

## 4.3 | Local Adaptation Drives Leaf Thermoregulation in *E. grandis*

The implications of local adaptation from the genomic analysis were supported by the climate-controlled experiment for *E. grandis* seedlings. We found that local adaptation to the climate of origin was likely responsible for the decline in predicted  $\Delta T_{\text{trait}}$  with temperature across the species distribution. This was despite the acclimation of some traits to temperature or VPD. Essentially, although leaf  $N_{\text{mass}}$  (a proxy for photosynthetic capacity) and leaf width showed plasticity to growth conditions, the net effect of this trait variation on predicted  $\Delta T_{\text{trait}}$  cancelled out. As a result, the variation in predicted  $\Delta T_{\text{trait}}$  was primarily driven by ecotypic variation in leaf width and water use efficiency. This does not mean that plasticity is unlikely to contribute to patterns of  $\Delta T_{\text{trait}}$  with temperature, as sensitivities to covarying environmental factors may differ across species and lead to different plastic and adaptive responses (Middleby, Cheesman, Hopkinson, et al. 2024). Interestingly, trait-based GDMs indicated that temperature had a greater relative importance for predicting phenotypic variation in  $\Delta T_{\text{trait}}$  than it did for underlying genetic variation, suggesting that acclimation may have contributed to trait differences in the field. However, in the glasshouse experiment, although individual traits showed plastic responses to temperature and humidity, there was no significant treatment effect on  $\Delta T_{\text{trait}}$  itself. This may reflect differences between the acclimation capacity of seedlings and mature trees.

Interestingly, we observed that  $g_1$  increased with MAT of origin in the glasshouse experiment for *E. grandis* and in the field measurements for all three species, indicating a decline in intrinsic water use efficiency and increased evaporative cooling in warmer-origin populations. Although temperature and VPD were positively correlated across our field sites, declining iWUE with increasing VPD would be unexpected under typical drought adaptation scenarios, where reduced stomatal conductance is generally favored to conserve water. However, in the Wet Tropics of Queensland, warmer areas tend to be wetter, as coastal lowlands receive higher annual rainfall than upland sites in the rain shadow. In this context, lower iWUE may reflect an adaptation to warm-wet conditions, where prioritizing transpirational cooling and carbon uptake is increased in the lowlands compared to the cooler but drier uplands. Our results suggest that temperature and/or soil moisture, rather than atmospheric dryness per se, may be the dominant selective force shaping ecotypic differences in stomatal behavior in *E. grandis*.

Moreover, the generalized dissimilarity modeling on outlier SNPs identified using GPA indicated that precipitation of the driest month was a more important explanatory variable than MAT. It is possible then that ecotypic variation observed in the glasshouse was driven by changes in precipitation rather than temperature. However, because precipitation of origin was positively correlated with temperature of origin in our sampled provenances, it is difficult to disentangle their individual effects.

#### 4.4 | Conclusions and Recommendations for Future Research

We found that across some of the species tested, local adaptation to climate significantly influences variation in leaf thermoregulatory traits. However, it remains unclear whether observed ecotypic variation is a response to thermal or moisture gradients, and whether leaf thermoregulation itself is under selection or if this is just a byproduct of adaptive variation to maintain carbon uptake or avoid water stress. Our findings indicate that limited homeothermy is present in some, but not all, tropical tree species, supporting growing evidence that although some species exhibit acclimation and/or adaptation in leaf thermal traits, patterns of intraspecific variation differ across species (Blonder et al. 2020; Kullberg and Feeley 2022; Middleby, Cheesman, and Cernusak 2024; Middleby, Cheesman, Hopkinson, et al. 2024; Tarvainen et al. 2022). As climate change continues to rapidly alter local temperature and moisture regimes, species that can increase their heat tolerance and/or heat avoidance may be less vulnerable to heat stress and better able to maintain carbon uptake and growth. Conversely, species lacking such strategies may face a heightened risk of decline or shifts in distribution (Fortier et al. 2024). This underscores the importance of considering intraspecific variation when assessing forest vulnerability to future climate change.

Future research should focus on expanding studies of plant thermoregulation by leveraging existing trait and genetic datasets to better understand the range of responses of tropical rainforest trees. Incorporating additional traits such as leaf angle and canopy architecture and accounting for dynamic rather than steady-state responses to fluctuating environments will also be important steps forward to more fully capture the processes influencing leaf thermal regulation strategies.

#### Author Contributions

**Kali B. Middleby:** conceptualization, formal analysis, funding acquisition, investigation, writing – original draft. **Rebecca Jordan:** methodology, validation, writing – review and editing. **Alexander W. Cheesman:** funding acquisition, investigation, writing – review and editing. **Maurizio Rossetto:** methodology, resources, writing – review and editing. **Martin F. Breed:** funding acquisition, supervision, writing – review and editing. **Darren M. Crayn:** funding acquisition, supervision, writing – review and editing. **Lucas A. Cernusak:** funding acquisition, supervision, writing – review and editing.

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#### Conflicts of Interest

The authors declare no conflicts of interest.

#### Data Availability Statement

The datasets underlying this study have been made publicly available on the Dryad data repository and can be accessed at the doi: [10.5061/dryad.wdbrv162h](https://doi.org/10.5061/dryad.wdbrv162h).

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## Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Data S1:** gcb70461-sup-0001-Supinfo.docx.