

Table 4. Proportion of simulations (of 1,000) that lead to a shift in Gene diversity equal to or even greater than the one observed in the Iberian brown bear long dataset between the different time periods

Ne	$\mu = 29.8\%$ subst./MY		$\mu = 10.0\%$ subst./MY	
	Holocene/Modern	Pleistocene/Holocene	Holocene/Modern	Pleistocene/Holocene
100	0.157	0.507	0.051	0.551
500	0.097	0.321	0.083	0.426
1,000	0.045	0.208	0.060	0.393
2,000	0.019	0.098	0.031	0.248
5,000	0.000	0.018	0.010	0.122
10,000	0.000	0.000	0.001	0.035
15,000	0.000	0.000	0.000	0.013
20,000	0.000	0.000	0.000	0.004
25,000	0.000	0.000	0.000	0.006
30,000	0.000	0.000	0.000	0.001
35,000	0.000	0.000	0.000	0.000
40,000	0.000	0.000	0.000	0.000
45,000	0.000	0.000	0.000	0.000

The simulations have been conducted for the large data set (177 nt) over a large space of possible effective size values, assuming (i) no demographic change over time, (ii) two possible mutation rates, and (iii) the age of the sample Asieko at 80 KY. Frequencies superior to 0.05 are shown in red.