

Supplementary material

Table S1. Study sites and characteristics of the adult populations of Polish larch in the two sample plots.

Sample Plot	Geographic Coordinates	Sample Size	Forest Compartment	Sample Plot Area (ha)	Population Density (ind./m ²)	Average Height (m)	Average Diameter (cm)
Plot A	50°53'02" N 21°06'41" E	126	A-1h,i	4.40	0.0029	29.50	69.48
Plot B	50°53'06" N 21°06'02" E	126	A-3c	3.30	0.0038	33.43	75.12

Table S2. The estimates of genotyping error rates obtained based on the full mating model and power-exponential kernel, using the NM π software.

Locus	Number of Alleles		Genotyping Error Rate					
	Plot A	Plot B	Plot A		Plot B		Both Plots Jointly	
LD31	11	14	0.05293	(0.00838)	0.03132	(0.00692)	0.04090	(0.00533)
LD42	7	6	0.02052	(0.00584)	0.03375	(0.00827)	0.02376	(0.00457)
LD45	9	8	0.03201	(0.00723)	0	-	0.01706	(0.00404)
LD50	9	12	0.02883	(0.00631)	0.00438	(0.00291)	0.01634	(0.00344)
LD56	9	8	0.05457	(0.00853)	0.01406	(0.00480)	0.03510	(0.00507)
LD101	5	6	0.02447	(0.00718)	0.01317	(0.00621)	0.01614	(0.00448)
LK189	10	11	0.03103	(0.00678)	0.01677	(0.00551)	0.02217	(0.00415)
LK211	21	23	0.03664	(0.00687)	0.00693	(0.00338)	0.02111	(0.00389)
LK228	13	13	0.06955	(0.00942)	0.03441	(0.00708)	0.05247	(0.00595)
LK229	9	10	0.09232	(0.01096)	0.09774	(0.01110)	0.09227	(0.00765)
LK263	16	18	0.13432	(0.01212)	0.11081	(0.01151)	0.12041	(0.00828)
Mean	10.82	11.73	0.0523		0.0330		0.0416	

Table S3. Mating system characteristics of individual mother trees (s —selfing; c —local outcrossing = $1-s-m$; m —background pollination; N_{epBAC} —effective number of background pollen parents; N_{epLOC} —effective number of local pollen parents; N_{ep} —overall effective number of pollen parents).

Mother Tree	s	c	m	N_{epBAC}	N_{epLOC}	N_{ep}
<i>Plot A mean</i>	0.042	0.565	0.393	26.506	6.681	10.227
13	0.008	0.708	0.284	41.112	11.919	18.480
25	0.063 *	0.494	0.443	40.575	7.811	13.100
33	0.008	<u>0.274</u>	0.718	25.750	6.231	10.034
42	0.008	<u>0.728</u>	0.263	23.721	1.091	2.086
51	0.035 *	0.647	0.318	17.109	5.263	8.050
61	0.099 *	0.649	0.252	11.426	8.966	10.048
66	0.041 *	0.582	0.377	14.160	3.882	6.093
84	0.060 *	0.486	0.454	25.676	9.323	13.679
92	0.087 *	0.441	0.471	36.647	7.759	12.806
114	0.008	0.640	0.352	28.882	4.570	7.891
<i>Plot B mean</i>	0.015	0.536	0.450	34.235	9.472	14.026
166	0.008	0.508	0.484	23.201	17.308	19.826
173	0.037 *	0.513	0.450	30.130	12.190	17.358
193	0.011	0.414	0.575	26.640	6.818	10.858
201	0.008	0.409	0.583	20.985	4.840	7.866
210	0.014	0.295	0.691	48.735	10.083	16.709
217	0.008	0.662	0.330	57.746	4.160	7.762
222	0.034 *	0.590	0.376	20.480	9.757	13.217
227	0.009	0.693	0.298	25.553	8.067	12.262
241	0.009	0.689	0.302	40.793	7.737	13.007
244	0.009	0.584	0.407	48.089	13.762	21.400
Total mean	0.028	0.550	0.421	30.370	8.077	12.127

* parameter s significantly different from 0 at $p < 0.05$.

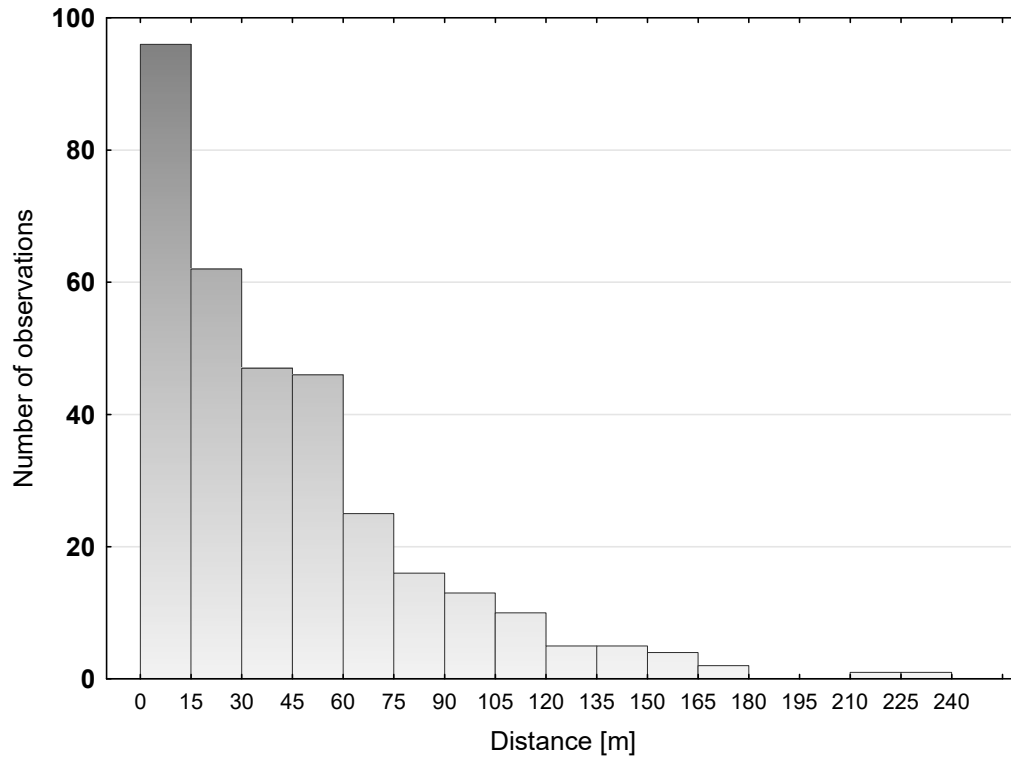


Figure S1. Frequency distribution of actual local pollen dispersal distances within neighborhoods calculated based on inferred genealogies.

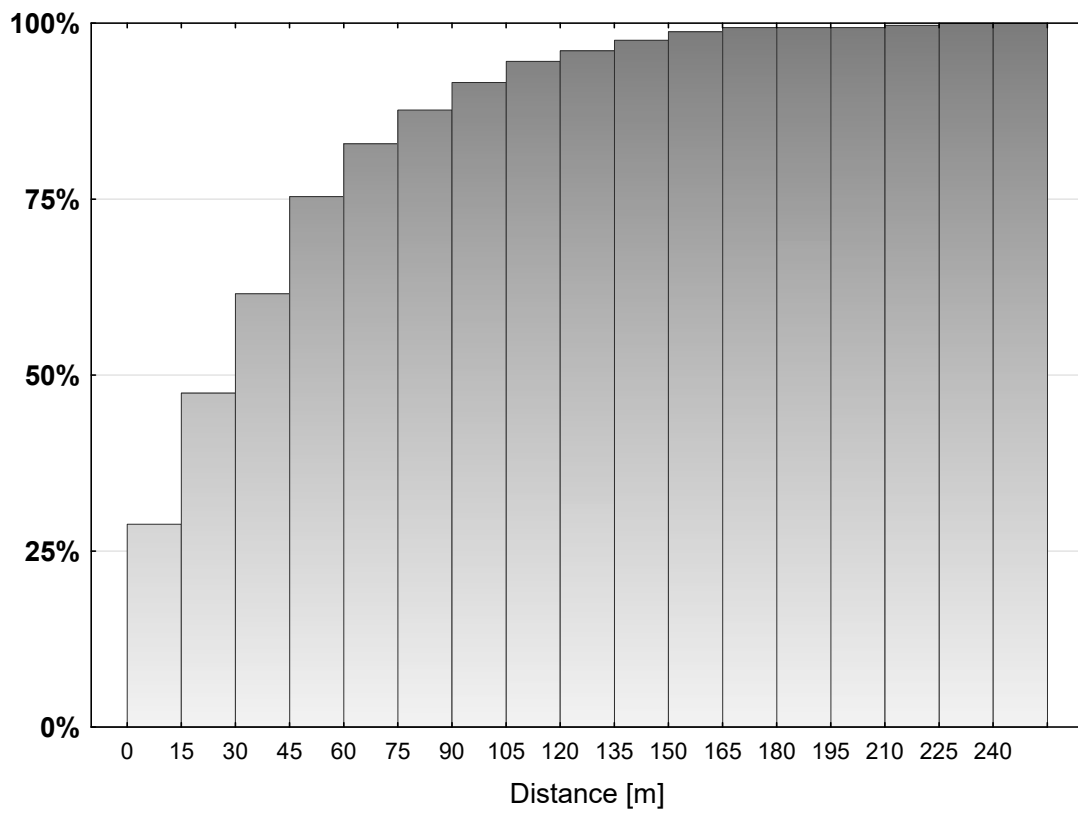


Figure S2. Cumulative distribution of actual local pollen dispersal distances within neighborhoods calculated based on inferred genealogies.

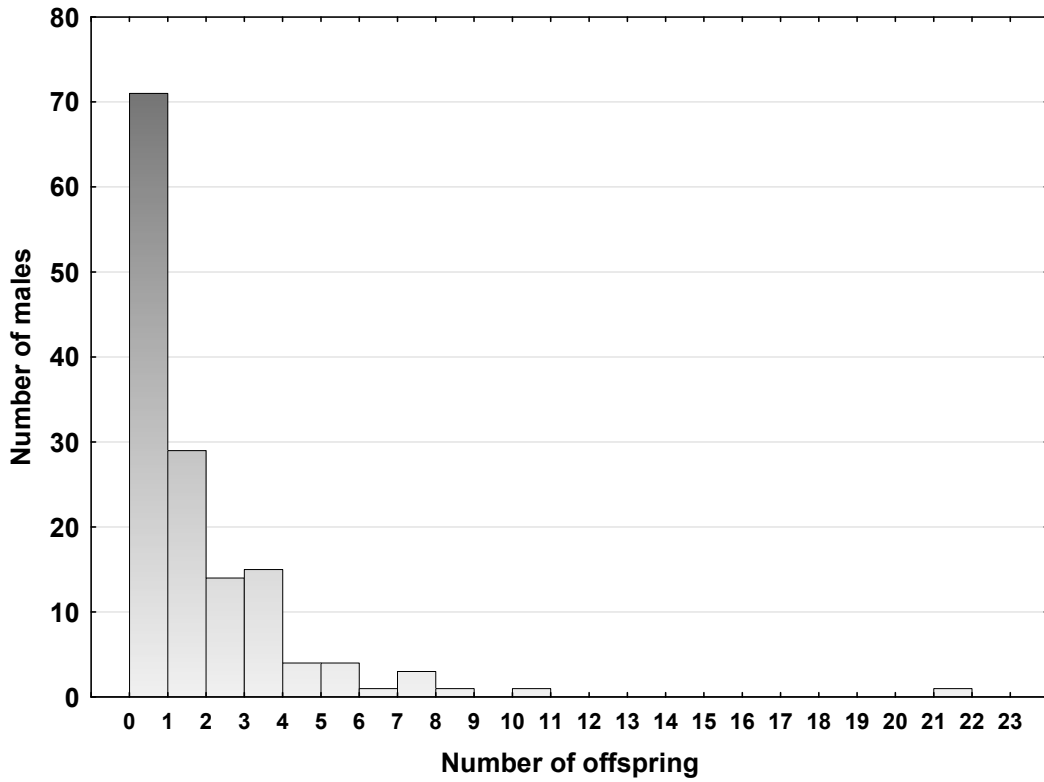


Figure S3. Frequency distribution of the number of offspring sired by individual males based on inferred genealogies.

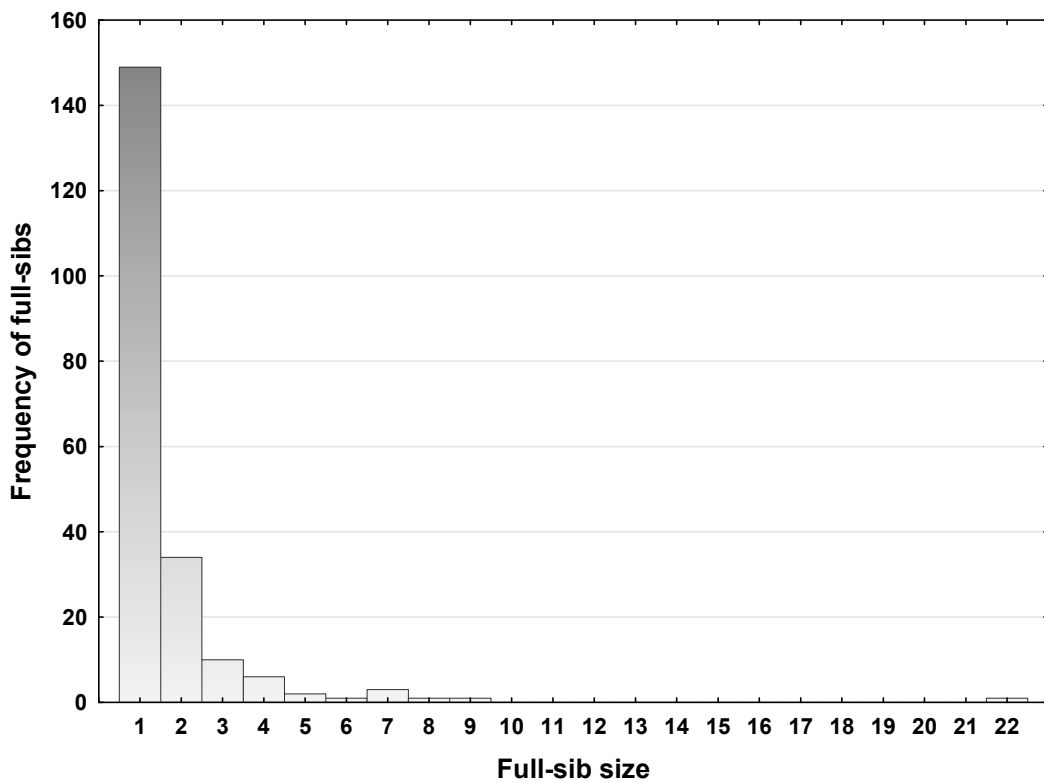


Figure S4. Frequency distribution of the number of offsprings per full-sib based on inferred genealogies.

