

Supplementary Materials:

Table S1. Location of the study subpopulations.

No.	Plot	Latitude (N)	Longitude (E)	Maternal lineage ¹	No.	Plot	Latitude (N)	Longitude (E)
1.	LB/RO	47.017	25.133	E	29.	ST54/PL	49.163	22.733
2.	SA/RO	47.467	24.817	E	30.	KA/SK	49.200	20.983
3.	SL/RO	47.467	25.667	E	31.	LU68/PL	49.246	22.665
4.	CM/RO	47.550	25.567	E	32.	RO/UA	49.250	22.967
5.	BM/RO	47.667	24.000	E	33.	LU69/PL	49.258	22.660
6.	DI/UA	47.933	24.217	E	34.	PA/SK	49.267	22.033
7.	KI/UA	47.950	25.783	E	35.	KM/PL	49.271	22.051
8.	PU/UA	48.000	25.283	E	36.	TR/UA	49.283	23.500
9.	LU/UA	48.033	24.533	E	37.	LU50/PL	49.305	22.623
10.	BU/UA	48.083	25.557	E	38.	LU52/PL	49.313	22.603
11.	MI/UA	48.167	25.400	E	39.	PI/UA	49.333	23.233
12.	KR/UA	48.200	24.733	E	40.	LZD120/PL	49.351	20.924
13.	BA/UA	48.217	25.233	E	41.	LZD106/PL	49.407	21.002
14.	UC/UA	48.333	23.950	W	42.	LZD96/PL	49.430	21.035
15.	MY/UA	48.417	24.617	W	43.	LZD21/PL	49.445	20.953
16.	BO/UA	48.500	24.700	W	44.	NW/PL	49.475	20.824
17.	KN/UA	48.550	24.900	W	45.	JL95/PL	49.546	19.366
18.	SO/UA	48.567	23.500	W	46.	BG/PL	49.322	22.198
19.	VO/UA	48.750	23.267	W	47.	WG22/PL	49.585	19.187
20.	RS/UA	48.767	24.400	W	48.	WG9/PL	49.590	19.219
21.	VP/UA	48.817	23.167	W	49.	LM219/PL	49.660	20.289
22.	TU/UA	48.900	23.467	W	50.	US61/PL	49.693	18.794
23.	KO/UA	48.933	22.583	W	51.	JL170/PL	49.697	19.378
24.	RY/UA	48.950	24.617	W	52.	JL171/PL	49.697	19.368
25.	RA/UA	49.017	24.033	W	53.	LM58/PL	49.698	20.256
26.	ST218/PL	49.133	22.716	W	54.	US74/PL	49.711	18.977
27.	MO/UA	49.150	23.883	W	55.	LM74/PL	49.714	20.198
28.	ST40/PL	49.162	22.722	W	56.	US5/PL	49.728	18.836

Notes: ¹ mtDNA haplotypes linked with glacial refugial areas in the southern Alps and northern Apennines (W) or north-western Greece (E).

Table S2. Parameters of genetic variation in the eastern (E) and western (W) maternal lineages.

No.	Plot	N _a	N _e	H _o	H _e	F _{IS}
Eastern lineages (n=13):						
1.	LB/RO	9.2	5.2	0.488	0.810	0.400
2.	SA/RO	9.8	5.5	0.495	0.814	0.398
3.	SL/RO	8.6	5.0	0.444	0.770	0.443
4.	CM/RO	9.6	6.0	0.617	0.816	0.265
5.	BM/RO	10.6	5.2	0.580	0.772	0.274
6.	DI/UA	10.2	6.6	0.606	0.785	0.250

7.	KI/UA	9.8	6.1	0.601	0.825	0.273
8.	PU/UA	9.0	5.5	0.521	0.791	0.366
9.	LU/UA	12.0	7.2	0.564	0.788	0.307
10.	BU/UA	10.2	6.5	0.608	0.819	0.267
11.	MI/UA	10.8	7.3	0.552	0.837	0.348
12.	KR/UA	10.8	5.9	0.593	0.782	0.251
13.	BA/UA	10.4	5.7	0.528	0.792	0.361
	Mean	10.1	6.0	0.554	0.800	0.323
	±SD	±0.9	±0.7	±0.053	±0.020	±0.063

Western lineage n = (43):

14.	UC/UA	8.6	4.4	0.629	0.770	0.180
15.	MY/UA	9.0	5.0	0.474	0.787	0.394
16.	BO/UA	8.8	5.0	0.609	0.792	0.236
17.	KN/UA	9.2	4.9	0.600	0.798	0.248
18.	SO/UA	8.8	4.9	0.582	0.773	0.250
19.	VO/UA	8.8	4.2	0.504	0.720	0.313
20.	RS/UA	8.0	4.1	0.563	0.755	0.253
21.	VP/UA	10.6	4.8	0.583	0.722	0.235
22.	TU/UA	7.8	4.1	0.442	0.700	0.430
23.	KO/UA	9.0	4.3	0.571	0.722	0.249
24.	RY/UA	8.4	4.2	0.480	0.722	0.360
25.	RA/UA	8.4	4.9	0.602	0.780	0.243
26.	ST218/PL	10.2	6.0	0.615	0.831	0.248
27.	MO/UA	9.2	4.2	0.613	0.754	0.193
28.	ST40/PL	9.6	5.1	0.652	0.786	0.165
29.	ST54/PL	11.0	4.5	0.605	0.788	0.218
30.	KA/SK	8.2	3.4	0.524	0.624	0.199
31.	LU68/PL	9.8	4.9	0.613	0.773	0.213
32.	RO/UA	9.8	5.1	0.605	0.790	0.242
33.	LU69/PL	9.6	5.4	0.610	0.774	0.222
34.	PA/SK	8.6	4.6	0.525	0.753	0.323
35.	KM/PL	8.8	4.5	0.619	0.746	0.173
36.	TR/UA	9.2	4.2	0.559	0.747	0.262
37.	LU50/PL	7.6	4.1	0.634	0.744	0.143
38.	LU52/PL	9.2	4.1	0.631	0.678	0.122
39.	PI/UA	7.2	3.4	0.459	0.675	0.342
40.	LZD120/PL	9.2	4.8	0.592	0.789	0.250
41.	LZD106/PL	9.4	4.8	0.613	0.722	0.169
42.	LZD96/PL	10.6	5.8	0.637	0.789	0.199
43.	LZD21/PL	9.8	4.6	0.635	0.751	0.160
44.	NW/PL	9.0	4.0	0.575	0.722	0.211
45.	JL95/PL	9.6	4.9	0.631	0.785	0.195
46.	BG/PL	8.4	4.4	0.583	0.753	0.228
47.	WG22/PL	11.2	5.0	0.527	0.791	0.347
48.	WG9/PL	8.0	4.5	0.562	0.717	0.240

49.	LM219/PL	9.0	5.0	0.562	0.736	0.249
50.	US61/PL	8.8	4.2	0.580	0.753	0.233
51.	JL170/PL	9.6	4.4	0.599	0.741	0.206
52.	JL171/PL	9.6	4.3	0.579	0.735	0.219
53.	LM58/PL	10.0	5.1	0.653	0.780	0.157
54.	US74/PL	9.4	4.9	0.603	0.726	0.196
55.	LM74/PL	8.8	4.4	0.610	0.718	0.171
56.	US5/PL	8.8	4.5	0.548	0.728	0.271
	Mean	9.1**	4.6***	0.581*	0.750***	0.236**
	±SD	±0.8	±0.5	±0.051	±0.039	±0.065

Eastern and western lineages (n=56)

Mean	9.3	4.9	0.575	0.761	0.256
±SD	±0.9	±0.8	±0.053	±0.041	±0.075

Notes: N_a — number of different alleles per locus, N_e — number of effective alleles per locus, H_o —observed heterozygosity, H_e —unbiased expected heterozygosity, F_{is} —inbreeding coefficient. The mean values denoted with asterisks (*, **, ***) are statistically different in the western and eastern lineages at the significance level <0.05, <0.01 and <0.001, respectively (two-sided permutation test).

Table S3. Characteristics of the five SSR loci for the eastern (E) and western (W) maternal lineages.

Maternal lineage	Locus	No. of alleles	N_a	N_e	H_o	H_e	F_{is}
E n=13	SF78	43	18.6	11.8	0.892	0.925	0.017
	SF239	10	6.4	3.5	0.283	0.711	0.599
	SF333	6	5.8	4.8	0.610	0.804	0.228
	SFb4	24	13.9	7.2	0.750	0.870	0.122
	SFb5	7	5.6	3.2	0.234	0.691	0.650
W n=43	SF78	55 (42,6)	15.7 **	7.2 ***	0.852	0.869 ***	0.024
	SF239	12 (9.9)	5.7	2.5 ***	0.283	0.560 **	0.488
	SF333	6 (6.0)	5.3 **	3.8 ***	0.538 *	0.742 ***	0.265
	SFb4	27 (23.3)	12.6 *	5.9 *	0.778	0.835 **	0.067
	SFb5	14 (10.8)	6.4 *	3.7	0.455 ***	0.721	0.369 ***

Notes as in Table S2. The number of alleles after rarefaction was given in brackets (mean from 100,000 random sub-samples without replacement for sample size n=13). The values denoted with asterisks are statistically different at the 0.05 significance level (two-sided permutation test with Holm-Bonferroni correction for multiple comparisons).

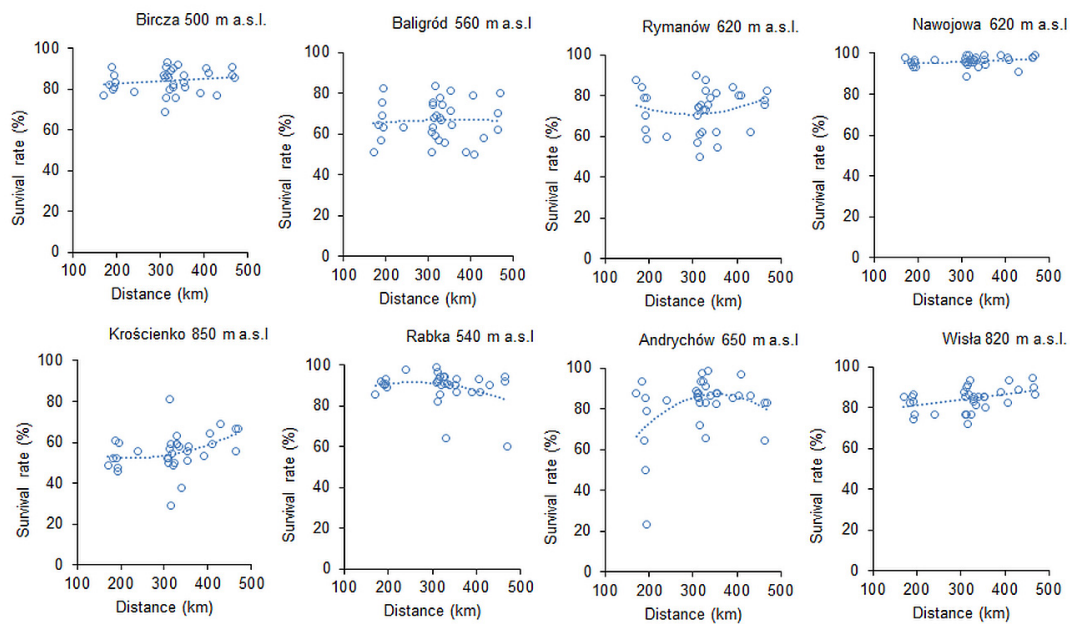


Figure S1. Relationships between the survival rate of the tested provenances after 15 years and the geographic distance between their origin sites and the meeting zone of the refugial lineages. The test sites are ordered concordant with their geographic location from east to west.

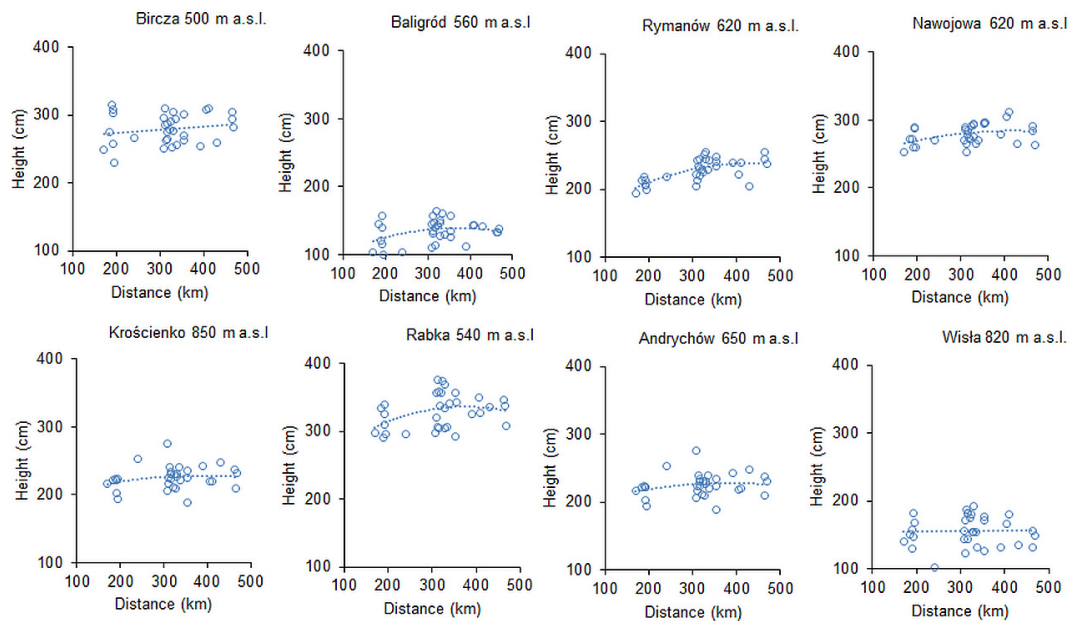


Figure S2. Relationships between the mean heights reached at age of 15 years by the tested provenances and the geographic distance between their origin sites and the meeting zone of the refugial lineages. The test sites are ordered concordant with their geographic location from east to west.