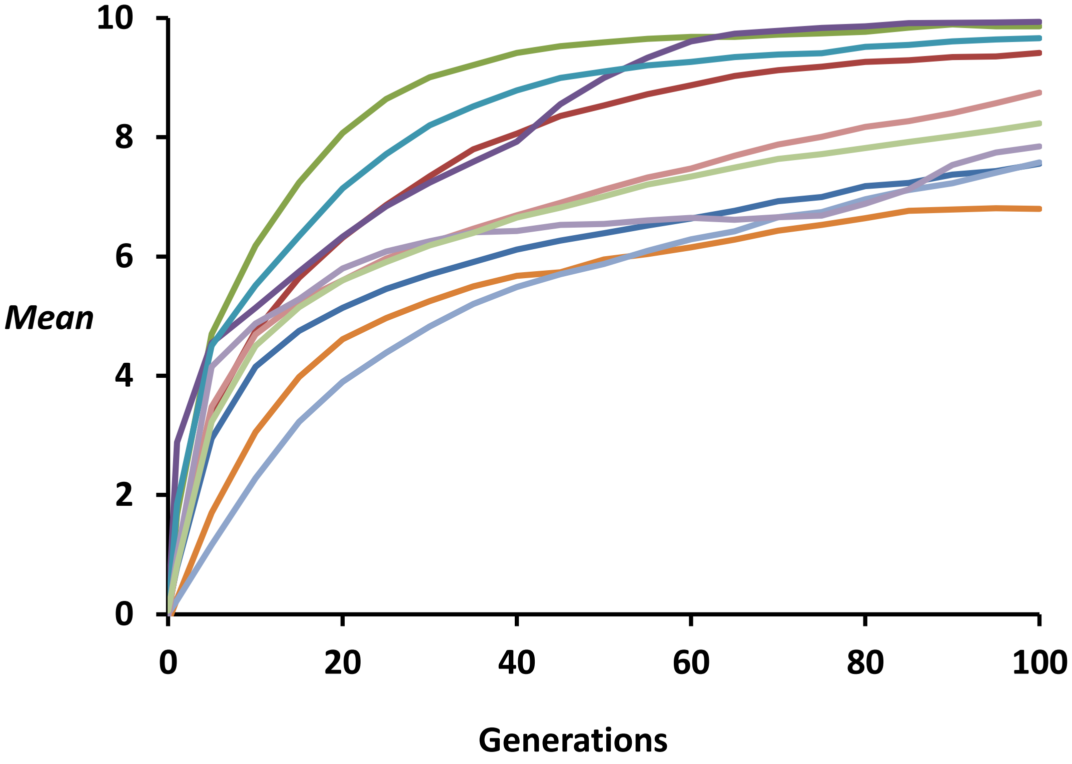

Figure S1 Example of simulated selection responses (change in the phenotypic mean for the selected quantitative trait) occurred after a change in the selection optimum in the population. The scenario refers to a subdivided population with n = 10 subpopulations, with a subpopulation census size randomly taken between 100 and 1000 and a migration rate among subpopulations randomly taken between 0.0001 and 0.1.

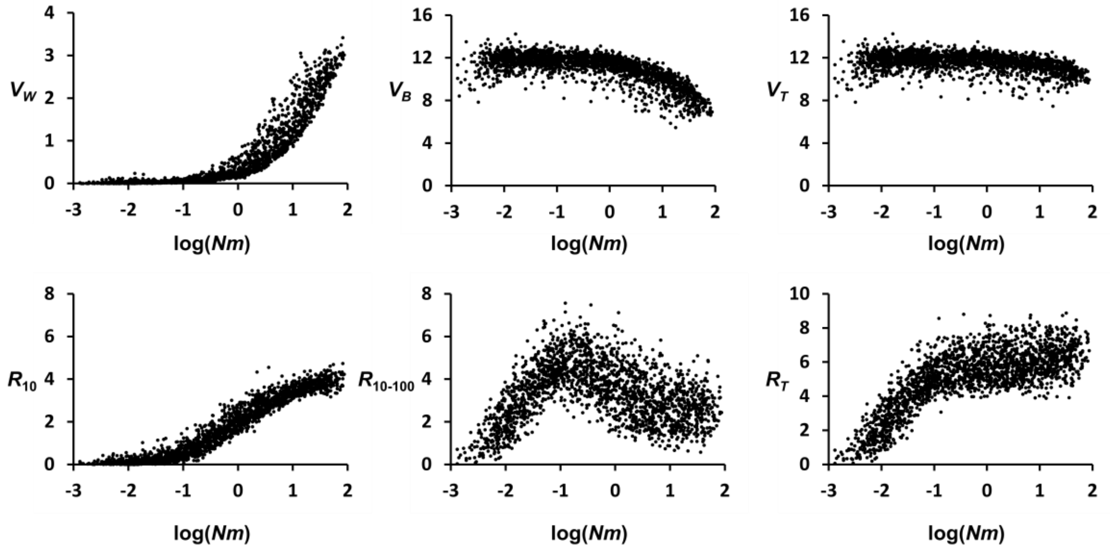

Figure S2 Initial quantitative trait variance components and responses to selection for the simulations plotted against the number of migrants per generation and subpopulation (*Nm*, in $\log_{10}$). The scenario refers to a subdivided population with $n = 10$ subpopulations, number of migrants per generation and subpopulation (*Nm*) either < 0.5 or > 0.5, mutation rate $u = 0.00001$ and strength of stabilising selection $\omega^2 = 25$. Results are based on 2,000 simulations varying the subpopulation size (*N*) randomly between 100 and 1000, and the migration rate (*m*) between 0.0001 and 0.1. V_W: Within-subpopulation genetic variance; V_B: Between-subpopulation genetic variance; V_T: Total genetic variance; R_{10}: response to selection until generation 10; $R_{10\text{-}100}$: response from generations 10 to 100; R_T: total response until generation 100.

The figure shows that whereas the short-term response (R_{10}) increases monotonically with *Nm*, the late response ($R_{10\text{-}100}$) increases with *Nm* for $\log(Nm) \approx -0.3$ ($Nm < {\sim}0.5$), and decreases thereafter. This indicates that, when subpopulations are considerably isolated from one another ($Nm < {\sim}0.5$, corresponding to an expected $F_{ST} > {\sim}1/3$), V_W is very low and V_B rather high, and late and total response increase with *Nm*, due to the slow but continuous increase of V_w at the expense of V_B. For higher levels of migration ($Nm > {\sim}0.5$; corresponding to $F_{ST} < {\sim}1/3$), V_W increases substantially with migration, implying an increase in the short-term response, but V_B and V_T decline consistently, implying a decline in late response.

Table S1 Ordinary correlation coefficients between initial population genetic diversity variables and response to selection for a structured population

		***Nm* < 0.5**			***Nm* > 0.5**		
		$\boldsymbol{R_{10}}$	$\boldsymbol{R_{10\text{-}100}}$	$\boldsymbol{R_{\mathrm{T}}}$	$\boldsymbol{R_{10}}$	$\boldsymbol{R_{10\text{-}100}}$	$\boldsymbol{R_{\mathrm{T}}}$
	V_W	0.786	0.269	0.450	0.839	–0.515	0.084
QT	V_B	–0.011	0.270	0.228	–0.715	0.543	0.052
	V_T	0.050	0.293	0.264	–0.455	0.468	0.178
	Q_{ST}	–0.774	–0.251	–0.431	–0.833	0.536	–0.055
QTL	H_S^*	0.738	0.487	0.623	0.726	–0.387	0.143
	D_G^*	–0.678	–0.417	–0.547	–0.930	0.581	–0.082
	H_T^*	–0.458	–0.268	–0.357	0.009	0.082	0.105
	G_{ST}^*	–0.830	–0.500	–0.659	–0.904	0.544	–0.104
	A_S^*	0.690	0.634	0.734	0.414	0.033	0.382
	D_A^*	–0.433	0.079	–0.054	–0.519	0.615	0.299
	A_T^*	0.443	0.598	0.635	0.249	0.175	0.414
	K_T^*	–0.385	0.009	–0.100	–0.097	0.428	0.427
	A_{ST}^*	–0.805	–0.672	–0.800	–0.749	0.613	0.107
	D^*	–0.621	–0.369	–0.490	–0.889	0.561	–0.072
Markers	H_S	0.660	0.690	0.774	0.248	0.165	0.401
	D_G	–0.779	–0.550	–0.689	–0.882	0.562	–0.065
	H_T	–0.483	–0.116	–0.234	–0.225	0.454	0.353
	G_{ST}	–0.782	–0.650	–0.774	–0.875	0.473	–0.165
	A_S	0.531	0.694	0.742	0.385	0.090	0.426
	D_A	–0.091	0.425	0.337	–0.368	0.561	0.360
	A_T	0.344	0.646	0.648	0.248	0.198	0.441
	K_T	–0.137	0.373	0.280	–0.150	0.458	0.419
	A_{ST}	–0.748	–0.710	–0.816	–0.895	0.601	–0.029
	D	–0.774	–0.521	–0.662	–0.881	0.568	–0.057

The scenario refers to a subdivided population with $n = 10$ subpopulations, *Nm* migrants per generation and subpopulation, mutation rate $u = 0.00001$ and strength of stabilising selection given by $\omega^2 = 25$. The variables included in the model are for quantitative trait (QT) and QTLs: V_W, V_B, V_T, Q_{ST}, H_S^*, D_G^*, H_T^*, G_{ST}^*, A_S^*, D_A^*, A_T^*, A_{ST}^*, D^* and K_T^*; and for neutral markers: H_S, D_G, H_T, G_{ST}, A_S, D_A, A_T, A_{ST}, D and K_T (see main text for definitions). R_{10}: response to selection until generation 10; $R_{10\text{-}100}$: response from generations 10 to 100; R_{T}: total response until generation 100. Average values (and its standard deviation) of K_T^* across runs was 3.6 (0.9) and that of K_T was 3.0 (0.8). The results are based on 5 sets of 2000 simulation runs varying the subpopulation size (N) randomly between 100 and 1000, and the migration rate (m) between 0.0001 and 0.1.

Table S2 Comparison between computer simulations and diffusion approximations (E[] in bold face) for different gene frequency and allelic diversity variables.

u = 0.00001

Nm	A_S	E[A_S]	D_A	E[D_A]	A_{ST}	E[A_{ST}]	K_T	E[K_T]
0	0.299	**0.301**	1.152	**1.146**	0.794	**0.792**	12.36	**68.198**
0.01	0.512	**0.547**	1.203	**1.174**	0.701	**0.682**	10.50	**37.366**
0.05	0.923	**1.059**	1.028	**0.969**	0.527	**0.478**	7.31	**16.269**
0.1	1.444	**1.277**	0.935	**0.749**	0.393	**0.370**	6.57	**11.208**
0.5	1.652	**1.483**	0.533	**0.385**	0.244	**0.206**	5.45	**6.223**
1	1.628	**1.574**	0.436	**0.330**	0.211	**0.173**	4.94	**5.515**
5	1.961	**1.909**	0.365	**0.280**	0.157	**0.128**	4.75	**4.928**
10	2.218	**2.080**	0.337	**0.269**	0.132	**0.115**	4.76	**4.853**
50	2.431	**2.464**	0.265	**0.248**	0.098	**0.092**	4.64	**4.792**
100	2.592	**2.598**	0.283	**0.236**	0.098	**0.083**	4.72	**4.785**
500	3.009	**2.782**	0.233	**0.180**	0.072	**0.061**	4.87	**4.779**
1000	3.110	**2.802**	0.217	**0.136**	0.065	**0.046**	4.91	**4.778**
u = 0.0002								
0	5.605	**4.887**	5.945	**4.382**	0.515	**0.473**	66.05	**112.854**
0.01	5.784	**5.058**	6.049	**4.435**	0.511	**0.467**	65.16	**110.190**
0.05	6.370	**5.782**	6.402	**4.683**	0.501	**0.448**	64.84	**101.763**
0.1	7.323	**6.552**	6.854	**4.872**	0.483	**0.427**	63.67	**94.500**
0.5	11.942	**10.520**	7.653	**5.352**	0.391	**0.337**	61.33	**74.240**
1	15.569	**13.205**	7.768	**5.389**	0.333	**0.290**	61.87	**68.030**
5	23.456	**20.803**	7.196	**5.249**	0.235	**0.202**	61.55	**61.392**
10	26.924	**24.416**	6.750	**5.222**	0.200	**0.176**	60.98	**60.419**
50	33.847	**32.129**	5.857	**4.880**	0.147	**0.132**	60.08	**59.614**
100	36.821	**34.941**	5.323	**4.777**	0.126	**0.120**	58.88	**59.511**
500	40.904	**38.592**	4.822	**3.610**	0.105	**0.086**	58.87	**59.429**
1000	43.009	**38.968**	4.649	**2.707**	0.098	**0.065**	59.92	**59.419**

The scenario considered refers to a subdivided population with n = 10 subpopulations, each of size N = 1000 individuals, mutation rate u, variable migration rate (m), and no sampling (all subpopulation individuals are analysed). See main text for definitions.

Table S3 Comparison between computer simulations and diffusion approximations (E[] in bold face) for different allelic diversity variables.

***u* = 0.00001**									
Nm	*g*	A_S	**E[A_S]**	D_A	**E[D_A]**	A_{ST}	**E[A_{ST}]**	K_T	**E[K_T]**
0	100	0.188	**0.207**	1.052	**1.072**	0.848	**0.838**	11.250	**44.151**
	50	0.182	**0.170**	1.047	**1.041**	0.852	**0.860**	11.224	**37.873**
	20	0.144	**0.129**	1.012	**1.007**	0.876	**0.887**	10.838	**29.597**
	10	0.119	**0.103**	0.990	**0.986**	0.893	**0.906**	10.596	**23.505**
1	100	1.293	**1.290**	0.368	**0.337**	0.221	**0.207**	3.950	**4.282**
	50	1.192	**1.168**	0.367	**0.345**	0.236	**0.228**	3.806	**4.012**
	20	0.980	**0.982**	0.350	**0.346**	0.264	**0.260**	3.460	**3.568**
	10	0.792	**0.806**	0.339	**0.347**	0.301	**0.301**	3.196	**3.231**
1000	100	1.968	**1.839**	0.250	**0.277**	0.113	**0.131**	3.870	**3.751**
	50	1.565	**1.569**	0.248	**0.277**	0.137	**0.150**	3.474	**3.487**
	20	1.189	**1.202**	0.249	**0.277**	0.173	**0.187**	3.084	**3.124**
	10	0.898	**0.923**	0.248	**0.278**	0.217	**0.231**	2.818	**2.848**
***u* = 0.0002**									
0	100	3.439	**3.274**	3.995	**3.431**	0.537	**0.512**	44.390	**69.487**
	50	2.900	**2.738**	3.510	**3.060**	0.548	**0.528**	39.004	**58.257**
	20	2.174	**2.085**	2.857	**2.609**	0.568	**0.556**	31.742	**43.646**
	10	1.629	**1.639**	2.366	**2.295**	0.592	**0.583**	26.290	**33.168**
1	100	9.441	**9.106**	5.608	**4.803**	0.373	**0.345**	41.140	**44.052**
	50	7.877	**7.366**	4.894	**4.392**	0.383	**0.374**	35.330	**38.171**
	20	5.580	**5.392**	3.955	**3.818**	0.415	**0.415**	28.250	**29.810**
	10	3.865	**3.786**	3.173	**3.180**	0.451	**0.457**	22.940	**23.658**
1000	100	20.181	**20.206**	4.847	**5.236**	0.194	**0.206**	39.390	**28.938**
	50	15.401	**15.320**	4.529	**5.044**	0.227	**0.248**	33.694	**33.583**
	20	9.451	**9.350**	3.957	**4.358**	0.295	**0.318**	26.608	**26.507**
	10	5.802	**5.758**	3.283	**3.600**	0.361	**0.385**	21.428	**21.271**

The scenario considered refers to a subdivided population with n = 10 subpopulations, each of size N = 1000 individuals, mutation rate u, variable migration rate (m), and g sampled genes per subpopulation. See main text for definitions.