Spatial gene drives and pushed genetic waves

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Gene drives have the potential to rapidly replace a harmful wild-type allele with a gene drive allele engineered to have desired functionalities. However, an accidental or premature release of a gene drive construct to the natural environment could damage an ecosystem irreversibly. Thus, it is important to understand the spatiotemporal consequences of the super-Mendelian population genetics before potential applications. Here, we use a reaction–diffusion model for sexually reproducing diploid organisms to study how a locally introduced gene drive allele spreads to replace the wild-type allele, although it possesses a selective disadvantage \( s > 0 \). Using methods developed by Barton and collaborators, we show that socially responsible gene drives require \( 0.5 < s < 0.697 \), a rather narrow range. In this “pushed wave” regime, the spatial spreading of gene drives will be initiated only when the initial frequency distribution is above a threshold profile called “critical propagule,” which acts as a safeguard against accidental release. We also study how the spatial spread of the pushed wave can be stopped by making gene drives uniquely vulnerable (“sensitizing drive”) in a way that is harmless for a wild-type allele. Finally, we show that appropriately sensitized drives in two dimensions can be stopped, even by imperfect barriers perforated by a series of gaps.

The development of the CRISPR-Cas9 system (1–4), derived from an adaptive immune system in prokaryotes (5), has received much recent attention, in part because of its exceptional versatility as a gene editor in sexually reproducing organisms compared with similar exploitations of homologous recombination, such as zinc-finger nucleases and the TALENS system (4, 6). Part of the appeal is the potential for introducing a novel gene into a population, allowing control of highly pesticide-resistant crop pests and disease vectors, such as mosquitoes (7–10). Although the genetic modifications typically introduce a fitness cost or a “selective disadvantage,” the enhanced inheritance rate embodied in CRISPR-Cas9 gene drives nevertheless allows edited genes to spread, even when the fitness cost of the inserted gene is large. The idea of using constructs that bias gene transmission rates to rapidly introduce novel genes into ecosystems has been discussed for many decades (11–16). Similar “homing endonuclease genes” (in the case of CRISPR-Cas9, the homing ability is provided by a guide RNA) were considered earlier by ecologists in the context of control of malaria in Africa (17, 18).

As a hypothetical example of a gene drive applied to a pathogen vector requiring both a vertebrate and an insect host, consider plasmodium, carried by mosquitoes and injected with its saliva into humans (Fig. 1). Female mosquitoes typically hatch from eggs in small standing pools of water and after mating, search for a human to feed on. They then lay their eggs and repeat the process, thus spreading the infection over a few gonotrophic cycles. A gene drive could alter the function of a protein manufactured in the salivary gland of female mosquitoes from, say, type a, anesthetizing nerve cells when it bites humans, to instead type A, clogging up essential chemoreceptors in plasmodium and thus killing these eukaryotes. In the absence of a gene drive, there would be a selective disadvantage or fitness cost \( s \) to losing this protein. Even if the fitness cost \( s \) was zero, it is unlikely that this new trait would be able to escape genetic drift in large populations. However, as we describe below, the trait could spread easily if linked to a gene drive that converts heterozygotes to homozygotes with efficiency \( c \) close to one (Fig. 1A). Remarkably, high conversion rates have already been achieved with the mutagenic chain reaction (MCR) realized by the CRISPR-Cas9 system (1–3) for yeast \((c_{\text{yeast}} > 0.995)\) (19), fruit flies \((c_{\text{flies}} \approx 0.97)\) (20), and the malaria vector mosquito, Anopheles stephensi, with engineered malaria resistance \((c_{\text{malaria}} \geq 0.98)\) (21).

However, the gene drives’ intrinsic nature of irreversibly altering wild-type (WT) populations raises biosafety concerns (9) and calls for confinement strategies to prevent unintentional escape and spread of the gene drive constructs (22). Although various genetic design or containment strategies have been discussed (9, 20, 23, 24) and a few computational simulations were conducted (17, 18, 25), the spatial spreading of the gene drive alleles has received less attention.

To understand such phenomena in a spatial context, we will exploit a methodology developed by Barton and coworkers (26–28) originally in an effort to understand adaptation and speciation of diploid sexually reproducing organisms in genetic hybrid zones. We apply these techniques to a spatial generalization of a model of diploid CRISPR-Cas9 population genetics proposed by Unkless et al. (29) and highlight two distinct ways in which gene drive alleles can spread spatially. The non-Mendelian (or “super-Mendelian”) (30) population genetics of gene drives are remarkable, because individuals homozygous for a gene drive can, in fact, spread into WT populations, even if they carry a positive selective disadvantage \( s \) (Fig. 1B). For small selective disadvantages \((0 < s < 0.5)\) in our case, the spatial spreading proceeds via a well-known Fisher–Kolmogorov–Petrovs’ky–Piskunov wave (31, 32). Such pulled genetic waves (33–35) are driven by growth

Significance

Gene constructs introduced into natural environments have been proposed to solve various ecological problems. The CRISPR-Cas9 technology greatly facilitates construction of gene drives that allow desired traits to rapidly replace wild types, even if these convey a selective growth rate disadvantage \( s > 0 \). However, accidental release of a gene drive could damage ecosystems irreversibly. We have modeled the spatial spread of gene drives and find a preferred range of selective disadvantages, \( 0.5 < s < 0.697 \). In this regime, gene drives spread but only when a nucleus exceeds a critical size and intensity. By making gene drives uniquely susceptible to a compound, their advance can be stopped in two dimensions by finite-width barriers, even when interrupted by gaps.

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and diffusive dispersal at the leading edge, and they are difficult to slow down and stop.

However, for somewhat larger selective disadvantages (0.5 < s < 0.697), we find that propagation proceeds instead via a pushed genetic wave (33–35), where the genetic wave advances via accentuated growth from populations somewhat behind the front that spills over the leading edge. These waves, characterized by a strong Allee effect (36, 37), are more socially responsible than the pulled Fisher waves, because (i) only inoculations with spatial size and density that exceed a critical nucleus or “critical propagule” (28) are able to spread spatially, thus providing protection against a premature or accidental release of a gene drive; (ii) the gene drive pushed waves can be stopped by making them uniquely vulnerable to a specific compound [“sensitizing drive” (9)], which is harmless for a WT allele; and (iii) appropriately sensitized gene drives can be stopped even by barriers punctuated by defects, analogous to regularly spaced fire breaks used to contain forest fires. Similar pushed or “excitable” waves also arise, for example, in neuroscience in simplified versions of the Hodgkin–Huxley model of action potentials (38). When the selective disadvantage associated with the gene drive is too large (s > 0.697 in our model), the excitable wave reverses direction, and the region occupied by the gene drive homozygotes collapses to zero.

The same mathematical analyses apply to spatial evolutionary games of two competing species in one dimension, which are governed by a class of reaction–diffusion equations that resemble the gene drive system. The fitness levels of the two interacting red and green species (w_r, w_c) are related to their frequencies [f(x, t), 1 − f(x, t)] by w_r(x, t) = g + α [1 − f(x, t)], w_c(x, t) = g + β f(x, t), where g is a background fitness, assumed identical for the two alleles for simplicity. The mutualistic regime α > 0, β > 0 in the first quadrant of Fig. 2 has been studied already (40), including the effect of genetic drift, with two lines of directed “percolation” transitions out of a mutualistic phase. Here, we apply the methods from ref. 28 to study the evolutionary dynamics near the line of first-order transitions that characterize the competitive exclusion regime in the third quadrant of Fig. 2. Because the mathematics parallels the analysis inspired by gene drive systems in the text, we relegate discussion of this topic to SI Appendix, which also has discussion of conversion efficiencies c < 1, an analogy with nucleation theory, and other matters.

**Mathematical Model of the CRISPR Gene Drives**

We start with a Hardy–Weinberg model (42) and incorporate an MCR with 100% conversion rate to construct a model for a well-mixed system. This model is the limiting case of “c = 1” in the work by Unckless et al. (29). Conversion efficiencies c < 1 can be handled by similar techniques. We consider a well-mixed diploid system with a WT allele a and a gene drive allele A with frequencies p = p(t) and q = q(t), respectively, at time t, with p(t) + q(t) = 1. Within a random mating model, the allele frequencies after one generation time τ are given by

\[(pa + qA)^2 = p^2g(a, a) + 2pq(a, A) + g^2(A, A),\]  

[1] and the ratios of fertilized eggs with diploid types (a, a), (a, A), and (A, A) are \(p^2 = 2pq = q^2\). In a heterozygous \((a, A)\) egg, the CRISPR-Cas9 machinery encoded on a gene drive allele A converts the WT allele a into a gene drive allele A. Here, we assume a perfect conversion rate \(a, A \rightleftharpoons 1\ MCR\) (A, A) in the embryo, which has been approximated already for yeast (19) and fruit flies (20). Genetic engineering will typically reduce the fitness of individuals carrying the gene drive alleles compared with WT organisms, which have already gone through natural evolution and may be near a fitness maximum.

The selective disadvantage of a gene drive allele \(s\) is defined by the ratio of the fitness \(w_{\text{wild}}\) of WT organisms \((a, a)\) to the fitness \(w_{\text{drive}}\) of \((A, A)\) individuals carrying the gene drive:

\[\frac{w_{\text{drive}}}{w_{\text{wild}}} = 1 - s,\quad 0 \leq s.\]  

[2] [In the limit \(c \rightarrow 1\), no heterozygous \((a, A)\) individuals are born (29).] Taking the fitness into account, the allele frequencies after one generation time \(τ\) are

\[p' = q' = \frac{w_{\text{wild}}p}{w_{\text{wild}}(1 - s)(q^2 + 2pq)},\]  

[3] where 

\[p' \equiv p(t + τ\gamma)\] and 
\[q' \equiv q(t + τ\gamma).\] On approximating \(q' = q = q(t + τ\gamma) - q(t)\) by \(τ\gamma dq/dt\), we obtain a differential equation

\[\frac{dq}{dt} = \frac{1 - s}{s} p - \frac{2q}{1 + s} q^2.\]
which governs population dynamics of the MCR with 100% conversion efficiency in a well-mixed system. To take spatial dynamics into account, we add a diffusion term (28) and obtain a deterministic reaction–diffusion equation for the MCR model, namely

\[
t_q = \frac{(1 - s)(q^2 + 2pq)}{p^2 + (1 - s)(q^2 + 2pq)} - q = \frac{sq(1 - q)(q - q^*)}{1 - sq(2 - q)}, \quad \text{where} \quad q^* = \frac{2s - 1}{s},
\]

which will be the main focus of this article. For later discussions, we name the reaction term of the reaction–diffusion equation

\[
f_{\text{MCR}}(q, s) = \frac{sq(1 - q)(q - q^*)}{1 - sq(2 - q)}.
\]

The reaction term reduces to a simpler cubic expression

\[
f_{\text{cubic}}(q, s) = sq(1 - q)(q - q^*)
\]

by ignoring \(-sq(2 - q)\) in the denominator, which is a reasonable approximation if the selective disadvantage \(s\) is small. This form of the reaction–diffusion equation has been well-studied, as reviewed in ref. 28.

Although population genetics is often studied in the limit of small \(s, s\) is, in fact, fairly large in the regime of pushed excitable waves of most interest to us here, \(0.5 < s < 1.0\). Hence, we will keep the denominator of the reaction term, which was also done in ref. 28 with a different reaction term. Comparison of results for the full nonlinear reaction term with those for the cubic approximation will give us a sense of the robustness of the cubic approximation.

Initiation of the Pushed Waves

The reaction terms \(f_{\text{MCR}}(q, s)\) and \(f_{\text{cubic}}(q, s)\) have three identical fixed points, \(q = 0, 1\) and \(q^* = (2s - 1)/s\). As discussed in SI Appendix in connection with classical nucleation theory in physics and following ref. 26, we can define the potential energy function

\[
U(q) = -\frac{1}{\tau_g} \int_0^q \frac{sq(1 - q')(q - q^*)}{1 - sq(2 - q')} dq',
\]

to identify qualitatively different parameter regimes. In a well-mixed system, without spatial structure, the gene drive frequency \(q(t)\) obeys Eq. 4 and evolves in time, so that it arrives at a local minimum of \(U(q)\). For the spatial model of interest here, \(q(x, t)\) shows qualitatively distinct behaviors in three parameter regimes depending on the selective disadvantage \(s\) (Fig. 3A). We plot the potential energy functions \(U(q)\) in these parameter regimes in Fig. 3B.

i) First, when \(s < s_{\text{min}} = 0.5\), fixation of a gene drive allele \(q(x) = 1\) for all \(x\) is the unique stable state, and there is no energy barrier to reach the ground state starting from \(q \approx 0\). In this regime, any finite frequency of gene drive allele locally introduced in space (provided it overcomes genetic drift) will spread and replace the WT allele. The frequency profile will evolve as a pushed traveling wave \(q(x, t) = Q(x - vt)\) with wave velocity \(v\). Such a wave was first found by Fisher (31) and Kolmogorov et al. (32) in the 1930s in studies of how locally introduced organisms with advantageous genes spatially spread and replace inferior genes. However, the thresholdlessness of initiation of population waves of engineered gene drives with relatively small selective disadvantages remains highly undesirable, because the accidental escape of a single gene drive construct can establish a population wave that spreads freely into the extended environment.

ii) There is a second regime for \(0.5 < s < 0.697\), in which the potential energy function \(U(q)\) exhibits an energy barrier between \(q = 0\) and \(q = 1\). In this regime, a pushed traveling wave can be excited only when a threshold gene drive allele frequency is introduced over a sufficiently broad region of

\[
A
s: \text{selective disadvantage}
\]

\[
0 0.2 0.4 0.6 0.8 1.
-0.08 -0.04 0.04 0.08
U(q)\tau_g

\[
B
0 0.2 0.4 0.6 0.8 1.
-0.08 -0.04 0.04 0.08
 Frequency q

\[
\text{Fig. 3.} \; (A) \; \text{Spatial dynamics of gene drives can be determined by both the selective disadvantage} \; s \; \text{and} \; (\text{when} \; 0.5 < s < 0.697) \text{the size and intensity of the initial condition.} \; (B) \; \text{The energy landscapes} \; U(q) \; \text{with various selective disadvantages} \; s. \; (i) \; \text{Pulled Fisher wave regime.} \; \text{When} \; s \; \text{is small,} \; s \leq s_{\text{min}} = 0.5 \; \text{red and yellow curves}, \; \text{fixation of the gene drive allele} \; (q = 1) \; \text{is the unique stable state, and there is no energy barrier between} \; q = 0 \; \text{and} \; 1. \; \text{Any finite introduction of a gene drive allele is sufficient to initiate a pushed Fisher population wave that spreads through space to saturate the system.} \; (ii) \; \text{Pushed excitable wave regime.} \; \text{When} \; s \; \text{is slightly larger (green curve) and satisfies} \; s_{\text{min}} = 0.5 < s < s_{\text{max}} = 0.697, \; q = 1 \; \text{is still the preferred stable state, but an energy barrier at} \; q = q^* \; \text{appears between} \; q = 0 \; \text{and} \; 1. \; \text{In this regime, the introduction of the gene drive allele at sufficient concentration and over a sufficiently large spatial extent is required for a pushed wave to spread to global fixation.} \; (iii) \; \text{Wave reverses direction.} \; \text{When} \; s \; \text{is large,} \; s > s_{\text{max}} = 0.697 \; \text{blue and purple curves}, \; q = 0 \; \text{is the unique ground state, and the gene drive species cannot establish a traveling population wave and therefore dies out.}
space that exceeds the size of a critical nucleus, which we investigate in the next section. The existence of this threshold acts as a safeguard against accidental release. In addition, such excitable waves are easier to stop, which we will discuss later. It seems that gene drives in this relatively narrow intermediate regime are the most desirable from a biosafety perspective.

iii) When \( s > s_{\text{max}} = 0.697 \), the fixation of a gene drive allele throughout space is no longer absolutely stable (Fig. 3B), and a gene drive population wave cannot be established. Indeed, the excitable wave reverses direction for \( s > s_{\text{max}} \). An implicit equation for \( s_{\text{max}} \) results from equating \( U'(0) = U(1) = 0 \), which yields

\[
0 = \int_{0}^{1} \frac{sg(1-q)(q-q^*)}{1-sq(2-q)} dq, \\
or \quad 0 = -2 + s_{\text{max}} + 2\sqrt{-1 + \frac{1}{2s_{\text{max}}} \arcsin(\sqrt{s_{\text{max}}})} \Rightarrow s_{\text{max}} \approx 0.697,
\]

where we used \( q^* = (2s - 1)/s \). When \( s > s_{\text{max}} \), the locally introduced gene drive allele contracts rather than expands relative to the WT allele and simply dies out. SI Appendix has the analogous results with an arbitrary conversion rate (0 < c < 1).

**Critical Nucleus in the Pushed Wave Regime**

When the selective disadvantage \( s \) is in the intermediate regime, \( s_{\text{min}} = 1/2 < s < s_{\text{max}} = 0.697, \) we can control initiation of the pushed excitable wave by the initial frequency profile of the gene drive allele \( q(x, 0) \) as shown in Fig. 4. For example, in Fig. 4A, an initially introduced gene drive allele (in the form of a Gaussian) diminishes and dies out, because the width of the initial frequency distribution \( q(x, 0) \) is not sufficient to excite the population wave. In contrast, the results in Fig. 4B show the successful establishment of the excitable wave starting from a sufficiently broad (Gaussian) initial distribution of a gene drive allele. Roughly speaking (provided \( 1/2 < s < s_{\text{max}} \)), two conditions must be satisfied to obtain a critical propagule. (i) The initial condition \( q(x, 0) \) at the center of the inoculant must exceed \( q^* = 2s - 1/s \), the local maximum of the function \( U(q) \) plotted in Fig. 3. (ii) The spatial spread \( \Delta x \) of the inoculant \( q(x, t=0) \) must satisfy \( \Delta x \geq \text{const} \sqrt{D/\tau g} \), where the dimensionless constant depends on \( s \). Thus, the initial width should exceed the width of the pushed wave that is being launched.

We show the spatial concentration profile \( q(x) \) that constitutes that (Gaussian) critical nucleus is just sufficient to initiate an excitable wave in Fig. 5. The solid lines in Fig. 5 represent numerically obtained critical nuclei of the MCR model. Note the consistency for \( s = 0.58 \) with the pushed excitable waves shown in Fig. 4. The dashed lines in Fig. 5 represent analytically derived critical propagules of the cubic model as a reference (details are in SI Appendix). Fig. 5 shows that the cubic model overestimates the height of critical propagule, particularly for larger \( s \). The difference between the reaction terms of the MCR model \( f_{\text{MCR}}(q) \) (Eq. 6) and those of its cubic approximation \( f_{\text{Cubic}}(q) \) (Eq. 7) arises from the term \(-sq(2-q)\) in the denominator of Eq. 5. In the biologically relevant regime \((0 < s < 1, 0 < q < 1)\), \( sq(2-q) \) is always positive, and \( f_{\text{MCR}}(q) > f_{\text{Cubic}}(q) \) is satisfied, which explains why there is a larger critical propagule in the cubic approximation and why the discrepancy is larger for larger \( s \). The critical nucleus with a step function-like circular boundary is studied both numerically and analytically in two dimensions in SI Appendix.

**Stopping of Pushed, Excitable Waves by a Selective Disadvantage Barrier**

Thus far, we have found that (i) we can control initiation of the spatial spread of a gene drive provided \( s_{\text{min}} = 0.5 < s < s_{\text{max}} = 0.697 \) and that (ii) the pushed population waves in this
regime slow down and eventually stop (and reverse direction) when $s > s_{\text{max}}$ (SI Appendix). In this section, we examine alternative ways to confine an excitable gene drive wave to attain greater control over its spread in this regime.

Imagine exploiting the CRISPR-Cas9 system to encode multiple functionalities into the gene drive machinery (1–3, 20). For example, one could produce genetically engineered mosquitoes that are not only resistant to malaria but also, specifically vulnerable to an insecticide that is harmless for the WT alleles. Such a gene drive, which is uniquely vulnerable to an otherwise harmless compound, is a sensitizing drive (9). The effect of laying down insecticide in a prescribed spatial pattern on a sensitizing drive can be incorporated in our model by increasing the selective disadvantage to a value $s_0(>s)$ within a “selective disadvantage barrier” region.

In Fig. 6, we numerically simulate the MCR model defined by Eq. 5 in one dimension with a barrier of strength $s_0 = 0.958$ placed in a region $25\sqrt{\tau_0 D} < x < 27\sqrt{\tau_0 D}$. When the selective disadvantage outside the barrier is small ($s < 0.5$) and the population wave travels as the pulled Fisher wave, even a tiny fraction of the MCR allele diffusing through the insecticide region can easily reestablish the population wave, which is shown in Fig. 6A. However, when the system is in the pushed wave regime $0.5 < s < 0.697$, the wave can be stopped provided that the spatial profile of the gene drive allele that leaks through does not constitute a critical nucleus, which is illustrated in Fig. 6B. SI Appendix has numerically calculated plots of the critical width and barrier selective disadvantage needed to stop pushed waves for various values of $s$.

![Fig. 6. Numerical simulations of pushed, excitable waves generated by Eq. 5 with barriers in one dimension, with time increments $\Delta t = 5.0\tau_0$. As the waves advance from left to right, the early time response is shown in red, with later times shown in blue. The fitness disadvantage inside the barrier is set to $s_0 = 0.958$ within a region $25\sqrt{\tau_0 D} < x < 27\sqrt{\tau_0 D}$ (shown as purple bars). The initial conditions are step function-like, $q(x, 0) = q_0/(1 + e^{(x-x_0)/\sqrt{\tau_0 D}})$, with $q_0 = 1.0$ and $x_0 = 5.0\sqrt{\tau_0 D}$, similar to the initial condition SI Appendix, Eq. S30 that we used in two dimensions (SI Appendix).
(A) In the case of a Fisher wave with $s = 0.479 < s_{\text{min}} = 0.5$, a small number of individuals diffuse through the barrier, which is sufficient to reestablish a robust traveling wave. (B) In the case of the excitable wave $s = 0.542 > s_{\text{min}} = 0.5$, a small number of individuals also diffuse through the barrier. However, because the tail of the penetrating wave front is insufficient to create a critical nucleus, the barrier causes the excitable wave to die out.](https://www.pnas.org/cgi/doi/10.1073/pnas.1705868114)

Excitable Wave Dynamics with Gapped Barriers in Two Dimensions

In the previous section, we showed that pushed excitable waves can be stopped by a selective disadvantage barrier in one dimension. However, in two dimensions, it may be difficult to make barriers without defects. Hence, we have also studied the effect of a gap in a 2D selective disadvantage barrier. We find that, although the gene drive population wave in the Fisher wave regime $s < 0.5$ always leaks through the gaps, the excitable wave with $0.5 < s < 0.697$ can be stopped, provided that the gap is comparable with or smaller than the width of the traveling wave front. In Fig. 7, we illustrate the gene drive dynamics for two different parameter choices. In Fig. 7, the strength of the selective disadvantage barrier is set to be $s_0 = 1.0$, and the width of the gap in the barrier is set to be $6\sqrt{\tau_0 D}$. The engineered selective disadvantage in the nonbarrier region $s$ differs in the two plots. In Fig. 7A, $s = 0.48 < 0.5$; therefore, the gene drive wave propagates as a pulled Fisher wave, and the wave easily leaks through the gap. If genetic drift can be neglected, we expect that Fisher wave excitations will leak through any gap, regardless of how small. However, when the selective disadvantage barrier is in the pushed wave regime $0.5 < s < 0.697$, the population wave can be stopped by a gapped selective disadvantage barrier as shown in Fig. 7B. To stop a pushed excitable wave, the gap dimensions must be smaller than the front width; alternatively, we can say that the gap must be smaller than size of the critical nucleus.

Discussion

The CRISPR-Cas9 system has greatly expanded the design space for genome editing and construction of MCRs with non-Mendelian inheritance. We analyzed the spatial spreading of gene drive constructs, applying reaction–diffusion formulations that have been developed to understand spatial genetic waves with bistable dynamics (26–28). For a continuous time and space version of the model by Unckless et al. (29), in the limit of 100% conversion efficiency, we found that a critical nucleus or propagule is required to establish a gene drive population wave when the selective disadvantage satisfies $0.5 < s < 0.697$. This range is even narrower when we relax the assumption of 100% conversion efficiency, so that $c < 1$ (SI Appendix). Our model led us to study termination of pushed gene drive waves using a barrier that acts only on gene drive homozygotes, corresponding to an insecticide in the case of mosquitoes. In this parameter...
regime, the properties of pushed waves allow safeguards against the accidental release and spreading of the gene drives. One can, in effect, construct switches that initiate and terminate the gene drive wave. In the future, it would be interesting to study the effect of additional mutations on an excitatory gene drive wave, particularly those that move the organism outside the preferred range 0.5 < s < 0.697. Finally, we address possible experimental tests of the theoretical predictions. Because it seems inadvisable to conduct field tests without thorough understanding of the system, laboratory experiments with microbes would be a good starting point. Recently, the transition from pushed to pulled waves was qualitatively investigated with haploid microbial populations (35). Because the MCR has already been realized in Saccharomyces cerevisiae (19), it may also be possible to test the theory in the context of range expansions on a petri dish, which has already been done for haploid mutualistic yeast strains in ref. 44. Here, the frontier approximates a 1D stepping stone model, and jostling of daughter cells at the frontier leads to an effective diffusion constant in one dimension (45, 46). Finally, as illustrated in SI Appendix, Fig. S2, the mathematics of the spatial evolutionary games in one dimension parallels the dynamics of diploid gene drives in the pushed wave regime, providing another arena for experimental tests, including the effects of genetic drift.

Materials and Methods
To simulate the dynamics governed by Eq. 5 in Figs. 4, 6, and 7 and SI Appendix, Fig. S6, we used the method of lines and discretized spatial variables to map the partial differential equation to a system of coupled ordinary differential equations (ODEs). Then, we solved the coupled ODEs with a standard ODE solver. The widths of the spatial grids were varied from 1/200/√πD to 1/20/√πD, always making sure that the mesh size was much smaller than the width of the fronts of the pushed and pulled genetic waves that we studied.

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