

File S3

Generation of individual-based data

We assumed that in each generation of each population the breeding population consists of 20 individuals. We assumed a hermaphrodite species and randomized the two parents for each propagule independently of each other (selfing allowed). To model gene flow among the populations, we assumed that the parent is an immigrant from one of the other populations with probability $\varepsilon=0.01$.

We assume a set of 32 loci determining the genotypic values among these traits, with 5 allelic variants in each locus, each having an equal frequency in the ancestral generation. We randomized the additive values of each allele in each locus from a two-dimensional multivariate normal distribution with mean zero and such a variance-covariance matrix (see Appendix A) that the expected amount of additive genetic variation in the ancestral generation was

$$E[\mathbf{G}^A] = \begin{pmatrix} 1.0 & 0.9 \\ 0.9 & 1.0 \end{pmatrix}.$$

The phenotypic value of individual i was modeled as the sum of the additive component and the environmental effect, i.e. $\mathbf{z}_i = \mathbf{a}_i + \mathbf{e}_i$, where the environmental effect \mathbf{e}_i was randomized from the two dimensional multivariate normal distribution with mean zero and variance-covariance matrix

$$\mathbf{V}_E = \begin{pmatrix} 0.5 & 0 \\ 0 & 0.5 \end{pmatrix}.$$

If modeling traits under selection, we let the populations become adapted locally to their environments by assuming that the environment experienced by a population X favored an optimal phenotype \mathbf{q}_X . We assumed that the \mathbf{q}_X values are distributed (i.i.d. among the populations) multnormally with mean zero and variance covariance matrix

$$\mathbf{V}_S = \begin{pmatrix} 5 & -4.5 \\ -4.5 & 5 \end{pmatrix},$$

and we thus have assumed that the expected direction of population divergence through the selective gradient is not proportional to \mathbf{G}^A .

We assume that the populations undergo weak selection, so that the initial number of propagules produced is high (ten times the actual population size), and selection operates through competition influencing survival. We define the fitness of an individual with phenotype \mathbf{z} in population j as

$$W_j(\mathbf{z}) = \exp(-(\mathbf{z} - \mathbf{q}_j)\mathbf{V}_F^{-1}(\mathbf{z} - \mathbf{q}_j))$$

where the variance-covariance matrix

$$\mathbf{V}_F = \begin{pmatrix} 0.5 & 0 \\ 0 & 0.5 \end{pmatrix}$$

describes the shape of the fitness landscape around the local optimum. We selected the 20 individuals that survived to form next generation among 200 propagules by sampling each individual with a probability that was proportional to its fitness value. In the case of no selection, the weights were set equal for all individuals.

To generate phenotypic data that allows for the estimation of genetic variability among and between populations, we assumed a breeding design in which five pairs of individuals were randomly sampled from each of the eight populations. We assumed a full-sib design with five offspring for each of the pairs, so that the total number of offspring was $8 \times 5 \times 5 = 200$. These individuals were assigned environmental effects as for the wild individuals, and their phenotypes were then recorded.

For neutral molecular markers, we also assumed a set of 32 loci with 5 alleles in each locus with equal frequencies in the ancestral population. We randomized the flow of the neutral alleles from the ancestral to the present generation, sampled ten individuals from each population, and genotyped these for the neutral molecular markers.