

Population genetic structure of *Picea engelmannii*, *P. glauca*
and their previously unrecognized hybrids in the central
Rocky Mountains

Supplemental material

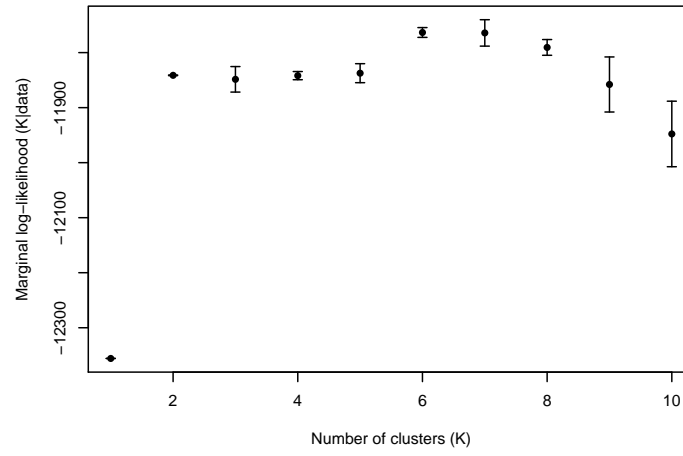
Table S1: Pairwise differentiation between parental (in italics) *P. glauca* (WBH, WAK, WON), *P. engelmannii* (EAZ, EMB) and focal (MLP, GTS, GTC, GTN, YSC, YSE, YSN, GSB, SLL, SSL, SDI, BHS, BHC) populations. p-values are shown above the diagonal and F_{ST} below, with significantly differentiated populations at the $\alpha=0.05$ level highlighted in bold.

		p-values																
Pop	EAZ	EMB	MLP	GTS	GTC	GTN	YSC	YSE	YSN	GSB	SLL	SSL	SDI	BHS	BHC	WBH	WAK	WON
<i>EAZ</i>	-	0.003	0.014	0.009	0.001	0.006	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
<i>EMB</i>	0.028	-	0.717	0.958	0.750	0.406	0.231	0.254	0.027	0.466	0.001	0.001	0.001	0.003	0.168	0.001	0.001	0.001
MLP	0.020	-0.004	-	0.186	0.235	0.209	0.024	0.015	0.014	0.344	0.001	0.001	0.001	0.001	0.476	0.001	0.001	0.001
GTS	0.032	-0.016	0.008	-	0.935	0.887	0.914	0.585	0.021	0.566	0.011	0.001	0.001	0.079	0.461	0.001	0.001	0.001
GTC	0.058	-0.007	0.006	-0.016	-	0.756	0.350	0.290	0.001	0.576	0.001	0.001	0.001	0.008	0.103	0.001	0.001	0.001
GTN	0.061	0.003	0.011	-0.025	-0.013	-	0.957	0.144	0.100	0.419	0.036	0.028	0.012	0.576	0.511	0.001	0.001	0.001
YSC	0.052	0.004	0.017	-0.011	0.002	-0.023	-	0.157	0.001	0.220	0.002	0.001	0.001	0.016	0.057	0.001	0.001	0.001
YSE	0.054	0.007	0.024	-0.004	0.005	0.020	0.009	-	0.001	0.054	0.001	0.001	0.001	0.001	0.016	0.001	0.001	0.001
YSN	0.039	0.012	0.013	0.015	0.038	0.018	0.022	0.038	-	0.021	0.083	0.003	0.001	0.001	0.506	0.001	0.001	0.001
GSB	0.048	0.001	0.003	-0.003	-0.004	0.003	0.007	0.025	0.024	-	0.004	0.001	0.001	0.021	0.103	0.001	0.001	0.001
SLL	0.083	0.050	0.051	0.035	0.067	0.035	0.037	0.076	0.012	0.058	-	0.293	0.005	0.013	0.134	0.001	0.001	0.001
SSL	0.101	0.049	0.045	0.046	0.067	0.036	0.040	0.082	0.031	0.061	0.004	0.054	0.001	0.001	0.011	0.001	0.001	0.001
SDI	0.080	0.063	0.052	0.061	0.078	0.067	0.070	0.042	0.012	0.023	0.024	0.021	-	0.003	0.001	0.001	0.001	0.001
BHS	0.056	0.020	0.021	0.010	0.022	-0.004	0.011	0.042	0.012	0.023	0.024	0.021	0.052	0.589	0.001	0.001	0.001	0.001
BHC	0.043	0.006	0.000	0.000	0.012	-0.002	0.012	0.026	0.000	0.014	0.010	0.019	0.042	-	0.001	0.001	0.001	0.001
<i>WBH</i>	0.167	0.129	0.118	0.143	0.158	0.140	0.129	0.170	0.065	0.154	0.066	0.053	0.110	0.079	0.080	-	0.001	0.001
<i>WAK</i>	0.223	0.192	0.176	0.193	0.223	0.197	0.170	0.233	0.098	0.221	0.099	0.067	0.143	0.112	0.128	0.045	-	0.004
<i>WON</i>	0.201	0.181	0.164	0.177	0.194	0.162	0.162	0.201	0.090	0.203	0.080	0.079	0.116	0.098	0.110	0.045	0.037	-

Table S2: Estimates of average linkage disequilibrium (LD; Δ) in 18 populations of parental *P. glauca* (WBH, WAK, WON), *P. engelmannii* (EAZ, EMB) and focal (MLP, GTS, GTC, GTN, YSC, YSE, YSN, GSB, SLL, SSL, SDI, BHS, BHC) populations.

Population	Mean	Max	90% quantile
EAZ	0.00460	0.0651	0.0105
EMB	0.00516	0.0378	0.0131
MLP	0.00594	0.0346	0.0118
GTS	0.00778	0.0473	0.0178
GTC	0.00516	0.0231	0.0124
GTN	0.00761	0.0600	0.0199
YSC	0.00631	0.0325	0.0137
YSE	0.01030	0.1100	0.0249
YSN	0.00523	0.0179	0.0098
GSB	0.00764	0.0469	0.0156
SLL	0.00807	0.0450	0.0199
SSL	0.00455	0.0300	0.0108
SDI	0.00624	0.0496	0.0138
BHS	0.00511	0.0204	0.0086
BHC	0.00886	0.0311	0.0161
WBH	0.00394	0.0311	0.0089
WAK	0.00338	0.0260	0.0081
WON	0.00517	0.0286	0.0146

A. Estimate of K based on L(K)



B. Estimate of K based on ΔK

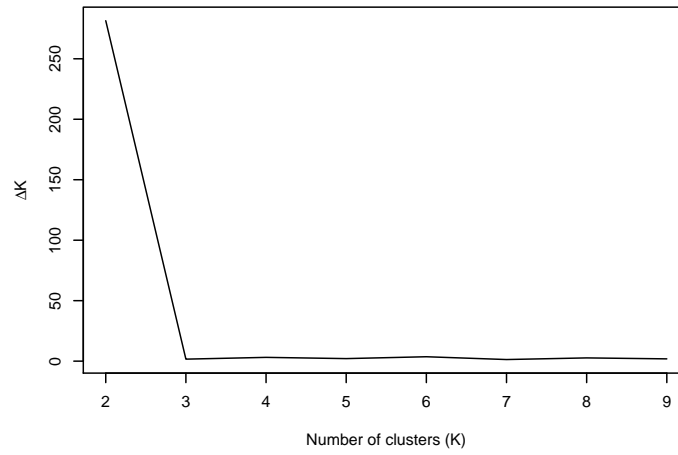


Figure S1: Estimates of $\ln(K | \text{data})$ in *structure*. A. Mean estimates of K ranging from 1–10 including standard error bars from 10 replicate runs of MCMC. B. Estimates of K based on ΔK (Evanno et al. 2005).

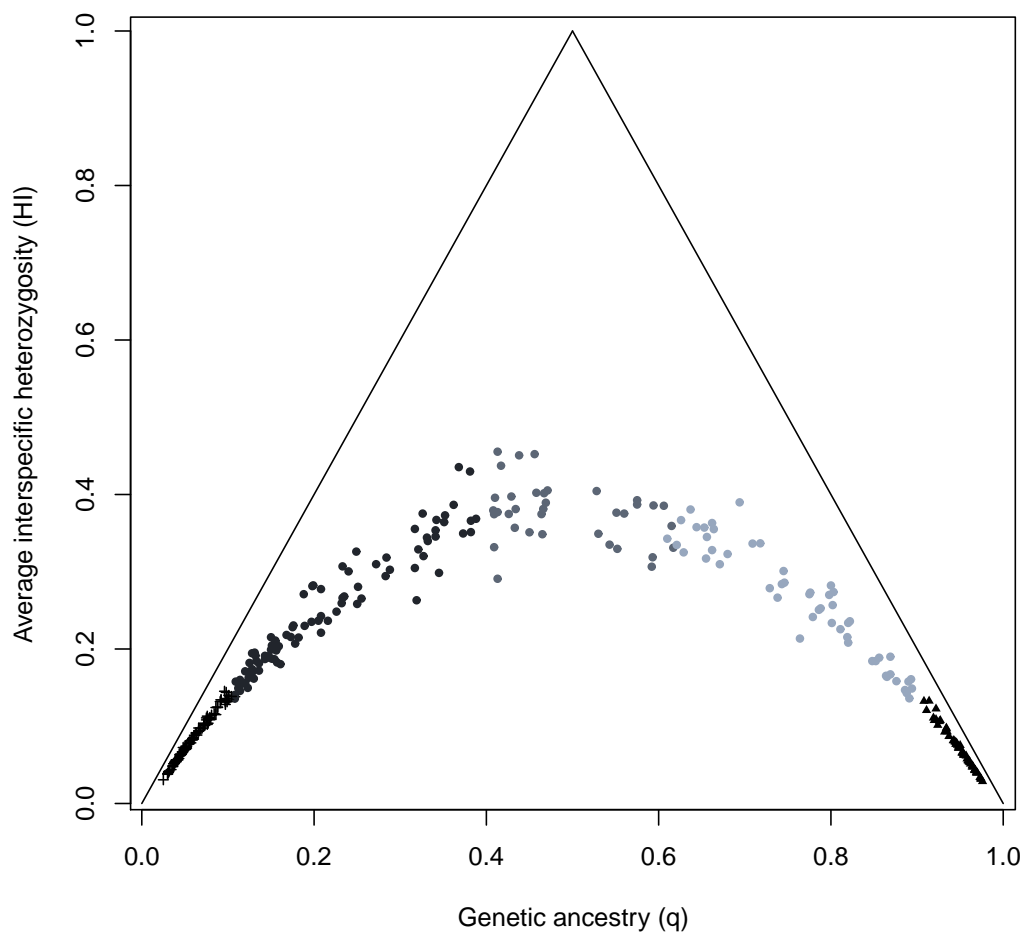


Figure S2: Genetic ancestry (q) versus average interspecific heterozygosity (H_I) for 336 individuals of parental *Picea engelmannii* and *P. glauca*, and focal individuals. Symbols represent each individual's genetic ancestry (q) detected using microsatellites during the course of this study: crosses (*P. engelmannii* ancestry), $q \leq 0.10$; dark grey circles, $0.11 \leq q \leq 0.39$; grey circles, $0.40 \leq q \leq 0.59$; light grey circles, $0.60 \leq q \leq 0.89$; triangles (*P. glauca* ancestry), $q \geq 0.90$.

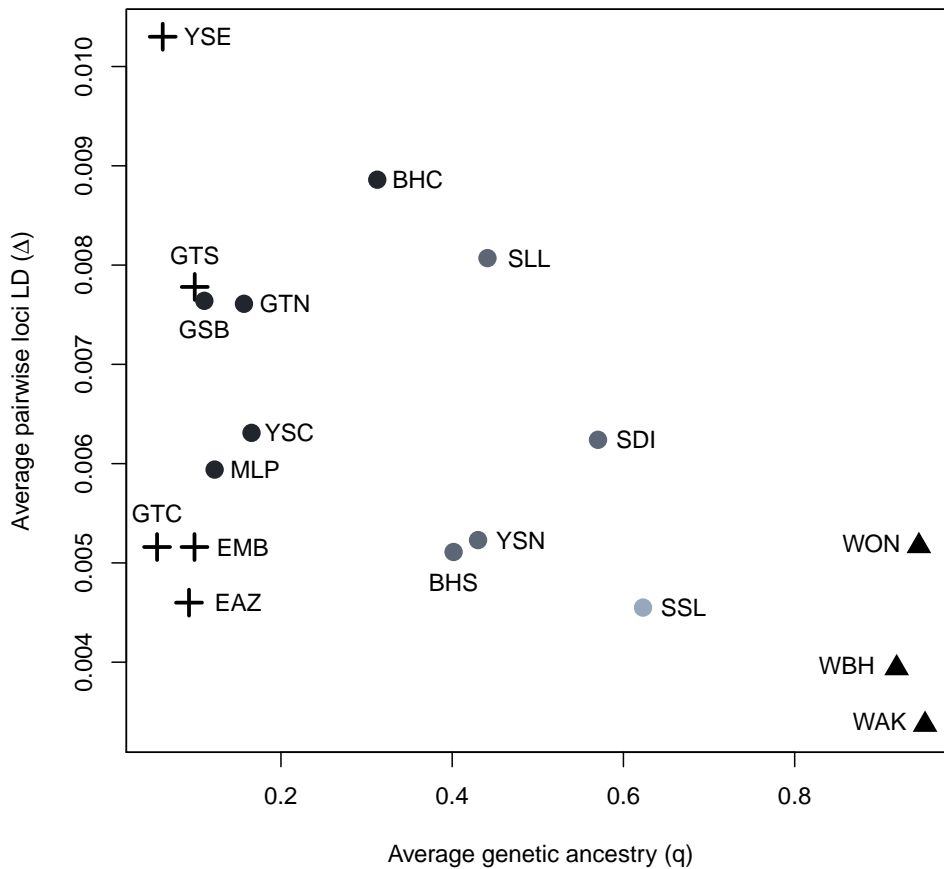


Figure S3: Average population genetic ancestry (q) versus average pairwise linkage disequilibrium (LD; Δ) of parental *P. glauca* (WBH, WAK, WON), *P. engelmannii* (EAZ, EMB) and focal (MLP, GTS, GTC, GTN, YSC, YSE, YSN, GSB, SLL, SSL, SDI, BHS, BHC) individuals. Symbols represent mean genetic ancestry (q) for each population detected using microsatellites during the course of this study: crosses (*P. engelmannii* ancestry), $q \leq 0.10$; dark grey circles, $0.11 \leq q \leq 0.39$; grey circles, $0.40 \leq q \leq 0.59$; light grey circles, $0.60 \leq q \leq 0.89$; triangles (*P. glauca* ancestry), $q \geq 0.90$.

References

Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* 14(8):2611–2620