

SUPPORTING INFORMATION

Appendix S1. Supplementary methods

Simulation model specification

We evaluated how sensitive climate change range projections might be to the effect of dispersal and competition on dispersal, establishment and extinction lags. We developed a 1-dimensional stepping stone model describing the assembly of a meta-community of one hundred species along a temperature (elevation) gradient, inspired by a Lotka-Volterra model of interspecific competition. In the model, we assume that a plant species' distribution along the elevation gradient is principally limited by abiotic factors at the colder range edge (Pellissier *et al.* 2013) and biotic interactions at the warmer edge (Vetaas 2002). As a consequence, we assume that the modelled extinction of alpine plant species under climate change only results from increased competition from colonizing species arriving from warmer areas. The 1-dimensional landscape contains 500 cells each containing a single community, forming a regular linear temperature gradient varying between 0 and 20 °C. The model is characterized by the following parameters:

Dispersal: each population in each cell exports a fraction d of its population to the neighbouring cells. The two cells at the extremes of the landscape only export a fraction $d/2$ of their populations to their unique neighbouring cell.

Growth rate: the growth rate of species i increases with temperature at a rate g_i . It is characterized by a value T_{min_i} , which is the lowest temperature at which species i has a positive growth rate in the absence of competition.

Sensitivity to competition: the relative growth rate of species i in a community decreases linearly with the total community plant biomass at a rate l_i . This can be interpreted as a consequence of overall competition for nutrients, light or space from both inter- and intra-specific competitors.

Intraspecific competition: the growth rate of species i decreases at a rate c_i with the biomass of conspecifics; an additional term for intraspecific competition is necessary to describe the greater niche overlap expected between conspecifics than heterospecifics that stabilizes coexistence (Chesson 2000).

Each species is thus characterized by four theoretical traits: g_i , $Tmin_i$, l_i and c_i . We assume that species can be placed on a single trade-off axis that contrasts fast-growing (high g_i), stress-sensitive (high $Tmin_i$), competitive species that are highly tolerant of neighbouring biomass (low l_i), and slow-growing, stress-tolerant, competition intolerant species (C to S axis; Grime 1977). As a consequence, the modelled species are distributed along a linear functional axis, where g_i and $Tmin_i$ are positively linearly related and l_i is negatively linearly related to $Tmin_i$. Such a trade-off is expected, since many alpine species have a stronger tolerance to climatic stress, have low growth rate and low tolerance to competition (Maestre *et al.* 2009; Alexander *et al.* 2015). We fixed c_i to the same value for all species (see Table S1 for parameters values).

The biomass of species i in cell j at time $t+1$, $P_{i,j,t+1}$, can be calculated from the population of species i in cell j at time t , $P_{i,j,t}$, in two successive operations. First, we derive the population size after dispersal between neighbouring cells:

$$P'_{i,j,t} = (1 - d) \times P_{i,j,t} + \frac{d}{2} \times (P_{i,j+1,t} + P_{i,j-1,t}) \quad (\text{Equation 1})$$

Cells at the extremity of the gradient have only a single neighbouring cell and thus disperse only a fraction $d/2$ of their population. Second, we derive population size after taking into account population growth and competitive interactions:

$$P_{i,j,t+1} = P'_{i,j,t} + \Delta t \times P'_{i,j,t} [g_i(T_j - T_{min_i}) - c_i P'_{i,j,t} - l_i \sum_k P'_{k,j,t}] \quad (\text{Equation 2})$$

We generated 500 species pools of 100 species: we first drew the parameters of the distribution of species trait values g_i and l_i (mean and range width, hereafter referred to as “variation”, Table S1). Then in each species pool, we drew T_{min_i} values from a uniform distribution (Table S1) and deduced the values of the other traits g_i and l_i , with which they were collinear. The dispersal rate was drawn from a log distribution (Table S1). Each community had all species at the same initial abundance of 0.02. We let the model run for 40,000 time steps until the meta-community converged to a stable state. We evaluated the structure of the initial meta-community by calculating its mean α -diversity and β -diversity based on the inverse of the Simpson index (Jost 2007) (results are detailed below in *Influence of dispersal and species pool structure on initial meta-community structure*). Then we simulated a warming of +3 °C across the landscape occurring over 20,000 demographic time steps. As local temperature rises, species increase their growth, can disperse to cells previously outside of their distribution, and can eventually replace local species through competition.

Computation and analysis of community turnover

We analysed turnover in the meta-community by measuring the pairwise β -diversity of each community between the beginning and the end of the warming period. The β -diversity was calculated according to the definition of “true β -diversity” (Jost 2007; Tuomisto 2010) as follows: P_1 is the vector of species’ initial relative abundances in a community; P_2 is the vector of species’ final relative abundances in a community; and P_{12} is the vector of species’ averaged relative

abundances in a community across both dates. D is the Simpson diversity function. For a vector $P = \{p_i\}$ of species' relative abundances in a community:

$$D(P) = \frac{1}{\sum_i p_i^2} \quad (\text{Equation 3})$$

The turnover (β -diversity) of a community across the two dates is then:

$$\beta = \frac{D(P_{12})}{[0.5(D(P_1)^{-1} + D(P_2)^{-1})]^{-1}} \quad (\text{Equation 4})$$

β varies between 1, where there is no change in the community between the two dates, and 2, where the community changed completely. We standardized this value by subtracting 1 so that β varies between 0 and 1 (Chao *et al.* 2012). The mathematical formula is not defined for cases where the community is empty on one or both of the two dates.

To establish the importance of different parameters to community turnover following warming, we used a linear mixed model that linked the community β -diversity to dispersal rate d , and the mean and coefficient of variation in l_i and g_i . The 500 different species pools were treated as a random effect. We excluded from the model communities with a temperature lower than 4. These communities were often empty at the beginning of the simulation and became colonized following warming, and therefore their β -diversity value could not be defined by our index. We also excluded communities from the model that had an initial temperature above 17. Following warming, these communities displayed a community structure that was dominated by an edge effect (i.e. there were no competitors from warmer communities that could invade these communities). We evaluated the goodness of fit of the model with the marginal R^2 of the model

for the fixed effects, and conditional R^2 accounting for variance explained by both random and fixed effects (Nakagawa & Schielzeth 2013).

Finally, to illustrate the magnitude of lags in community turnover, we compared β -diversity from the simulations to the β -diversity obtained assuming that species track climate change without dispersal, establishment or extinction lags, and assuming that community abundance structure is left unchanged by this tracking. This is analogous to results that would be obtained by simply stacking species distribution model (SDM) projections. Under this scenario, we simply projected initial community structure “higher” along the gradient, so that communities occupy the same temperature after warming, and then quantified the β -diversity of each cell before and after the warming period.

Influence of dispersal and species pool structure on initial meta-community structure

To assess collinearity between the initial meta-community structure and the simulation parameters, we analysed the initial structure of the meta-community generated by our simulations by measuring its mean α -diversity and spatial β -diversity. β -diversity was derived from the inverse of the Simpson index, which accounts for species' relative abundances (Jost 2007; Tuomisto 2010). We then used linear models to explain variation in mean α -diversity and spatial β -diversity across our simulations from the dispersal rate and species pool structure (Table S2). The meta-community becomes more diverse (high mean α -diversity) and with a greater turnover along the gradient (high β -diversity) with increasing variation in g_i and l_i . When the mean of g_i and l_i were high, the meta-community was less diverse and displayed a weaker spatial turnover, likely because these high rates favour competitive exclusion (species tends to have both a high growth rate and to be sensitive to competition). Finally when there was a high dispersal rate, the meta-community was less diverse and displayed a lower spatial turnover. This is likely because

species are able to persist in cells with a temperature lower than the minimum temperature they can tolerate through source-sink dynamics, thus decreasing turnover and exerting competitive interference with less competitive, more stress-adapted species.

Supplementary references

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Table S1. The parameter distributions used within or across simulations.

Parameter	Values
Initial cell temperature range	[0, 20]
N	100
$\log_{10}(d)$	U[-4, -1]
$Tmin_i$	U[4 16.5]
Mean g_i	U[0.2, 0.5]
Coefficient of variation in g_i	U[0.1, $1/\sqrt{3}$]
Mean l_i	U[0.7, 1.5]
Coefficient of variation in l_i	U[0.1, $1/\sqrt{3}$]
c_i	0.2
Δt	0.025

Table S2. Parameter estimates (\pm SD) from the linear models linking initial community mean α -diversity and β -diversity to dispersal rate, mean/coefficient of variation in growth rate and sensitivity to competition. R^2 for the models of α -diversity and β -diversity were 0.33 and 0.78, respectively. Because all covariates and response variables were standardized, the parameter estimates are also effect sizes (***) $P < 0.001$). For all parameters, d.f. = 1 and residual d.f. = 494.

Parameter	Mean α-diversity (Estimate \pm SD)	β-diversity (Estimate \pm SD)
Intercept	0.000 (0.037)	0.000 (0.013)
Mean of g_i	-0.450 (0.037)	0.0379 (0.0131)***
Coefficient of variation in g_i	0.469 (0.371)***	0.922 (0.013)***
Mean of l_i	-0.188 (0.370)***	0.0307 (0.013)
Coefficient of variation in l_i	-0.215 (0.370)***	0.132 (0.013)***
Dispersal (log transformed)	-0.0403 (0.037)	-0.230 (0.013)***

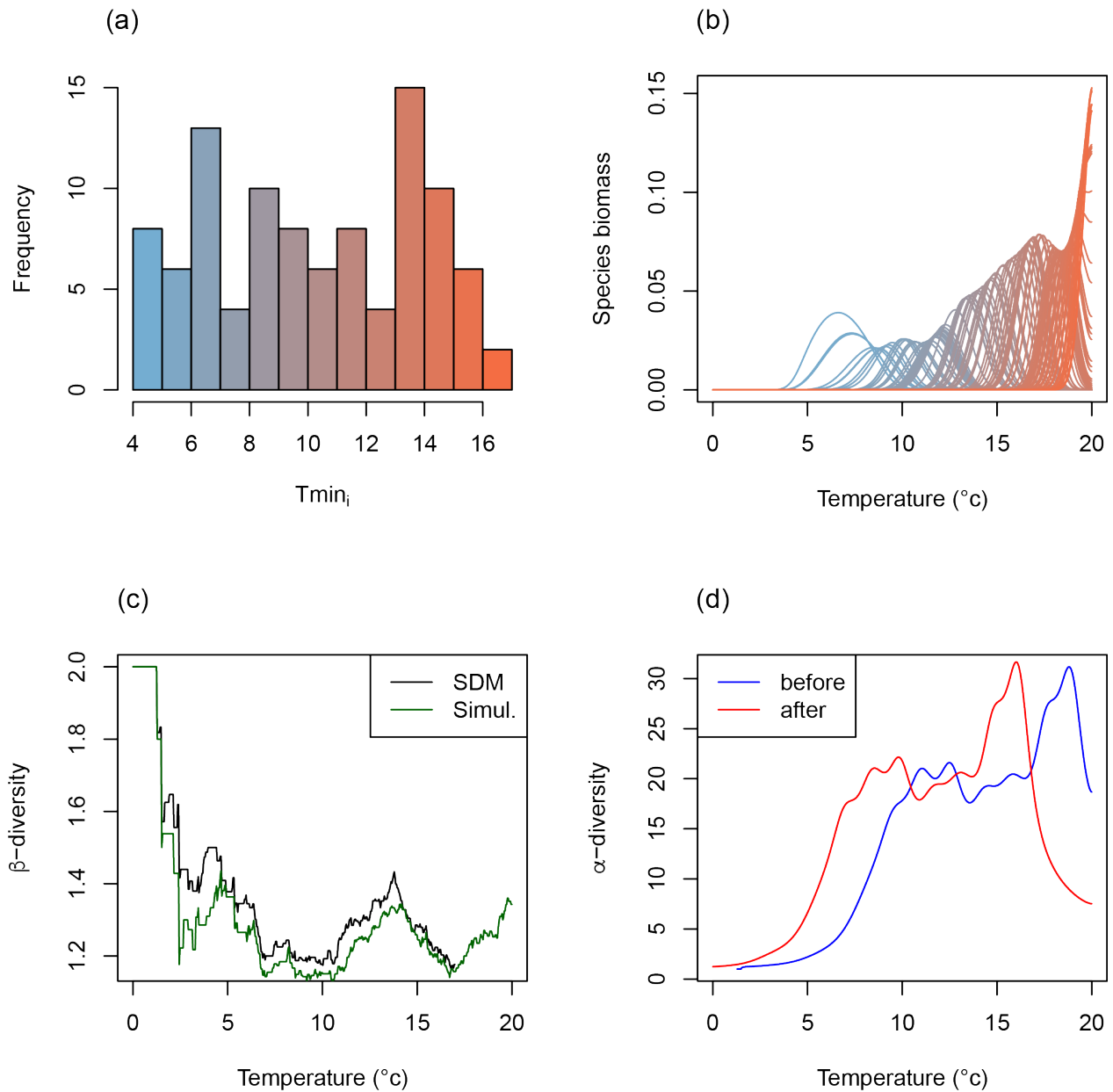


Figure S1. An example of a meta-community generated with the averages of the parameter values shown in Table S1: (a) the distribution of $Tmin$ values (sampled from a uniform distribution); (b) the initial distribution of species' biomass along the temperature gradient, where species found growing in low temperature sites have a lower biomass than species from higher temperature conditions (colour [blue–red] reflects the value of $Tmin$ [low–high] for each species). (c) Community turnover due to warming (β -diversity), contrasting the prediction of our model (green) with the “SDM-like” prediction (black; see main text), and (d) community α -diversity (calculated as the inverse of Simpson's index) before (blue) and after (red) warming.

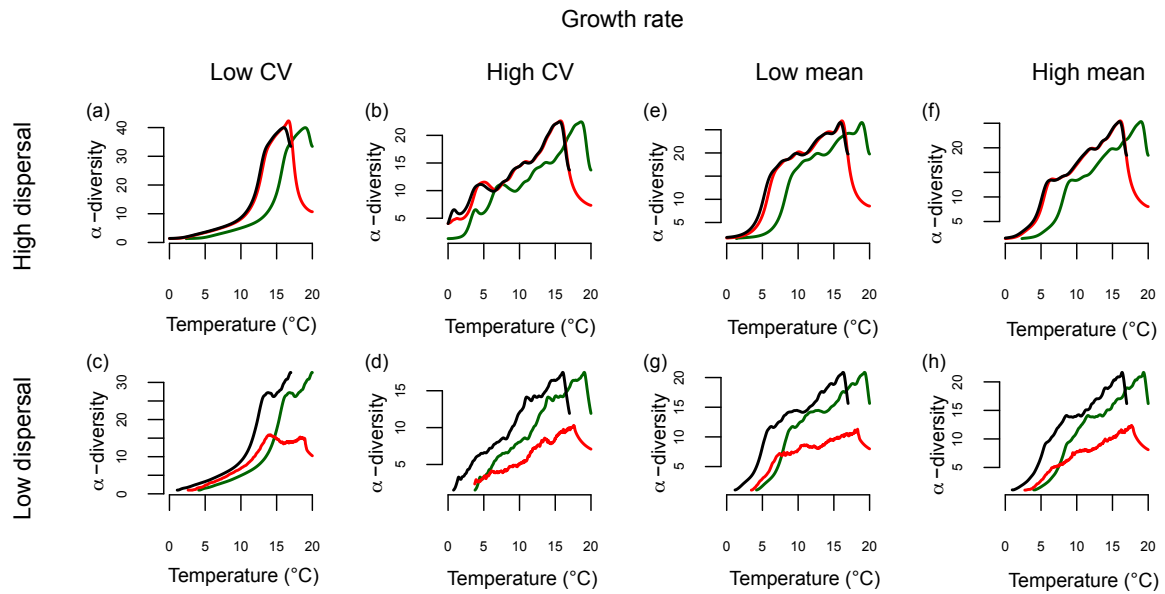


Figure S2. Species diversity along an elevation temperature gradient (α -diversity, calculated as the inverse of Simpson's index) before (green) and after climate warming, according to projections from simulations (red) and from stacked species distribution model projections (black). Shown are eight scenarios that differ depending on dispersal ability (rows) and growth rate within the species pool (a, e: coefficient of variation [CV] = 0.1; b, f: CV = $1/\sqrt{3}$; c, g: mean = 0.7; d, h: mean = 1.5; a-d: $d = 10^{-1}$; e-h: $d = 10^{-4}$). In each panel, all other parameters except the ones specified in the header of their line and column were set to the average value of their respective distribution (see Table S1).

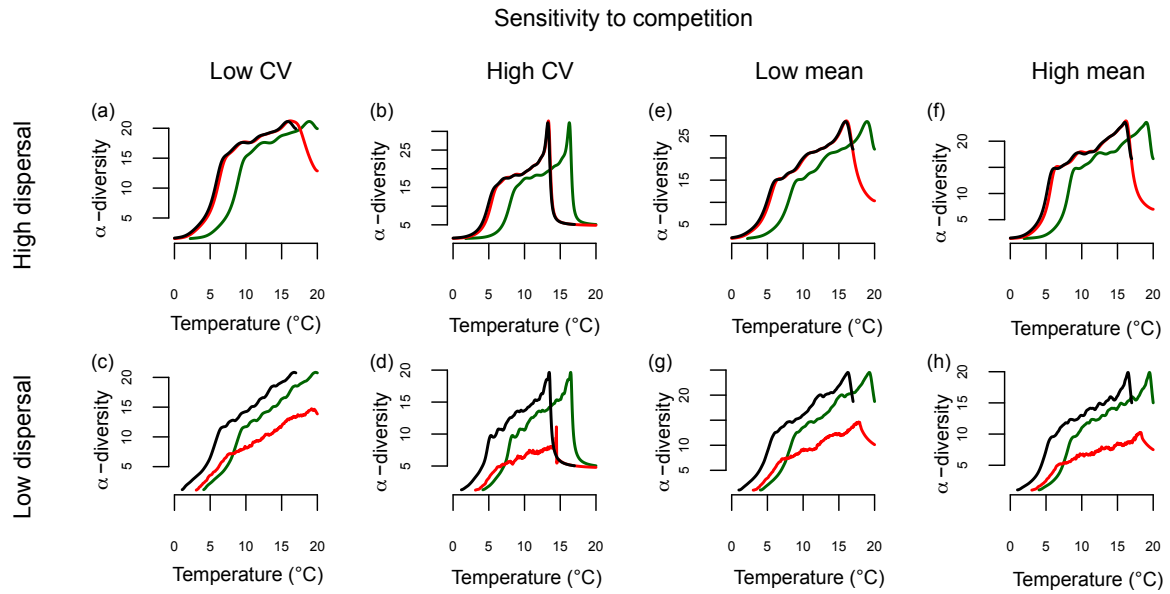


Figure S3. Species diversity along an elevation temperature gradient (α -diversity, calculated as the inverse of Simpson's index) before (green) and after climate warming, according to projections from simulations (red) and from stacked species distribution model projections (black). Shown are eight scenarios that differ depending on dispersal ability (rows) and sensitivity to competition within the species pool (a, e: coefficient of variation [CV] = 0.1; b, f: CV = $1/\sqrt{3}$; c, g: mean = 0.7; d, h: mean = 1.5; a-d: $d = 10^{-1}$; e-h: $d = 10^{-4}$). In each panel, all other parameters except the ones specified in the header of their line and column were set to the average value of their respective distribution (see Table S1).