

Supplementary Information for

Smith AL, Hodkinson TR, Vilellas J, Catford JA, Csergő AM, Blomberg SP, Crone EE, Ehrlén J, Garcia MB, Laine A-L, Roach DA, Salguero-Gómez R, Wardle G, Childs DZ, Elderd BD, Finn A, Munné-Bosch S, Baudraz MEA, Bódis J, Brearley FQ, Bucharova A, Caruso CM, Duncan RP, Dwyer JM, Gooden B, Groenteman R, Hamre LN, Helm A, Kelly R, Laanisto L, Lonati M, Moore JL, Morales M, Olsen SL, Pärtel M, Petry WK, Ramula S, Rasmussen PU, Enri SR, Roeder A, Roscher C, Saastamoinen M, Tack AJM, Töpper JP, Vose GE, Wandrag EM, Wingler A, Buckley YM (2020). Global gene flow releases invasive plants from environmental constraints on genetic diversity. *Proceedings of the National Academy of Sciences USA*, www.pnas.org/cgi/doi/10.1073/pnas.1915848117

Correspondence: Annabel Smith
Email: annabel.smith@uq.edu.au

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Figures S1 to S6
Table S1

Other supplementary materials for this manuscript include the following:

Dataset S1
Data and code (Zenodo Repository): <https://zenodo.org/record/3626288>

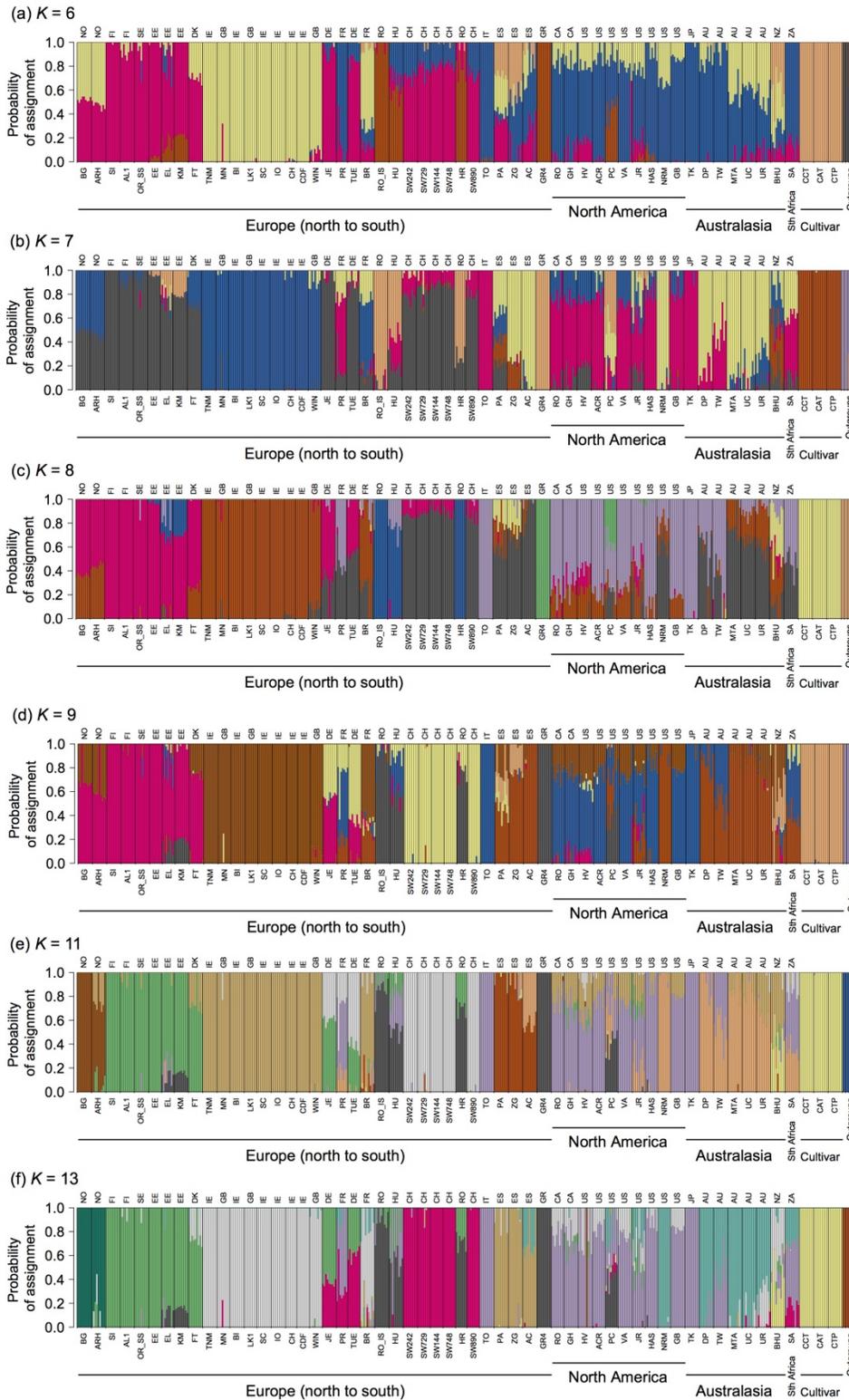


Fig. S1. Probabilities of assignment for 491 *Plantago lanceolata* individuals to genomic clusters identified by fastSTRUCTURE, grouped by site within region. Model complexity which maximised marginal likelihood in the data was six and 13 model components were used to explain structure in the data. The figure presents a representative set of results from $K = 6, 7, 8, 9, 11$ and 13 . Country codes are indicated above the bars and site codes (Table S1) are below.

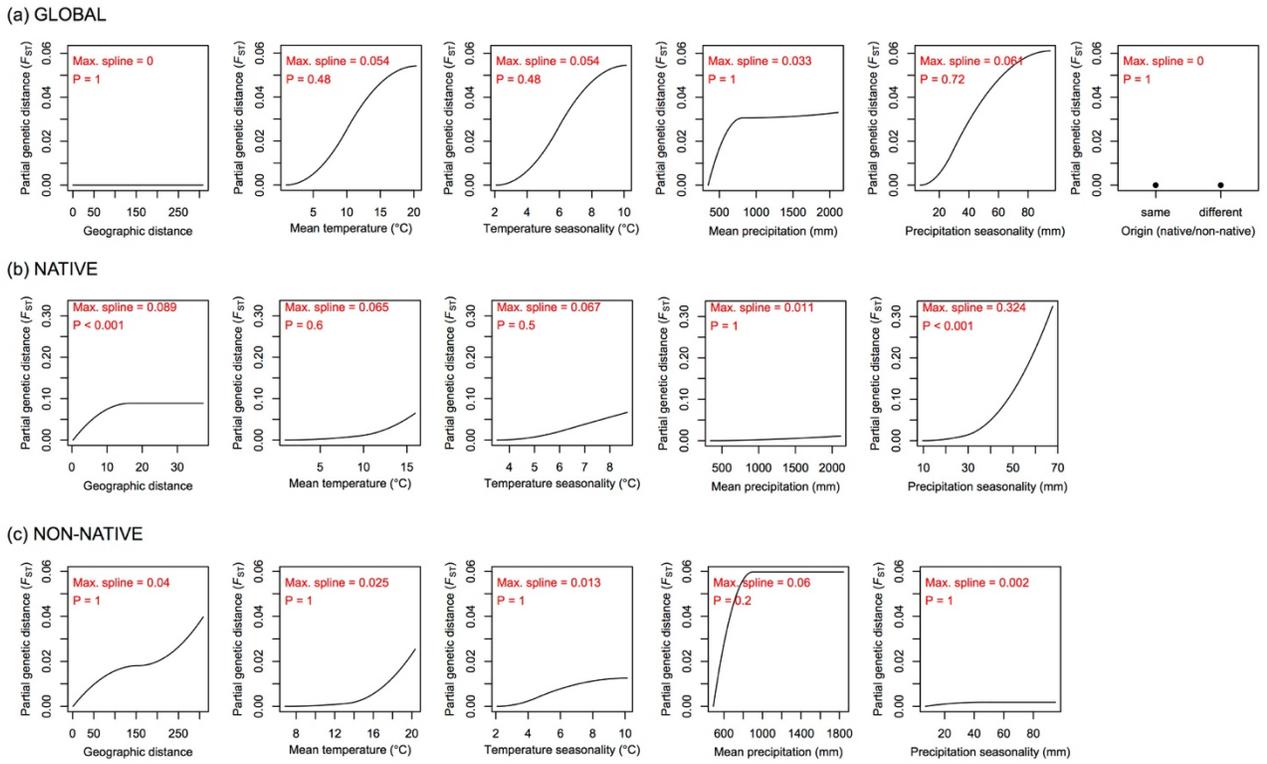


Fig. S2. Results from three separate generalised dissimilarity models investigating the influence of environmental variables on partial genetic distance (F_{ST}) among populations of *Plantago lanceolata*. (a) The global population including native and non-native populations (deviance explained 10.9%), (b) the native European range (deviance explained 74.3%) and (c) the non-native range (deviance explained 23.1%). The splines indicate the partial influence of each variable along the gradient, given all other variables in the model, and the P values (Bonferroni-adjusted for each model) indicate their importance. The shape of each spline indicates the rate of change in allele frequencies along the gradient. Note, the y-axis varies spans a much higher range in panel (b) ($F_{ST} = 0-0.3$), reflecting the stronger influence of environmental variables on F_{ST} in the native range.

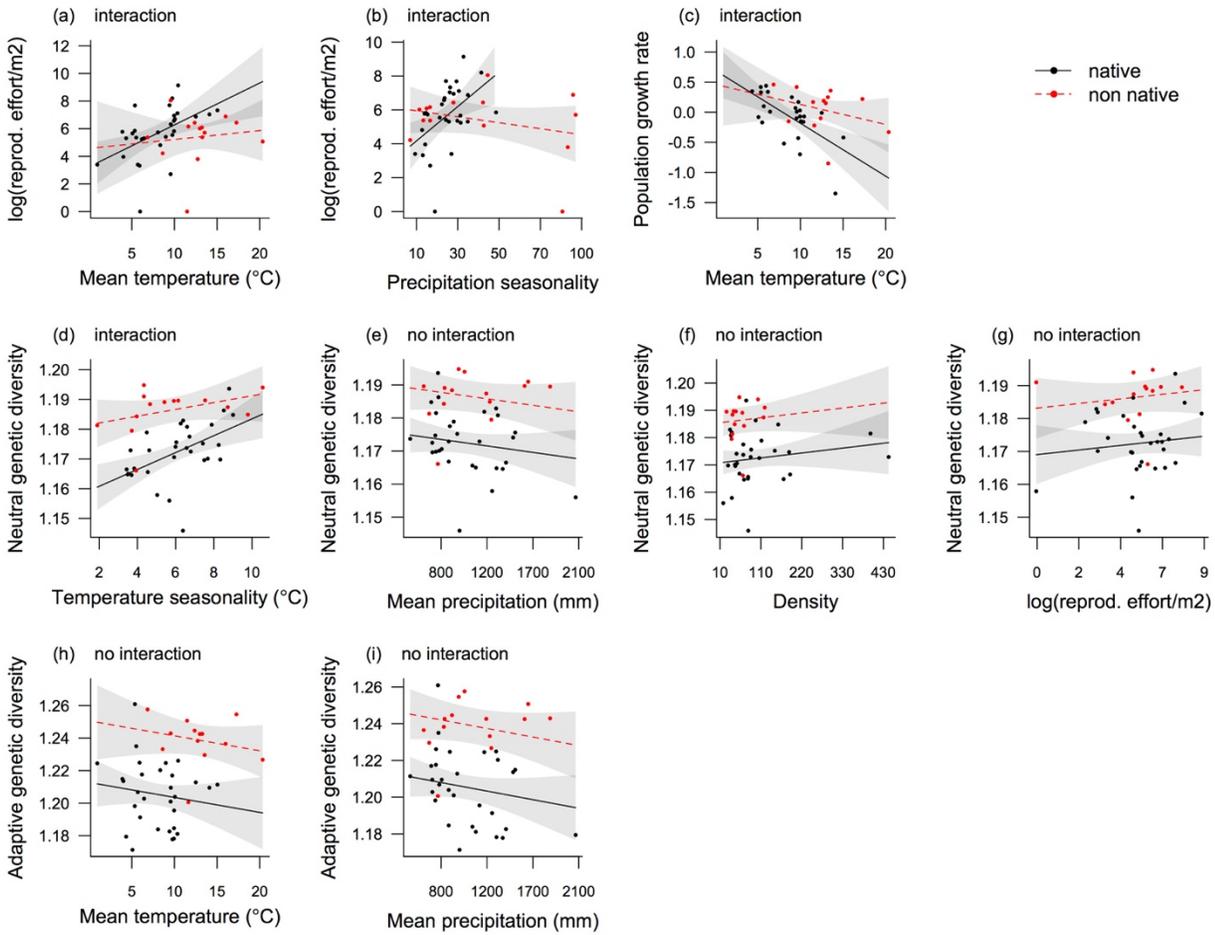


Fig. S3. Models with support from the data. All models except (b) were ranked lower than the first. (b) For the influence of precipitation seasonality on reproductive effort, the only supported model was interactive (AICc weight = 0.65) but was not interpretable because the native and non-native ranges did not have comparable values. First-ranked models are in Fig. 5 in the main document and Dataset S1 includes rankings and coefficients. Effects of range (native/non-native) in these models were either additive or interactive. Model estimates and 95% confidence intervals are shown over the raw data. Temperature seasonality is the standard deviation of annual mean temperature at each site.

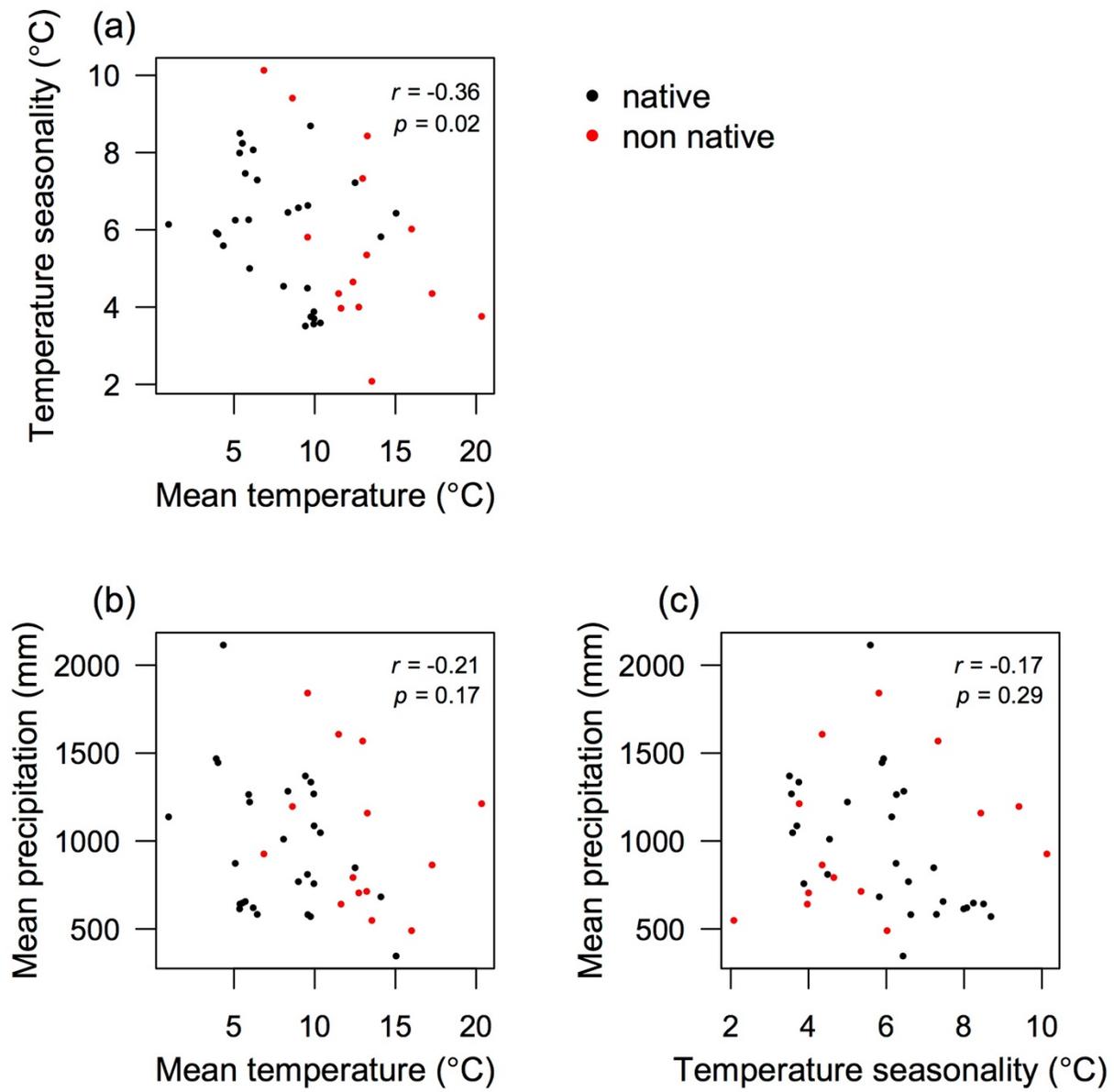


Fig. S4. Relationships among environmental variables that affected demography or genetic diversity.

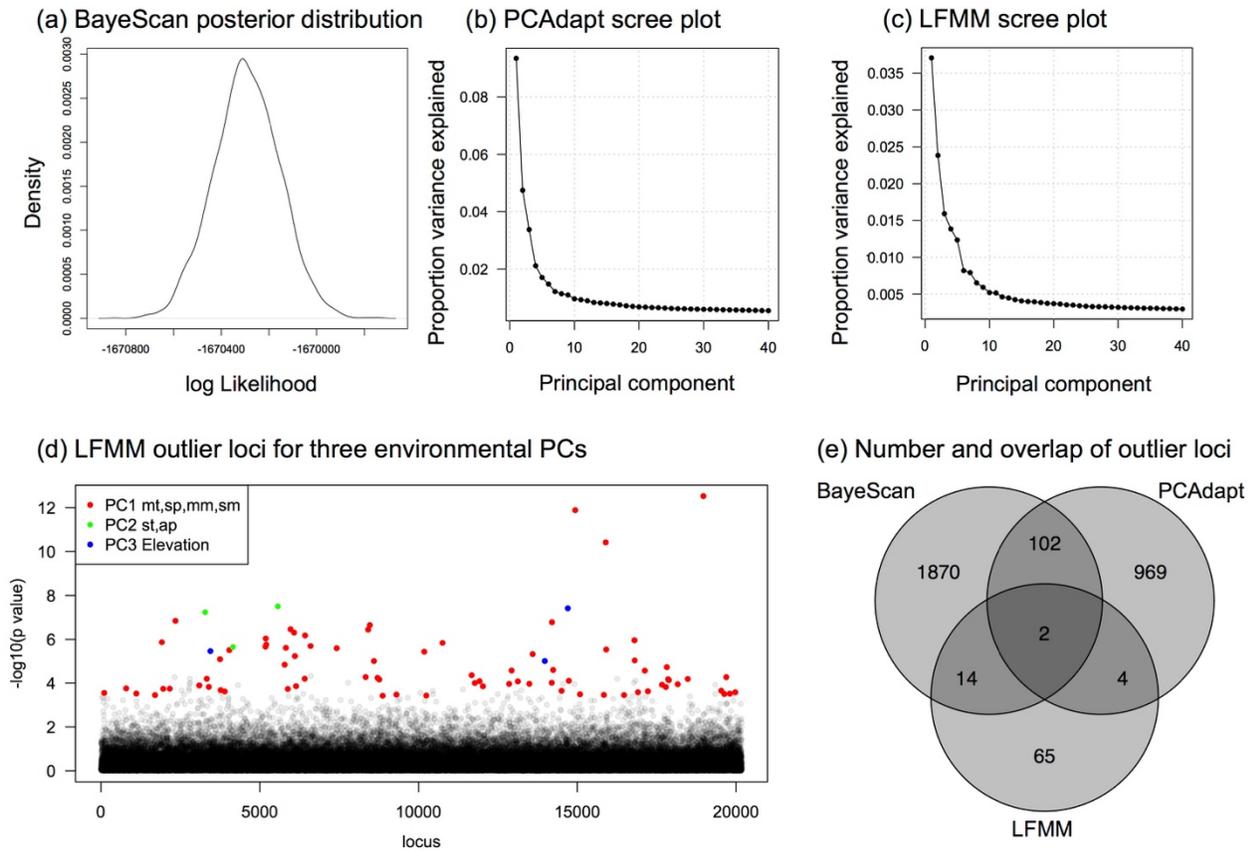


Fig. S5. Diagnostics and results from outlier tests to detect SNPs putatively under selection. (a) The posterior distribution of 100,000 MCMC iterations from BayeScan model; (b) scree plot of principal components in PCAadapt model; (c) scree plot of principal components in LFMM model; (d) LFMM outlier loci (in colours) plotted over non-outliers (in black) in relation to three environmental principal components: PC1 (red) had high loadings on mean temperature (mt), precipitation seasonality (sp), mean moisture (mm) and moisture seasonality (sm), PC2 (green) had high loadings on temperature seasonality (st) and mean precipitation (ap), PC3 (blue) had a high loading on elevation; (e) in total, 3024 SNPs were identified as outliers using all three methods, with little overlap among methods.

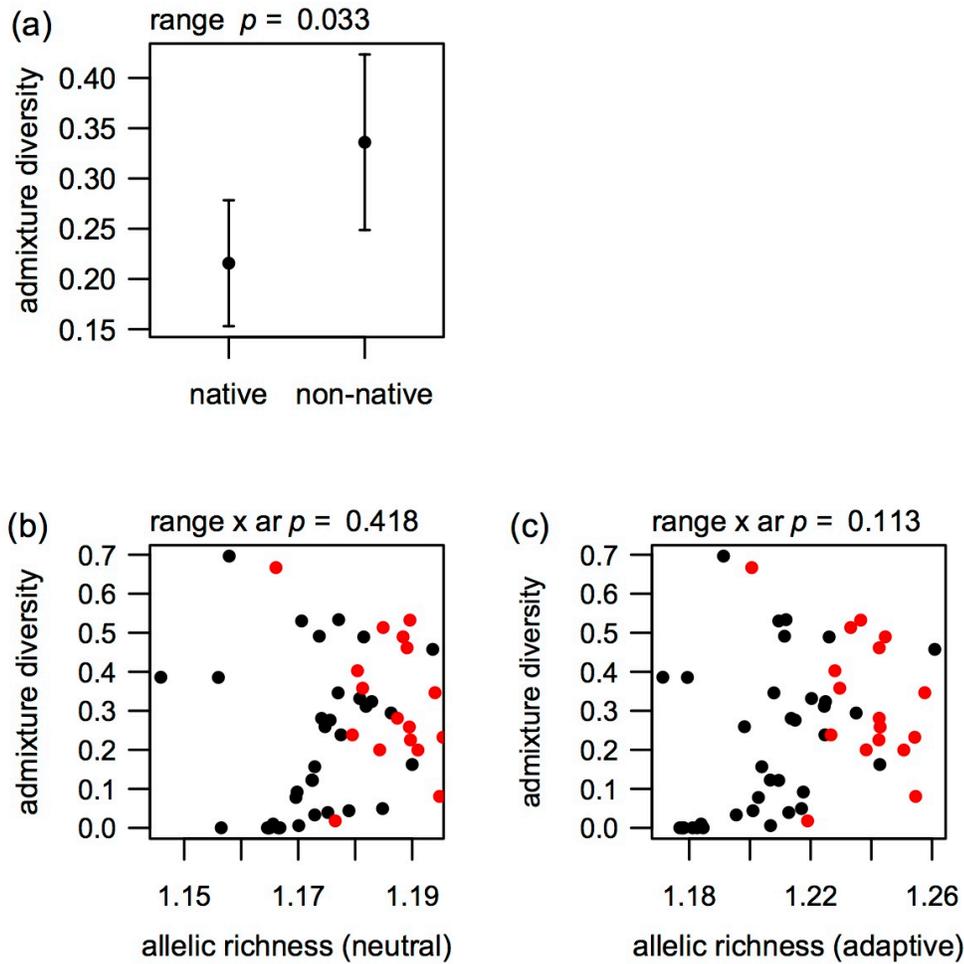


Fig. S6. Admixture diversity score (DS) in *Plantago lanceolata*, calculated from the assignment probabilities of fastSTRUCTURE analysis. (a) Estimates and 95% confidence intervals from a linear mixed model of individual DS in native and non-native ranges. (b–c) Relationship between site-level allelic richness and mean DS . Black points = native, red points = non-native. DS gives complementary information to the within-population genetic diversity as high genetic admixture does not always equal high genetic diversity.

Table S1. Summary of *Plantago lanceolata* sites included in genetic (all sites, n = 53) and demographic (n = 44) analyses. Genetic analyses included additional samples from cultivar lines and outgroups (Fig. 1 in main document). He = expected heterozygosity, AR = allelic richness.

Range	Country	Site code	Latitude	Longitude	N individuals genotyped	Genetic diversity					Demographic census		
						He	AR neutral	AR adaptive	Admixture diversity (DS)	N private alleles	Census	Year 0	No. years sampled
Native	Estonia	EE	58.7171	23.7716	8	0.166	1.170	1.218	0.0919	0	yes	2015	2
	Estonia	EL	58.2597	26.3513	8	0.188	1.194	1.261	0.4575	1	yes	2015	2
	Estonia	KM	57.7349	26.5331	9	0.182	1.186	1.235	0.2944	0	yes	2015	2
	Finland	SI	60.2370	21.9598	9	0.165	1.170	1.207	0.0059	0	yes	2015	2
	Germany	JE	50.9519	11.6228	9	0.167	1.173	1.210	0.1218	0	yes	2015	2
	Germany	TUE	48.5397	9.0368	8	0.172	1.178	1.225	0.2384	0	yes	2015	3
	Hungary	HU	46.7493	17.2373	9	0.181	1.182	1.226	0.4892	2	yes	2015	2
	Ireland	TNM	55.2456	-7.6174	9	0.161	1.167	1.183	0.0002	0	yes	2015	3
	Ireland	BI	53.3724	-6.1682	9	0.161	1.167	1.185	0.0002	0	yes	2016	2
	Ireland	SC	53.0723	-8.9923	9	0.160	1.165	1.178	0.0002	0	yes	2015	3
	Ireland	IO	53.0571	-9.5167	9	0.160	1.165	1.178	0.0002	1	yes	2015	2
	Ireland	CH	52.1443	-8.9484	7	0.172	1.173	1.196	0.0332	0	yes	2015	3
	Ireland	CDF	51.8996	-8.4859	8	0.160	1.165	1.181	0.0002	0	yes	2016	2
	Italy	TO	45.0650	7.5895	9	0.172	1.175	1.213	0.0394	1	yes	2015	3
	Norway	BG	61.4481	7.4807	9	0.143	1.146	1.171	0.3860	0	yes	2015	2
	Norway	ARH	60.6652	6.3374	9	0.151	1.156	1.179	0.3855	0	yes	2015	2
	Romania	RO_IS	47.1849	27.5569	9	0.188	1.185	1.217	0.0494	3	yes	2016	2
	Romania	HR	46.3447	25.6170	7	0.179	1.175	1.198	0.2592	1	yes	2015	2
	Spain	PA	42.7574	-0.2367	9	0.153	1.158	1.191	0.6964	3	yes	2014	2
	Spain	ZG	41.6895	-0.9324	9	0.169	1.174	1.211	0.4911	0	yes	2016	2
	Spain	AC	41.3179	1.9500	9	0.169	1.171	1.210	0.5303	0	yes	2015	2
	Sweden	OR_SS	59.2692	18.1011	9	0.164	1.170	1.203	0.0779	0	yes	2015	2
	Switzerland	SW242	46.4453	6.9315	9	0.175	1.181	1.220	0.3316	0	yes	2017	1
	Switzerland	SW729	46.4048	7.0620	8	0.176	1.182	1.225	0.3115	0	yes	2017	1
	Switzerland	SW144	46.3809	7.0676	8	0.171	1.176	1.215	0.2761	0	yes	2017	1
	Switzerland	SW748	46.3688	7.1228	8	0.170	1.174	1.214	0.2806	0	yes	2017	1
	Switzerland	SW890	46.2583	7.0845	8	0.178	1.183	1.225	0.3236	0	yes	2017	1
	UK	MN	53.3798	-2.2161	8	0.172	1.179	1.201	0.0440	0	yes	2016	2
	UK	LK1	53.1924	-1.7624	8	0.161	1.166	1.184	0.0099	0	yes	2016	2
	UK	WIN	51.0432	-1.3082	8	0.168	1.173	1.204	0.1567	0	yes	2016	2
	Denmark	FT	55.6194	10.2951	9	0.171	1.177	1.208	0.3460	0	no	NA	NA
	Finland	AL1	60.2200	19.5410	9	0.166	1.172	1.207	0.1226	0	no	NA	NA
	France	PR	48.8526	2.3504	7	0.185	1.190	1.243	0.1624	0	no	NA	NA
France	BR	47.9994	-4.3463	9	0.171	1.177	1.212	0.5335	0	no	NA	NA	
Greece	GR4	38.3243	21.8793	9	0.151	1.157	1.177	0.0002	58	no	NA	NA	
Non-native	Australia	UR	-37.1910	144.3836	9	0.181	1.188	1.245	0.4895	0	yes	2016	2
	Australia	UC	-35.2343	149.0851	9	0.182	1.189	1.243	0.4614	0	yes	2015	2
	Australia	TW	-27.5811	151.9878	9	0.189	1.195	1.255	0.0807	0	yes	2015	2
	Australia	DP	-27.4984	153.0260	9	0.175	1.180	1.227	0.2383	0	yes	2015	2
	Canada	RO	49.2874	-121.6696	8	0.184	1.190	1.243	0.2585	0	yes	2015	2
	Canada	GH	43.5347	-80.2117	9	0.188	1.194	1.258	0.3464	0	yes	2015	2
	New Zealand	BHU	-43.6500	172.4561	9	0.162	1.166	1.201	0.6669	2	yes	2015	2
	USA	HV	42.4857	-71.5687	9	0.179	1.185	1.233	0.5134	1	yes	2014	2
	USA	ACR	39.7132	-123.6518	8	0.187	1.191	1.251	0.1995	0	yes	2015	2

USA	PC	38.5177	-121.7643	8	0.188	1.190	1.237	0.5324	27	yes	2016	1
USA	VA	37.9674	-78.4740	9	0.186	1.187	1.243	0.2810	0	yes	2016	2
USA	HAS	36.3787	-121.5672	8	0.182	1.184	1.238	0.1999	0	yes	2015	2
USA	NRM	35.5244	-121.0738	8	0.176	1.181	1.230	0.3580	0	yes	2015	2
USA	GB	35.2291	-83.3903	9	0.187	1.190	1.243	0.2254	0	yes	2015	3
Australia	MTA	-34.0704	150.7679	9	0.175	1.180	1.228	0.4027	0	no	NA	NA
Japan	TK	35.6607	139.6849	9	0.174	1.177	1.219	0.0179	6	no	NA	NA
South Africa	SA	-33.9416	18.8731	9	0.189	1.195	1.254	0.2322	0	no	NA	NA
USA	JR	37.4080	-122.2275	8	0.196	1.202	1.271	0.5446	0	no	NA	NA

Dataset S1 (separate Excel file). Results from analysis of environmental and demographic effects on genetic diversity, including AICc rankings and top-model coefficients.

Data and code (Zenodo Repository): Smith, AL. (2020) annabellisa/PLANTPOPNET_genetics: PLANTPOPNET data and scripts v1.2 (Version v1.2). Zenodo. <http://doi.org/10.5281/zenodo.3626288>