

Estimates of historical effective population size from computer simulations

We used the software SLiM3 to simulate a genome nucleotide sequence of 200 Mb for a population of a sexually reproducing diploid species with random mating and non-overlapping generations with population size $N = 1000$ or $10,000$ run for $10,000$ generations. Neutral mutations were assumed to occur with rate 0.5×10^{-8} per nucleotide and generation, with a recombination frequency between consecutive nucleotides of 2.5×10^{-8} , thus implying an average rate of recombination of 2.5 cM / Mb, analogous to that found in the fish species analysed in the main text. Ten and five generations before the last one (for the scenarios of $N = 1000$ and $N = 10,000$, respectively) a sudden drop in population size down to $N = 100$ and $N = 50$ individuals occurred, and this population size was maintained for the last nine and four generations, respectively. In the last generation, the genotypes of $20,000$ SNPs in the 100 individuals were analysed for linkage disequilibrium to obtain historical estimates of the effective size with the programs GONE and the previous method from Hayes et al. [5]. Twenty simulated replicates were carried out.

The results are shown in Figure S3. The estimated historical N_e obtained with the program GONE was able to infer the drastic drops to $N = 100$ (Figure S3a) and $N = 50$ (Figure S3b) individuals in the last ten and five generations (respectively), although with some variation around this value. With respect to the estimation of the ancestral N_e (before the sudden drop), the estimates were unbiased with a certain variation around the true value in the case with an ancestral population of size $N = 1000$ individuals. However, estimates of the ancestral N_e in the case of $N = 10,000$ showed a tendency to be upwardly biased, with values in some replicates up to around $50,000$ individuals.

Estimates obtained by the method of Hayes et al. [5] were unable to detect the drastic drop in N_e , and showed a linear decline (curvilinear because of the logarithmic scale). In the earliest generation showed in the figure (generation 100 in the past), the estimates of the ancestral N_e were much lower than the true ones.

Figure S3. Estimates of N_e (logarithmic scale) obtained by computer simulations with the LD methods of Hayes et al. [5] and Santiago et al. [6] for the scenarios of 1000 (a) and 10,000 (b) individuals simulated, respectively. Red solid line: real data; black solid lines: Hayes et al. [5]; black dotted lines: Santiago et al. [6].

