

Figure S1 The number of alleles (n , left y-axis) and average fitness (\bar{w} , right y-axis) as a function of time for two levels of gene flow (m) and three different population sizes (N) for individual simulations. The black, interrupted line indicates n and the grey continue line indicates \bar{w} .

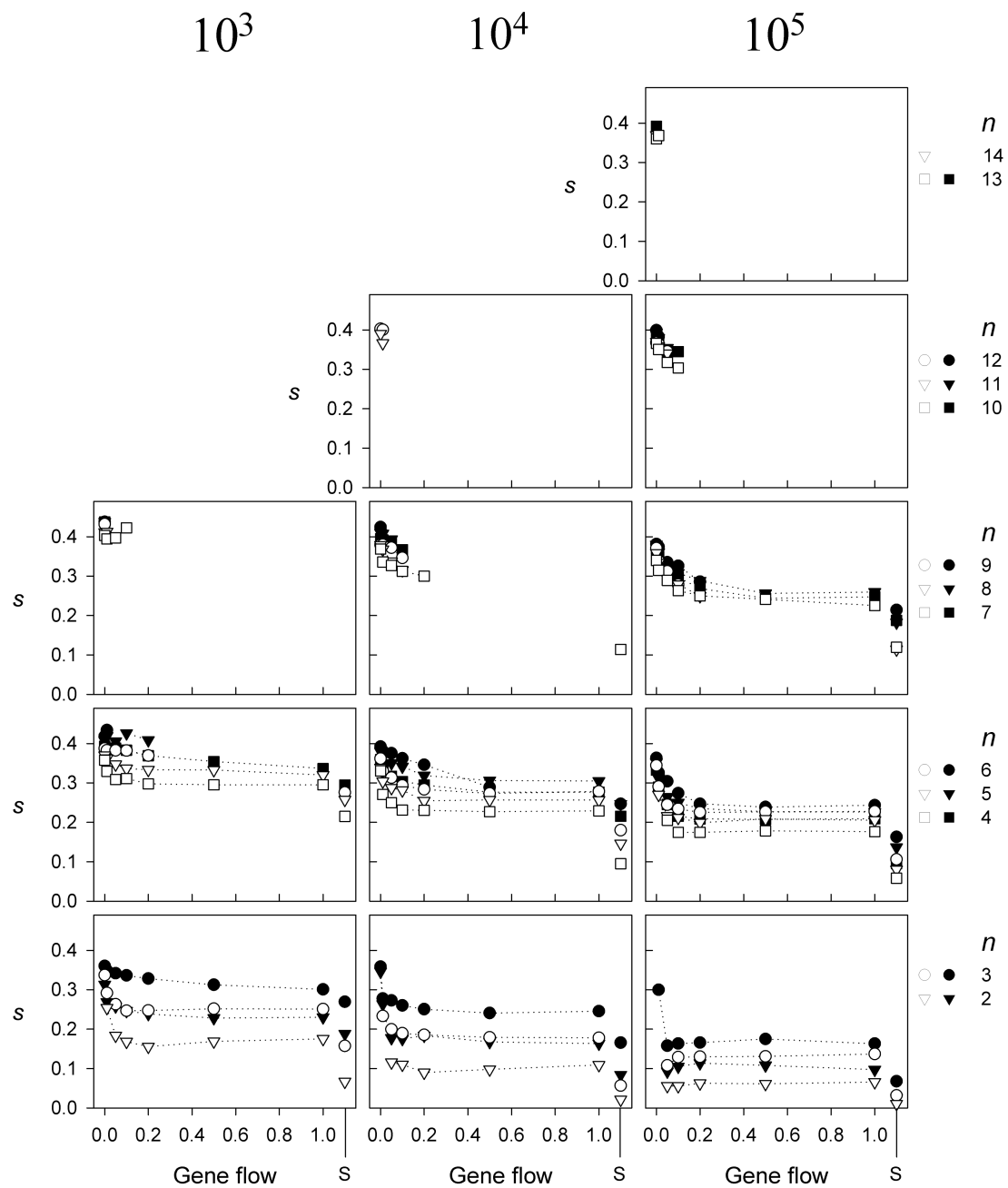


Figure S2 The level of selection strength (s) for genotypes with common alleles (i.e., with frequencies of over 5%) after 10,000 generations as a function of gene flow for three different total population sizes (N) and $n > 1$. Standard errors are small (< 0.03) and omitted for clarity. The black symbols indicate the results for populations with random drift whereas the white symbols indicate those without. The letter S on the x-axis indicates the results for single-deme populations. Only combinations of N , m and n are shown for which at least 10 replicates were found.

File S1

Spatial Selection Model

Available for download at www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.149781/-/DC1.