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Supplementary file

Table S1. Genetic differentiation (F_{ST}) between Scots pine populations from Poland at nSSR loci (* $P \le 0.05$, ** $P \le 0.01$, *** $P \le 0.001$).

	PL1	PL8	PL9	PL10	PL13	PL14	PL2	PL3	PL4	PL5	PL6	PL7	PL11	PL12	PL15
PL1															
PL8	0.0318														
PL9	0.0134	0.0351*													
PL10	0.0295	0.0202	0.0095												
PL13	0.0104	0.0132	0.0140	0.0021											
PL14	0.0084	0.0187	0.0133	0.0037	0.0044										
PL2	0.0081	0.0218	0.0322***	0.0073	0.0004	0.0005									
PL3	0.0154	0.0386**	0.0243	0.0223*	0.0177	0.0079	0.0172*								
PL4	0.0198	0.0337*	0.0133*	0.0088	0.0134	0.0039	0.0185	0.0191							
PL5	0.0084	0.0580**	0.0326*	0.0291	0.0233	0.0090	0.0169	0.0322	0.0153						
PL6	0.0254	0.0169*	0.0293	0.0155	0.0218	0.0253	0.0087	0.0289*	0.0325*	0.0499					
PL7	0.0145	0.0271	0.0076	-0.0094	-0.0045	-0.0028	0.0036	0.0168	-0.0048	0.0153	0.0212				
PL11	0.0259	0.0232	0.0209	0.0109	0.0139	0.0003	0.0152	0.0160	0.0061	0.0231	0.0206	0.0022			
PL12	0.0240	0.0218	0.0232	0.0071	0.0078	0.0082	0.0092	0.0222	0.0047	0.0220	0.0098	0.0009	-0.0028		
PL15	0.0216	0.0387*	0.0258**	0.0051	0.0038	-0.0030	0.0025	0.0177	0.0114	0.0153	0.0285	-0.0007	0.0141	0.0164	
PL16	0.0219	0.0245	0.0318*	0.0096	0.0064	0.0043	-0.0100	0.0112	0.0223	0.0373	0.0089	0.0122	0.0137	0.0187	0.0047



Fig. S1. The results of LOSITAN analysis of ten nuclear microsatellite loci. The red and yellow areas represent confidence intervals for expected distributions of loci under selection. A candidate locus for positive selection (psyl25) is marked.



Fig. S2. Lack of relationship between pairwise F_{ST} (for nSSR) and geographic distances (r = 0.138, $P \le 0.11$) between 16 Polish populations of Scots pine used in the study.



Fig. S3. Relationship between pairwise F_{ST} (for nSSR) and geographic distances (r = 0.602, p ≤ 0.01) between 23 populations of Scots pine used in the study.



Fig. S4. Principal coordinates plot showing genetic relationship of Scots pine populations based on variation at chloroplast microsatellites loci.

The proportion of variance accounted for by the first two axes was 67,41%.



Fig. S5. Assignment of Scots pine populations to the four genetic clusters (K=4) found in the STRUCTURE analysis based on chloroplast microsatellite markers. Population acronyms are as in Table 1.



Fig. S6. Relationship between Nei's genetic distances (for cpSSRs) and geographic distances (r = 0.437, p ≤ 0.05) between 23 populations of Scots pine used in the study.



Fig. S7. Relationship between Nei's genetic distances (for cpSSRs) and geographic distances (r = 0.284, p ≤ 0.05) between 16 Polish populations of Scots pine.