Drivers of thermal tolerance breadth of plants across contrasting biomes: do mean or
seasonality in climate indices matter more?

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Acknowledgements

We acknowledge the Traditional Custodians of Country throughout Australia, especially across

the lands on which this study took place, and recognise their continuing connection to these lands,

waters and natural communities. We pay our respects to Aboriginal and Torres Strait Islander

cultures and to Elders past, present and emerging. We thank the National Parks and Wildlife

Service for assistance and support, with special thanks to M. Hams, S. Doak and R. Bjork at

Gundabooka National Park, M. Schroder at Kosciuszko National Park, and J. Erskine, J. Lemmon

and P. Nagle at Royal National Park and Illawarra State Conservation Area. We thank the

following for assistance in the field: C. Bellotto, Z. Brown, A. Crimmins, C. Cunningham, P.

Cunningham, L. Danzey, M. Davies, L. Fuller, J.M. Hoskins, T. Salisbury, E. Rogers and K.

Spooner. This study was conducted under approval from the NSW Department of Planning,

Industry and Environment (Scientific Licence SL102330). The work was supported by an

Australian Research Council Linkage Project grant (LP180100942) in partnership with the Save

our Species program, New South Wales Government Department of Planning, Industry and

Environment.

Author Contributions

VFB, AMC, SKCJ, ABN, LABR and AL designed the study, PAA, RVG, VGB and AMC

collated and analysed the data. All authors contributed to intellectual conceptualisation, data

collection, interpretation of results, and writing. All authors meet all criteria for authorship.

Data availability statement

Data will be made available on the Dryad Digital Repository on acceptance of publication.

Conflict of interest statement

The authors have no conflicts of interest to disclose.

Abstract

1. The Climate Variability Hypothesis (CVH) predicts that species from environments with

more variable temperatures should have wide thermal tolerance breadth. We addressed this

question in plants and asked which local climate predictors (including precipitation, mean

and extreme temperatures and thermal variability) best predict species physiological

thermal limits.

2. Measures of low ($T_{crit\text{-}cold}$) and high ($T_{crit\text{-}hot}$) photosystem II thermal tolerance thresholds

were used to determine thermal tolerance breadth (TTB), along with ice nucleation

temperature ($T_{nucleation}$, freezing tolerance) of 69 plant species sampled from three

contrasting biomes: alpine, desert and wet temperate.

3. Thermal tolerance metrics $T_{crit\text{-}cold}$, $T_{nucleation}$, $T_{crit\text{-}hot}$ and TTB all differed among biomes.

Notably, desert species had the most cold and heat tolerant leaves, and therefore the widest

TTB, whereas species in alpine and temperate biomes had similar TTB. For plants in all

biomes, TTB exceeded the thermal range of their local climate.

4. Overall, two Principal Component axes of local climate drivers explained substantial

variation in all tolerance metrics. Extreme hot, dry climates improved freezing and heat

tolerance. High thermal variability and low minimum temperatures also improved freezing

tolerance, but were unrelated to heat tolerance or TTB. Species explained a significant

amount of variation among all metrics, but this was not due to phylogenetic relatedness. A

small portion of the variation in physiological thermal thresholds was explained by growth

form. Unexplained variation could be due to microclimate-driven plasticity, leaf traits or

thermoregulatory mechanisms.

5. **Synthesis**. Our results provide some support for the climate variability hypothesis in plants:

photosynthetic thermal tolerance breadth was greatest in more thermally variable biomes.

This relationship was largely driven by cold tolerance, with variation in heat tolerance

explained better by mean and extreme temperatures. Therefore, we conclude that, the CVH

alone is not sufficient to explain variation in plant thermal tolerance, with many aspects of

climate being potentially important drivers.

Introduction

Desert and alpine plant species live at the thermal limits of biological processes. Unlike those in

temperate regions, plants living in extreme environments are exposed to both very low and very

high temperatures and thus to a wide thermal range and highly variable thermal regimes, both

among days and seasons. Given the important influence of temperature in shaping species

distributions (Garcia-Pichel et al., 2013, Tattersall et al., 2012), the innate thermal tolerance

thresholds (lowest and highest temperature that a species can withstand) and thermal tolerance

breadths (range of temperature between upper and lower thermal tolerance thresholds) of species

might be expected to reflect the temperature variation characterising their environment. The

climate variability hypothesis (CVH; Janzen, 1967) predicts that species with *wide* thermal

tolerance ranges are likely to evolve in environments with *variable* temperatures compared to

thermal specialists with *narrow* tolerance ranges that evolved in thermally *stable* environments.

This hypothesis is a cornerstone of thermal ecology, but to date has been primarily explored in

animals (Addo-Bediako et al., 2000, Calosi et al., 2010, Compton et al., 2007, Baudier et al., 2018).

Cold and heat tolerance thresholds are rarely studied concomitantly. In natural systems, cold

tolerance studies predominate in alpine environments where plants can withstand very low

temperatures and tolerate extracellular ice formation and the resulting cytoplasmic dehydration

(Sakai and Larcher, 1987, Larcher, 2003). Heat tolerance studies have historically been primarily

focussed on warm and desert environments (with notable exceptions, e.g., Buchner et al., 2015).

In a range of desert species, heat tolerance has been associated with native microhabitat conditions

(Curtis et al., 2016), although such differences are sometimes less marked under common garden

conditions (Downton et al., 1984, Knight and Ackerly, 2002). Despite great progress, a recent

systematic review revealed that less than 5% of more than 3000 studies examining thermal

tolerance of plants considered both heat and cold tolerance thresholds together (Geange et al.,

2021). This focus on either cold or heat tolerance overlooks the fact that plants in extreme biomes

can experience both cold and heat stress. In addition, unlike in the animal kingdom, we lack an

understanding of plant thermal tolerance breadth (TTB) based on concomitant measurements of

heat and cold tolerance. The magnitude of TTB and the ecological drivers thereof are almost

entirely unknown for plants.

Until recently, most research has focussed on agricultural species (Geange et al., 2021), limiting

our understanding of plant thermal tolerance in a wider, ecological context. Temperature increases

with climate change have motivated an increase in studies on plant heat tolerance, particularly in

relation to climate variability and the occurrence of unseasonal extreme events (Rummukainen,

2012, Seneviratne et al., 2012). However, field sampling studies rarely encompass multiple biomes

or a broad range of thermal environments across landscapes. There remains a critical gap in our

understanding of how plants in extreme *vs* benign environments tolerate both heat and cold stress

in situ, which limits our capacity to predict where the most thermally sensitive species occur.

Differing patterns of climate among contrasting biomes provide an opportunity to explore the role

of climate variability in upper and lower thermal thresholds and on thermal tolerance breadth. Of

the few studies that have compared thermal thresholds among biomes, Smillie and Nott (1979)

found that heat tolerance was lower in alpine species, followed by temperate and tropical species.

In a rare study considering both upper and lower thermal thresholds together, Cunningham and

Read (2006) found that, in common garden conditions, temperate origin species have lower heat

and higher cold tolerance than tropical species. Meta-analytical studies across a wide range of

species and biomes suggest that heat tolerance decreases and cold tolerance increases with latitude;

however, these shifts in tolerance do not keep pace with an observed latitudinal temperature

gradient (Lancaster and Humphreys, 2020). Further, predictors of thermal tolerance variation with

latitude may include mean maximum temperature of the warmest month and mean annual

temperature (O'Sullivan et al., 2017, Lancaster and Humphreys, 2020), but threshold-based

predictors (e.g. number of days over 35˚C per year; Maher et al., 2019) are suggested to be drivers

of heat tolerance (Mora et al., 2015). Given that water availability influences plant heat tolerance

(Curtis et al., 2016, Marchin et al., 2022) and freezing tolerance (Sierra-Almeida et al., 2016),

precipitation parameters are also likely to affect thermal thresholds. Further, upper and lower

thermal thresholds can vary in relation to the methods used (Lancaster and Humphreys, 2020,

PerezFeeley et al., 2021), impairing the capacity for large-scale meta-analyses to capture such

sources of variation and limiting their power for generalisable conclusions. Finally, although we

have evidence that climate variables influence plant heat and cold thermal tolerance thresholds

independently, the climate predictors of thermal tolerance breadth, are virtually unknown. If we

can reveal general patterns underlying variation in, and the climate drivers of, physiological

thermal tolerance thresholds among co-occurring plant species within and among biomes, we can

strengthen predictions of which and where species are likely to be most vulnerable to changing

thermal conditions.

Here we sought to determine the climate drivers of leaf-level physiological thermal tolerance

thresholds and thermal tolerance breadth of plant species in extreme and benign environments in

the context of the climate variability hypothesis. We used chlorophyll fluorescence to determine

the low and high photosystem II (PSII) thermal tolerance thresholds and TTB of 22 alpine, 24

desert and 23 wet temperate rainforest species (temperate hereafter) during the growing season.

We also determined ice nucleation temperatures to examine freezing tolerance in all species. To

examine the relationships between climate variability and physiological thresholds, we extracted

long-term, locally downscaled climate parameters for each sampling locality. Aim 1 was to

determine how the thermal tolerance thresholds and TTB of a broad range of plant species differed

among the contrasting biomes. We hypothesised that thermal thresholds would be skewed towards

the extremes of the biomes; colder threshold temperatures in the alpine and hotter in the desert,

with temperate species having milder cold and heat tolerance thresholds. Aim 2 was to test whether

species from more the thermally variable alpine and desert biomes would have greater tolerance

to both heat and cold, and thus wider thermal tolerance breadth than temperate biome species, in

accordance with the CVH. Aim 3 was to assess whether variation in thermal tolerance thresholds

and TTB could be explained by local climate variables, and whether the relationships were linear

or not. We hypothesised that climate extremes and variability would have a stronger association

with thermal tolerance thresholds and TTB than mean climate values, supporting the CVH.

Materials and Methods

Study locations

Sites used in this study were designated to one of three biomes in New South Wales,

Australia: alpine (Monaro Ngarigo, Ngunnawal, Wiradjuri and Walgalu Country, Kosciuszko

National Park), desert (Ngemba and Barkindji Country, Gundabooka National Park), and

temperate (wet temperate rainforests of Dharawal, Wadi Wadi and Yuin Country in the Illawarra

Region: Royal National Park, Illawarra State Conservation Area and Bass Point Conservation

Area). Sampling sites incorporated a range of vegetation types sampled in each biome (mean

climatic details from sites are inset in Fig. 1).

Fig. 1. Locations of study sites across three biomes in NSW, Australia. Desert sites (red) in Gundabooka National Park (GNP), wet temperate rainforest sites (green) in the Illawarra Region (temperate), and alpine sites (blue) in Kosciuszko (KNP). GNP sites spanned open eucalypt woodland, mulga and chenopod shrublands between elevations of 100 to 224 m a.s.l. KNP sites encompassed feldmark, herbfields and sphagnum bog vegetation formations between 1792 and 1855 m a.s.l. In the temperate environments, collections were conducted across the Illawarra, including the tall open forest and rainforest communities between 100 to 400 m. a.s.l. MAP = mean annual precipitation, MAT = mean annual temperature, MinT = mean minimum temperature of the coldest month, MaxT = mean maximum temperature of the warmest month, T_{range} = MaxT - MinT).

Species selection

A total of 69 species (22 alpine, 24 desert and 23 temperate species) were selected to encompass a representative sample of growth forms and plant families and where possible, included

congeneric and/or con-familial species between two or more biomes (Table S1). We included

community dominants and a range of less abundant species to represent a cross section of species

occupying each biome. Species replicates were sampled across days within each sampling period

to incorporate daily variation in thermal tolerance thresholds.

Leaf sample collection

Mature, fully expanded leaves were harvested from five to seven individuals per species. For

shrubs and trees, small branches were collected from the northern facing side of the plant at a

height of 1-1.5 m. For smaller growth forms, entire individuals or rosettes were collected. Samples

were kept in cool sealed plastic bags with moistened paper towel until they were processed

(approximately 1-2 h after collection). In the field laboratory, leaves (size ranging 0.25 cm^2 to

5 cm^2) were cut (or combined) to fit an approximate area of 1 cm^2 and kept on wet florist foam in

humid dark containers until thermal tolerance assays were performed. Measurements occurred

during January 2020, March 2020 and December 2020 for the desert, temperate and alpine biomes,

respectively. Sampling periods were selected to capture peak growing season in each region.

Thermal tolerance threshold assays

The photosynthetic machinery, specifically photosystem II (PSII), embedded in the thylakoid

membrane has long been recognised as a thermally sensitive structure (Schreiber and Berry, 1977,

Berry and Bjorkman, 1980, Seemann et al., 1984). The temperature at which the PSII are disrupted

causes a rise in minimal chlorophyll *a* fluorescence (F_0) as a leaf is heated or cooled (Schreiber

and Berry, 1977, Neuner and Pramsohler, 2006). This critical temperature indicates a threshold

beyond which physiological and photochemical systems become increasingly impaired and

damage can occur if temperatures are sustained.

Lower and upper thresholds of PSII ($T_{crit-cold}$ and $T_{crit-hot}$)

The critical low and high temperature thresholds of PSII ($T_{crit-cold}$ and $T_{crit-hot}$) were measured using

T-F_0 curves, i.e., the rise in F_0 (Neuner and Pramsohler, 2006, Arnold et al., 2021) with set heating

or cooling rates. One leaf per individual (or several small leaves abutting one another) was used

for each of the heating and cooling assays with n = 5-7 replicates per species. For each assay run,

45 samples were secured with double-sided tape to paper on a Peltier plate (CP-121HT; TE-

Technology, Inc., Michigan, USA), used to cool or heat samples at a set rate using LabView-based

control software (National Instruments, Texas, USA) and adapted code from TE-Technology, Inc.

A vacuum sealed double-glazed glass was placed on top of the leaf samples on the plate to avoid

water condensation, particularly at freezing temperatures, and compress samples to ensure

maximum leaf contact with the Peltier plate (see Arnold et al., 2021 for more details).

Chlorophyll fluorescence was measured with a Pulse Amplitude Modulated (PAM) chlorophyll

fluorescence imaging system (Maxi-Imaging-PAM; Heinz Walz GmbH, Effeltrich, Germany)

mounted above the Peltier plate. Leaves were first dark-adapted, and the PSII photochemistry

maximum quantum efficiency (F_V/F_M) measured to check starting function of leaves before

another dark adaption for 15min prior to assay. Circular areas of interest were created in the middle

of leaf samples avoiding edges for F_0 measurements using the Maxi-Imaging-PAM software.

During temperature ramping, F_0 was measured every 20 s with a weak blue low frequency (1 Hz)

pulse modulated measuring light (0.5 μmol photons m^{-2} s^{-1}). Leaf temperatures were

simultaneously measured with 40-gauge type-T thermocouples (OMEGA Engineering, Singapore)

attached to undersides of leaves and logged with a multi-channel DT85 Datataker datalogger

(Lontek, Australia). For hot T-F_0 measurements, samples were heated to 60 °C at a rate of 30 °C

h^{-1} (0.5 °C min^{-1}). For cold T-F_0 measurements, the leaves were cooled down to -20 °C or -25 °C

when logistically possible, at a rate of 15 °C h^{-1} (0.25 °C min^{-1}). Temperature rates were selected

as moderate temperature changes following Arnold et al. (2021). The starting temperature of each

heating/cooling assay depended on average field lab temperature, generally 15 °C for alpine and

temperate, and 20 °C for desert measurements.

$T_{crit-cold}$ and $T_{crit-hot}$ were determined as inflection points on the T-F_0 curves, using the *segmented* R

package (Muggeo, 2017) (code available from https://github.com/pieterarnold/Tcrit-extraction).

For further description of T-F_0 curve see Arnold et al. (2021). $T_{crit-cold}$ and $T_{crit-hot}$ were used to

represent the lower and upper bounds of the PSII thermal tolerance breadth, TTB (TTB = $T_{crit-hot}$ -

$T_{crit-cold}$).

Ice nucleation temperatures

Freezing tolerance is tied to the temperatures at which ice formation occurs, the ice nucleation

temperature ($T_{nucleation}$). Measuring $T_{nucleation}$ is required to understand whether temperature-

dependent damage to photosynthetic machinery occurs in association with ice formation. $T_{nucleation}$

was estimated from the leaf temperature data collected during $T_{crit-cold}$ measurements, where

freezing exotherms can be identified visually as small increases in temperature when leaf

temperature for each sample is plotted against time. The temperature at which the exotherm began

was recorded as $T_{nucleation}$ (Larcher, 2003).

Local climate variables for sampling locations

Climate data were obtained from gridded datasets at 1 km resolution based on spatial interpolations

of long-term (1981-2010) conditions accessed from the CHELSA v2.1 database (Karger et al.,

2017). For each species, we extracted the following local climate variables for each species at leaf

collection sites: mean annual precipitation (MAP), mean annual temperature (MAT), mean

minimum temperature of the coldest month (MinT), mean maximum temperature of the warmest

month (MaxT), and calculated the annual thermal range (T_{range} = MaxT - MinT). Table S2 includes

a complete list of species and sampling locations, which are also shown on Fig. 1.

Statistical analyses

All analyses and data visualisations were conducted in the R Environment for Statistical

Computing version 4.3.1 (R Core Team, 2023). To address aims 1 and 2, we calculated summary

statistics (means and standard errors) for each thermal tolerance threshold metric by biome and

species to evaluate their differences. Pairwise Tukey's Honest Significant Differences were used

to compare means among biomes. To address aim 3, we first generated a correlation matrix for the

five key local climate variables (MAP, MAT, MinT, MaxT, T_{range}) using the R package *corrplot*

(Wei and Simko, 2021). All local climate variables were moderately to strongly correlated with

each other (Fig. 1A); therefore, we elected to conduct a Principal Components Analysis (PCA)

with the variables. The first two Principal Component axes (PC1 and PC2, respectively) explained

99.6% of the variation among the five climate variables (Table 1), therefore we used these two

axes as local climate variables in analyses.

Prior to model fitting, we assessed if the shared evolutionary history across our 69 species may

also explain differences in thermal tolerance thresholds. We generated a phylogenetic tree using

the R package *V.phylomaker* (Jin and Qian, 2022) and calculated the phylogenetic signal and

statistical significance for $T_{crit-hot}$, $T_{crit-cold}$, $T_{nucleation}$ and TTB using four methods: Albouheif's

C_{mean}, Moran's I, Blomberg's K and Pagel's λ using the *phylosignal* package (Keck et al., 2016).

We analysed our thermal tolerance threshold data using linear mixed effects regression models

with correlated random effects structure using the *Almer* function from the *evolvability* R package

(Bolstad et al., 2014). The *Almer* function is built on the *lmer* function from *lme4* (Bates et al.,

2015) but incorporates a correlated random effects structure *A*, which we used to fit a phylogenetic

variance-covariance matrix to account for phylogenetic relatedness among species. For each

response variable ($T_{crit-hot}$, $T_{crit-cold}$, $T_{nucleation}$ and TTB), we fit four candidate models that included

fixed effects of both climate variables, PC1 and PC2, as either linear or second-degree (quadratic)

polynomial terms in combination (i.e., fixed effects in model 1 = PC1 + PC2; model 2 = PC1 +

$PC1^2$ + PC2; model 3 = PC1 + PC2 + $PC2^2$; model 4 = PC1 + $PC1^2$ + PC2 + $PC2^2$). Each candidate

model included three random effects: species (69 levels), growth form (10 levels), and a structured

phylogenetic matrix. Variance explained by differences among species was therefore separated

from phylogenetic relatedness. We calculated Akaike's Information Criterion (AIC) values for

each model fit by maximum likelihood to allow for model comparisons, and then calculated

Akaike's weights using the *MuMIn* R package (Bartoń, 2023) to identify the most parsimonious

model for each thermal tolerance threshold response variable. The final model was refit with

restricted estimate maximum likelihood and its parameters reported, including R^2_{GLMM} values

(Johnson, 2014) to calculate the variance explained by fixed effects (marginal R^2; mR^2) and the

variance explained by both fixed and random effects (conditional R^2; cR^2).

Results

Local climate analysis

Local climate variables were strongly correlated with each other (Fig. 2A) and PCA described

99.6% of the climate space among the three biomes along two axes (Fig. 2B). PC1 explained

77.2% of the variation among the five climate variables and was strongly loaded positively by

MAP and negatively by MAT and MaxT (Fig. 2C). Negative PC1 values can be reasonably

interpreted as cooler and wetter climate, while positive PC1 values indicate a hotter (mean and

extreme temperatures) and drier climate (Fig. 2B). PC2 explained 22.4% of the variation among

the five climate variables and was strongly loaded positively by T_{range} and negatively by MinT

(Fig. 2D). Positive PC2 values can be reasonably interpreted as a climate with colder extremes and

greater range in thermal extremes across the year, while negative PC2 values indicate a climate

with less extreme cold temperatures and greater thermal stability through the year (Fig. 2B).

Fig. 2. Correlations and Principal Component (PC) composition of local climate variables (MAP

= mean annual precipitation, MAT = mean annual temperature, MinT = mean minimum

temperature of the coldest month, MaxT = mean maximum temperature of the warmest month,

T_{range} = annual thermal range (MaxT - MinT)). (A) Correlation matrix of local climate variables,

(B) Principal Components Analysis biplot of PC1 and PC2 showing biome position in climate PC

space, contribution of individual local climate variables to (C) PC1 and (D) PC2.

Biome differences in thermal tolerance

There were clear differences among biomes for all thermal tolerance thresholds (Fig. 3A-C). Unexpectedly, desert species exhibited the most extreme cold thresholds $T_{crit-cold}$ (-13.3 ± 0.3 °C), followed by alpine (-10.9 ± 0.4 °C) and then temperate species (-8.8 ± 0.3 °C), all of which differed significantly from one another (Fig. 3A). Similar to the response of $T_{crit-cold}$, $T_{nucleation}$ values were lowest in desert species (-16.1 ± 0.4 °C), followed by alpine (-10.8 ± 0.5 °C) and warmest in temperate species (-7.5 ± 0.4 °C); again, these differed significantly from one another (Fig. 3B). Interestingly, $T_{crit-cold}$ values for alpine and temperate species were very close to their $T_{nucleation}$, whereas in desert species, ice formation occurred at markedly lower temperatures than $T_{crit-cold}$ (Fig. 3A-B). As predicted, desert species had significantly higher heat tolerance $T_{crit-hot}$ (49.3 ± 0.5 °C), followed by temperate (46.5 ± 0.4 °C) and then alpine (43.1 ± 0.4 °C) species (Fig. 3C). Thermal tolerance breadth (TTB) was significantly wider in desert species (62.5 ± 0.6 °C) than temperate (55.3 ± 0.5 °C) or alpine species (53.9 ± 0.6 °C), but alpine and temperate species had similar TTB (Fig. 3D).

Fig. 3. Thermal tolerance thresholds and breadth across the three biomes. (A) Cold tolerance threshold ($T_{crit-cold}$), (B) ice nucleation temperature ($T_{nucleation}$), (C) heat tolerance threshold ($T_{crit-hot}$) and (D) thermal tolerance breadth (TTB = $T_{crit-hot}$ - $T_{crit-cold}$), where desert has n = 24 species, temperate has n = 23 species and alpine has n = 22 species. Small transparent points represent individual replicates and large solid points represent biome means ± SE. Lowercase letters inset in each plot denote significant differences among biomes from post-hoc Tukey's Honest Significant Differences tests within each thermal tolerance metric.

Species clearly differed in their tolerance thresholds, where the most and least tolerant species

aligned with the respective characteristics of their biome. The temperate species *Oplismenus*

hirtellus was the least cold tolerant ($T_{crit-cold}$ = -4.0 ºC), whereas two alpine species, *Epacris*

paludosa and *Hovea montana*, were most cold tolerant ($T_{crit-cold}$ = -18.5 ºC) and the desert species

Atriplex stipitata had the most extreme ice nucleation temperature ($T_{nucleation}$ = -20.5 °C). The

alpine species *Pimelea ligustrina* was the least heat tolerant ($T_{crit-hot}$ = 38.1 ºC) and the desert

species *Rhagodia spinescens* was the most heat tolerant ($T_{crit-hot}$ = 54.9 ºC). A full list of species

and their individual thermal tolerance thresholds and breadth is presented in Table S1. There was

considerable variation among species within biomes (Fig. 4). Within the desert biome, TTB was

more similar across species (lower variability; TTB range = 56.2 – 70.3 °C; Δ14.1 °C), compared

to the alpine biome, which had the greatest variation among species (TTB range = 45.9 – 63.1 °C;

Δ17.2 °C), followed by the temperate biome (TTB range = 44.8 – 60.4 °C; Δ15.6 °C). The rank

order of species' TTB from widest to narrowest generally reflects their biome, where 17 of the top

20 widest TTBs were all desert species (Fig. 4). By contrast, 10 of the 20 narrowest TTBs were

alpine species, and temperate species had generally moderate to narrow TTB (Fig. 4).

Fig. 4. Thermal tolerance breadth (TTB = $T_{crit-hot}$-$T_{crit-cold}$) for 69 species across three biomes. Species are sorted top to bottom from widest to narrowest TTB, with lines connecting the mean $T_{crit-cold}$ to the mean $T_{crit-hot}$ for each species (length of line = TTB). Red squares and lines represent desert species (n = 24 species), green triangles and lines represent temperate species (n = 23 species) and blue circles and lines represent alpine species (n = 22 species). Cross symbols (×) represent the mean $T_{nucleation}$ for each species. The light blue vertical dashed line represents 0 °C. Each species has n = 5-6 replicates for each thermal tolerance threshold value.

Consistent across all three biomes, TTB was much wider than the extreme temperature range

calculated for the sampling sites; thus, most thermal tolerance thresholds extended well beyond

the minimum and maximum temperatures expected for each species in their local environment.

The only notable exception was for the alpine biome species, where the cold threshold was closer

to the minimum temperatures representing our alpine sites (Fig. 5). Notably, TTB was wider in

species from desert biomes, which are exposed to considerably greater seasonality and extremes,

higher MAT, MaxT and wider T_{range} than those in alpine and temperate environments (Fig. 5).

Fig. 5. Mean thermal tolerance breadth (TTB = $T_{crit-hot}$ - $T_{crit-cold}$) for the alpine, temperate and desert

biomes, relative to the mean thermal range of the local environments (T_{range} = MaxT - MinT). Red

squares and lines represent desert, green triangles and lines represent temperate and blue circles

and lines represent alpine biomes. Cross (×) symbols represent the mean $T_{nucleation}$ and plus (+)

symbols represent the mean annual temperature for each biome. Solid lines connect the mean T_{crit-}

$_{cold}$ to the mean $T_{crit-hot}$ (large symbols) for each biome (length of line = TTB). Dashed lines connect

the mean MinT to the mean MaxT (small symbols) for each biome (length of line = T_{range}). The

light blue vertical dashed line represents 0 °C. Each species has n = 5-6 replicates for each thermal

tolerance threshold value.

Local climate drivers of variation in thermal tolerance thresholds and breadth

We investigated the relationships between the Principal Components of climate variables at the

local site of plant sampling and each of the thermal tolerance thresholds. $T_{crit-cold}$ had a significant

non-linear relationship with PC1 but no significant relationship with PC2 (Table 1, Fig. 6A, B).

Cold tolerance was greatest in plants from both ends of the PC1 axis: the extreme cold and wet

(alpine) as well as the hot and dry (desert), with less cold tolerant plants in between (temperate).

Ice nucleation temperature had a significant linear relationship with PC1 and significant non-linear

relationship with PC2 (Table 1, Fig. 6C, D); $T_{nucleation}$ was greatest in plants from the hottest and

driest climate, which worsened in increasingly cool and wet climates (Fig. 6C). Desert species had

consistently greater freezing tolerance, which drove the $T_{nucleation}$ relationship with PC1 to be more

linear than it was for $T_{crit-cold}$ (Fig. 6A, C). Freezing tolerance was worse in plants from thermally

stable and less extreme climates (temperate) but increased sharply toward climates with colder

extremes and greater range in thermal extremes across the year (Fig. 6D). Species from

environments with greater seasonality therefore froze at lower temperatures than species in

environments where temperature is more stable (Fig. 6D).

Heat tolerance had a significant linear relationship with PC1 but not PC2 (Table 1); $T_{crit-hot}$ was

highest in plants from hot, dry climate, and declined significantly as climate become increasingly

cool and wet (Fig. 6E), but it was unrelated to PC2 (thermal range and minimum temperature; Fig.

6F). Thermal tolerance breadth had a significant non-linear relationship with PC1 but was not

associated with PC2 (Table 1, Fig. 6G-H); TTB was highest in hot, dry climates and it declined

non-linearly as climates became cooler and wetter, where TTB was not different between alpine

and temperate species (Fig. 3D and 6G). For all thermal tolerance thresholds, among-species

differences explained a substantial proportion of variance ($T_{crit-cold}$ = 27.7%, $T_{nucleation}$ = 46.5%,

$T_{crit-hot}$ = 24.7%, TTB = 26.8%). Among-species differences were not attributable to phylogenetic

relatedness. Only $T_{crit-cold}$ was non-zero with phylogeny, explaining just 0.1% of variance

(Table 1), and all four phylogenetic signal metrics consistently identified no evidence of

phylogenetic signal in the thermal tolerance thresholds or breadth (Table S4). Plant growth form

explained additional variance, which was greatest for TTB ($T_{crit-cold}$ = 8.9%, $T_{nucleation}$ = 4.0%, $T_{crit-hot}$ = 1.6%, TTB = 9.6%).

hot = 1.6%, TTB = 9.6%).

Table 1. Model output summaries for Principal Components (PC1 and PC2; see Fig. 2) of local

climate drivers of physiological thermal thresholds.

			$T_{crit-cold}$ (°C)				
Fixed	**Coefficient ± SE**	*t-value*	*p-value*	**Random**	**Coefficient**	*$R^{2\,*}$*	*R^2*
Intercept	-10.586 ± 1.241	-8.529	**<0.001**	Growth form	1.042	mR^2	0.206
PC1	-16.605 ± 6.603	-2.515	**0.012**	Species	1.836	cR^2	0.498
PC2	-36.351 ± 15.670	-2.320	**0.021**	Phylogeny	0.092	$cR^2 - mR^2$	0.292
PC2²	0.349 ± 0.785	0.445	0.657	Residual	2.772		
			$T_{nucleation}$ (°C)				
Fixed	**Coefficient ± SE**	*t-value*	*p-value*	**Random**	**Coefficient**	*R^2*	*R^2*
Intercept	-11.504 ± 0.484	-23.745	**<0.001**	Growth form	0.762	mR^2	0.444
PC1	-0.970 ± 0.200	-4.840	**<0.001**	Species	2.595	cR^2	0.725
PC2	-49.776 ± 7.001	-7.110	**<0.001**	Phylogeny	0.000	$cR^2 - mR^2$	0.281
PC2²	-15.997 ± 6.578	-2.432	**0.016**	Residual	2.674		
			$T_{crit-hot}$ (°C)				
Fixed	**Coefficient ± SE**	*t-value*	*p-value*	**Random**	**Coefficient**	*R^2*	*R^2*
Intercept	46.371 ± 0.427	108.578	**<0.001**	Growth form	0.568	mR^2	0.251
PC1	1.319 ± 0.186	7.110	**<0.001**	Species	2.231	cR^2	0.448
PC2	-0.172 ± 0.330	-0.520	0.603	Phylogeny	0.000	$cR^2 - mR^2$	0.197
				Residual	3.855		
			TTB (°C)				
Fixed	**Coefficient ± SE**	*t-value*	*p-value*	**Random**	**Coefficient**	*R^2*	*R^2*
Intercept	57.461 ± 0.894	64.268	**<0.001**	Growth form	1.906	mR^2	0.276
PC1	65.669 ± 10.560	6.218	**<0.001**	Species	3.187	cR^2	0.548
PC1²	48.643 ± 24.509	1.985	**0.048**	Phylogeny	0.000	$cR^2 - mR^2$	0.272
PC2	-1.070 ± 1.223	-0.875	0.382	Residual	4.788		

*mR^2 represents the variance explained by all fixed effects and $cR^2 - mR^2$ represents the variance
explained by all random effects.

Fig. 6. Local climate variables (Principal Components, PC1 and PC2; see Fig. 2) that predict

variation in thermal tolerance thresholds across all biomes. Regressions between (A) $T_{crit-cold}$ and

PC1, (B) $T_{crit-cold}$ and PC2, (C) $T_{nucleation}$ and PC1, (D) $T_{nucleation}$ and PC2, (E) $T_{crit-hot}$ and PC1, (F)

$T_{crit-hot}$ and PC2, (G) TTB and PC1 and (H) TTB and PC2. Arrows and annotations indicate climate

variable loadings on PC1 and PC2 axes: positive PC1 values = hotter and drier climate (+MAT, -

MAP, +MaxT); negative PC1 values = cooler and wetter climate (-MAT, +MAP, -MaxT). Positive

PC2 values = greater range in thermal extremes across the year and colder extremes (+T_{range}, -

MinT) negative PC2 values = greater annual thermal stability and less extreme cold temperatures

(-T_{range}, +MinT), see Fig. 2 and Table S3. Large solid points are species-level means ± SE and

small transparent points are individual replicates. Points are coloured by biome and regressions

are predicted model fits ± SE from the best models reported in Table 1, where solid regression

lines represent significant relationships.

Discussion

The climate variability hypothesis predicts that species will evolve wider thermal tolerance

breadths in environments with more variable temperatures and be selected for thermal

specialisation (narrow TTB) in thermally stable environments, a concept largely supported in

animals (i.e., Compton et al., 2007, Sunday et al., 2011). In plants, a recent study found that the

TTB of alpine species in temperate latitudes was not generally wider than the TTB of tropical

latitude species (though not all these measurements were conducted concomitantly or with the

same methods) (Sklenář et al., 2023). Other studies exploring CVH in plants have investigated

phenotypic plasticity increase with latitude (Molina-Montenegro and Naya, 2012), species

distribution range with seasonality across elevation (Mumladze et al., 2017) and photosynthetic

strategy with environmental temperature variability (Perez et al., 2023). Here we explored the

CVH for plants by measuring photosynthetic heat and cold tolerance thresholds concurrently to

determine TTB of species growing in two extreme and more thermally variable (desert and alpine),

one benign and more thermally stable (temperate).

Based on the CVH framework, we hypothesised that the thermal tolerance thresholds of alpine and

desert species would be skewed to their respective habitat extremes (aim 1). Also, we expected

that these skewed tolerances in the thermally variable, extreme environments would drive wider

TTB than the more stable, benign temperate environment (aim 2). We found that variation in TTB

in the more variable and extreme desert and alpine environments was indeed wider than temperate

species, with desert TTB values skewed towards higher temperatures, alpine TTB values skewed

towards colder temperatures and temperate TTB sitting in between. However, the mean TTB of

alpine and temperate species were similar to one another, whereas desert species had both greater

heat and cold thresholds. Finally, we assessed whether climate extremes and variability, rather

than means, explained more variation in thermal tolerance and TTB (aim 3). We found that mean

and maximum temperatures and precipitation (PC1 axis) had a stronger relationship with TTB than

thermal variability and cold extremes (PC2 axis), which provides only partial support the CVH.

When we explored the climate drivers of thermal tolerance thresholds, we found that thermal range

(within PC2), a proxy for climate variability, was only a strong driver for freezing tolerance

($T_{nucleation}$). Below we explore our findings in terms of physiology and the ecological implications

of these results for species persistence in a changing climate.

TTB well exceeds thermal ranges in each biome and varies within biomes

Thermal tolerance breadth values of PSII reported here are notably wide; wider than the thermal

ranges in each environment and larger than measures of TTB in many other organisms. For

instance, across a range of marine and terrestrial ectotherm taxa, the widest recorded TTB was

60 °C in terrestrial arthropods (Sunday et al., 2011), while the widest TTB in our dataset was 70.3

°C in the desert species *Rhagodia spinescens*, with several other desert species also exceeding 60

°C. Within each biome, we found species with a range of wide and narrow TTB (Fig. 4). For

example, several alpine species across growth forms had relatively narrow TTB, such as the snow

bed species *Psychrophila introloba* (48.9 °C TTB) and the tree line species *Eucalyptus pauciflora*

subsp. *niphophila* (47.7 °C TTB). The narrow TTB of some alpine species was mainly driven by

their low heat tolerance ($T_{crit-hot} \approx 40$ °C), whereas other co-occurring species, *Hovea montana* and

Epacris paludosa had TTB values similar to those of many desert species (~63 °C), driven by

extreme cold tolerance (around -18 °C). This within-biome variation in TTB might be due to

variation among species microclimatic niche, which can override broad-scale climate drivers of

physiological tolerance (Curtis et al., 2016, Curtis et al., 2019, Aparecido et al., 2020).

Although thermal seasonality was greater in alpine than temperate regions sampled here, the

average TTB for these two biomes was remarkably similar (Fig. 3D). Temperate species appeared

to tolerate colder temperatures than expected, and it is possible that their relatively wide thermal

tolerance is a legacy of exposure to climate extremes through geological time (Byrne et al., 2008).

The climate legacy effect on thermal tolerance is suggested to be stronger for cold than heat

tolerances across both animal and plant taxa (Bennett et al., 2021) and might explain why some

temperate and desert species have greater freezing tolerance than expected by their current climate

parameters. Although metrics based on air temperatures for our alpine biome (e.g., MAT, thermal

range) confirm that thermal range and seasonality are large in this biome, mountain plants spend

4-5 months under the insulating cover of snow, which stabilises temperatures (Briceño et al.,

2014). This dampening of climate extremes might contribute to the similarity between alpine and

temperate species thermal tolerance breadth.

Heat and cold thermal limits vary among biomes

Plants exposed to drought and/or freezing share a similar physiological response: cell dehydration

(Anisko and Lindstrom, 1996, Blake and Hill, 1996, Lintunen et al., 2013). The physiological

response to drought conditions may partially explain our apparently counterintuitive result that

desert species were more freezing tolerant (more extreme $T_{crit-cold}$ and $T_{nucleation}$) than either alpine

or temperate species. Plants can use osmotic adjustments to offset water loss from cells along the

water potential gradient caused by both drying and freezing (Larcher, 2003, Siminovitch and

Cloutier, 1983). Thus, the ability of desert species to cope with dehydration induced by long

periods of drought might also confer the ability to cope with freezing, even though these desert

species are unlikely to ever be exposed to such extreme freezing temperatures. In addition, leaf

adaptations to aridity such as small leaves, thick cuticles, smaller, more densely packed cells,

thicker cell walls with small capillary structures and small xylem vessel diameter (Dörken et al.,

2020) also can prevent ice formation, which increases supercooling capacity and freezing tolerance

(Lintunen et al., 2013). Such mechanisms may reflect that species living in environments where

freezing temperatures are rare use supercooling as a mechanism to avoid freezing damage, whereas

in alpine environments, species tolerate ice formation. Indeed, the desert species studied here

generally had nucleation temperatures much lower than their $T_{crit-cold}$, from which we can infer a

high supercooling capacity that effectively serves to delay freezing. Indeed, Andean alpine

species' low $T_{nucleation}$ at the end of the growing season are attributed to low soil moisture and thus

potential water stress, rather than low temperatures (Sierra-Almeida et al., 2016). Drought also

improves both heat and cold tolerance in an Australian alpine grass (Sumner et al., 2022).

Likewise, drought exposure can increase heat tolerance through raising intracellular sugar

contents, which stabilise thylakoid membranes (Hüve et al., 2006, Brestic et al., 2012). The

extreme freezing, cold and heat tolerances found in our desert species might reflect a secondary

outcome of plant adaptation to aridity.

The relatively high $T_{crit-hot}$ of some of our alpine species may seem surprising; however, these heat

tolerance ranges are similar to recent measures of heat tolerance in other alpine species (43-55°C,

Sumner and Venn, 2022). Alpine plants can be exposed to very high temperatures, especially those

with prostrate growth forms (Körner, 2003). Leaf temperatures of European alpine species can

reach up to 50 °C in summer, especially on calm sunny days, and leaf heat tolerances can be higher

than 50 °C (Buchner and Neuner, 2003). Maximum leaf temperature has been measured at nearly

40 °C in early summer in Australian alpine species (Bird et al., 2023, unpublished data) and may

yet be much higher in hot and still conditions in late summer. Therefore, thermal tolerance

thresholds could be breached in alpine species if the combination of heat with other environmental

stress, such as high light, caused heat tolerance to decrease, as found for some European alpine

species (Buchner et al., 2015, Buchner and Neuner, 2003).

Heat and cold thermal limits relate to different climatic variables

Predicting plant responses to changing temperature regimes is a significant global challenge and

requires a mechanistic understanding of how temperature affects species physiology and

distributions. Although the physiological mechanisms underpinning freezing and cold tolerance

(Guy, 2003) and heat tolerance (Wahid et al., 2007) have been established in model plants,

responses of species exposed to natural conditions remain understudied. While the thermal limits

of plants have recently been shown to broadly vary with latitude (O'Sullivan et al., 2017, Lancaster

and Humphreys, 2020), comparisons employing standard techniques across multiple biomes

remain rare, particularly for both heat and cold tolerance concomitantly (Geange et al., 2021).

Importantly, the capacity to predict thermal tolerance from key bioclimatic parameters such as

MAT and MAP remains complex (Perez and Feeley, 2021). For our cross-biome dataset, we used

a PCA approach due to the strong correlations among local climate variables, which means that

we cannot state explicitly that MAT or MAP or T_{range} are strong explanatory variables individually

per se. Rather, these biomes are defined clearly by climate variables in combination: PC1 from

cool and wet to extreme hot and dry; and PC2 from thermally stable and benign minimum

temperatures to thermally variable and cold minimum temperatures. The combination of mean

annual temperature, precipitation and maximum temperatures explained considerable variation in

$T_{crit-cold}$ and $T_{nucleation}$. However, because desert species had much lower $T_{nucleation}$ than $T_{crit-cold}$, the

patterns with the climate axes differed slightly. These contrasting alpine and desert cold threshold

responses suggest that $T_{nucleation}$ is more strongly associated with aridity and minimum

temperatures than $T_{crit-cold}$, supporting the idea of shared mechanisms of tolerance to freezing and

dehydration under drought.

Although plants growing in extreme hot and dry environments have higher heat tolerance, due to

the high correlation of MAP with both MAT and MaxT, the role of temperature *vs* precipitation

cannot be completely separated. For a range of common-grown Australian *Acacia* species from

broad climatic and geographic origin, precipitation does not strongly drive variation in $T_{crit-hot}$

(Andrew et al., 2023). Yet, drought or low water availability might drastically reduce stomatal

conductance and therefore cooling capacity during exposure to heat, thus increasing both leaf

temperature and heat tolerance (Cook et al., 2021), demonstrating that water availability and

temperature are intrinsically linked. Local climate, and particularly temperature, seems to play a

significant role in driving variation in $T_{crit-hot}$ in our field study. Our findings contrast with another

common garden study of 123 taxonomically diverse species, for which climate variables generally

had very weak predictive power (<5%) for heat tolerance (Perez and Feeley, 2021).

Despite some clear macroclimatic patterns in our study, a large proportion of the variation in cold

and, to a lesser extent, heat tolerance was attributable to among-species differences, unrelated to

phylogeny (cold: 27.7 - 46.5%, heat: 24.7%). The contribution of species differences could reflect

their different leaf traits, particularly those contributing to variation in leaf temperature, the signal

of which may be amplified when sampled *in situ*. Mahan and Upchurch (1988) proposed that the

lower limit of temperature for a plant is controlled by its environment, while the upper limit can

be controlled by the plant, suggesting that plants are 'limited homeotherms'. Recent studies have

shown that what drives variation in heat tolerance is leaf temperature, rather than air temperature

(Cook et al., 2021, Perez and Feeley, 2020). Leaves can avoid heat stress through different

mechanisms that decouple leaf from air temperature, such as anatomical traits (Leigh et al., 2017,

Leigh et al., 2012, Tserej and Feeley, 2021), patterns of display such as leaf inclination (Ball et al.,

1988) and transpirational cooling through stomatal conductance (Deva et al., 2020, Drake et al.,

2018), all of which can vary among co-existing species (Urban et al., 2017, Marchin et al., 2022).

Leaf-to-air temperature decoupling (Blonder et al., 2020) might also explain why relationships

between heat tolerance and latitude are smaller than expected for the air temperature span

considered (O'Sullivan et al., 2017, Curtis et al., 2016, Lancaster and Humphreys, 2020).

Thermal tolerance breadth captures both lower and upper limits. Unlike for animals, global

patterns of variation in the TTB of plants have received little attention. Despite the existence of

large thermal tolerance datasets, the lack of paired, concurrently measured low and high thermal

tolerance thresholds has hampered the ability to adequately assess thermal tolerance breadth in

plants. In our study, TTB increased non-linearly (hyper-allometrically) with increasing PC1:

species exposed to the high mean temperatures, coupled with aridity and heat extremes in our

desert biome had much wider thermal tolerance breadth than temperate or alpine plants (Fig. 6B).

However, although we found that species played a role in explaining variation in TTB, the capacity

for different species to respond to increasingly extreme and variable temperatures by changing

their TTB is only recently emerging. Thermal tolerance breadth of temperate and tropical alpine

species appears to differ only at the end of the temperate growing season, due to an increase in

cold acclimation (Sklenář et al., 2023). For common-grown seedlings from the same biomes that

were tested here, TTB became narrower when exposed to a combination of heat and freezing

temperatures in controlled climate chambers (Harris et al., *in press*). However, the same authors

found that the effect of biome is minimal, which contrasts the clear biome-based differences in

thermal thresholds observed here in plants *in situ*. The distinct responses between these contexts

implies that life stage and current growing conditions are likely to be important modifiers of

thermal tolerance. A recent study in an alpine species found that growth conditions far outweighed

other environmental and genetic sources of variation in trait changes (Arnold et al., 2024).

Research into what influences the capacity for species to shift their TTB in response to

environment is ongoing. Current research generally suggests that the evolution of plant niches is

constrained by heat tolerance (Araujo et al., 2013), supported by evidence of reduced variation in

heat tolerance across landscapes (Lancaster and Humphreys, 2020). However, we found the

opposite, with heat tolerance having greater among-species variability (~30 °C) than cold tolerance

(~20 °C) across our diverse biomes. This disparity points to the need for examination into whether

wider TTB or more extreme thermal thresholds contribute to greater plasticity to warming and

future climate extremes.

Narrow physiological thermal limits have been identified as a feature of species vulnerability to

climate change (Pacifici et al., 2015, Williams et al., 2008). Nevertheless, the use of PSII thermal

tolerance metrics determined at the leaf-level, requires careful interpretation. When leaves reach

their critical thermal limits, damage to PSII can occur, leading to decreased electron transport rate

and photosynthetic failure, thus compromising leaf survival. The likelihood that such damage

compromises whole plant survival, however, is less clear. PerezSocha et al. (2021) found heat

tolerance thresholds to correlate with carbon assimilation limits and therefore are linked to plant

productivity. To further unpick these patterns, we need to better understand the relationship

between physiological thermal limits of modular components of the whole plant with plant survival

and fitness across the plant life cycle. Further, to explain additional variation in these thermal

tolerance thresholds, explorations of the plasticity in both cold and heat tolerance across space and

time are also warranted.

Concluding summary

Thermal tolerance breadth (TTB), a parameter broadly used in animal thermal biology literature,

has rarely been measured using a consistent method in such a diverse range of plant species and

environments. To explore the climate variability hypothesis, we concomitantly measured the lower

($T_{crit\text{-}cold}$ and $T_{nucleation}$) and upper ($T_{crit\text{-}hot}$) photosystem thermal thresholds and TTB of 69 plant

species across three biomes: two climatically extreme (alpine and desert) and one more stable

(temperate). Considering climate from a discreet biome perspective, our results provide only

partial support for the CVH, with plants from the climatically variable desert biome having the

widest TTB. Across local climate variables, we found limited support for the CVH, with some

evidence that ice nucleation temperature was driven by thermal range and minimum temperature,

but heat tolerance was not, and substantial variation was explained by species. TTB of leaves was

extremely wide; much wider than the air temperature extremes to which plants are exposed in these

biomes. It is important to remember that sustained stressful temperatures within critical limits

could still have far-reaching effects, depending on species life history, morphological traits and

plasticity, as well as microclimatic and temporal heterogeneity. While local climate may partially

explain variability in plant thermal tolerance and breadth, incorporating species traits,

incorporating leaf temperature and microhabitat information is an important next step to better

understand the vulnerability of different vegetation communities to climate extremes.

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Supporting Information

Table S1. Selected species in each biome, family, growth form and mean thermal tolerance thresholds.

Species	Family	Growth form	$T_{crit-cold}$ (°C)	$T_{nucleation}$ (°C)	$T_{crit-hot}$ (°C)	TTB (°C)
Alpine						
Aciphylla glacialis	Apiaceae	Herb	-7.3±0.4	-7.2±0.3	39.5±1.2	46.8±1.4
Astelia alpina	Asteliaceae	Herb	-13.9±0.7	-9.8±0.5	46.4±1.0	60.4±0.8
Carex breviculmis	Cyperaceae	Sedge	-12.0±1.2	-15.3±1.7	47.0±0.8	59.4±0.7
Celmisia costiniana	Asteraceae	Herb	-9.6±0.7	-7.6±0.7	44.9±0.4	54.4±0.9
Epacris paludosa	Ericaceae	Shrub	-18.2±1.2	-19.4±1.1	45.2±1.7	63.0±2.5
Eucalyptus pauciflora (ssp niphophila)	Myrtaceae	Tree	-8.7±0.3	-9.1±0.4	39.0±0.7	47.7±0.8
Ewartia nubigena	Asteraceae	Mat	-13.1±1.8	-11.9±1.9	43.0±0.9	56.1±2.2
Grevillea australis	Proteaceae	Shrub	-11.3±1.1	-10.8±1.8	44.1±1.4	55.4±1.9
Hovea montana	Fabaceae	Shrub	-18.5±0.3	-8.0±2.5	44.6±1.3	63.1±1.3
Luzula acutifolia	Juncaceae	Rush	-8.6±0.4	-10.3±1.3	44.2±2.3	52.9±2.3
Nematolepis ovatifolia	Rutaceae	Shrub	-7.5±0.4	-8.1±0.3	45.5±3.4	53.0±3.7
Olearia brevipedunculata	Asteraceae	Shrub	-14.3±1.3	-11.9±1.7	43.6±0.6	57.9±1.4
Orites lancifolius	Proteaceae	Shrub	-8.6±0.4	-8.5±0.5	45.2±1.7	53.8±1.7
Oxylobium ellipticum	Fabaceae	Shrub	-16.2±1.6	-19.4±1.3	42.3±1.2	58.5±2.4
Pimelea ligustrina	Thymelaeaceae	Shrub	-9.6±0.6	-8.6±0.6	37.1±0.4	46.6±0.6
Plantago muelleri	Plantaginaceae	Herb	-6.0±0.4	-5.5±0.4	39.9±2.9	45.9±3.1
Podocarpus lawrencei	Podocarpaceae	Shrub	-10.3±0.6	-13.7±1.7	45.8±1.2	56.0±1.2
Prostanthera cuneata	Lamiaceae	Shrub	-12.5±1.5	-15.9±1.7	39.1±2.0	51.7±1.5
Psychrophila introloba	Ranuculaceae	Herb	-7.3±0.4	-6.8±0.5	41.6±0.5	48.9±0.8
Richea continentis	Ericaceae	Shrub	-13.0±1.4	-14.4±2.3	43.6±0.4	56.7±1.3
Tasmannia xerophila	Winteraceae	Shrub	-8.4±0.5	-8.69±0.4	44.1±0.7	52.4±1.1
Viola betonicifolia	Violaceae	Herb	-6.6±1.0	-7.7±0.7	43.5±0.4	50.1±1.3
Temperate						
Acacia binervata	Fabaceae	Tree	-12.0±0.7	-11.8±0.9	39.8±1.5	51.8±1.0
Acacia longifolia	Fabaceae	Tree	-10.2±0.7	-10.3±0.6	43.7±1.7	53.8±2.2
Acmena smithii	Myrtaceae	Tree	-11.5±0.8	-6.3±1.6	48.0±0.7	59.4±1.0
Backhousia myrtifolia	Myrtaceae	Tree	-8.5±0.8	-6.8±1.0	48.0±0.4	56.5±1.1
Banksia integrifolia	Proteaceae	Tree	-6.7±0.5	-5.1±0.3	38.1±1.8	44.8±2.2
Brachychiton acerifolius	Malvaceae	Tree	-6.6±0.8	-7.7±0.5	48.6±0.4	55.2±0.7
Carex appressa	Cyperaceae	Sedge	-9.3±0.3	-5.0±0.7	50.1±1.2	59.4±1.1
Cayratia clematidea	Vitaceae	Climber	-8.0±0.8	-8.0±0.5	46.5±0.2	54.6±0.9
Ceratopetalum apetalum	Cunoniaceae	Tree	-10.8±1.0	-8.5±1.8	47.3±2.0	58.1±3.0
Cryptocarya microneura	Lauraceae	Tree	-8.5±1.1	-11.9±0.3	45.4±1.2	53.9±1.7
Doryphora sassafras	Atherospermataceae	Tree	-8.4±0.7	-5.1±0.7	47.6±0.8	55.9±1.1
Ficus coronata	Moraceae	tree	-8.7±0.6	-5.8±0.7	46.5±0.5	55.2±0.8
Guioa semiglauca	Sapindaceae	Tree	-7.7±0.3	-5.3±0.9	50.8±0.4	58.5±0.5
Lomandra longifolia	Asparagaceae	Sedge	-10.9±1.1	-6.7±1.2	49.5±1.6	60.4±2.3
Luzuriaga cymosum	Luzuriagaceae	Climber	-10.1±1.7	-10.9±1.3	48.8±0.2	58.9±1.7
Myoporum acuminatum	Scrophulariaceae	Tree	-9.4±0.6	-7.3±1.7	49.0±0.9	58.4±0.9
Oplismenus hirtellus	Poaceae	Grass	-4.0±0.7	-6.2±1.2	43.8±1.0	47.8±1.0

Species	Family	Form				
Pittosporum undulatum	Pittosporaceae	Tree	-10.5±1.2	-8.5±1.4	45.2±1.4	55.7±2.2
Podocarpus elatus	Podocarpaceae	Tree	-8.8±1.1	-6.6±1.1	48.2±0.9	57.1±1.9
Stephania japonica	Menispermaceae	Climber	-7.1±0.5	-5.7±1.1	48.3±0.6	55.4±1.0
Tasmannia insipida	Winteraceae	Shrub	-11.7±1.3	-14.1±0.7	48.0±0.6	59.7±0.8
Trochocarpa laurina	Ericaceae	Shrub	-6.2±0.6	-3.2±0.5	47.9±1.4	54.2±1.4
Viola banksii	Violaceae	Herb	-7.1±1.6	-6.0±0.6	42.2±0.7	49.3±1.6
Desert						
Acacia aneura	Fabaceae	Tree	-13.0±2.2	-16.2±1.2	53.0±4.0	66.0±4.0
Acacia salicina	Fabaceae	Tree	-13.8±0.8	-13.6±1.1	49.6±0.8	63.3±0.9
Acacia victoriae	Fabaceae	Tree	-15.6±1.9	-18.3±0.4	45.1±1.8	60.7±3.3
Alectryon oleifolius	Sapindaceae	Tree	-13.0±0.9	-13.5±1.1	50.3±1.9	63.4±2.1
Atriplex stipitata	Amaranthaceae	Subshrub	-16.7±0.6	-20.5±0.4	47.2±0.5	63.9±1.1
Brachychiton populneus	Malvaceae	Tree	-8.8±1.2	-13.9±1.4	47.4±1.9	56.2±2.1
Capparis mitchellii	Capparaceae	Tree	-13.1±0.6	-14.7±1.8	49.5±1.3	62.6±1.5
Casuarina pauper	Casuarinaceae	Tree	-14.9±0.3	-18.0±0.4	48.7±0.9	63.6±1.3
Dodonaea viscosa	Sapindaceae	Shrub	-12.4±1.4	-14.8±0.7	45.4±0.5	57.8±1.6
Eremophila latrobei	Scrophulariaceae	Shrub	-11.6±0.8	-18.3±1.1	48.5±2.0	60.2±2.1
Eremophila sturtii	Scrophulariaceae	Shrub	-12.7±1.5	-14.3±1.4	51.3±1.8	64.1±2.9
Eucalyptus coolabah	Myrtaceae	Tree	-13.3±2.0	-17.8±0.8	46.3±2.4	59.6±3.7
Eucalyptus largiflorens	Myrtaceae	Tree	-14.3±1.2	-13.9±0.5	45.9±3.1	60.2±2.5
Flindersia maculosa	Rutaceae	Tree	-13.7±0.7	-14.9±1.3	51.7±4.0	65.4±3.6
Geijera parviflora	Rutaceae	Tree	-11.3±1.4	-15.0±1.1	51.4±2.2	62.8±3.2
Grevillea striata	Proteaceae	Shrub	-15.0±1.2	-17.6±0.3	47.6±4.2	62.7±4.3
Myoporum montanum	Scrophulariaceae	Shrub	-13.9±0.4	-16.2±1.1	48.4±0.9	62.2±1.1
Pimelea microcephala	Thymelaeaceae	Shrub	-12.2±2.9	-15.6±0.8	48.7±2.1	60.9±2.1
Ptilotus sessilifolius	Amaranthaceae	Subshrub	-12.7±3.4	-17.2±2.2	51.8±0.5	64.6±3.6
Rhagodia spinescens	Amaranthaceae	Subshrub	-15.4±2.2	-18.1±1.2	54.9±3.4	70.3±4.5
Sclerolaena birchii	Amaranthaceae	Subshrub	-13.9±1.5	-15.4±0.7	48.6±1.6	62.5±2.8
Senna artemisioides	Fabaceae	Shrub	-13.4±2.2	-18.1±0.6	51.9±1.0	65.3±2.7
Sida fibulifera	Malvaceae	Subshrub	-13.1±2.1	-15.2±0.9	50.5±0.9	63.6±2.0
Solanum esuriale	Solanaceae	Herb	-11.9±0.9	-13.5±1.5	49.3±1.1	61.2±0.8

Table S2. Climate data extracted for species locations across all biomes used in initial models (see associated spreadsheet).

Table S3. Loadings and variance explained by the first and second Principal Components (PC1 and PC2) that explain 99.6% of the variance among local climate variables. Bold indicates dominant variables.

	Loadings	
Local climate variable	**PC1**	**PC2**
MAP	**-0.498**	-0.158
MinT	0.382	**-0.624**
MaxT	**0.506**	0.098
Trange	0.334	**0.713**
MAT	**0.489**	-0.261
Variance explained	76.5%	23.1%
Cumulative variance	76.5%	99.6%

Table S4. Model AIC and weights for each physiological thermal tolerance threshold and TTB.

Trait	Model fixed effect structure	*npar*	AIC	Weight
$T_{crit-cold}$	PC1 + PC2	7	1928.7	0.065
	PC1 + PC1^2 + PC2	8	1924.8	**0.458**
	PC1 + PC2 + PC2^2	8	1926.1	0.236
	PC1 + PC1^2 + PC2 + PC2^2	9	1926.1	0.241
$T_{nucleation}$	PC1 + PC2	7	1806.6	0.080
	PC1 + PC1^2 + PC2	8	1805.9	0.113
	PC1 + PC2 + PC2^2	8	1802.6	**0.586**
	PC1 + PC1^2 + PC2 + PC2^2	9	1804.6	0.221
$T_{crit-hot}$	PC1 + PC2	7	2126.6	**0.525**
	PC1 + PC1^2 + PC2	8	2128.5	0.203
	PC1 + PC2 + PC2^2	8	2128.6	0.194
	PC1 + PC1^2 + PC2 + PC2^2	9	2130.4	0.078
TTB	PC1 + PC2	7	2307.7	0.203
	PC1 + PC1^2 + PC2	8	2306.0	**0.463**
	PC1 + PC2 + PC2^2	8	2308.1	0.164
	PC1 + PC1^2 + PC2 + PC2^2	9	2308.0	0.170

Table S5. Phylogenetic signal in physiological thermal tolerance thresholds.

Trait	C_{mean}	*p*-value	I	*p*-value	K	*p*-value	λ	*p*-value
$T_{crit-cold}$	0.112	0.075	0.007	0.235	0.111	0.454	0.560	0.316
$T_{nucleation}$	0.052	0.222	-0.013	0.473	0.095	0.595	0.253	1.000
$T_{crit-hot}$	-0.181	0.987	-0.063	0.950	0.048	0.957	0.000	1.000
TTB	-0.103	0.854	-0.005	0.378	0.126	0.295	0.000	1.000