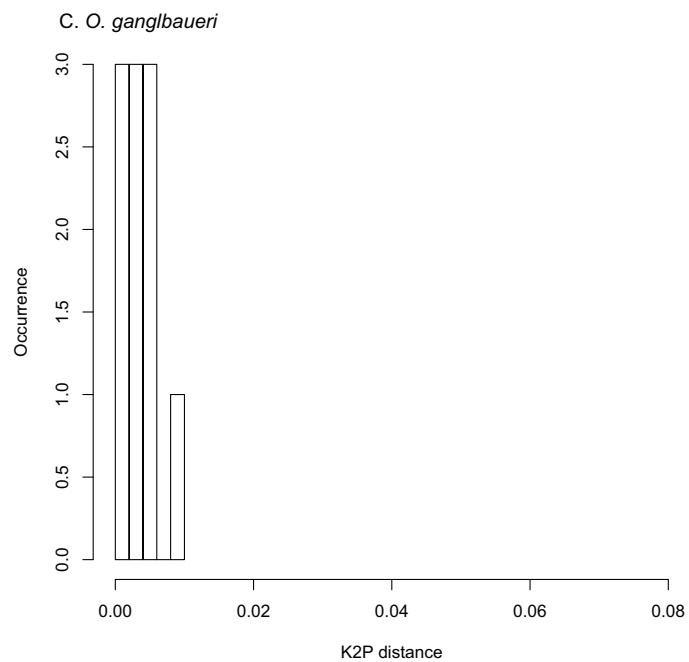
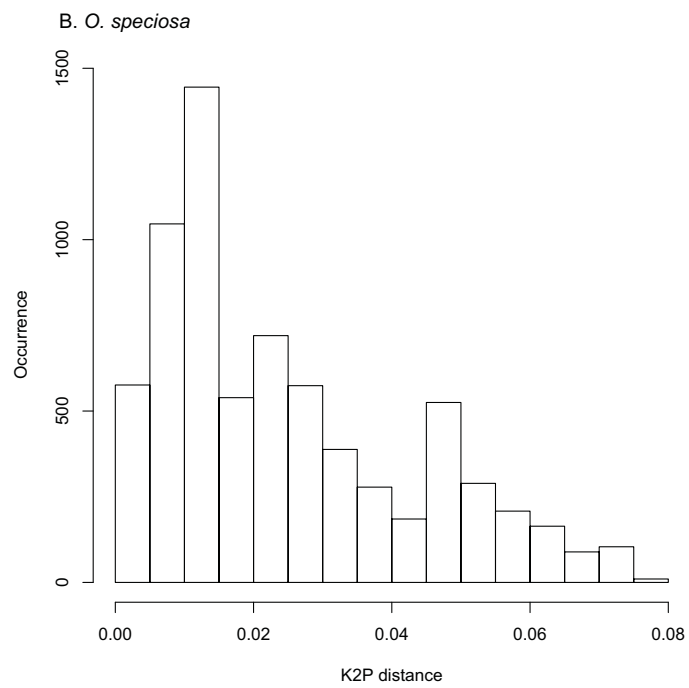
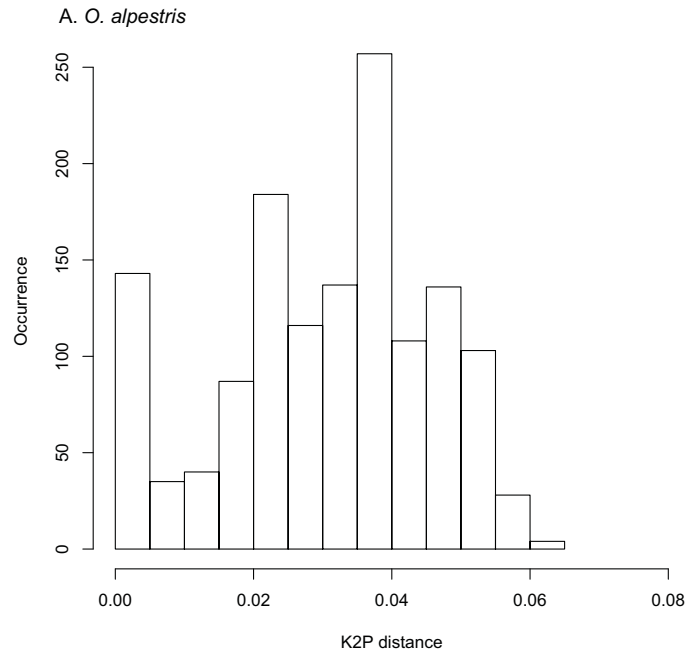


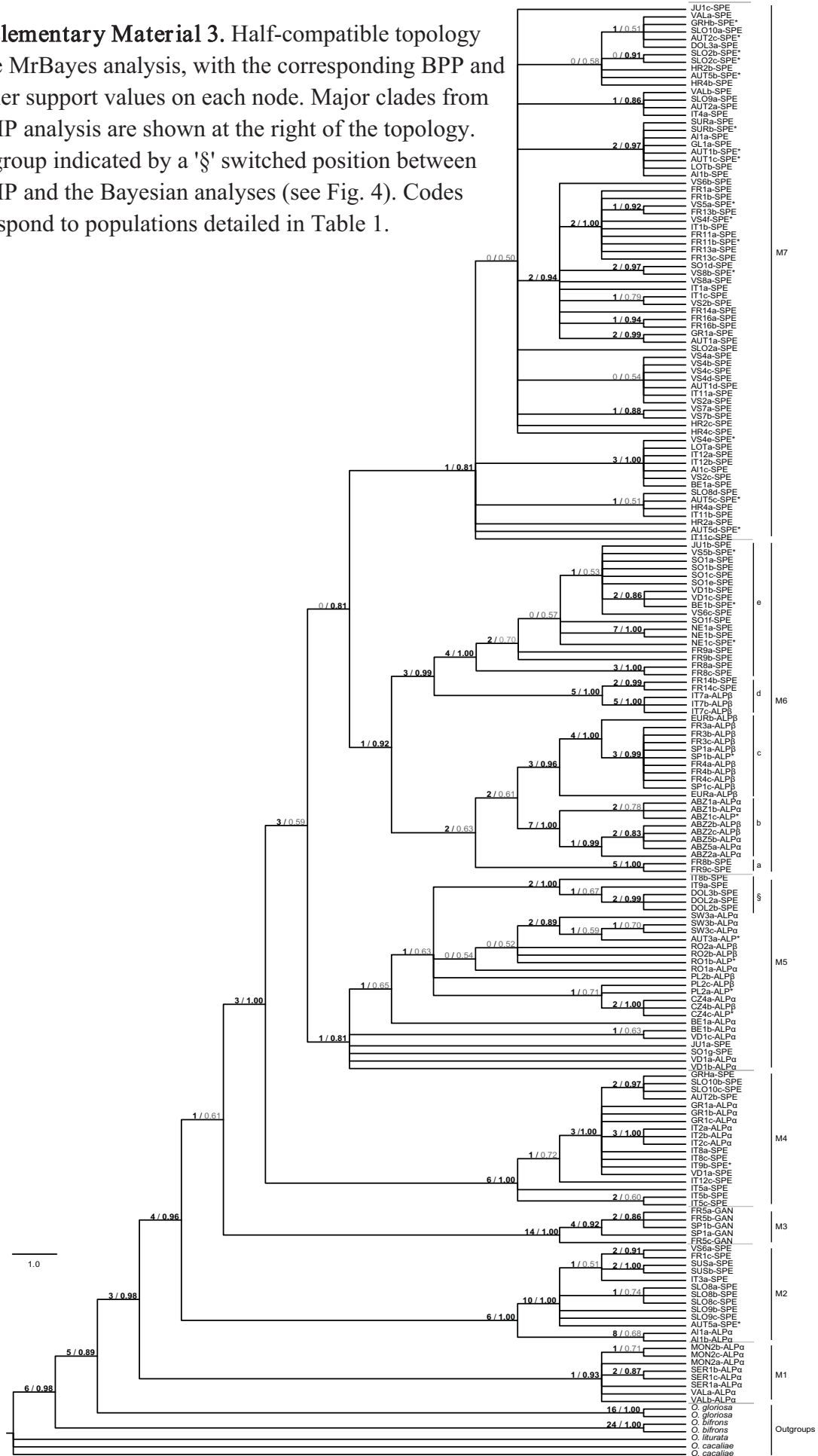
Supplementary Material 1. Contingency table showing the number of individuals cross-classified by morphological categories, mtDNA and nuclear phylogenetic clades.

<i>ITS2</i> clustering	genitalic morphology	mtDNA clustering							Total
		M1	M2	M3	M4	M5	M6	M7	
N0	alpestris α			1			5		6
	alpestris β						15		15
	speciosa			9	11	2	19	61	102
Total N0				10	11	2	39	61	123
N1	ganglbaueri		5						5
Total N1			5						5
N2	alpestris α	8		1	6	10			25
	alpestris β					5			5
Total N2		8		1	6	15			30
Total		8	5	11	17	17	39	61	158

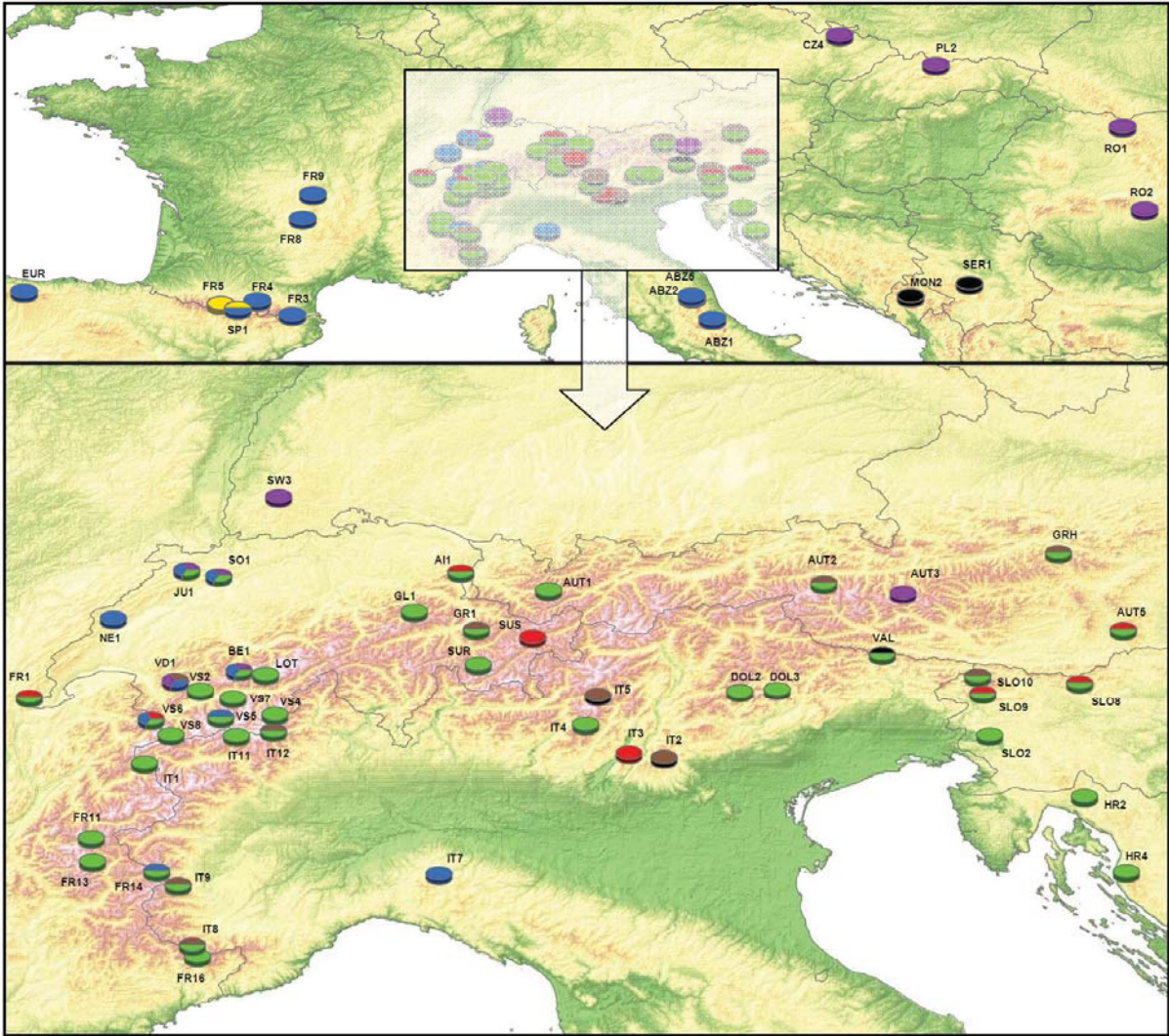
Supplementary Material 2. Detailed K2P barcoding distances within each species (*O. alpestris*, *O. speciosa*, *O. ganglbaueri*).



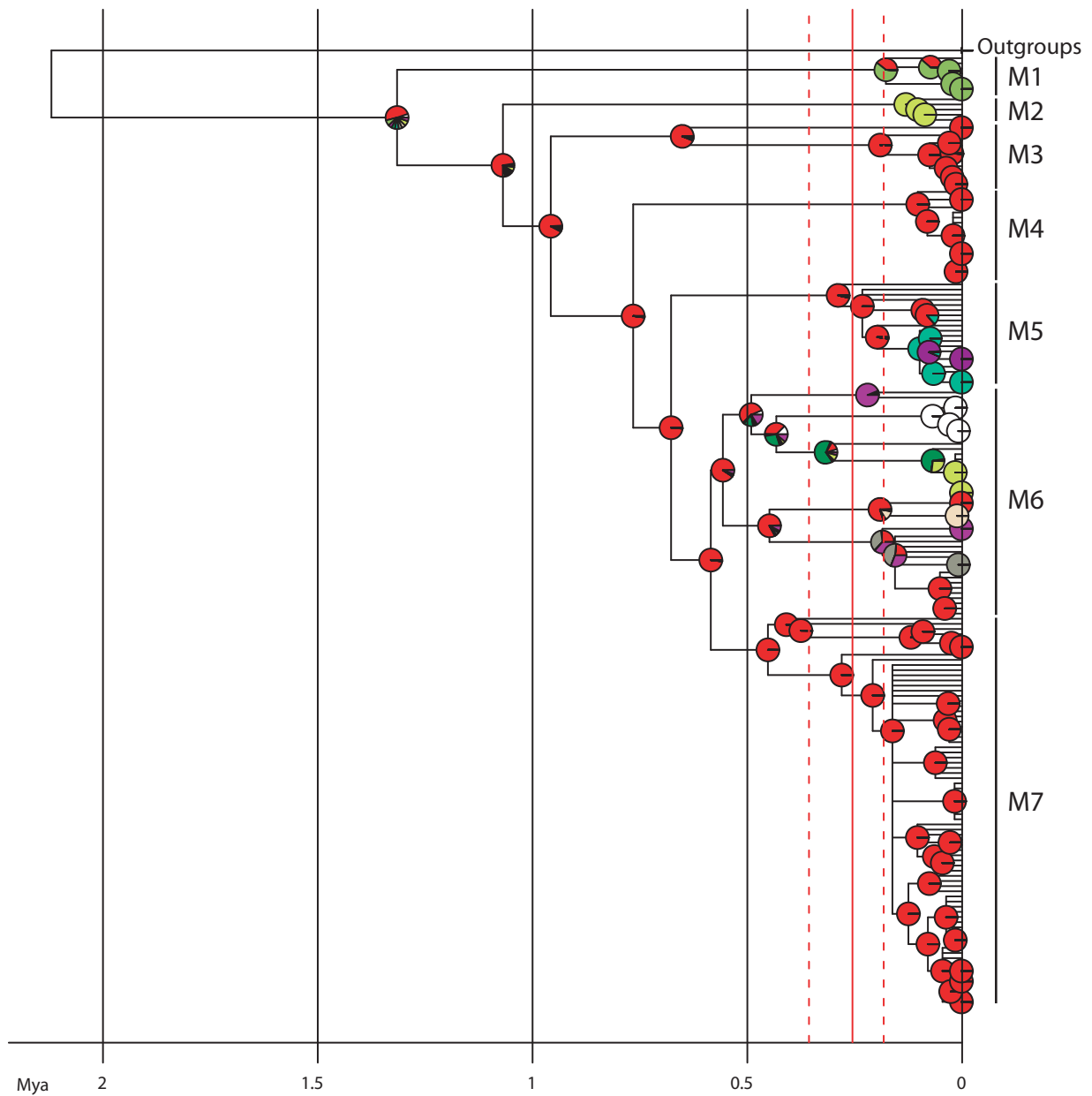
Supplementary Material 3. Half-compatible topology of the MrBayes analysis, with the corresponding BPP and Bremer support values on each node. Major clades from the MP analysis are shown at the right of the topology. The group indicated by a '\$' switched position between the MP and the Bayesian analyses (see Fig. 4). Codes correspond to populations detailed in Table 1.



Supplementary Material 4. All-in-one geographical distribution of each mtDNA clade identified in the MP analysis (see Fig. 4). Colors refer to clades as in Figure 4 and codes correspond to populations detailed in Table 1.



Supplementary Material 5. Biogeographic history of the *Oreina* AGS complex inferred from the likelihood method implemented in Mesquite and represented on the PL dated Majority-rule consensus tree. On each node is represented a pie-chart indicating the ancestral reconstruction of biogeographic areas (see text for more details). See Fig. 4 for clade definition and color legends. The red lines represent the mean and 95% interval of confidence for the shift in diversification rate (see Fig. 8).



Supplementary Material 6. Summary of the biogeographic scenarios of the *Oreina* AGS complex inferred from the MP-DIVA and Mesquite ancestral area reconstructions (see text for more details on the protocol to extract biogeographic events from the reconstructions). The table is subdivided into two parts: (A) “main story” from the root to the definition of the clades and (B) “within-clade” summarizing events occurring in clades M1 to M7. This table was used to reconstruct the biogeographic scenario from Fig. 7 where only events shared by the two methods (in bold) were represented. Abbreviations: in roman: events unique to one of the method; in grey: events not represented on Fig. 7 due to their high level of uncertainty; in bold: events shared between the two methods (represented on Fig. 7). Finally the star (*) indicates events that are shared between the two methods but occurred at different time scales: either the main story for MP-DIVA or within-clade for Mesquite. These events were represented on Fig. 7 using dashed lines. The occurrence of each event is represented in the column “Times”. See Fig. 4 for area definitions.

Clade	MP-DIVA		Mesquite	
	Event	Times	Event	Times
Main story	B-->C (clade 1)	1	B-->C (clade 1)	1
	B-->I (clade 2)	1	B-->I (clade 2)	1
	B-->G (clade 5)	1	-	-
	B-->A (clade 6)	1	-	-
	B-->E (clade 6)	1	-	-
	B-->J (clade 6)	1	-	-
Clade M1	-	-	C-->B	2
Clade M2	Stays in I	-	Stays in I	-
Clade M3	B-->G	1	B-->G	1
Clade M4	Stays in B	-	Stays in B	-
Clade M5	B-->F	2	B-->F	3
	B-->G	1	B-->G	2
	D-->B	1	D-->B	1
	F-->D	1	F-->D	1
Clade M6	A-->J	1	-	-
	-	-	B-->A	1
	-	-	B-->E	1
	-	-	B-->G	2
	B-->H	1	B-->H	1
	B-->J	1	B-->J	2
	E-->I	1	E-->I	1
	E-->J	1	-	-
	G-->B	1	G-->B	2
	-	-	G-->J	2
J-->G	1	J-->G	1	
Clade M7	B-->C	2	B-->C	6
	B-->G	2	B-->G	4
Number of dispersals:		23	35	

Supplementary Material 7.

Tajima's D test parameters for each biogeographic region. All tests were non-significant, indicating no signature of recent range expansion or retraction.

Neutrality test	Abruzzi Appenines	Alps	Balkan Range	Black Forest	Cantabric Range	Carpathians & Sudetes	Jura	Ligurian Appenines	Pyrenees	Massif Central	Mean	Standard deviation
Sample size	8	112	12	3	2	10	16	3	14	6	18.6	33.17027
S	5	152	29	1	14	10	67	1	40	26	34.5	46.10435
Pi	2.143	19.799	11.061	1.333	14.000	3.689	17.500	0.667	17.813	11.533	9.954	7.428
Tajima's D	0.504	-1.053	0.682	0.000	0.000	-0.058	-0.570	0.000	1.810	0.081	0.140	0.763
Tajima's D p-value	0.754	0.129	0.789	0.989	1	0.525	0.285	0.986	0.987	0.534	0.6978	0.31709

Supplementary Material 8.

Geographic events for each of the ten nodes included in the 5-95% inflexion-point interval of the diversification rate (see Figure 8), as highlighted in Figure 4. Areas' codes also refer to codes used in Figure 4. Both events that arose from the anterior node and events that happened towards the posterior node(s) are addressed, respectively on the left and on the right of the column informing on the focal node (in bold in the centre). We distinguished among three different types of geographical events: dispersal, vicariance, and no change. When for a given node, there was a high level of biogeographic uncertainty (i.e., the maximum probability of the most likely area was not higher than 0.5), no events could be inferred. Besides each area, the DIVA probability is given in brackets. In three cases (in italics), we did not duplicate information and just referred to the line above. In total, we could retrieve six vicariance and four dispersal events, all but one implying the Alps (b).

anterior node Areas [DIVA probability]	« from » event	5-95% inflexion point interval		« to » event	posterior node(s)
		Node (clade)	Areas [DIVA probability]		Areas [DIVA probability]
b [1]	dispersal (b → c)	I (M7)	bc [1]	vicariance (b c)	c [1] b [0.927]
b [1]	no biogeographic change	II (M7)	b [1]	<i>see « from » event to node I just above</i>	
j [0.724]	no inference possible	III (M6)	high level of biogeographic uncertainty	no inference possible	g [1] j [1] j [1] g [1] g [1] b [1] bg [0.51]
high level of biogeographic uncertainty	no inference possible	IV (M6)	bh [1]	vicariance (b h)	b [1] h [1]
high level of biogeographic uncertainty	no inference possible	V (M6)	ae [1]	vicariance (a e)	e [1] a [1]
high level of biogeographic uncertainty	no inference possible	VI (M6)	a [1]	no biogeographic change	a [1] a [1] a [1]
b [0.947]	dispersal (b → f)	VII (M5)	bf [1]	vicariance (b f)	b [1] f [1]
bg [0.969]	vicariance (b g)	VIII (M5)	b [0.947]	<i>see « from » event to node VII just above</i> dispersal (b → g) no biogeographic change	bg [0.612] b [1] b [1] b [1]
b [0.974]	dispersal (b → g)	IX (M5)	bg [0.969]	<i>see « from » event to node VIII just above</i>	
bi [1]	vicariance (b i)	X (M2)	i [1]	no biogeographic change	i [1] i [1]