

Development of a SNaPshot assay for the genotyping of organellar SNPs in four closely related pines

Supplementary Material

Table S1. List of 12 populations used in this study

Acronym	N	Population/group	Species	Coordinates	
F1	12	Joutsa, Finland	<i>P. sylvestris</i>	26.140	61.740
So	12	Sokolica, Poland	<i>P. sylvestris</i>	20.441	49.418
TAR	12	Tarnawa, Poland	<i>P. sylvestris</i>	22.830	49.113
M2	12	Dolina Pięciu Stawów, Poland	<i>P. mugo</i>	20.031	49.131
M6	11	Semkovo, Bulgaria	<i>P. mugo</i>	23.300	42.040
M10	12	Kamniška Bistrica, Slovenia	<i>P. mugo</i>	14.375	46.051
Bat	15	Wielkie Torfowisko Batorowskie, Poland	<i>P. uliginosa</i>	16.384	50.458
WGB	12	Węgliniec, Poland	<i>P. uliginosa</i>	15.226	51.294
WLB	12	Węglowiec, Poland	<i>P. uliginosa</i>	15.192	51.298
UNC1	12	Vall de Ransol, Andora	<i>P. uncinata</i>	1.382	42.350
UNC3	12	Vall de Nuria, Spain	<i>P. uncinata</i>	2.015	42.205
UNC8	12	Valdelinares, Spain	<i>P. uncinata</i>	-0.415	40.285

Table S2. mtDNA haplotypes with occurrence in each population and haplotype frequency (samples with each haplotype/all samples)

H. a	H. s	Bat	WGB	WLB	M2	M6	M10	F1	So	TAR	UNC1	UNC3	UNC8	Frequency %
H4	GAGTCGGGGGG	0	3	1	6	0	0	0	12	10	0	0	0	21.92
H1	TCTGATTTGTG	15	0	1	1	0	0	10	0	0	0	0	0	18.49
H6	GCGGCGGGGGG	0	0	0	5	11	9	0	0	0	0	0	0	17.12
H10	GCGGCGGGGGC	0	0	0	0	0	0	0	0	0	12	9	3	16.44
H3	GCGTCGGGGGG	0	8	6	0	0	0	1	0	1	0	0	0	10.96
H12	GCGGCGGGTGC	0	0	0	0	0	0	0	0	0	0	0	9	6.16
H5	TCTTATTTGTG	0	0	4	0	0	2	0	0	0	0	0	0	4.11
H11	GCGTCGGGGGC	0	0	0	0	0	0	0	0	0	0	3	0	2.05
H2	TCGGCGGGGGG	0	1	0	0	0	0	0	0	0	0	0	0	0.68
H7	GCGGCGTG GGG	0	0	0	0	0	1	0	0	0	0	0	0	0.68
H8	GCTGAGTTGTG	0	0	0	0	0	0	1	0	0	0	0	0	0.68
H9	TCTGAGTTGTG	0	0	0	0	0	0	0	0	1	0	0	0	0.68

H. a – haplotype acronym; H. s – haplotype sequence. Haplotype sequences are concatenated mtDNA SNPs in following order: PR5, PR7, PR15, PR19, PR21, PR24, PR25, PR29, PR30, PR31 and PR32.