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

Nm	g	A_S	**E[A_S]**	D_A	**E[D_A]**	A_{ST}	**E[A_{ST}]**	K_T	**E[K_T]**
***u* = 0.00001**									
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.