Population dynamics of underdominance gene drive systems in continuous space

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SUPPORTING INFORMATION

Validation of our framework in a two-panmictic-demes model

To present a basic overview of underdominance drive dynamics, we study a simple scenario of two panmictic demes linked by migration (Figure S1A). This has been the most common model investigated in previous studies of underdominance systems, and we recapitulate part of these studies here as a basic introduction to the performance of these systems in this standard model.

We assumed that two panmictic populations have equal carrying capacity \( K = 10,000 \) and are linked by symmetric migration at rate \( M \). The scenario was initialized by introducing 10,000 wild-type individuals to each population, and then homozygotes for the gene drive alleles (or heterozygotes for the two different drive alleles in the 1L2T system) were added to the existing individuals in the first population so that they represented 80% of that population at the time of release. This frequency was selected because it is usually well above the expected invasion frequency thresholds in a single panmictic population for each of the four underdominance systems, even with strong fitness costs.

We analyzed the population dynamics of the four underdominance systems over a grid of parameter values in which we varied the fitness parameter \( F \) of each system from 0.6 to 1.0 and the migration frequency \( m \) from 0.0 to 0.1. To assess the ability of the drive to persist in the release population, we recorded the final drive frequencies in the release population after 20 generations, at which point most simulations had reached an equilibrium. To assess the ability of the drive system to invade a separate population of wild-type individuals, we recorded the final drive frequency in the other population.

Consistent with previous studies, we found that as long as fitness costs and migration rates were sufficiently low, all four underdominance systems were able to persist in the release population (Figure S1B-E). The RCT system had more trouble persisting in the presence of high migration than the 1L1T system, presumably due to its lower ability to remove wild-type alleles. As expected, the 1L2T system was the most sensitive to migration of all the underdominance systems because of its high introduction threshold, where even low immigration rates of wild-type individuals often sufficed to push the drive below its threshold in the release population. The 2L2T system was the most persistent in the face of migration, even when fitness costs were high. Moreover, when fitness costs were sufficiently small and migration sufficiently high, this system was able to invade the adjoining population (Figure S1F).
Figure S1. Two-deme introduction. (A) Two panmictic demes of 10,000 individuals are linked by migration. Drive individuals are introduced into one population at 80% frequency. (B)-(E) Ability of the four underdominance systems to persist in the release population after 20 generations. (F) Ability of the 2L2T system to invade the adjoining population. The graphs below each heatmap show drive frequency trajectories from individual simulations for parameter settings marked by the circles on the heatmaps with corresponding colors. Color gradients show final drive frequencies in the drive release (blue) and other (red) populations. Persistence and invasion heatmaps for all four systems and comparison to a non-driving allele are shown in Figure S2.
Figure S2. **Two-deme introduction.** Heatmaps for all drives and a normal allele with the same scale and scenario as Figure S1 for (A) persistence and (B) invasion.

Figure S3. **Symmetric scenario.** Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 3 for (A) persistence and (B) invasion.
Figure S4. **Circle release scenario.** Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 4 for (A) persistence and (B) invasion.

Figure S5. **Circle release scenario with variable introduction radius.** Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 5 for (A) persistence and (B) invasion.
Figure S6. Panmictic release scenario compared to random release spatial scenario. Drive individuals with $F=1$ were randomly introduced into either a panmictic or a spatial population of 10,000 individuals. The final frequency of the drive is shown after 20 generations.

Figure S7. High-density circle release scenario, variable drive homozygote fitness and dispersal. Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 6 for (A) persistence and (B) invasion.
Figure S8. High-density circle release scenario, variable drive homozygote fitness and relative central density. Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 6 for (A) persistence and (B) invasion.

Figure S9. High-density circular release scenario, variable dispersal and relative central density. Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 6 for (A) persistence and (B) invasion.
Figure S10. Migration-corridor scenario, variable drive homozygote fitness and dispersal. Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 7 for (A) persistence and (B) invasion.

Figure S11. Migration-corridor scenario, variable drive homozygote fitness and corridor width. Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 7 for (A) persistence and (B) invasion.
Figure S12. Migration-corridor scenario, variable dispersal and corridor width. Heatmaps for all drives and a normal allele with the same scale and scenario as Figure 7 for (A) persistence and (B) invasion.
Figure S13. Two panmictic populations linked by migration scenario. (A) Two panmictic populations with 5,000 individuals are linked by symmetric migration. Drive individuals start in one population and wild-type in the other. (B)-(E) Ability of the four underdominance systems to persist after 20 generations. (F) Ability of the 2L2T system to invade after 20 generations. Color gradients show final drive frequencies in the initial drive (blue) and wild-type (red) populations. Persistence and invasion heatmaps for all four systems and a non-driving allele are shown in Figure S12.

Figure S14. Panmictic demes linked by migration scenario. Heatmaps for all drives and a normal allele with the same scale and scenario as Figure S8 for (A) persistence and (B) invasion.
Figure S15. Comparison of invasiveness of the 2L2T system between the two-panmictic-demes scenario and the migration-corridor scenario. Same as Figure 8, but results are shown for several different corridor widths. We also display final allele frequencies after 100 generations to show a broader range of outcomes. Comparing the corridor width of 0.1 in this figure to Figure 8, we see that the allele frequency drastically increases between 100 and 200 generations. This is because after the barrier of the corridor is overcome, invasion in the rest of the population proceeds rapidly. Additionally, we see that for all corridor widths except 0.2, there is an optimal level of migration (indicated by the intermediate normal allele invasion frequency level) for successful invasion. Larger migration rates (corresponding to higher dispersal) mean more population exchange between the right deme and the adjacent region of the corridor, thus making the “barrier” at the end of the corridor more difficult to overcome. Note that scenarios where the 2L2T invasion frequency is very low (~5% or lower, for small corridor widths) typically represent an equilibrium where the drive remains confined to the corridor (and a small area around it in the right deme). Higher levels usually represent an ongoing successful invasion that will eventually spread through the entire deme.