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Supplementary Information for
Red-listed plants are contracting their elevational range faster than common plants in the European Alps

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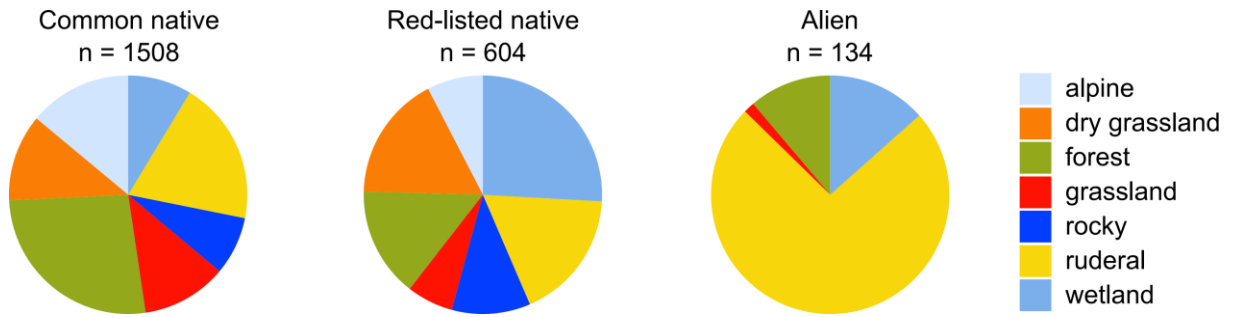
This PDF file includes:

Fig S1. Proportion of species belonging to each habitat preference category for common native, red-listed native and alien species.

Fig. S2 Study area. Trento Province located in NE Italy, covering 6'207 km^2 over an elevational range of 66–3'769 m a.s.l.
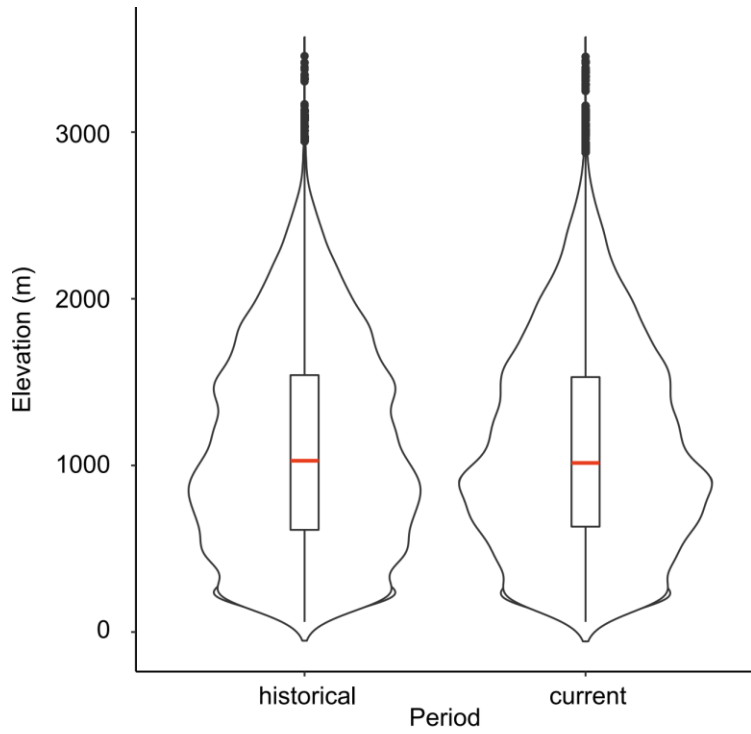
Fig. S3. Violin plots describing the record distribution along the elevational gradient in the historical and current period (1990-2004 vs. 2005-2019). The box indicates the interquartile range, with the black vertical lines showing the lower (25%) and upper quartiles (75%) and the red horizontal line indicating record median elevation.
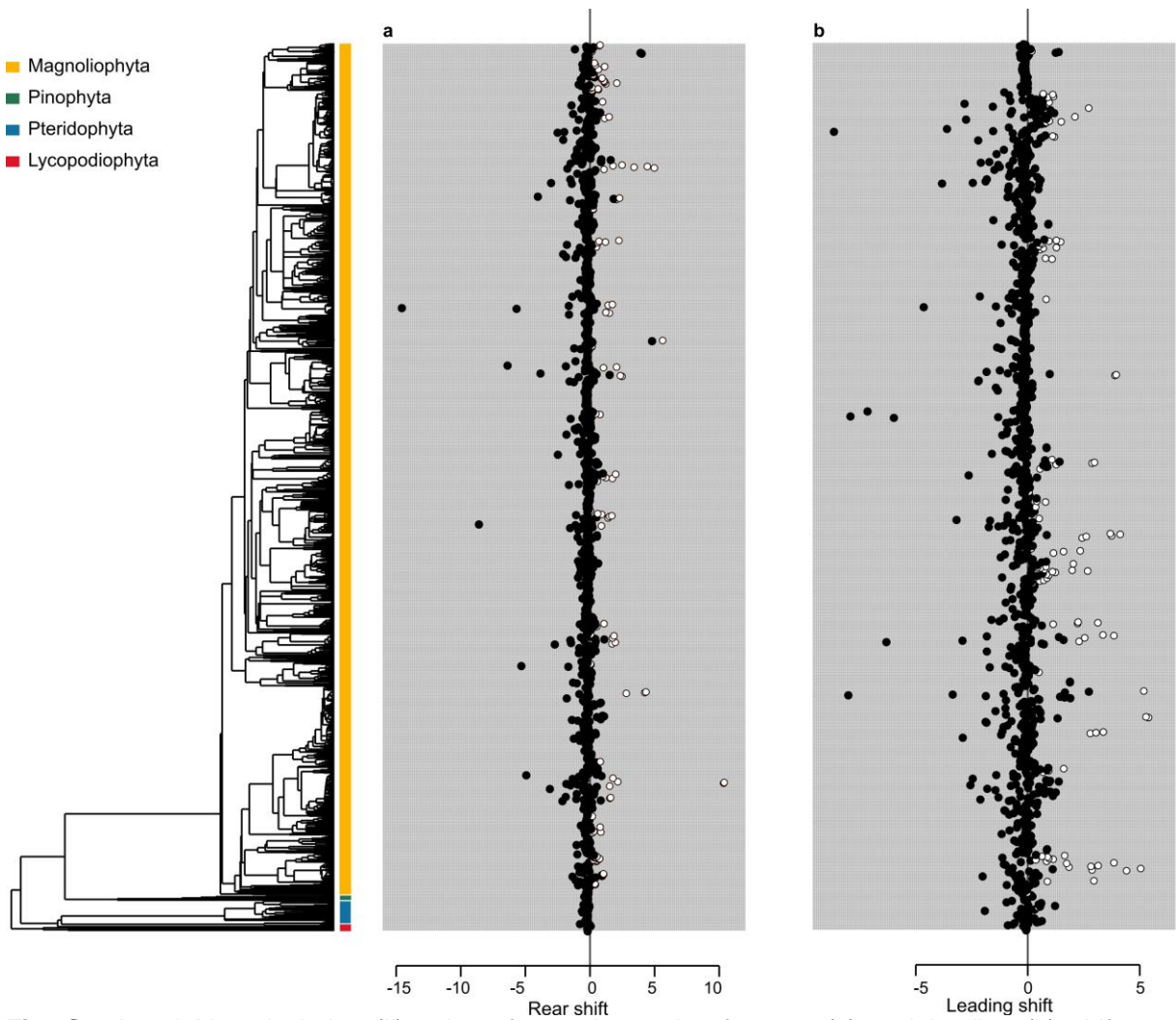
Fig. S4. Local Moran's index (Ii) values for each species for rear (a) and leading (b) shift computed with lipaMoran and plotted with dotplot.phylo4d. White points indicate significant Ii values. Different colours highlight different phyla along the phylogenetic tree. Overall, we observed only weak positive phylogenetic correlation in a few clusters. Global metrics suggested a weak phylogenetic signal (Table S3).
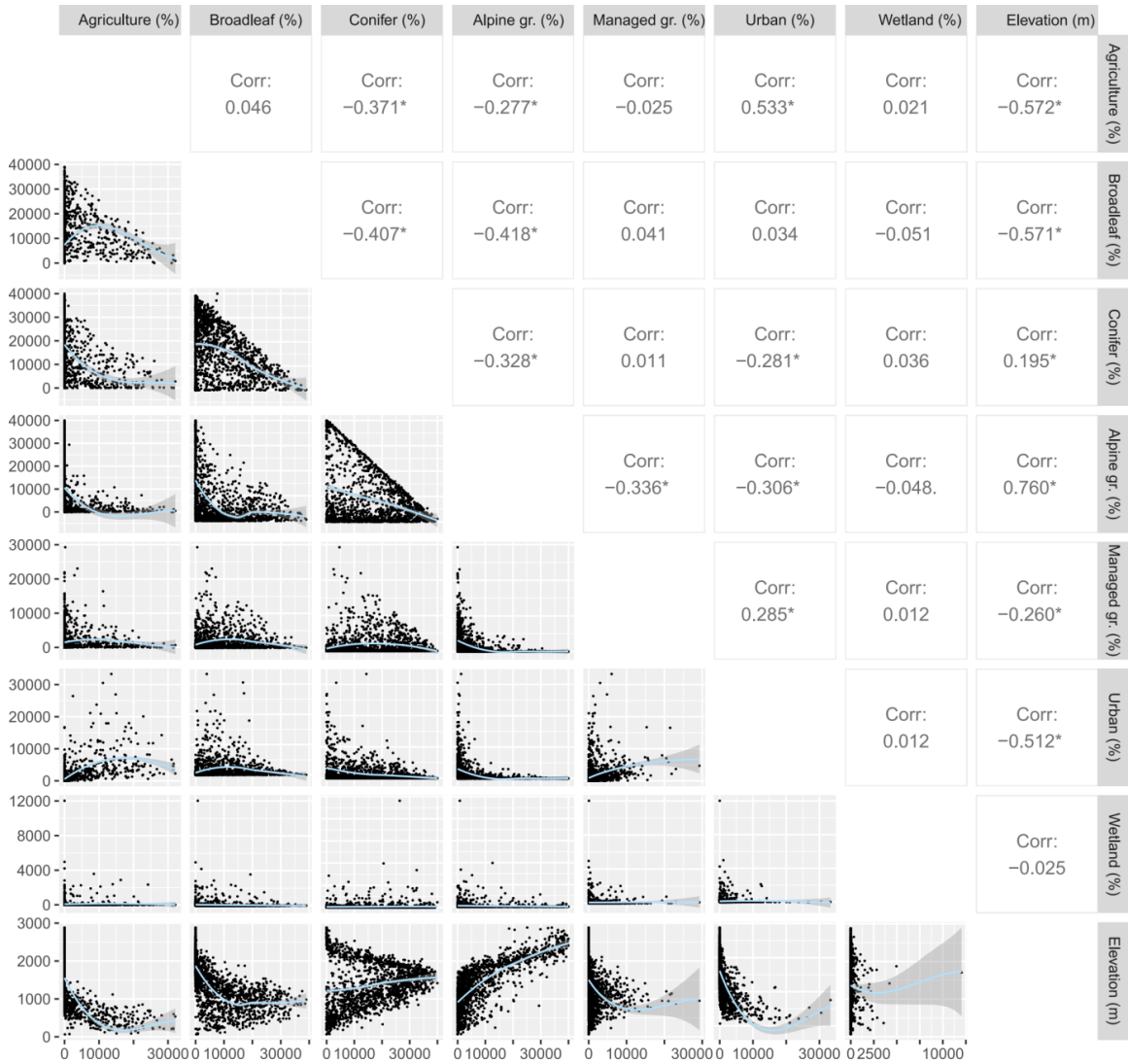
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Fig. S5. Correlation between mean elevation and cover of agriculture, broadleaf forest, conifer forest, alpine grassland, managed grassland, urban, and wetland quantified (ha) in each grid cell (2 × 2 km^2). Light blue lines indicate a smooth local regression. Corr indicates the Pearson's correlation coefficient.

Table S1. Effect of status (common native red-listed native and alien), edge type (rear and leading) and their interaction on rate of range shift. We fitted a non-parametric permutation test with species as random effect (N permutations = 1000) using the aovp function in the lmPerm package with default settings. N = 1,479 species.

Fixed effect	df	SS	P-value
Status	2	26	1.000
Edge type	1	467	1.000
Status × Edge type	2	1098	<0.001

Table S2. Effect of status (common native red-listed native and alien), edge type (rear and leading) and their interaction on rate of range shift. We fitted a non-parametric permutation two-way between-within subjects ANOVA with species as random effect using the function bwtrim() in the R package WRS2. N permutations = 1000. The response variable shift was transformed by trimming means by 5 %, 10 %, 20 % and 30 % (two tails). N = 1,479 species.

Trim level for the mean (%)	Fixed effect	Q	P-value
0.05	Status	0.332	0.718
	Edge type	0.188	0.665
	Status × Edge type	19.810	<0.01
0.10	Status	0.839	0.435
	Edge type	0.110	0.741
	Status × Edge type	25.829	<0.01
0.20	Status	1.477	0.234
	Edge type	0.015	0.903
	Status × Edge type	29.227	<0.01
0.30	Status	2.053	0.137
	Edge type	0.112	0.739
	Status × Edge type	28.737	<0.01

Table S3. Results from tests of a phylogenetic signal in the distribution of the leading and rear shift. C_{mean} = the Abouheif's Cmean index; I = the Moran's I index; K = Blomberg's K, K* = Blomberg's K *and λ = Pagel's λ. We used the function phyloSignal() of the R package phylosignal (see Methods for details). N = 1,234 species. Moran's I and Abouheif's Cmean are autocorrelation indices not based on an evolutionary model, whereas, Blomberg's K, K * and Pagel's λ assume a Brownian motion of trait evolution (Münkemüller et al., 2012). Hence, a value of K, K* or λ close to zero indicates phylogenetic independence and a value of one indicates that species' traits are distributed under Brownian motion. Reported values for the distribution of the leading and rear shift are close to 0 and, therefore, indicate phylogenetic independence. Overall, all indices usually show high uncertainties in P-values for random trait distributions and they are strongly influenced by sample size (Münkemüller et al., 2012). This explains the high variability and small values of the observed P-values. The index most affected by sample size is Moran's I, while the least affected is Pagel's λ. In addition, Pagel's λ shows the smallest type I error when testing for phylogenetic signal against random expectations. Here, Pagel's λ reported no phylogenetic signal for both leading and rear shift distribution.

Response variable	Test	Statistic	P-value
Leading shift	C_{mean}	0.032	0.048
	I	0.001	0.067
	K	0.024	0.394
	K*	0.057	0.692
	λ	0.028	1.000
Rear shift	C_{mean}	0.057	0.004
	I	0.003	0.012
	K	0.022	0.775
	K*	0.056	0.699
	λ	<0.001	1.000

Reference
Münkemüller, T., Lavergne, S., Bzeznik, B., Dray, S., Jombart, T., Schiffers, K., & Thuiller, W. (2012). How to measure and test phylogenetic signal. Methods in Ecology and Evolution, 3, 743-756.