**Appendix S3 – Generalization of the framework to include a simple one-generation founder event**

The framework can be generalized to include a simple one-generation founder event, and thus results in the form of Tables 1-3 would show the proportion of allelic diversity expected to be retained following the founder event and population expansion until migration-drift balance is reached. The generalization is based on similar simulations as described in the main text, only including different initial conditions for the model. This can account for instances in which the allele was not lost during the founding event, but rather was present in the newly founded population at a certain frequency.

When using the model formulated in equation 2 and an initial condition , the simulation can be performed in the same manner as presented in the main text. The analysis can be repeated, and a new parameter  can be computed. For initial condition , we will denote the  value obtained using the simulation framework as (the  value described in the main text is  under this notation). It is possible to calculate the probability that, given a simple one-generation founder event with initial population size , the initial frequency of the allele is  using a binomial distribution:

 .

Thus, following Denniston [1], the probability of the allele’s presence at equilibrium, taking into consideration the founder event, denoted as , can be calculated under the presented framework as:

 .

 values are attained through simulations, such as the ones described in the main text, with different initial conditions.

Note that for , the allele is most likely lost during the founder event (i.e., ), and therefore

 .

For higher *Q* values, but still low values not much larger than ,  is dominated by the first few terms of equation 8. Thus, only simulations with initial conditions  for small *i* values need to be considered. For these values, it is reasonable to assume that in most individual simulation runs, the allele will be lost due to drift in the first few generations of the simulation, before new alleles arrive from the source population (the expected time to reappearance of the allele is , which is long for low *Q* values). Thus, most of these runs will converge with runs that effectively begin with , although for different demographic functions (same growth rate *r* and carrying capacity *K* values, only different initial population size values). Therefore, for the first few relevant terms in equation 8, , and again equation 9 holds.

The analysis presented in the main text (such as presented in Table 1 and Table 2) can consequently be used as an approximation for the actual proportion of alleles retained, taking into consideration the founder effect, only given that *Qc*(the cut-off frequency) is  or at least is not much larger than . Otherwise, further simulations are needed to attain more  for as many terms needed in equation 8. For *Q* values close to 0.5, probably all terms are needed for a good approximation. In any case, in order to increase the accuracy of the estimation, calculating all  is recommended.

The generalization of the framework described above considers only a simple one-generation founder event, but there are more complicated descriptions of population founder events. While equation 7 does not hold for founder events other than a simple one-generation founder event, if  for all  can be attained using other means (e.g., mathematical formulations or simulations), then equation 8 will still hold, and the framework can accommodate these generalizations as well. Such probabilities have been described for more general types of founder events by other authors (e.g. [2–10]).

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