

Genetic drift scenarios simulated with a coalescent backward approach in SIMCOAL2, assuming a founder population of $N_e = 300$ splitting into five populations of $N_e = 60$ and constant size, 20 generations ago. We simulated independent chromosomes and a mutation rate of 10^{-4} in an IAM model constrained to 15 alleles. The right column states the proportion of pairwise comparisons that is significant after correction for multiple tests. Ten independent simulations of three migration rates ($m = 0.05$; 0.1; 0.2) revealing comparable F_{ST} 's with observed values are given below.

Migration	Mean pairwise $F_{ST}(\theta)$	\pm SD	P	% P < 0.05	% Sign. FDR
0,01	0,0675	0,0106	< 0,0001	100	100
0,05 ^(a)	0,0126	0,0038	< 0,0113	100	100
0,1 ^(b)	0,0048	0,0026	< 0,3902	50	27
0,2 ^(c)	0,0021	0,0024	< 0,8077	18	6
0,3	0,0030	0,0032	< 0,9219	30	10
0,4	0,0008	0,0019	< 0,9824	10	0
0,5	0,0007	0,0011	< 0,9727	0	0
0,99	0,0020	0,0020	< 0,9121	0	0

* a,b,c; mean over 10 simulations (below)

