Plant Communications, Volume *1*

Supplemental Information

Demographic Processes Linked to Genetic Diversity and Positive Selection across a Species' Range

Yvonne Willi, Marco Fracassetti, Olivier Bachmann, and Josh Van Buskirk

Table S1. Population information with the columns (from left to right): population identity; latitude North [°];longitude West [°]; $\log_{10}$-transformed population census size; mating system (O: outcrossing, S: selfing); membership in ancestral genetic cluster (E: east, W: west); geographic distance from the core (for a detailed description see Methods) [km]; evidence for admixture (1:yes, 0: no); the three genomic diversity estimates of Tajima's π, Watterson's θ and Tajima's D for intergenic regions, intron regions and coding DNA sequences of the genome; the two genomic estimates of a signature of positive selection, fraction of genes with positive McDonald-Kreitman test and the fraction of substitutions driven to fixation by positive selection at non-synonymous sites, α, based on aMK testing.

								Intergenic regions			Intron regions			CDS			Positive selection	
Pop.	Lat.	Long.	lPS	MS	Clu.	Dist.	Admix.	π	θ	D	π	θ	D	π	θ	D	F_{genes}posSel	α
NC1	35.25	-83.08	2.3	S	E	868	0	0.0019	0.0018	0.3198	0.0004	0.0003	0.5953	0.0003	0.0003	0.6060	0.0015	-0.1867
NC2	36.04	-81.16	4.4	O	E	686	0	0.0021	0.0020	0.2488	0.0005	0.0004	0.5981	0.0004	0.0004	0.5966	0.0020	-0.1345
NC3	36.11	-81.66	3.2	O	E	710	0	0.0029	0.0026	0.3979	0.0008	0.0007	0.7371	0.0007	0.0005	0.7299	0.0011	-0.0913
NC4	36.41	-79.96	3.5	O	E	593	0	0.0028	0.0026	0.1305	0.0008	0.0007	0.4989	0.0007	0.0006	0.4660	0.0011	-0.0514
VA1	37.42	-77.02	2.8	O	E	404	0	0.0048	0.0049	-0.0912	0.0017	0.0016	0.2643	0.0013	0.0012	0.2828	0.0028	0.1805
VA2	37.81	-77.12	1.8	S	E	364	0	0.0031	0.0028	0.4347	0.0011	0.0009	0.7859	0.0008	0.0007	0.7723	0.0000	-0.0682
MD1	38.86	-75.84	2.6	O	E	289	0	0.0043	0.0039	0.4490	0.0016	0.0013	0.7746	0.0012	0.0010	0.7946	0.0028	0.1042
MD2	38.99	-77.25	2.9	O	E	231	0	0.0055	0.0057	-0.1222	0.0021	0.0019	0.3640	0.0016	0.0014	0.4048	0.0049	0.1870
MD3	39.49	-78.93	2.1	O	E	290	0	0.0036	0.0034	0.2707	0.0013	0.0011	0.6666	0.0010	0.0008	0.6542	0.0019	0.0185
MD4	39.70	-76.19	3.7	O	E	201	0	0.0059	0.0069	-0.4831	0.0021	0.0021	0.0453	0.0016	0.0016	0.1004	0.0021	0.1830
WV1	38.96	-79.29	3.0	O	E	342	0	0.0045	0.0043	0.1517	0.0016	0.0014	0.5286	0.0012	0.0011	0.4919	0.0021	0.0058
NJ1	40.44	-73.99	2.1	O	E	172	0	0.0041	0.0038	0.3076	0.0016	0.0013	0.7891	0.0012	0.0010	0.8075	0.0015	0.0715

PA1	40.51	-80.36	2.1	O	E	402	0	0.0043	0.0043	0.0351	0.0017	0.0015	0.4048	0.0013	0.0012	0.3941	0.0015	0.0899
PA2	40.57	-75.40	3.9	O	E	250	0	0.0027	0.0025	0.3187	0.0007	0.0006	0.6489	0.0005	0.0005	0.6779	0.0014	0.0293
PA3	41.28	-77.87	3.0	O	E	230	0	0.0049	0.0053	-0.2802	0.0020	0.0020	0.1459	0.0015	0.0015	0.1276	0.0014	0.2135
NY1	41.30	-73.98	2.6	O	E	193	0	0.0051	0.0056	-0.3721	0.0021	0.0022	0.0278	0.0016	0.0016	0.0672	0.0006	0.2121
NY2	41.32	-73.99	2.3	O	E	194	0	0.0047	0.0046	0.1117	0.0018	0.0016	0.5512	0.0014	0.0012	0.5881	0.0031	0.1628
NY3	41.73	-73.56	5.6	O	E	240	0	0.0031	0.0029	0.3819	0.0012	0.0010	0.7617	0.0009	0.0008	0.7485	0.0026	-0.0103
NY4	42.35	-76.39	3.2	O	E	274	0	0.0051	0.0053	-0.1268	0.0018	0.0017	0.3775	0.0014	0.0013	0.3912	0.0020	0.1603
NY5	42.66	-74.02	2.2	O	E	401	0	0.0051	0.0053	-0.1228	0.0019	0.0018	0.3426	0.0015	0.0013	0.3626	0.0030	0.1216
NY6	43.00	-76.09	2.8	O	E	348	0	0.0050	0.0053	-0.2173	0.0020	0.0019	0.2466	0.0015	0.0014	0.2697	0.0028	0.1542
MO1	37.72	-92.06	3.3	O	W	893	0	0.0019	0.0018	0.2269	0.0005	0.0004	0.5056	0.0004	0.0004	0.5015	0.0015	-0.0713
MO2	38.47	-90.71	2.1	S	W	791	0	0.0005	0.0005	0.2205	0.0000	0.0000	0.4514	0.0000	0.0000	0.5549	0.0000	-0.1864
MO3	39.59	-91.92	3.6	O	W	690	1	0.0033	0.0032	0.1386	0.0013	0.0012	0.4043	0.0009	0.0009	0.4022	0.0000	0.1756
IL1	41.00	-87.56	1.9	O	W	872	0	0.0019	0.0018	0.3313	0.0006	0.0005	0.7753	0.0005	0.0004	0.7731	0.0000	-0.1634
IL2	42.42	-87.80	6.8	O	W	604	0	0.0037	0.0037	0.0313	0.0014	0.0013	0.4980	0.0011	0.0010	0.5097	0.0004	0.0755
IN1	41.61	-87.19	5.2	O	W	761	0	0.0034	0.0036	-0.1801	0.0014	0.0013	0.2700	0.0010	0.0010	0.2702	0.0012	0.0193
OH1	41.62	-83.79	4.2	S	W	819	0	0.0007	0.0008	0.1723	0.0000	0.0000	0.7956	0.0000	0.0000	0.8222	0.0000	-0.1218
IA1	41.97	-90.37	2.2	O	W	402	1	0.0040	0.0039	0.2051	0.0016	0.0015	0.4739	0.0012	0.0011	0.4776	0.0036	0.1077
IA2	43.36	-91.84	2.0	O	W	304	1	0.0036	0.0034	0.3213	0.0013	0.0011	0.6918	0.0010	0.0008	0.7058	0.0025	0.0754
PA4	42.17	-80.07	5.5	O	W	1040	1	0.0029	0.0026	0.3684	0.0010	0.0008	0.7836	0.0007	0.0006	0.7970	0.0024	-0.0340
MI1	42.70	-86.20	5.2	O	W	618	0	0.0033	0.0035	-0.1618	0.0013	0.0013	0.2302	0.0010	0.0010	0.2208	0.0005	0.0405
MI2	44.01	-86.49	7.0	O	W	499	0	0.0034	0.0035	-0.1023	0.0013	0.0012	0.3655	0.0010	0.0009	0.3857	0.0005	0.0350
MI3	45.75	-85.50	4.6	O	W	480	0	0.0033	0.0034	-0.0694	0.0013	0.0012	0.3692	0.0010	0.0009	0.3512	0.0020	0.0649
MI4	46.67	-86.02	2.8	O	W	624	0	0.0022	0.0022	0.0906	0.0007	0.0006	0.5842	0.0006	0.0005	0.5858	0.0007	-0.1216
MI5	47.38	-87.96	3.1	S	W	238	0	0.0020	0.0019	0.2573	0.0007	0.0006	0.7669	0.0005	0.0004	0.7834	0.0000	-0.0839
MI6	48.16	-88.45	3.0	S	W	331	0	0.0015	0.0016	0.0462	0.0003	0.0003	0.4148	0.0002	0.0002	0.4250	0.0000	-0.1667
WI1	43.83	-89.72	3.3	O	W	213	0	0.0048	0.0061	-0.8135	0.0020	0.0024	-0.4234	0.0016	0.0018	-0.3599	0.0038	0.2058
WI2	46.11	-92.08	1.7	O	W	218	0	0.0041	0.0044	-0.2143	0.0017	0.0016	0.1503	0.0013	0.0013	0.1888	0.0014	0.1205
WI3	46.73	-90.81	3.8	O	W	196	0	0.0037	0.0036	0.1003	0.0015	0.0013	0.5002	0.0011	0.0010	0.5214	0.0027	0.1579
ON1	42.87	-79.18	1.8	S	W	1105	1	0.0013	0.0013	0.3233	0.0001	0.0001	0.6676	0.0001	0.0001	0.6879	0.0010	-0.1307
ON2	42.58	-80.39	3.5	S	W	997	1	0.0010	0.0011	-0.3272	0.0001	0.0001	-0.4252	0.0001	0.0001	-0.4264	0.0021	-0.1797

ON3	43.26	-81.84	5.9	O	W	872	0	0.0028	0.0028	-0.0354	0.0009	0.0008	0.3158	0.0007	0.0006	0.3286	0.0023	-0.0535
ON4	42.26	-81.85	6.3	S	W	936	1	0.0014	0.0014	0.1265	0.0003	0.0003	0.5654	0.0002	0.0002	0.5577	0.0047	0.0078
ON5	45.60	-82.14	4.1	O	W	699	0	0.0030	0.0028	0.2785	0.0010	0.0008	0.7956	0.0008	0.0006	0.7891	0.0014	0.1435
ON6	45.79	-82.75	2.2	O	W	662	0	0.0027	0.0027	0.0092	0.0009	0.0009	0.3959	0.0007	0.0006	0.3999	0.0011	-0.0467
ON7	45.78	-82.75	2.1	O	W	662	0	0.0024	0.0024	0.0875	0.0008	0.0007	0.6258	0.0006	0.0006	0.6461	0.0007	-0.0344
ON8	47.93	-84.85	2.9	O	W	479	0	0.0028	0.0025	0.3553	0.0009	0.0008	0.8746	0.0007	0.0006	0.8800	0.0021	-0.0517
ON9	47.79	-84.90	2.7	O	W	467	0	0.0029	0.0026	0.3906	0.0010	0.0008	0.8207	0.0007	0.0006	0.8323	0.0012	-0.0643
ON10	48.60	-86.30	4.7	O	W	486	0	0.0028	0.0026	0.2655	0.0010	0.0008	0.7345	0.0008	0.0006	0.7428	0.0006	0.0158
ON11	48.77	-87.13	1.5	S	W	417	0	0.0003	0.0003	-0.0851	0.0000	0.0000	-0.2173	0.0000	0.0000	-0.2141	0.0000	0.1146
ON12	49.65	-94.92	3.1	O	W	691	0	0.0029	0.0029	0.0589	0.0011	0.0010	0.5815	0.0009	0.0007	0.5801	0.0005	-0.0727
Outcrossing, mean								*0.0036*	*0.0036*	*0.0636*	*0.0013*	*0.0012*	*0.4785*	*0.0010*	*0.0009*	*0.4878*	*0.0018*	*0.0507*
Selfing, mean								*0.0014*	*0.0013*	*0.1488*	*0.0003*	*0.0003*	*0.4401*	*0.0002*	*0.0002*	*0.4569*	*0.0009*	*-0.1002*
Average								*0.0032*	*0.0032*	*0.0800*	*0.0011*	*0.0010*	*0.4711*	*0.0009*	*0.0008*	*0.4818*	*0.0016*	*0.0217*

Table S2. Test statistics of the four-population test for treeness. Clade 1 was [NJ1,PA1], clade 2 was[ON3,X], where X is a western population in an area formerly covered by the Laurentide ice sheet. Tests are sorted by the *Z* score; only tests with significant positive *Z* scores support the hypothesis of past gene flow.

Populations	F4 statistic	Standard error	*Z* score	*P*
NJ1,PA1;ON3,PA4	0.00875	0.00134	6.54	6.25E-11
NJ1,PA1;ON3,ON2	0.00663	0.00140	4.74	2.14E-6
NJ1,PA1;ON3,ON1	0.00659	0.00140	4.72	2.35E-6
NJ1,PA1;ON3,ON4	0.00437	0.00116	3.78	0.000155
NJ1,PA1;ON3,IL1	0.00100	0.00098	1.02	0.307
NJ1,PA1;ON3,OH1	0.000809	0.00101	0.804	0.421
NJ1,PA1;ON3,WI2	0.000174	0.000921	0.189	0.850
NJ1,PA1;ON3,IL2	-0.000261	0.00113	-0.231	0.817
NJ1,PA1;ON3,IN1	-0.000355	0.000832	-0.427	0.669
NJ1,PA1;ON3,MI2	-0.000431	0.000847	-0.509	0.611
NJ1,PA1;ON3,MI1	-0.000577	0.000878	-0.657	0.511
NJ1,PA1;ON3,WI3	-0.000988	0.00101	-0.983	0.326
NJ1,PA1;ON3,MI3	-0.00108	0.000878	-1.23	0.220
NJ1,PA1;ON3,ON5	-0.00186	0.000937	-1.99	0.0471
NJ1,PA1;ON3,ON8	-0.00227	0.00113	-2.02	0.0436
NJ1,PA1;ON3,MI5	-0.00236	0.00114	-2.07	0.0387
NJ1,PA1;ON3,ON7	-0.00230	0.00110	-2.09	0.0368
NJ1,PA1;ON3,ON12	-0.00238	0.000985	-2.42	0.0157
NJ1,PA1;ON3,ON6	-0.00258	0.00101	-2.57	0.0102
NJ1,PA1;ON3,MI4	-0.00249	0.000947	-2.63	0.00858
NJ1,PA1;ON3,ON9	-0.00345	0.00102	-3.38	0.000734
NJ1,PA1;ON3,MI6	-0.00542	0.00143	-3.79	0.000149
NJ1,PA1;ON3,ON10	-0.00378	0.000928	-4.07	4.73E-5
NJ1,PA1;ON3,ON11	-0.00607	0.00140	-4.35	1.39E-5

Table S3. Test statistics of the four-population test for treeness. Clade 1 was [MO1,MO2], clade 2 was [WI3,X], where X is a western population. Tests are sorted by the *Z* score; only tests with significant positive *Z* scores support the hypothesis of past gene flow.

Populations	F4 statistic	Standard error	*Z* score	*P*
MO2,MO1;WI3,MO3	0.00603	0.00175	3.44	0.000577
MO2,MO1;WI3,IA1	0.00294	0.00133	2.21	2.71E-2
MO2,MO1;WI3,IA2	0.00313	0.00149	2.10	3.54E-2
MO2,MO1;WI3,PA4	0.00112	0.00156	0.716	0.474
MO2,MO1;WI3,WI2	0.000541	0.000957	0.565	0.572
MO2,MO1;WI3,MI5	-0.000397	0.00133	-0.298	0.766
MO2,MO1;WI3,WI1	-0.000556	0.000944	-0.589	0.556
MO2,MO1;WI3,ON2	-0.00107	0.00166	-0.644	0.519
MO2,MO1;WI3,ON1	-0.00143	0.00168	-0.853	0.394
MO2,MO1;WI3,ON12	-0.00277	0.00143	-1.94	0.0526
MO2,MO1;WI3,ON4	-0.00379	0.00153	-2.47	0.0134
MO2,MO1;WI3,ON8	-0.00439	0.00127	-3.45	0.000565
MO2,MO1;WI3,ON10	-0.00441	0.00120	-3.69	0.000224
MO2,MO1;WI3,ON9	-0.00477	0.00126	-3.79	1.53E-4
MO2,MO1;WI3,ON11	-0.00623	0.00157	-3.97	7.30E-5
MO2,MO1;WI3,MI3	-0.00528	0.00129	-4.08	4.53E-5
MO2,MO1;WI3,MI6	-0.00601	0.00142	-4.22	2.41E-5
MO2,MO1;WI3,MI4	-0.00737	0.00142	-5.19	2.05E-7
MO2,MO1;WI3,IL2	-0.00621	0.00114	-5.45	5.01E-8
MO2,MO1;WI3,ON5	-0.00741	0.00128	-5.77	8.08E-009
MO2,MO1;WI3,ON7	-0.00894	0.0015	-5.97	2.39E-009
MO2,MO1;WI3,ON6	-0.00829	0.00139	-5.98	2.20E-009
MO2,MO1;WI3,MI2	-0.00837	0.00116	-7.22	5.14E-013
MO2,MO1;WI3,IN1	-0.00892	0.00119	-7.50	6.36E-014
MO2,MO1;WI3,OH1	-0.0130	0.00173	-7.51	6.01E-014
MO2,MO1;WI3,ON3	-0.0104	0.00135	-7.73	1.09E-014
MO2,MO1;WI3,IL1	-0.0106	0.00131	-8.11	5.14E-016
MO2,MO1;WI3,MI1	-0.00988	0.00116	-8.50	1.84E-017

Table S4. Linear model testing relationships between genomic diversity and census size, mating system, ancestral cluster, distance to cluster core, and admixture. Genomic diversity is represented by the weighted medians of Tajima's *D* of intergenic and CDS regions (windows of 5000 bp). Sample size for all models was 52 populations. Variation explained by the models were: intergenic *D*: $R^2 = 0.13$; CDS *D*: $R^2 = 0.04$. Estimated intercept and coefficients, and variation explained are reported. Significance is indicated: *, $0.01 < P \leq 0.05$; **, $0.001 < P \leq 0.01$; ***, $P \leq 0.001$.

	D, intergenic regions		*D*, CDS regions	
Source	Estimate	Var. [%]	Estimate	Var. [%]
Intercept	0.1248		0.5357***	
log1$_0$(census size)	-0.0296	1.65	-0.0122	0.13
Mating system (selfing)	0.0175	0.78	-0.0623	0.40
Ancestral cluster (west)	-0.0920	1.22	-0.0583	0.47
log$_{10}$(distance to core)	0.4047*	8.06	0.3117	3.20
Admixture (yes)	0.0498	0.95	-0.0531	0.27

Table S5. Observed Watterson's θ from intergenic regions for pairs of selfing (S) and nearby outcrossing (O) populations were compared to test whether differences in N_e of selfing populations exceeded the predicted reduction relative to a random outcrossing population. The predicted reduction is (1 + F_{IS} of the selfing population) (Pollack 1987). The last column lists the relative deviation of the observed θ in selfing populations from their expected θ based on the θ of the nearby outcrossing populations.

Population S	F_{IS}	$\theta_{S\ obs}$	Population O	$\theta_{O\ obs}$	$\theta_{S\ predicted}$	Deviations$_{S\ obs}$
MI6	0.673	0.0016	ON12	0.0029	0.0017	-0.10
MO2	0.677	0.0005	MO1	0.0018	0.0011	-0.50
NC1	0.442	0.0018	NC2	0.0020	0.0014	0.29
OH1	0.680	0.0008	IL1	0.0018	0.0011	-0.28
ON1	0.700	0.0013	PA4	0.0026	0.0015	-0.18
ON11	0.950	0.0003	ON10	0.0026	0.0014	-0.74
ON2	0.615	0.0011	PA4	0.0026	0.0016	-0.31
ON4	0.458	0.0014	ON3	0.0028	0.0019	-0.26
Average						*-0.26*

Table S6. Pearson correlation coefficients for pairs of genetic diversity estimates based on microsatellites (expected heterozygosity, H_e, and allelic richness, A) and on single-nucleotide polymorphisms for intergenic regions, intron regions, and coding DNA sequences (CDS) (Tajima's π, and Watterson's θ). Sample size was 52 populations. P-values were <0.001 for all pairwise tests.

	π, intergen.	π, intron	π, CDS	A	θ, intergen.	θ, intron	θ, CDS
H_e	0.892	0.925	0.924	0.919	0.894	0.919	0.919
π, intergenic		0.983	0.984	0.850	0.981	0.964	0.966
π, intron			0.999	0.879	0.972	0.987	0.986
π, CDS				0.877	0.973	0.985	0.987
A					0.907	0.921	0.921
θ, intergenic						0.983	0.984
θ, intron							0.999

Figure S1

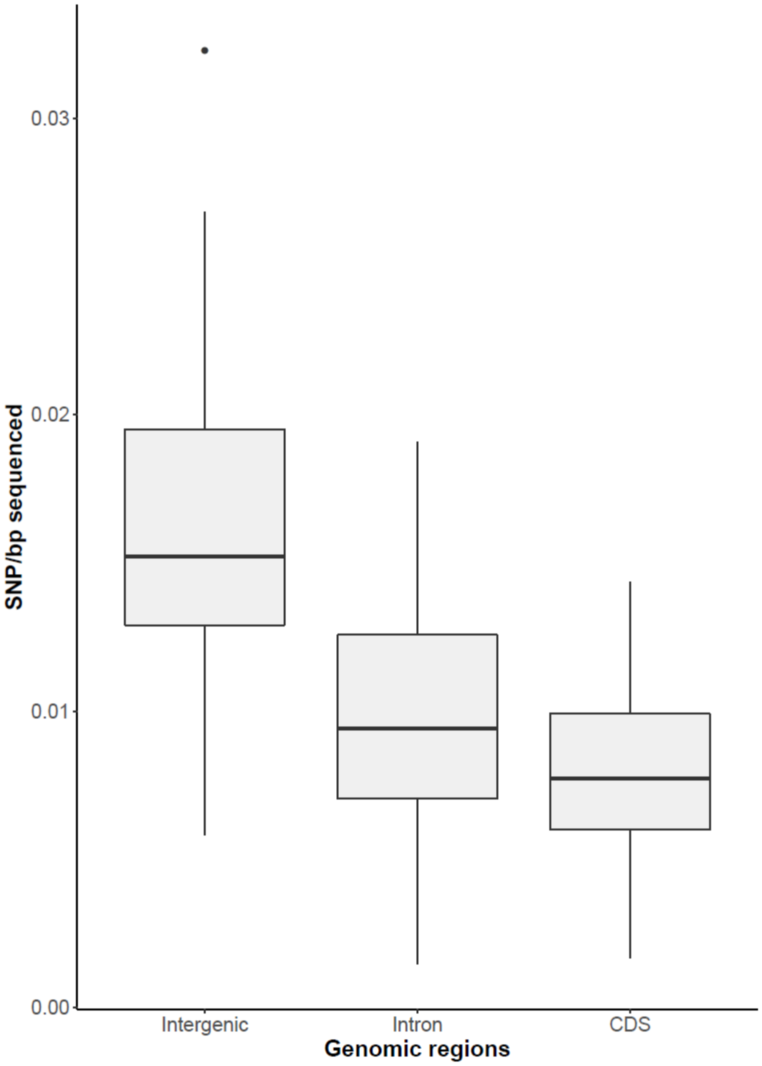

Fig. S1. Boxplot of the fraction of SNPs relative to base pairs sequenced for intergenic regions, intron regions and coding DNA sequences (CDS) (*N* = 52 populations). The thick horizontal line represents the median, the hinges are the first and third quartile, and whiskers extend to the most extreme data point no more than 1.5x the interquartile range from the box.

Figure S2

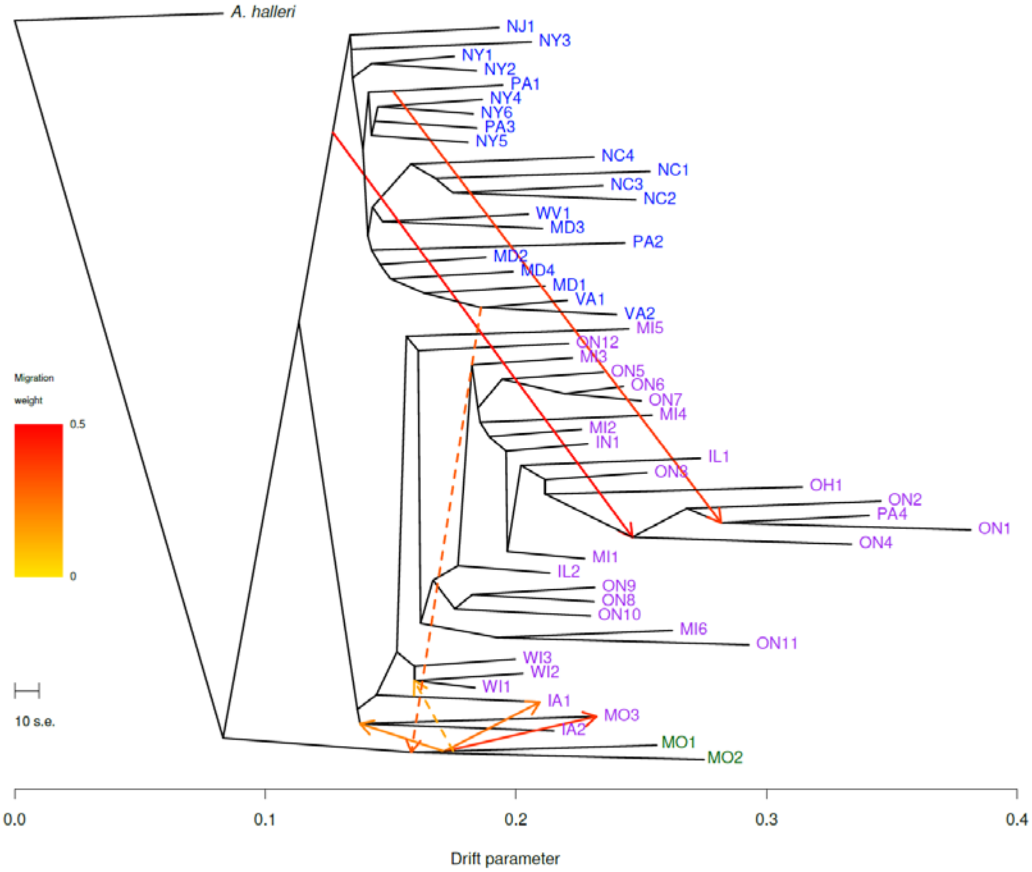

Fig. S2. Relatedness tree of *A. lyrata* populations, using *A. halleri* as an outgroup. The branch lengths are proportional to the drift parameter of time over $2N_e$. The populations of the Ozarks clade are indicated by green tip labels, those of the mid-western clade are in purple and those of the eastern clade in blue. The solid arrows indicate migration events with support by the four-population test for treeness, the dotted arrows indicate migration events without support by the four-population test or that could not be tested.

Figure S3

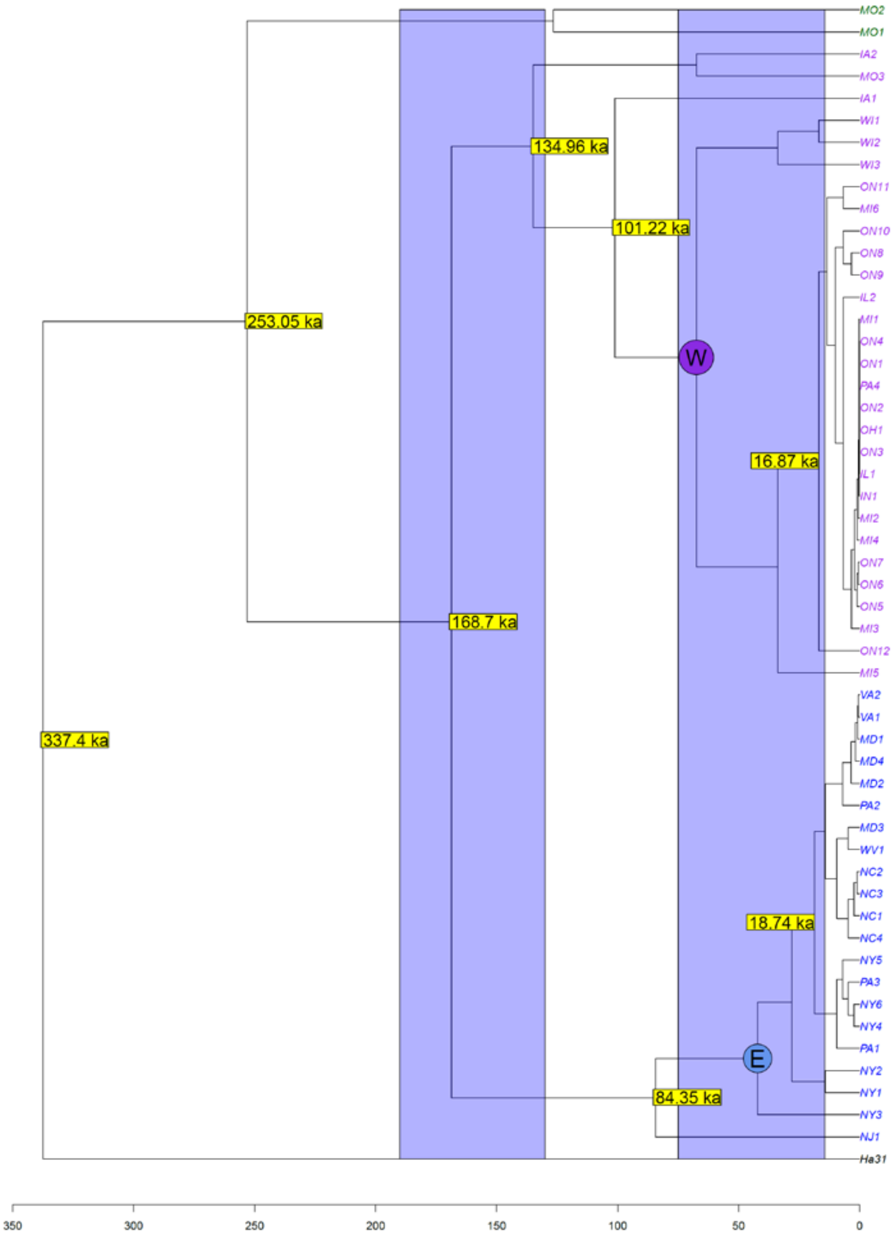

Fig. S3. Time-calibrated tree of *Arabidopsis lyrata* populations produced with Treemix. The purple rectangles indicate periods of glaciation (Illinoian 190,000-130,000 years ago; Wisconsin 75,000-14,500 years ago). The populations of the Ozarks clade are indicated by green tip labels, those of the mid-western clade are in purple, and those of the eastern clade are in blue. The two circles indicate the nodes from which expansion was assumed to have happened since the last glacial maximum. Populations with older splits were located in areas not covered by ice during the LGM. Estimated divergence times are in yellow boxes. The scale on the bottom indicates number of years (×10^3) before present.

Figure S4

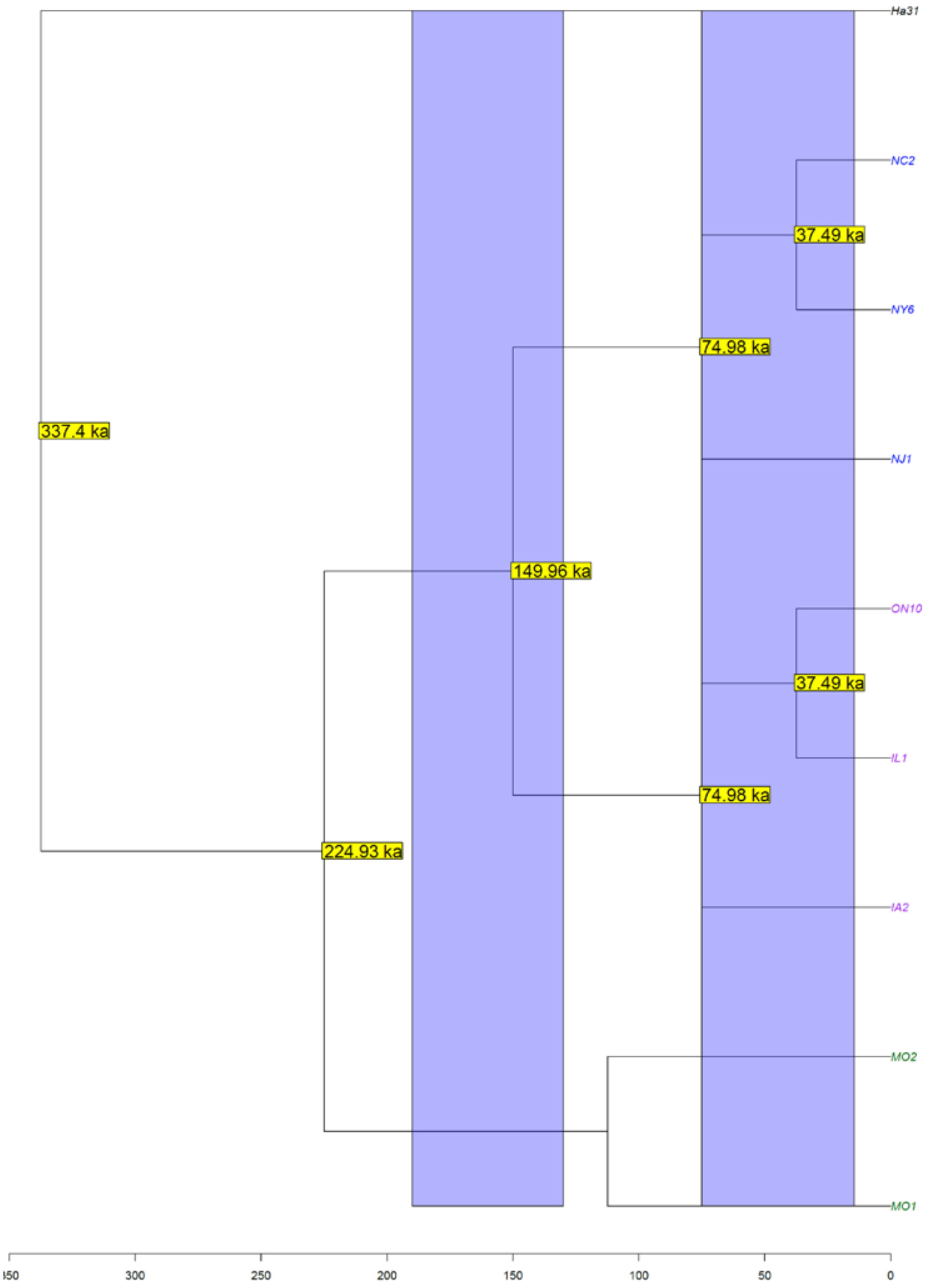

Fig. S4. Time-calibrated tree of a subsample of *A. lyrata* populations produced with revPoMo. The purple rectangles indicate periods of glaciation (Illinoian 190,000-130,000 years ago; Wisconsin 75,000-14,500 years ago). The populations of the Ozarks clade are indicated by green tip labels, those of the mid-western clade are in purple, and those of the eastern clade are in blue. Estimated divergence times are in yellow boxes. The scale on the bottom indicates number of years (×10^3) before present.