Supplementary materials

Contents

1. Supplementary methods

Methods S1: *Variance-covariance matrices for random terms defined under the linear mixed model*

Under the general linear mixed model defined in Equation (1), the joint distribution of the random terms was assumed to be multivariate normal, with means and (co)variances:

$$\begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} \sim N\left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{G} & \mathbf{0} \\ \mathbf{0} & \mathbf{R} \end{bmatrix} \right)$$

where $\mathbf{0}$ is a null matrix, $\mathbf{G}$ and $\mathbf{R}$ are (co)variance matrices corresponding to $\mathbf{u}$ and $\mathbf{e}$, respectively. Different model terms in $\mathbf{u}$ were assumed to be mutually independent.

Under a univariate model, $\mathbf{G} = \mathbf{I}_{n_p}\sigma^2_{prov} \oplus \mathbf{A}\sigma^2_a$, where $\mathbf{I}_{n_p}$ is an identity matrix of dimension n_p x n_p (n_p = number of provenances), $\mathbf{A}$ is the matrix of additive genetic relationship coefficients among all individuals in the pedigree (i.e. base population parents and their progeny, which was tested in a common-garden trial), σ^2_{prov} is the variance of provenance effects, σ^2_a is the variance of additive genetic effects within provenances, and $\oplus$ is the direct sum operation. The matrix $\mathbf{A}$ was modified to take into account a selfing rate of 10% for *E. pauciflora* [1] and a base-level population inbreeding of 0.067 [2]. The residual effects were defined by $\mathbf{R} = \mathbf{I}_n\sigma^2_e$, where $\mathbf{I}_n$ is an identity matrix of dimension n x n (n = number of trees tested in a common-garden trial), and σ^2_e is the residual variance.

Under a bivariate model, the (co)variance matrices $\mathbf{G}$ and $\mathbf{R}$ were defined as:

$$\mathbf{G} = \begin{bmatrix} \mathbf{I}_{n_p}\sigma^2_{prov_k} & \mathbf{I}_{n_p}\sigma_{prov_{k,l}} \\ \mathbf{I}_{n_p}\sigma_{prov_{k,l}} & \mathbf{I}_{n_p}\sigma^2_{prov_l} \end{bmatrix} \oplus \begin{bmatrix} \mathbf{A}\sigma^2_{a_k} & \mathbf{A}\sigma_{a_{k,l}} \\ \mathbf{A}\sigma_{a_{k,l}} & \mathbf{A}\sigma^2_{a_l} \end{bmatrix}$$

$$\mathbf{R} = \begin{bmatrix} \mathbf{I}_n\sigma^2_{e_k} & \mathbf{I}_n\sigma_{e_{k,l}} \\ \mathbf{I}_n\sigma_{e_{k,l}} & \mathbf{I}_n\sigma^2_{e_l} \end{bmatrix}$$

where k and l refer to two traits; $\sigma_{k,l}$ denotes the covariance between the two traits for a given random term; and σ^2_{prov}, σ^2_a, σ^2_e, $\mathbf{A}$, $\mathbf{I}$, n_p, n and $\oplus$ are defined as before.

Methods S2: *Verification of model assumptions*

(Co)variance components and genetic parameters

For HT and LIGD, preliminary analyses based on a linear mixed model fitting the intercept and replicates as fixed effects (plus STMD used as a covariate in modelling LIGD), and provenances and families within provenances as random effects, provided residual distributions that approached normality well, as indicated by the visual inspection of the histogram and the quantile-quantile plot of conditional studentized residuals. However, the residual distribution from the linear mixed model was skewed for PET, although the observed asymmetry did not appear to be severe.

To assess whether a Gaussian-based approximation of the residual distribution from the above-mentioned analysis of PET was inaccurate for hypothesis testing of model parameters, we also fitted a generalized linear mixed model (GLMM) in which PET was assumed to follow a Beta distribution. As indicated by Ferrari and Cribari-Neto [3], the flexibility of the Beta distribution makes it useful for modelling continuous variables such as proportions - that assume values in the open unit interval (0, 1) - enabling to naturally accommodate

heteroscedasticity and asymmetry in the data. The GLMM fitted the same predictor variables (i.e. fixed and random effects) as described before and, following [3], the Beta density was parameterized in terms of a location parameter μ (i.e. mean response) and a scale parameter ϕ (i.e. precision); the logit link was used as a link function for modelling μ (i.e. to relate the mean response to the predictor variables), while ϕ was fitted as a nuisance parameter. Prior to analysis, the observed percentage values of PET were converted into proportions. The beta-distributed model assumes that the response variable comprises observations from a continuous bounded scale within the open unit interval (0, 1): the proportions for PET were reasonably continuous in this interval, varying between 0.08 and 0.93. When comparing variance component estimates, the ratio of the provenance variance relative to the family variance (or vice-versa) obtained on the logit scale under the GLMM was similar to that obtained on the observed trait scale under a linear mixed model assuming normality. Concerning hypothesis tests, calculated likelihood-ratio test statistics were comparable between the two models, and provided the same conclusions regarding the statistical significance of the provenance and family variance estimates; the two models also provided the same conclusions with respect to Wald *F*-tests that were conducted to determine whether differences among replicate fixed effects were statistically significant. In conclusion, we found adequate to present the results obtained from a variance component analysis of PET assuming a normal distribution, due to: (i) their analogy with the outcomes from the GLMM assuming a (more flexible) Beta distribution; and (ii) the simplicity of interpreting genetic parameters (e.g. heritabilities and genetic correlations) derived from (co)variances estimated on the observed trait scale.

Selection analysis

As an indicator to assess the degree of multicollinearity in the performed multiple-trait regression analysis, the condition number did not exceed 2.3, and thus was well below the value (i.e. 10) at which the presence of multicollinearity starts to be a concern for parameter estimation and testing [4]. Using studentized deleted residuals from either single- or multiple-trait regression models, histograms and quantile-quantile plots indicated that the residual distributions approximated reasonably well the normal distribution, and evidence of heteroscedasticity was not identified by plots of residuals against fitted values [also corroborated by the White [5] statistical test, which did not detect significant departures from homoscedasticity]. Although five observations were found in general to be associated with large studentized deleted residuals (i.e. ranging between 2.5 and 3, in absolute value), they were not considered to be statistically significant outliers, as their absolute magnitude did not exceed a *t*-distribution critical value corresponding to a Bonferroni-adjusted alpha level (i.e. $0.05/n$) and n-p-1 degrees of freedom (n = number of observations; p = number of independent variables in the regression model).

Methods S3: *Notes on the interpretation of selection differentials and gradients*

Under a single-trait regression model using individual phenotypic values, an estimated standardized selection differential measures the total effects of selection that will modify the phenotypic trait distribution within the given generation, and thus is unable to distinguish between direct selection on the focal trait and selection acting indirectly through other (measured or unmeasured) traits, that also affect fitness and may be phenotypically correlated with the focal trait [6]. In this sense, a directional selection differential quantifies the magnitude of the total effects of linear selection favouring higher or lower trait mean values

[6, 7]. By enabling the estimation of partial regression coefficients, a multiple-trait regression model provides estimates of selection gradients that quantify the effects of selection acting directly on a trait or on a pairwise combination of traits, implying that the effects of indirect selection operating through the other modelled traits have been removed [6]. In this sense, a selection gradient estimates direct selection for a given trait, as the effects of the other measured traits included in the model are held constant. Nevertheless, the multiple-trait regression approach does not preclude the possibility that selection may occur for a measured trait via indirect selection acting on unmeasured characters, which may themselves be subject to selection and also be phenotypically correlated with the measured traits [6, 8].

Using family means in place of individual phenotypic values enables to estimate selection differentials and/or gradients that are less likely to be affected by bias attributed to environmental covariances between fitness and traits, which may be introduced by the individual's microsite when applying a standard phenotypic selection analysis [9, 10, 11]. A requirement for pursuing this approach is that both fitness components and targeted traits are genetically variable, and thus heritable [9, 10]. When compared with the classical method evaluating selection on individual phenotypic variation (i.e. as referred above, and described by Lande and Arnold [6]), selection gradients estimated by using family mean values as observations are less likely to be biased by the omission of important unmeasured traits: to influence estimates of selection gradients, unmeasured traits covarying with fitness (and thus potentially subject to selection) must be both genetically variable and genetically correlated with the measured focal traits [9, 10].

As mentioned in the Materials and Methods section, standardized linear and non-linear selection gradients were estimated separately from first- and second-order polynomial regression models. This separated estimation procedure follows the suggestion of Lande and Arnold [6] in the sense that, when a second-order polynomial model includes linear and

quadratic terms that are correlated, valid estimates of directional selection may be obtained only from a first-order polynomial model. Nevertheless, including linear regression terms in a second-order polynomial model will contribute to remove putative changes caused by directional selection when evaluating the effects of non-linear selection (e.g. influence on the (co)variances of the traits; Lande and Arnold [6]).

2. Supplementary figures

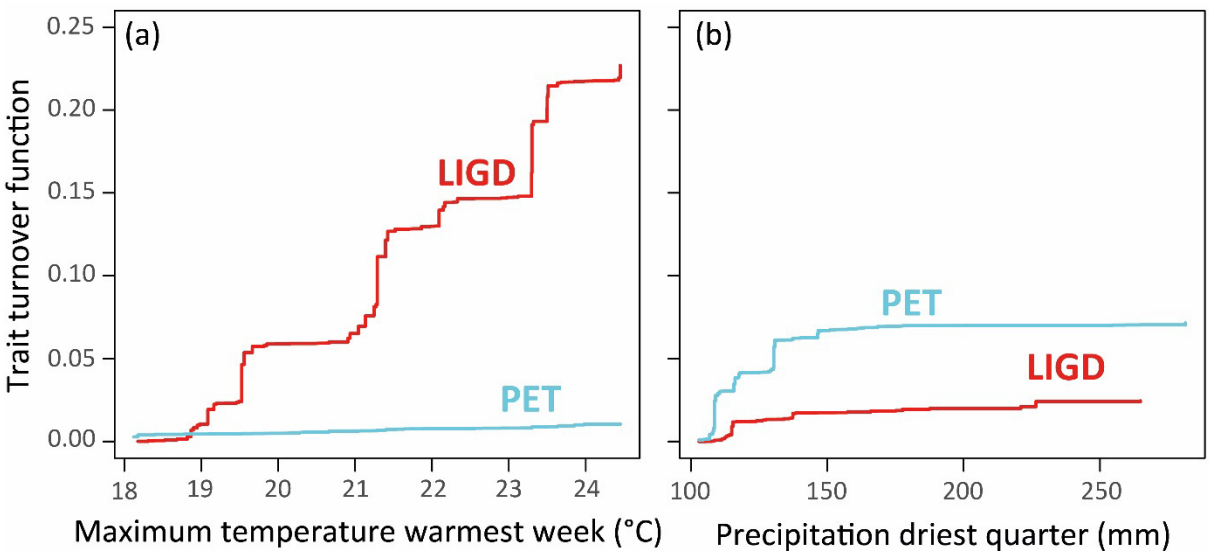

Figure S1. Focal trait turnover functions for the (a) maximum temperature of the warmest week (TMXWW) and (b) precipitation of the driest quarter (RDRYQ) gradients, derived from the gradient forests model fitted as a function of climate (see Table S1) and space/latent environmental variation (Moran's eigenvector map variables; MEMs). The two focal traits (i.e. dependent variables) pertain to lignotuber diameter at the cotyledonary node (LIGD; red line) and percentage of nodes expanded at six months of age which had petiolate leaves (PET; blue line). The maximum curve value obtained along the y-axis for each trait indicates the cumulative importance of the *i*th independent variable whilst averaging the effect of all other independent variables. The cumulative importance is scaled by the weighted conditional importance (R^2_{fi}) for the trait and standardised by the density of observations along the gradient [12]. Steep changes in the curve reflect the location of important changes in trait values along the gradient. The common y-axis visually aids the identification of traits that are changing the most along the gradient [12]. In the present case, LIGD obtains the highest R^2_{fLIGD} with strong change points occurring between 19°C and 24°C.

3. Supplementary tables

Table S1. Bioclimatic variables used in a principal component (PC) analysis to summarise the variation in home-site contemporary climate for the provenances translocated to the studied trial site, as well as to derive the contemporary and growing period climates for this site.

Code	Variable	Contemporary climate at the trial site	Incremental change in the growing period climate relative to the contemporary climate at the trial site	PC1 (54%)	PC2 (18%)	PC3 (16%)	PC4 (7%)
TANN	Annual mean temperature (°C)	11.4	0.5	**0.76**	**-0.60**	-0.22	-0.02
TMDR	Mean diurnal temperature range (°C)	12.3	0.6	**0.65**	0.44	**-0.54**	-0.29
TISO	Isothermality (TMDR/TSPAN)	0.5	0.3	**0.74**	-0.10	-0.30	-0.48
TCVAR	Temperature seasonality (Coefficient of variation)	1.3	0.1	0.35	**0.73**	**-0.55**	-0.06
TMXWW	Max temperature of warmest week (°C)	24.5	1.1	**0.85**	-0.16	-0.47	-0.12
TMNCW	Min temperature of coldest week (°C)	0.8	-0.1	0.48	**-0.87**	0.05	0.08
TSPAN	Temperature annual range (°C)	23.7	1.1	**0.55**	**0.57**	**-0.58**	-0.20
TWETQ	Mean temperature of wettest quarter (°C)	7.5	-0.6	**0.69**	-0.34	0.28	-0.49
TDRYQ	Mean temperature of driest quarter (°C)	15.4	2.2	0.18	-0.21	**-0.65**	**0.54**
TWMQ	Mean temperature of warmest quarter (°C)	16.3	0.7	**0.81**	-0.48	-0.31	-0.02
TCLQ	Mean temperature of coldest quarter (°C)	6.6	-0.1	**0.68**	**-0.71**	-0.12	0.00
RANN	Annual precipitation (mm)	609	-56	**-0.91**	-0.23	-0.31	-0.15
RWETW	Precipitation of wettest week (mm)	16	1	**-0.86**	-0.24	-0.43	-0.04
RDRYW	Precipitation of driest week (mm)	7	0	**-0.91**	-0.16	-0.08	-0.31
RCVAR	Precipitation seasonality (Coefficient of variation)	19	0.3	**-0.40**	-0.12	**-0.76**	0.28
RWETQ	Precipitation of wettest quarter (mm)	190	-23	**-0.87**	-0.22	-0.41	-0.10
RDRYQ	Precipitation of driest quarter (mm)	118	-9	**-0.92**	-0.21	-0.08	-0.28
RWMQ	Precipitation of warmest quarter (mm)	122	-7	**-0.90**	-0.20	-0.05	-0.33
RCLQ	Precipitation of coldest quarter (mm)	179	-21	**-0.87**	-0.24	-0.42	-0.02
Latitude	Decimal degrees south of equator (˚)			-0.12	-0.18	-0.41	0.43
Longitude	Decimal degrees west of the standard meridian (˚)			0.52	-0.26	0.44	0.05
Altitude	Elevation above sea level (m)			**-0.77**	**0.55**	0.28	0.07

Tabulated are: (i) the code and description for each of the 19 bioclimatic variables; (ii) their mean contemporary (1976 - 2005) values for the trial site, and the incremental change (i.e. climate anomaly) during the growing period (2014 - 2018) at the trial site relative to the mean contemporary value; (iii) the Pearson's correlation of the bioclimatic variables (i.e. the variable loadings) to the retained first four principal components (PC1 to PC4); and (iv) the Pearson's correlation of latitude, longitude and altitude with the first four PCs (bold correlations are significantly different from zero at $P < 0.001$). The percentage of variation accounted for by each PC is shown in parenthesis, with the first four PCs explaining 95% of the total variation in the climate data across the 37 native provenances of *Eucalyptus pauciflora* in Tasmania, Australia. Red text indicates the variable within each class of climatic variables (temperature and precipitation) that had the highest correlation with a PC axis, and was relatively independent from other PC axes at the $|r| < 0.7$ level. Growing period bioclimatic variables were calculated by firstly downloading minimum and maximum daily temperature and daily precipitation values for the trial site obtained from the Australian Bureau of Meteorology (http://www.bom.gov.au/jsp/awap/, accessed on the 12 of August, 2018). Daily climate for the trial site was then used to calculate yearly bioclimatic variables in the AUSClim package in R (unpublished R package), and then the yearly bioclimatic variables were averaged over the growing period. The growing period climate mean was then subtracted from the contemporary climate mean for each bioclimatic variable to give the incremental change in climate at the trial site. Notable is the increased heat (positive TMXWW and TDRYQ increments) and decreased water availability (negative RANN increments) experienced during the growing period relative to the contemporary climate for the trial site.

Table S2. Summary statistics for the focal functional traits and fitness surrogate measured in *E. pauciflora*.

	Mean	Phenotypic standard deviation	Family-mean standard deviation
Functional traits			
LIGD (mm)	9.3	2.55	2.09
PET (%)	64.0	14.68	10.75
Fitness surrogate			
HT (m)	3.4	1.22	0.86

LIGD = lignotuber diameter at the cotyledonary node; PET = percentage of nodes expanded at six months of age which had petiolate leaves; HT = total tree height at age 44 months.

4. Supplementary references

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