

Black poplar establishment on alluvial bars: seed rain homogeneity over a few kilometres

Supplementary Material

Table S1. Details of the SSR markers used for genotyping

Name	LeftPrimer -F	RightPrimer -R	Length	Length range	Motif	Tm °C
WPMS22	ACATGCTACGTGTTTGAATG	ATCGTATGGATGTAATTGTCTTA	129	75–148	TGA	55
ORPM221	TGGAGGCTGTCTGTTTGTG	AGATTTGAGCGACTCCGAAA	211	192–242	(AG) ¹⁷	55
WPMS13	GATCCTGAACAATGTCGTACTTC	ACGATAACCTGCGAGAAATGT	141	101–142	GT	55
WPMS07	ACTAAGGAGAATTGTTGACTAC	TATCTGGTTTCCTCTTATGTG	258	218–270	GT	55
PMGC14	TTCAGAATGTGCATGATGG	GTGATGATCTCACCCTTTG	210	203–224	CTT	49
PMGC93	ATCATGCGTTCGGCTACAGC	CTCAAACTCCAAGTGTATAAC	350	335–374	CTT	55
PMGC2578	GAGAACTCGGTGACTGACTG	CAGCAACATCCACATATTAGC	194	165–194	GA	55
PMGC14	TTCAGAATGTGCATGATGG	GTGATGATCTCACCCTTTG	210	203–224	CTT	49
WPMS16	CTCGTACTATTTCCGATGATGACC	AGATTATTAGGTGGGCCAAGGACT	158	140–161	GTC 8(ATCCTC) ⁵	55
WPMS20	GTGCGCACATCTATGACTATCG	ATCTTGTAATTCTCCGGGCATCT	252	222–252	(TTCTGG) ⁸	60
WPMS09	CTGCTTGCTACCGTGGAACA	AAGCAATTGGGTCTGAGTATCTG	295	246–298	GT (GA)	60
WPMS06	GTATAACGATGACCCACGAAGAC	TATAAATAAAGGCATGACCAGACA	205	182–226	GT	60

Table S2. Matrix with *F_{st}* (multilocus) for each pair of patches sampled (A, B, C and D). Each associated p.value were non-significant <0.001

	A	B	C	D
A	0.000			
B	0.000	0.000		
C	0.006	0.007	0.000	
D	0.007	0.007	0.006	0.000

Table S3. Population genetic parameters for each locus and all loci combined (multilocus). *N* = number of individuals; *N_a* = total number of alleles; *N_{ae}* = effective number of alleles (Nielsen et al., 2003); *H_e* and *H_o* = expected and observed heterozygosities, respectively; *F_{is}* = inbreeding coefficient; *P* (*F_{is}* ≠ 0) = the p-value of the permutation test.

Locus	N	N _a	N _{ae}	H _e	H _o	F _{is}	P (F _{is} ≠0)
WPMS13	368	17	7.75	0.871	0.858	0.015	0.430
WPMS14	368	22	7.21	0.861	0.851	0.013	0.533
WPMS20	368	7	3.91	0.744	0.729	0.021	0.477
PMGC93	368	7	3.52	0.716	0.730	−0.020	0.508
PMGC2578	368	20	6.51	0.847	0.826	0.024	0.238
ORPM221	368	19	9.30	0.893	0.902	−0.011	0.534
Multilocus	368	15.33	6.37	0.822	0.816	0.007	0.441

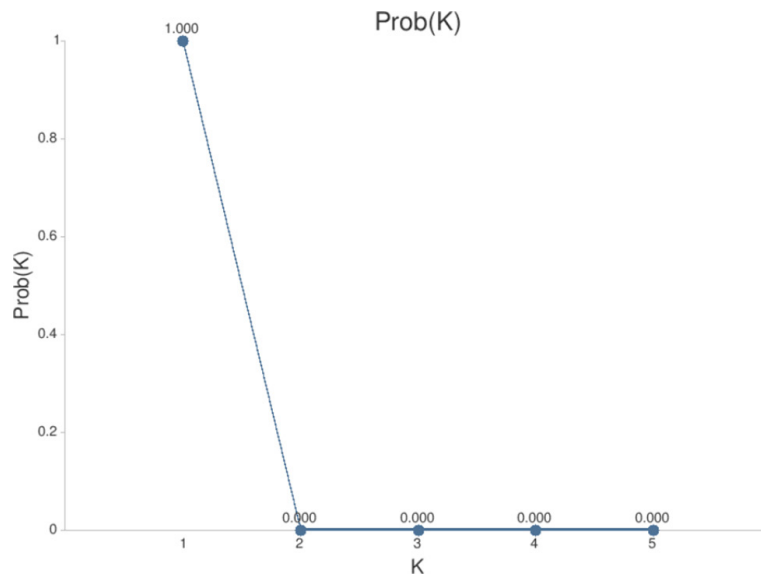


Fig. S1. Probability By K graph. Using median values of $\text{Ln}(\text{Pr Data})$ the k for which $\text{Pr}(K=k)$ is highest: 1

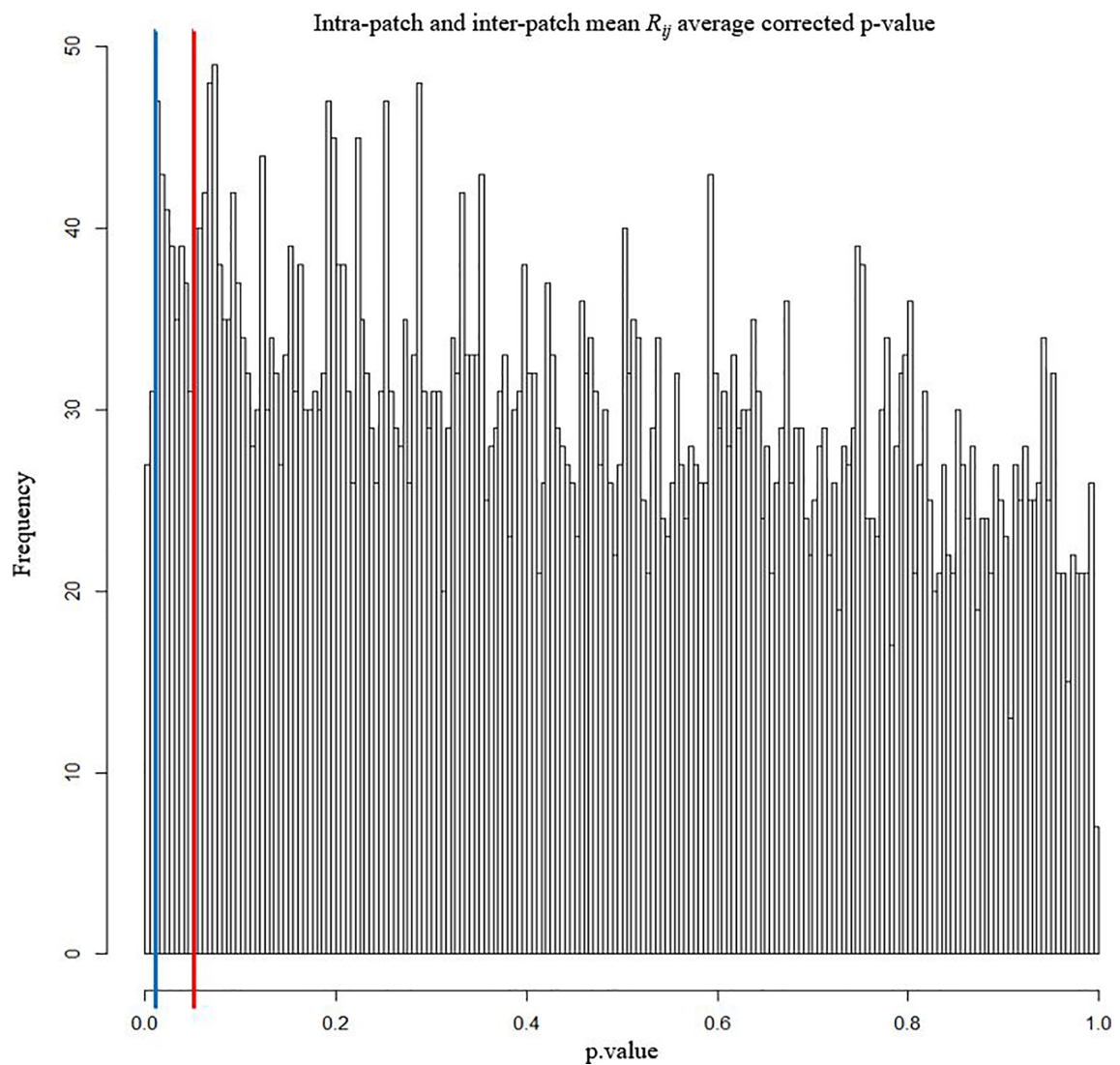


Fig. S2. Pairwise R_{ij} (inter patch vs. intra patch) average corrected p-value and the percentage of tests passing the significance level: $\alpha = 0.05$ red vertical line; and $\alpha = 0.01$ blue vertical line