

Supplementary material

Appendix 1. Parameters of genetic diversity for each microsatellite locus estimated for *Dactylorhiza majalis* subsp. *majalis*: A - mean number of alleles per locus; A_e - effective number of alleles; H_o - observed heterozygosity; H_e - expected heterozygosity; F_{IS} - inbreeding coefficient; [P] - significance level for the hypothesis of HWE equilibrium.

Locus name	A	A_e	H_o	H_e	F_{IS}	[P]
ms3	8	1.86	0.475	0.476	0.002	>0.001
ms8	9	2.61	0.590	0.636	0.073	0.001
ms10	3	1.07	0.044	0.069	0.367	0.001
ms11	3	1.55	0.304	0.370	0.179	0.001
ms13	7	2.20	0.520	0.562	0.075	0.001
Means	6.00	1.86	0.387	0.423	0.139	-

Appendix 2. Analysis of molecular variance (AMOVA) for nuclear microsatellite data considering *Dactylorhiza majalis* subsp. *majalis* populations.

Source of variation	df	Sum of squares	Variance components	Percentage of variation	P
Between populations	21	88.35	0.103	10.61	0.001
Between individuals within populations	333	305.84	0.054	5.54	0.001
Within individuals	355	288.00	0.811	83.85	0.001