SUPPORTING INFORMATION

Climate oscillations and species interactions: large scale congruence but regional differences in the phylogeographic structures of an alpine plant and its monophagous insect

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Appendix S1 Sampled populations of *Oreina gloriosa* and *Peucedanum ostruthium* with their geographical coordinates and the number of analysed individuals.

					Number of analysed individuals	
Country	**Code**	**Population**	**Elevation (m)**	**Geographical coordinates**	***Oreina* sequencing/AFLP**	***Peucedanum* AFLP**
France	AFR	Ailefroide	1700	44°53'N, 06°26'E	3/3	3
Switzerland	BOG	Bosco Gurin	1858	46°18'N, 08°27'E	1/1	3
France	BOR	Le Boréon	1795	44°06’N, 07°18’E	1/2	2
Italy	BRC	Breuil-Cervinia	2149	45°55’N, 07°37’E	3/3	3
Italy	BRE	Vallon du Breuil	1996	45°42’N, 06°52’E	2/2	2
Switzerland	CDM	Col des Mosses	1843	46°23’N, 07°07’E	2/2	2
Switzerland	CHA	Chandolin	1945	46°14'N, 07°36'E	2/1	3
Switzerland	EMO	Lac de l’Emosson	1949	46°03'N, 06°55'E	3/3	2
France	GAL	Col du Galibier	1658	45°05'N, 06°26'E	3/3	2
Austria	GKO	Graukogel	1647	47°06’N, 13°09’E	3/3	2
Switzerland	GLT	Gletsch	1634	46°33'N, 08°21'E	2/2	1
Switzerland	GON	Gondo	1554	46°09’N, 80°06’E	3/3	3
Italy	HEI	Madonna di Senale	1559	46°43’N, 10°51’E	2/2	3
France	ISE	Col de l’Iseran	1818	45°23'N, 07°02'E	2/2	3
France	ISO	Isola 2000	1855	44°11'N, 07°08'E	2/2	1
Switzerland	LAF	La Fouly	1571	45°56'N, 07°05'E	3/3	2
Switzerland	LDT	Lai da Tuma	1997	46°39'N, 08°40'E	2/2	3
Germany	OBE	Oberstdorf	1496	47°24’N, 10°20’E	2/2	3
France	PAL	Lac Palluel	1855	44°44'N, 06°26'E	2/2	3
Switzerland	PES	Alp Pesca	1900	46°13'N, 10°04'E	2/2	3
Switzerland	SAG	Saas Grund	1639	46°06'N, 07°56'E	3/3	1
Italy	VDD	Valle di Daone	1319	46°01'N, 10°30'E	1/1	3

Appendix S2 Cross-check of Procrustes results with a non-model based approach.

The Procrustes rotation analysis allowed comparison of the phylogeography of *Oreina gloriosa* with that of its host plant *Peucedanum ostruthium*. The procedure was initially applied using STRUCTURE 2.2 (Falush *et al*., 2007) assignment probabilities as an input. In order to validate these results with a non-model based approach, we performed a Procrustes rotation analysis using inter-population differentiations (G_{ST}), computed from the Shannon diversity index. The procedure worked as follows. (1) The Shannon index was applied to measure the total genetic diversity and its partitions within- and between populations (Equation 1). (2) The population differentiation (i.e. G_{ST}) was then measured as the proportion of diversity occurring between populations, in regard to the total genetic diversity (Equation 2). (3) Applying the procedure in pairwise manner allowed the construction of a distance matrix of G_{ST} values between populations. (4) This distance matrix was finally projected on principal component axes (using a principal coordinates analysis) to compute centroid coordinates for each population. (5) The Procrustes rotation analysis was applied on the centroid coordinates obtained from the *O. gloriosa* and *P. osthrutium* AFLP datasets.

Equation 1

$$Shan_x = -\sum_{1}^{nloci} p_{xi} \cdot \ln(p_{xi}) \;,\; S_{within} = Shan_x + Shan_y \;,\; S_{Total} = Shan_{x \cup y},\; S_{between} = S_{Total} - S_{within}$$

where $Shan_x$ is the Shannon diversity index of population *x*, *nloci* is the number of AFLP loci in the dataset, p_{xi} is the band presence frequency of the ith locus in population *x*. $Shan_x$ and $Shan_y$ are the respective Shannon diversity indices of populations *x* and *y*, $Shan_{x \cup y}$ is the Shannon diversity of the union of population *x* and *y* (i.e. the data of both populations are merged into a single group for which the Shannon diversity is computed).

Equation 2

$$G_{ST} = \frac{S_{between}}{S_{Total}}$$

The results obtained using STRUCTURE assignment probabilities or Shannon-based G_{ST} values were largely congruent (Fig. S1) and only results of the former approach were presented in the manuscript.

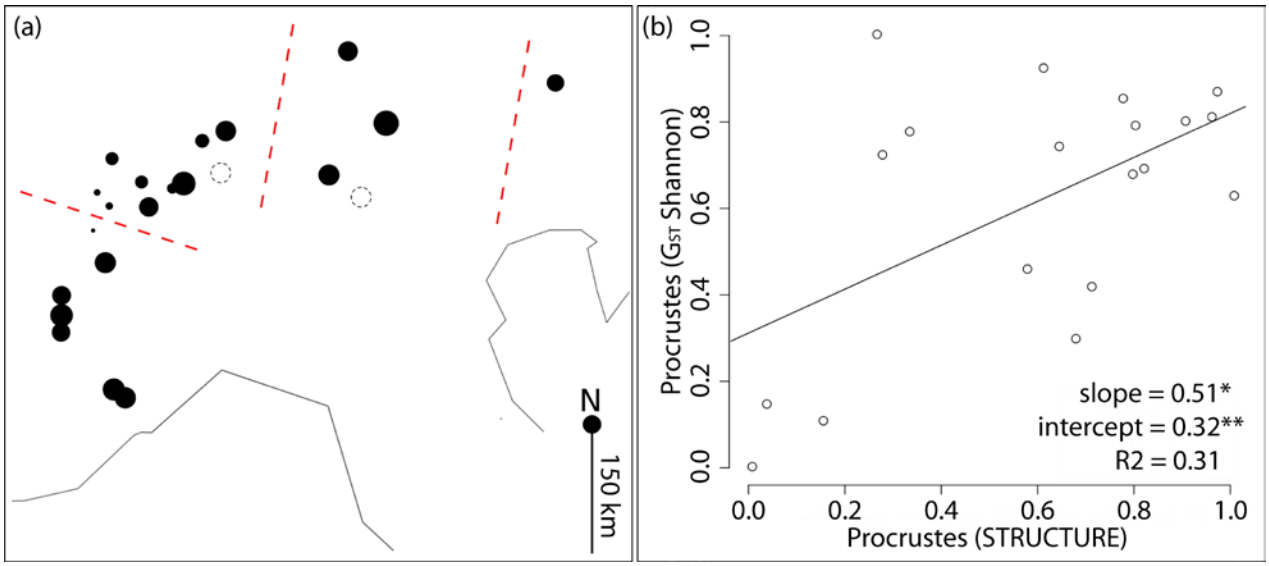


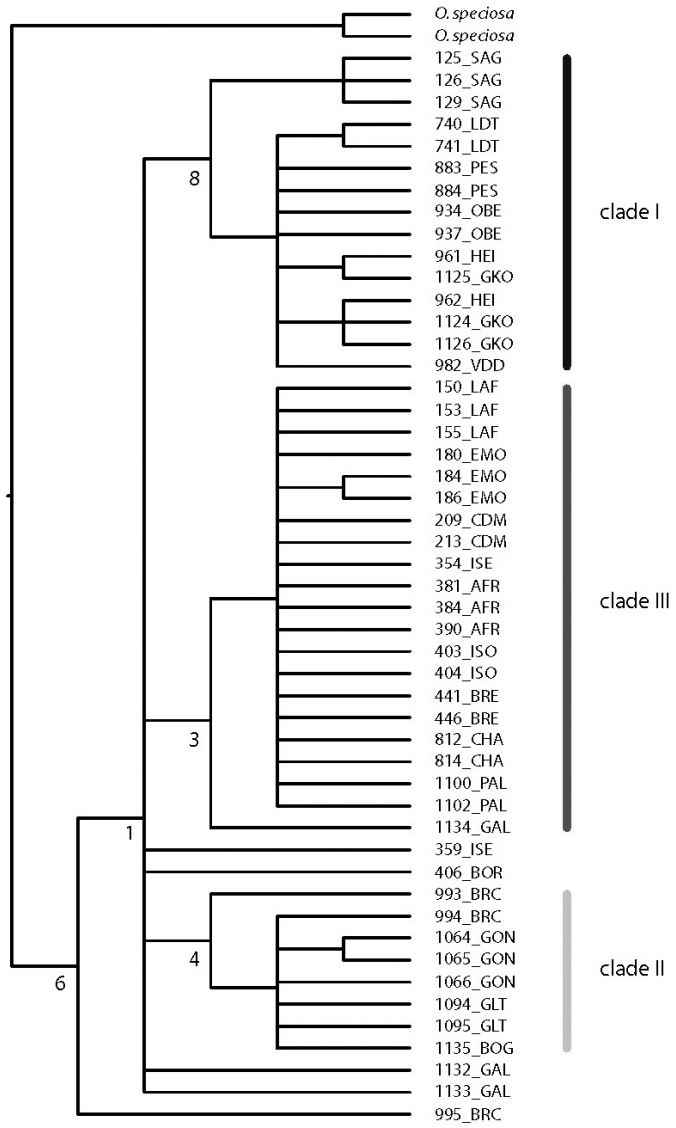
Figure S1 (a) Procrustes analysis, as obtained using inter-population G_{ST} values. (b) Comparison of Procrustes analysis results obtained using either STRUCTURE-based probability assignments (*x*-axis) or inter-population G_{ST} values (*y*-axis). The slope, intercept, R^2 and the significance levels (* *P*-value < 0.05, ** *P*-value < 0.01) of the linear model are provided. Note that two populations (i.e. BOG and VDD) were excluded from comparisons, due to insufficient sampling efforts in the *O. gloriosa* AFLP dataset (indicated as dashed circles in A).

REFERENCE

Falush, D., Stephens, M. & Pritchard, J.K. (2007) Inference of population structure using multilocus genotype data: dominant markers and null alleles. *Molecular Ecology Notes*, **7**, 574-578.

Appendix S3 Supplementary results: (a) strict consensus tree of the maximum parsimony analysis for the *Oreina gloriosa* sequence dataset, and (b) contingency table comparing the grouping of *O. gloriosa* individuals using AFLP and mtDNA data.

(a) Strict consensus tree of the maximum parsimony analysis for the *Oreina gloriosa* sequence dataset. The three well defined clades, also illustrated in the Bayesian approach (Fig. 2), are circumscribed and node supports are given by Bremer supports (decay index).



(b) Contingency table comparing the grouping of *Oreina gloriosa* individuals by AFLP-based STRUCTURE 2.2 clustering (in columns) and mitochondrial (mt) DNA clades retrieved using BEAST (in rows) for samples that were placed in both a defined mtDNA clade and in a STRUCTURE group. Group names refer to colour codes in Figs 1 & 2. Matching percentages for the three mtDNA clades and the main three STRUCTURE groups (in bold) are 77%, 56% and 85%, for clades I, II and III, respectively.

	STRUCTURE groups						
mtDNA clade	**purple**	**yellow**	**green**	light blue	red	black	Total
clade I (black)	**10**	2		1			13
clade II (grey)		**5**				1	6
clade III (white)		1	**17**		2		20
Total	10	8	17	1	2	1	39