

Requirements for driving anti-pathogen effector genes into populations of disease vectors by homing

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ABSTRACT There is a need for new interventions against the ongoing burden of vector-borne diseases such as malaria and dengue. One suggestion has been to develop genes encoding effector molecules that block parasite development within the vector, and then use the nuclease-based homing reaction as a form of gene drive to spread those genes through target populations. If the effector gene reduces the fitness of the mosquito and does not contribute to the drive, then loss-of-function mutations in the effector will eventually replace functional copies, but protection may nonetheless persist sufficiently long to provide a public health benefit. Here we present a quantitative model allowing one to predict the duration of protection as a function of the probabilities of different molecular processes during the homing reaction, various fitness effects, and the efficacy of the effector in blocking transmission. Factors that increase the duration of protection include reducing the frequency of pre-existing resistant alleles, the probability of non-recombinational DNA repair, the probability of homing-associated loss of the effector, the fitness costs of the nuclease and effector, and the completeness of parasite blocking. For target species that extend over an area much larger than the typical dispersal distance, the duration of protection is expected to be highest at the release site, and decrease away from there, eventually falling to zero, as effector-less drive constructs replace effector-containing ones. We also model an alternative strategy of using the nuclease to target an essential gene, and then linking the effector to a sequence that restores the essential function and is resistant to the nuclease. Depending upon parameter values, this approach can prolong the duration of protection. Our models highlight the key design criteria needed to achieve a desired level of public health benefit.

KEYWORDS gene drive; population genetic engineering; pest control; homing; malaria

Introduction

Many human diseases are transmitted indirectly, by vectors such as mosquitoes (e.g., malaria, dengue fever, yellow fever, lymphatic filariasis), sandflies (leishmaniasis), tsetse flies (African trypanosomiasis), black flies (onchocerciasis), ticks (Lyme disease, relapsing fever), and many others. The on-going burden of disease – estimated at more than a billion cases and a million deaths every year (World Health Organization) – indicates an on-going need for more effective interventions. One approach

that has been much discussed, at least in the context of malaria and dengue control, is to genetically engineer the vectors to contain one or more novel ‘effector’ genes that block the development of the pathogen, and then use the process of gene drive to spread those effectors through the vector population (Burt 2014; Champer *et al.* 2016). In the context of malaria, effectors that have been shown to at least partially inhibit transmission include anti-microbial peptides, single-chain antibodies, immune system activators, and peptides that bind to mosquito proteins (putative parasite receptors) in the midgut or salivary glands (Wang and Jacobs-Lorena 2013; Adelman *et al.* 2016).

Gene drive is a natural process of preferential inheritance which allows transposable elements, gamete killers, B chromosomes, homing endonuclease genes and many other types of genetic elements to spread through populations over successive generations even if they cause some harm to the host organism

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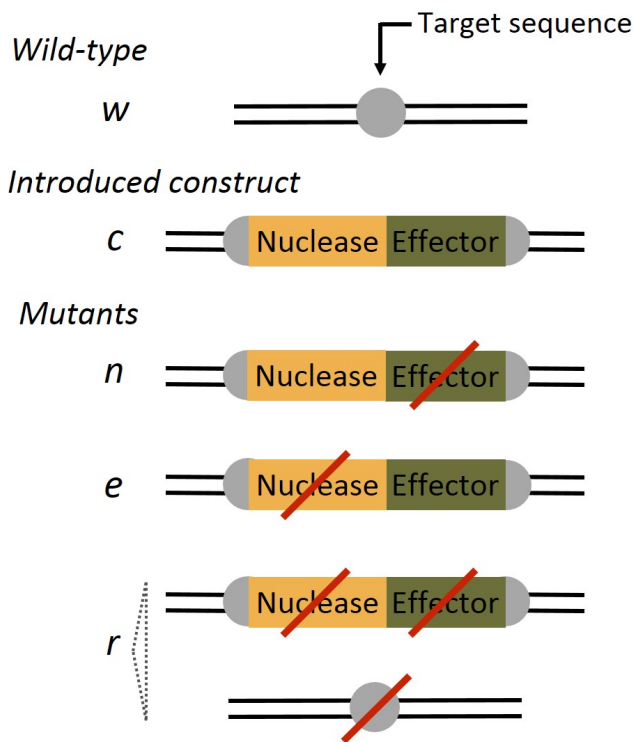


Figure 1 Five alleles in Model I. *w*: wild-type allele with sequence (typically 15-20bp) recognised by the nuclease. *c*: complete construct that contains genes encoding the nuclease engineered to recognise the target sequence and the effector. In *w/c* heterozygotes the nuclease is expressed in the germline and cleaves the target sequence and the construct can ‘home’ across to the cut chromosome during the repair process; the presence of the construct in the middle of its target sequence protects the *c* allele from being cut. *n*: nuclease-only constructs formed by loss of the effector gene during homing. *e*: effector-only construct formed by loss of the nuclease gene during homing. *r*: resistant allele that does not code for anything and is not cut by the nuclease; they can be formed by loss of the genes during homing, or by non-HR of *w* alleles following cleavage.

(Burt and Trivers 2006). Many different approaches have been proposed for making synthetic gene drive constructs able to spread effector genes through a vector population (Marshall and Akbari 2016). One such approach uses genes encoding enzymes (nucleases) that recognize and cleave a specific DNA sequence (Burt 2003). If the gene is inserted in the middle of its own recognition sequence, thereby protecting the chromosome it is on from being cut, then it can catalyse the homing reaction, in which individuals that are heterozygous for the presence of the gene are converted to homozygotes, as the cut chromosome uses the intact one as a template for repair. The gene is then transmitted to all the progeny, rather than the Mendelian 50%, allowing it to rapidly increase in frequency in a population over successive generations. If an effector gene is linked to the nuclease gene, then it could also spread through the population. Proof-of-principle demonstrations of homing constructs carrying a cargo gene have been published in *Drosophila* and *Anopheles* using a natural homing endonuclease and engineered zinc finger, TALE, and CRISPR nucleases (Chan et al. 2011, 2013a,b; Simoni et al.

2014; Gantz and Bier 2015; Gantz et al. 2015; Hammond et al. 2016).

The homing reaction depends upon cleavage of the target DNA followed by recombinational repair using the construct-containing homologous chromosome as a template. This reaction is not 100% effective: for example, there are other pathways for repairing broken chromosomes, including non-homologous end-joining and micro-homology mediated end joining (Symington and Gautier 2011), and these other processes can produce ‘resistant’ alleles that neither contain the nuclease gene nor are recognized by the nuclease. Moreover, mutations can occur in the construct while it is being copied during the homing reaction, and there is some evidence that the fidelity of copying at this stage may be lower than for normal DNA replication (Hicks et al. 2010; Simoni et al. 2014; Rodgers and McVey 2016). If mutations were to occur in the effector gene that rendered it nonfunctional, effectively ‘losing the cargo’, then it is possible a nuclease-only construct could spread through a population, with no effect on disease transmission.

Population modeling can be used to identify the key molecular and demographic parameters determining the fate of a gene drive construct after release and its impact on pathogen transmission. It can therefore be useful both for designing constructs and for determining whether lab results for a particular construct are sufficiently promising to consider proceeding to the field. Since the idea of using nucleases for population genetic engineering was first proposed (Burt 2003), there has been some modeling of simpler homing constructs designed to knock-out a target gene in the vector (Deredec et al. 2008, 2011; North et al. 2013; Bull 2016; Unckless et al. 2016), but less of constructs designed to knock-in a novel effector gene.

In this paper we first model the simplest strategy of linking the effector directly to the nuclease, and explore how the duration of protection is affected by the probabilities of different molecular processes, by the fitness costs of the nuclease and the effector, and by the efficacy of the effector. We then explore the spatial dynamics, and find that the duration of protection is expected to decrease away from the release site, eventually to zero. Finally, we model an alternative strategy in which a nuclease is designed to target an essential gene, and the effector is linked to a sequence that restores the essential function but is resistant to the nuclease (Burt 2003), and find that in some circumstances it can prolong the duration of protection. Our modeling will help guide the design and assessment of homing-based constructs for population-wide knock-in of novel transmission-blocking genes.

Model I. Linking an effector to the nuclease

Genetics

The first model considers five alleles (Figure 1): the wild-type sequence (denoted *w*); the complete construct that has both an intact nuclease gene and an intact effector gene (*c*); nuclease-only constructs that have an intact nuclease gene but defective effector (*n*); effector-only constructs that have an intact effector gene but defective nuclease (*e*); and resistant alleles that are not recognized by the nuclease, and do not have either an intact nuclease gene or effector (*r*). We assume the population starts predominantly with the wildtype allele, and a certain number of individuals homozygous for complete constructs are introduced into it. Nuclease-only and effector-only alleles arise due to mutations during homologous repair (HR) events, while resistant alleles can arise in multiple ways: they may pre-exist in

the population before release (due to sequence polymorphisms at the target site); they may arise from non-HR events after nuclease-induced cleavage (e.g., nonhomologous end joining or micro-homology-mediated repair); or they may arise due to mutations during HR events. Resistance alleles may therefore differ substantially in their primary sequence (as n and e alleles may also differ in sequence depending on the underlying mutation), but we shall consider them all to have the same transmission rates and effects on fitness.

Cleavage and homing can occur in the germlines of two genotypes, w/c and w/n . In w/c heterozygotes we suppose cleavage of the target site occurs with probability k_c , and therefore the w allele is left uncleaved with probability $1 - k_c$; cleaved alleles are repaired by non-HR (producing an r allele) with probability k_j , and by HR with probability $1 - k_j$; and HR leads to a mutation that disrupts the nuclease gene only (producing an e allele) with probability k_n , a mutation that disrupts the effector gene only (producing an n allele) with probability k_e , a mutation that disrupts both genes (producing an r allele) with probability k_{ne} , or no mutation in either gene (producing a c allele) with probability $1 - k_n - k_e - k_{ne}$. In w/n heterozygotes we assume all probabilities are the same as above, except if cleavage is followed by HR, then there are only two options: a mutation disrupts the nuclease gene (producing an r allele, probability k_n), or there is no mutation, leading to an n allele (probability $1 - k_n$). In all other individuals transmission is assumed to be Mendelian. The frequencies of each allele in the gametes of each genotype are shown in Supplementary Table S1.

Population Biology

We assume the vector population consists of equal numbers of males and females, and that all genetic and fitness parameters are the same between them, so allele and genotype frequencies will be the same in the two sexes. For simplicity, we further assume that adults give rise to adults directly, without modeling the juvenile stages (eggs, larvae, pupae). New adults are recruited (born) according to a logistic density-dependent rate, and die at a constant rate. Each newly recruited adult is formed from a random mating event immediately previously (i.e., we ignore sperm retention – see Beaghton *et al.* (2016)).

With five alleles there are 15 different diploid genotypes, and their fitnesses are denoted relative to the wildtype homozygote (w/w), which has a fitness of 1. Rather than have 14 different parameters for these fitnesses, we model them as functions of just six parameters: s_d , s_n and s_e are the homozygous fitness costs of disrupting the target sequence (s_d), of expressing the nuclease (s_n), and of expressing the effector (s_e), and h_d , h_n , and h_e are the corresponding dominance coefficients. s_d , s_n and s_e range from 0 (no cost) to 1 (lethal), and h_d , h_n , and h_e from 0 (completely recessive cost) to 1 (completely dominant). Each genotype has a fitness value associated with how many of its target sites are disrupted, how many nuclease genes it is expressing, and how many effector genes it is expressing (0, 1, or 2 in each case), and the overall fitness of the genotype is calculated as the product of these three values (Supplementary Table S1). Differences in fitness are manifest as differences in the contribution of each genotype to the overall recruitment rate. We further assume the population is large enough that stochastic effects can be ignored and the dynamics of allele frequencies and genotype abundances can be modeled using deterministic differential equations. The system of 15 equations is given in File S1, and is solved numerically using Wolfram Mathematica

(Wolfram Research, Inc. 2015).

The effect of a release on disease transmission will depend on the abundances of the different genotypes and on the reduction in vector competence when the effector is present in one (heterozygote) or two (homozygote) copies ($h_{rc}r_c$ and r_c , respectively; again, the degree of refractoriness r_c ranges from 0 [no effect] to 1 [complete blockage], and the dominance coefficient for refractoriness h_{rc} varies from 0 [recessive] to 1 [dominant]). We quantify the overall effect of the intervention at time t as the proportionate reduction in the vectorial capacity: $\Lambda[t] = 1 - V[t]/V_0$, where $V[t]$ is the vectorial capacity at time t , calculated as the sum of the numbers of the different genotypes, weighted by their vector competence, and V_0 is the initial, pre-release vectorial capacity (see SI for further details). The spread of genes with fitness costs can reduce the total density of females, which will contribute to the reduction in vectorial capacity, but for most of the parameter values we consider in this paper the vast majority of the effect is through the increased proportion of individuals carrying the effector.

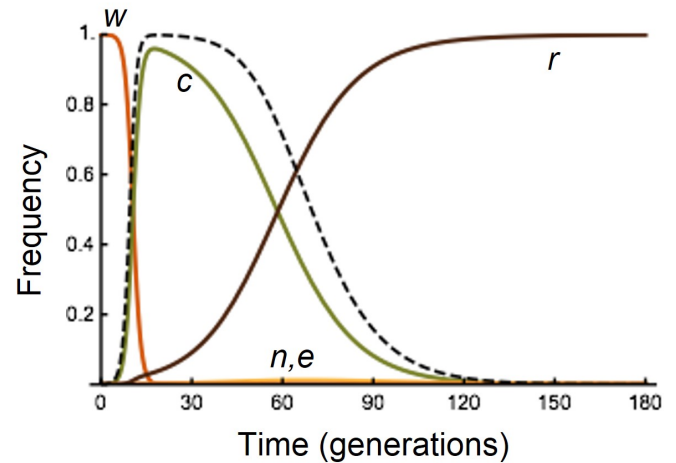


Figure 2 Allele frequency dynamics in Model I for the baseline set of parameter values. The complete construct (c) rapidly increases in frequency, replacing the wild type allele (w), but then is itself replaced by the resistant allele (r). The nuclease-only (n) and effector-only (e) alleles never reach appreciable frequencies with these parameter values. The dashed line shows $\Lambda[t]$, the proportionate reduction in vectorial capacity.

Results

There are 17 parameters in the model, defining the various aspects of demography, molecular biology, fitness and vector competence effects, and initial allele frequencies (Table 1). These are expected to vary according to the target species and molecular construct. To gain insight into the model we have chosen an exemplar set of parameter values that is consistent with the most extensive published work on mosquitoes (Hammond *et al.* 2016), hypothetical homozygous fitness costs for nuclease expression of 5% and effector expression of 10%, with dominance coefficients for both of 0.5, and an effector that completely blocks transmission even in the heterozygous state (see Table 1 for other baseline parameter values). We then vary each of the parameters individually, while keeping the others at their baseline values, to determine which parameters are the most important in affecting the efficacy of the intervention. The homing rates in our

Table 1 Parameters and baseline values

Symbol	Parameter ^a	Baseline value ^b
λ	Density-independent recruitment rate	6
γ	Density-dependent recruitment rate	1
r_0	Initial frequency of resistance	0
cc_0, wn_0, ee_0	Initial release frequencies	10^{-4}
k_c	Probability of cleavage	0.995
k_j	Probability of non-HR	0.02
k_n	Probability nuclease gene lost during homing	10^{-4}
k_e	Probability effector lost during homing (I)	10^{-4}
k_{ne}	Probability nuclease and effector lost during homing (I)	10^{-4}
k_r	Probability that non-HR of w produces functional r allele (II)	0
h_d	Dominance coef. for target site disruption	0.5 / 0.03
s_d	Cost of target site disruption	0 / 1
h_n	Dominance coef. for nuclease expression	0.5
s_n	Cost of nuclease expression	0.05
h_e	Dominance coef. for effector expression	0.5
s_e	Cost of effector expression	0.1
h_{rc}	Dominance coefficient for refractoriness	1
r_c	Homozygous degree of refractoriness	1
m_w	Probability of spontaneous mutation of wild type allele (II)	10^{-5}
m_n	Probability of spontaneous mutation of nuclease allele (II)	10^{-5}
m_e	Probability of spontaneous mutation of effector allele (II)	10^{-5}

^a I - Model I only; II - Model II only^b Given as Model I / Model II if different

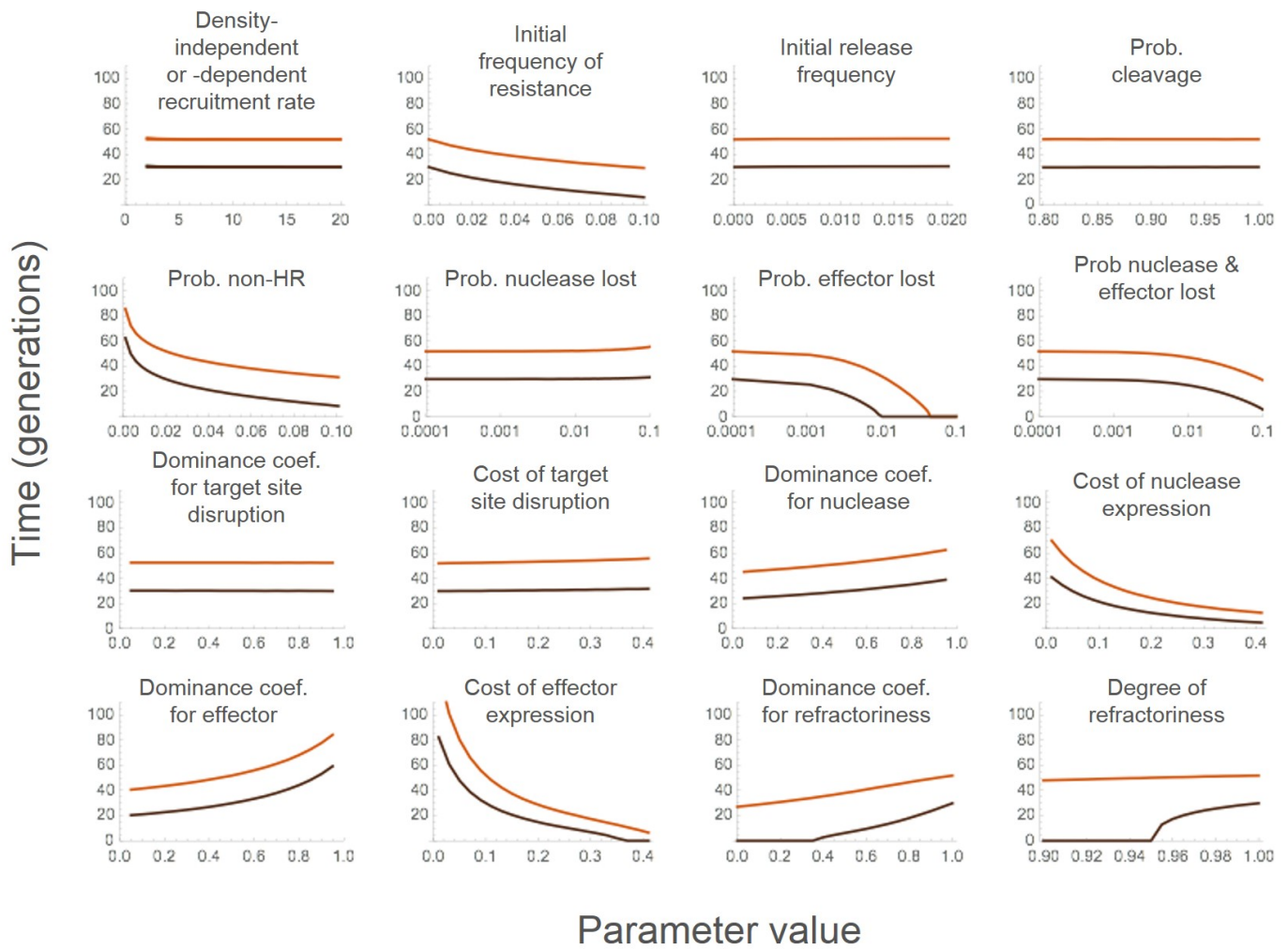


Figure 3 Duration of 67% and 95% protection (top and bottom lines in each graph) as each of the underlying parameters is varied, holding all others at their baseline values. When varying h_d , s_d was set equal to 0.1.

baseline model are high ($k_c(1 - k_j)(1 - k_n - k_e - k_{ne}) = 97.5\%$), and therefore the construct increases rapidly in the population, replacing the wild-type (Figure 2). However, resistant alleles are produced after $k_j + (1 - k_j)k_{ne} = 2.01\%$ of these initial cleavage events, and because they do not suffer the costs of nuclease and effector expression, they gradually replace the complete constructs. Nuclease-only or effector-only alleles are produced after only 0.01% of cleavage events, and never attain a significant frequency. The proportionate reduction in vectorial capacity increases to a maximum of $\Lambda[t] = 99.8\%$, and then falls back to 0. To quantify the duration of protection, we calculate the number of generations for which $\Lambda[t]$ is greater than 95% and 67% – and for our baseline parameter values this is 30 and 52 generations, respectively. To put these numbers into context, *Anopheles gambiae* mosquitoes may have 10-18 generations per year, depending on temperature (Depinay et al. 2004; Mordecai et al. 2013).

To see which parameters are most important in determining this duration of impact, we varied each one over what seemed a reasonable range while keeping the other parameters fixed at their baseline values (Figure 3). A number of parameters have little or no effect on the duration of efficacy, including the birth

rate parameters (λ and γ , because we are monitoring the *proportion* of individuals with one or two effectors, rather than the total number); the initial release frequency of the construct (at least up to 1%); the cleavage rate (at least down to $k_c = 80\%$); the probability of homing-induced loss of the nuclease (k_n); and the selection coefficients associated with disruption of the target locus (h_d and s_d , as long as they are not so high that the construct cannot spread). This last result follows from the fact that all the non-wildtype sequences suffer this cost, and so it does not affect the rate at which the effector-less alleles replace the effector-containing alleles. Factors that reduce the duration of protection include increasing (i) the frequency of pre-existing resistant alleles (r_0), (ii) the probability of non-HR (k_j), (iii) the probability of homing-associated loss of the effector (k_e); (iv) the selection coefficient against the nuclease (s_n); and (v) the selection coefficient against the effector (s_e); and decreasing (vi) the completeness of blockage by the effector (r_c and h_{rc}). Interestingly, the more dominant the costs of nuclease and effector expression, the longer the duration of protection, because then the selective benefit of the resistant allele is recessive, and selection for rare recessives is slow. It is also possible to investigate how simultaneous variation in multiple parameters affects the

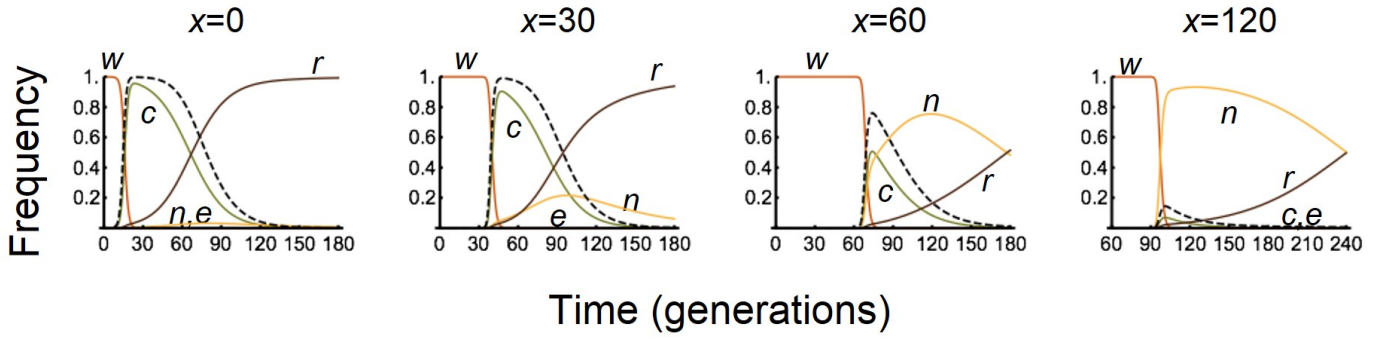


Figure 4 Allele frequency dynamics at different distances (x) from the release site in the spatial version of Model I. Distances are measured in units of the average movement per generation. The dashed line shows Δ , the proportionate reduction in vectorial capacity. Note time axis is shifted in the last panel.

duration of protection. As an example, Supplementary Figure S1 shows contour plots for the duration of 67% or 95% reductions in vectorial capacity as a function of the homozygous fitness cost of the nuclease and of the effector (assumed to be equal, $s_e = s_n = s$) and the rate of non-HR (k_j).

Supplementary File S2 is a Wolfram CDF document that allows users to define their own parameter values and visualize the resulting allele frequency dynamics and duration of protection (CDF player is available for free download from [Wolfram](https://www.wolfram.com/cdf/)). While for many parameter values the dynamics are qualitatively similar to those shown in Figure 3, it is also possible to get more complex behaviour, including apparent cycles (Supplementary Figure S2).

Spatial analysis

The c (complete) and n (nuclease-only) alleles in our model can only spread in the presence of the w (wildtype) allele. The n allele has homing rate equal to the c allele, and imposes less of a fitness cost, and therefore the ratio of $n:c$ alleles increases monotonically with time. However, with the baseline parameter values the n allele reaches a maximum frequency of only 1.3% because it is not present at the time of release; it is formed relatively rarely; and the c allele consumes the w alleles so quickly that there is not enough time for n to significantly replace c before the resource upon which they depend (w) is exhausted and they both disappear, replaced by r . This model considered a single well-mixed population; in a spatial model with local dispersal and a single release site, the genes may spread out spatially from the release site, which would extend the competition between n and c alleles. One might therefore expect that n alleles will become more prominent away from the release site, and the intervention less effective.

To investigate this effect quantitatively, we formulate a system of reaction-diffusion equations for genotype dynamics that extends the model to two spatial dimensions (Fisher 1937; Shigesada and Kawasaki 1997; Beaghton *et al.* 2016). The main additional assumptions of the model are that organisms move randomly and are distributed continuously across a homogeneous environment much larger than the typical dispersal distance. Further details are given in Supplementary File S1.

Analysis of the model shows that, as expected, it takes time for constructs released at one site to reach and have an effect at another site (Figure 4). Moreover, the n allele becomes (transiently) more prominent away from the release site, replacing

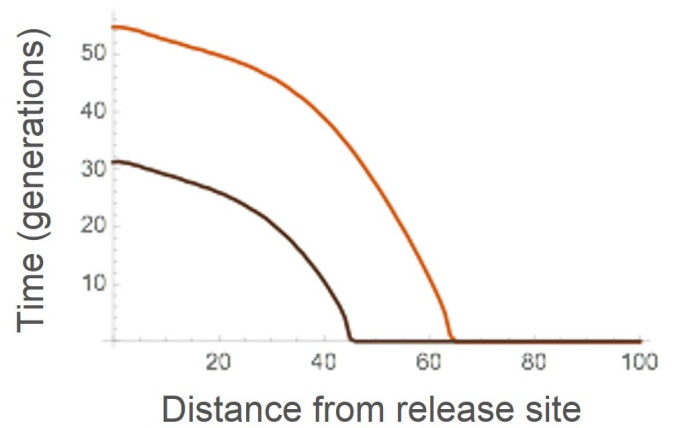


Figure 5 Duration of 67% (top line) and 95% (bottom) protection as a function of distance from the release site.

the c allele, before itself being replaced by the r allele. As a result, the c allele reaches a lower maximum frequency, and the duration of protection is reduced (Figure 5). At sufficiently great distances, the effector never reaches an appreciable frequency, and the intervention has no protective effect.

Model II. Linking the effector to a resistant gene

Genetics

As we have seen, if the effector is linked to the nuclease, the complete construct can spread rapidly, but it is then susceptible to being replaced by resistant alleles. The speed with which this second replacement occurs (and thus the speed with which protection is lost) depends upon the rate at which r alleles appear and their fitness advantage relative to c alleles. r alleles can appear relatively frequently (by non-HR), and their fitness advantage is larger because the effector is linked to the nuclease, which may have its own costs. An alternative approach that addresses these issues is to release a homing construct that targets a gene important for the host (e.g., an essential gene), and a separate construct that is resistant to the nuclease, functional for the host, and has the effector linked to it (Figure 6). In principle, the advantages of this approach are that the effector-less functional resistant sequence will arise at a lower rate than in

the previous model, and will be less strongly selected, which together should prolong the protection. For this approach to work, the knock-out phenotype (e.g., death) must be recessive; non-HR events must not typically produce resistant alleles that are functional for the host; and yet it still must be possible to create a resistant sequence in the lab that is functional.

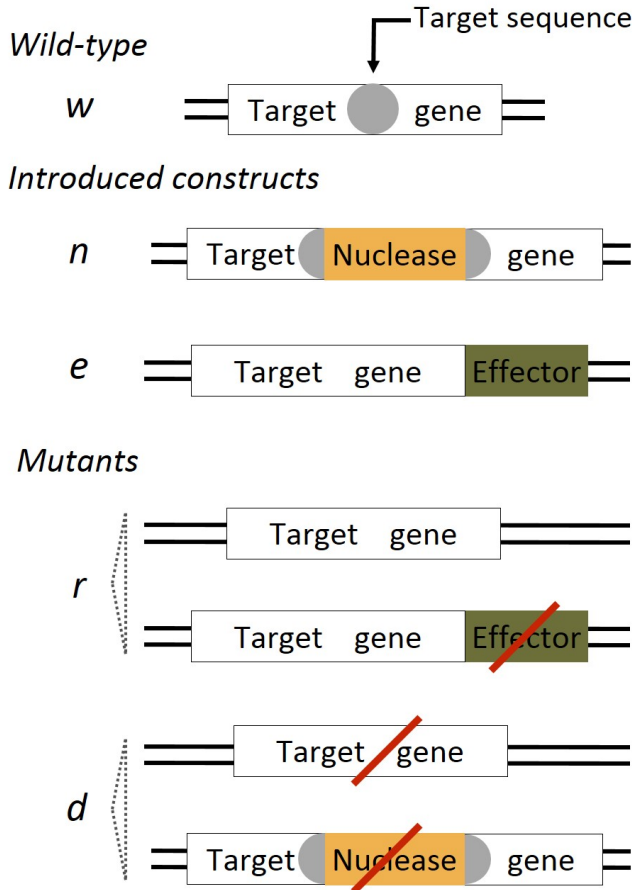


Figure 6 Five alleles in Model II. w : wild-type allele with target genes containing sequence recognized by the nuclease. n : allele with nuclease gene inserted in the middle of the target sequence, protecting the chromosome from being cut but also disrupting the target gene. e : effector gene linked to a target gene in which the recognition sequence has been changed so it is no longer recognized by the nuclease. d : disrupted target gene formed by non-HR of w alleles or by loss of nuclease from n alleles. r : functional target gene that is also resistant to cleavage due to not having the target sequence; can be formed by non-HR of w alleles or by loss of the effector gene of e alleles. Note that other alleles are possible, such as effector with disrupted target gene (e.g., formed by spontaneous mutation of e alleles), or effector with functional target gene with target sequence (e.g., formed by recombination between w and e alleles). These are expected to be rare because they are formed rarely and are not selected for.

To quantify the duration of protection with this alternative approach, we constructed another model, again with five alleles: wildtype (w), nuclease only (n), effector with functional resistance (e), defective alleles that are resistant to cleavage but non-functional (d), and functional resistant alleles (r). For sim-

plicity, we assume the r allele is fully functional, with no fitness cost. The population is assumed to start predominantly with w alleles, and a relatively small number of n heterozygotes and e homozygotes are introduced into it. Again, there are 15 different diploid genotypes. Homing can only occur in w/n heterozygotes, and is governed by the same processes as before, with parameters k_c , k_j , and k_n , except for those gametes formed by non-HR: we let a fraction k_r of them be functional resistant r alleles, with the remainder being defective d alleles (probability $1-k_r$). We also now allow for loss of function of the nuclease, effector and target genes by spontaneous mutation (i.e., not associated with homing), with baseline values for each of these set at 10^{-5} (Table 1). Such mutations are assumed to occur in the germline before homing. For simplicity we continue assuming the target population is large enough we do not have to worry about stochastic effects. Further details of the model are given in Supplementary File S1 and Tables S2, S3 and S4.

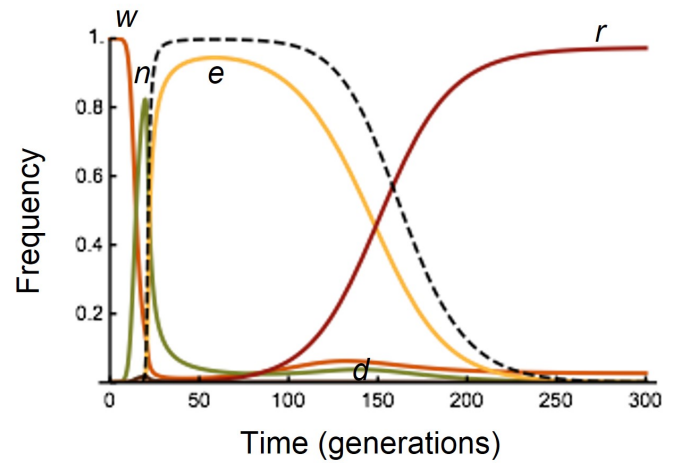


Figure 7 Allele frequency dynamics for Model II for the baseline set of parameter values. The nuclease allele (n) rapidly increases in frequency, replacing the wild type allele (w), but then is itself replaced by the effector-containing allele (e), which in turn is eventually replaced by the resistant allele (r). The disrupted allele (d) alleles never reaches an appreciable frequencies with these parameter values. The dashed line shows $\Delta[t]$, the proportionate reduction in vectorial capacity.

Results

The trajectories of allele frequencies and the protection provided with the baseline parameter values are shown in Figure 7. The wildtype allele is rapidly replaced by the nuclease-only construct, which is then rapidly replaced by the resistant allele carrying the effector, which is then eventually replaced by the effector-less resistant allele. For these particular parameter values, the maximum level of protection is 99.7%, and protection remains above 95% and 67% for 90 and 129 generations, respectively. The effect of varying each parameter individually on the duration of protection is shown in Figure 8. As expected, in addition to the efficacy of the effector, the most important parameters are the fitness cost of the effector (h_e and s_e), and the probability an effector-less resistant allele arises either by non-HR (k_r) or by spontaneous mutation (m_e). The Supplementary Information again includes an interactive Wolfram CDF document (File S3), allowing users to define their own parameter values and

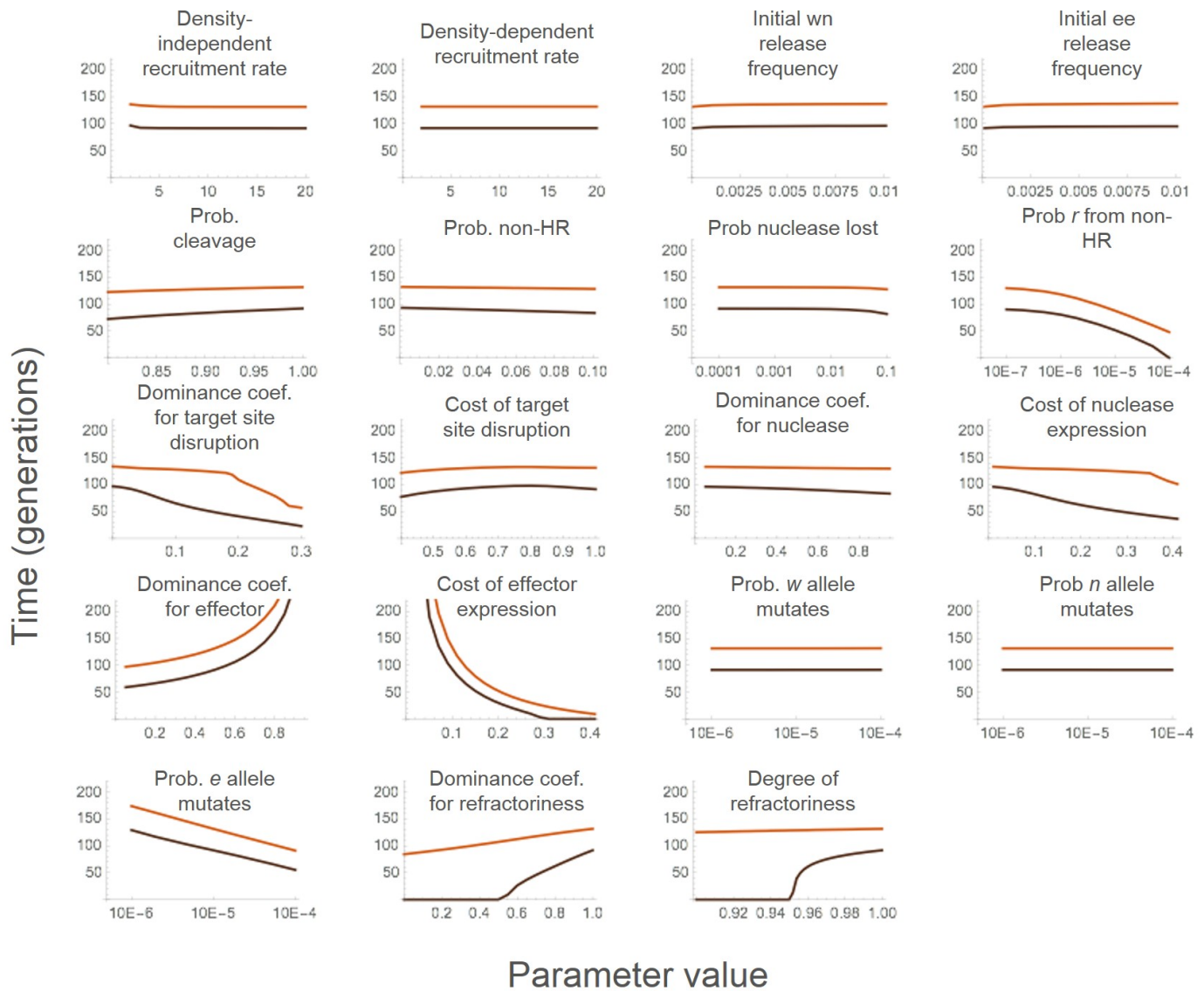


Figure 8 Duration of 67% and 95% protection (top and bottom lines in each graph) for Model II as each of the underlying parameters is varied, holding all others at their baseline values.

visualize the results. In general, the duration of protection is greater under Model II than under Model I, if the construct can be designed such that r alleles are sufficiently unlikely to arise from non-HR, but the extent of the advantage varies widely (e.g., 20% to 4-fold), depending on the assumptions made.

Discussion

Drive can spread a gene through a population even if it is harmful to the organisms carrying it, but if a gene is both harmful and does not contribute to the drive, as with the effectors considered here, then loss-of-function mutations will eventually replace the functional gene. While an intervention may not be evolutionarily stable in the face of such mutations, the protection may nonetheless persist sufficiently long as to be worthwhile from a public health perspective. In this paper we have presented a quantitative framework which indicates the design criteria needed to achieve a desired level of efficacy for two alternative

approaches using the homing reaction to drive an effector gene through a vector population.

With both approaches, three types of parameters are important in determining the duration of protection: the probabilities of different molecular processes, the various fitness effects, and the efficacy of the effector in blocking transmission. Unfortunately, all of these may be challenging to measure, considering that performance in the field may be different than that in the lab (particularly for the effects on fitness and vector competence; [Adelman *et al.* \(2016\)](#)). Field releases of effectors not associated with a drive system may be one source of useful information on these parameters.

Our modeling shows that the protection offered by the effector will be limited not only in time, but also in space, declining away from the release site. This is because in the time taken for the construct to reach a distant site, there will have been more opportunity for effector-less constructs to replace effector-containing ones. At sufficient distances from the release

site, only effector-less drive constructs are expected to spread through the population. The quantitative details of this effect will depend upon the spatial distribution and dispersal patterns of the target species. Unfortunately, for many vector species these are poorly known; we have used a simple model of uniform distribution and random movement, but other possibilities should be considered.

The modeling presented here may be useful in designing gene drive constructs. For the simpler approach of linking the effector to the nuclease, the probability of non-HR is a key parameter to be minimized, and there is still much to learn about how best to do this. For example, different nuclease architectures leave different types of ends at the cleavage site, which may affect the repair pathway (Simoni *et al.* 2014). The choice of promoter used to drive nuclease expression will affect the cell type in which cleavage occurs, and can also affect the relative probabilities of different repair pathways (Chan *et al.* 2011, 2013a,b). Genomic context may also have an effect – for example, if there are repeats near the target site, this can stimulate micro-homology mediated repair (Nakade *et al.* 2014). With CRISPR-based nucleases, there is the option of using multiple gRNAs (Esvelt *et al.* 2014), and what effect this will have on the relative likelihood of HR needs investigating. It is also important to minimize the probability that homing leads to transfer of the nuclease gene but loss of the effector. For CRISPR-mediated drive, some incomplete HR events can occur if the gRNA locus is used as a template for repair (Hammond *et al.* 2016), and it may help to put the effector between the gRNA and Cas9 genes.

With the alternative approach of using the nuclease to target an essential gene, and linking the effector to a resistant allele, the probability of non-HR may be less important, but other parameters are critical, including targeting an important gene (s_d high), where the knock-out is recessive (h_d low), and it is possible to have a functional resistant allele, yet it is unlikely to arise by non-HR (k_r low). In principle one could also combine the two approaches and link the effector both to the nuclease and to the resistant allele. Other variants are also possible, such as linking the effector to a trans-acting suppressor (e.g., based on RNAi) or a mutator (e.g., Wu *et al.* (2016)) of the gene drive construct, either of which could be inserted elsewhere in the genome and could spread by natural selection. If no resistant, suppressor, or mutator allele was released, the nuclease will impose a load upon the population, which can lead to population suppression, or even elimination, yet another way to reduce disease transmission (Burt 2003; Deredec *et al.* 2008, 2011; Eckhoff *et al.* 2017). The possibility of eventually combining population suppression and population modification approaches should be considered. Yet other approaches to synthetic gene drive systems do not use the homing reaction, such as those mimicking MEDEA elements or based on under-dominance (Marshall and Akbari 2016), and these will have their own design criteria for maximising the duration of protection.

The models presented here could be extended in several directions. We have only considered the spread of a single effector gene, whereas it is possible that more than one will be needed for complete blockage (e.g., Isaacs *et al.* (2012)), and these could be in the same construct or in separate ones. It will also be useful to allow for sex-specific molecular and fitness parameters, as these may well differ between males and females (e.g., if the effector is expressed only in females). We have also assumed that only the intended genotypes are released (i.e., there is some way to prevent resistant genotypes from accumulating in the insectary).

Our model also assumes an effectively infinite population, and allowing for some stochasticity may be particularly important for Model II, where our baseline rate for creation of functional resistant alleles is 10^{-5} . In finite populations there may be a nontrivial waiting time for such an allele to arise and survive stochastic loss, in which case protection would last longer than our current model indicates. We have also modeled the fitness cost of the effector as a constant, whereas if it acts early enough to block infection of the vector, and the pathogen is both common and harmful to the vector, then the effector may have low cost initially, and then increase in cost as the pathogen decreases in abundance. Finally, we have also treated the efficacy of the effector as a constant, and not included the possibility that the pathogen population might evolve in response to it. *Plasmodium*, for example, is a highly polymorphic pathogen whose sequence diversity has been shown to be relevant to the partial protection seen in a recent vaccine trial (Neafsey *et al.* 2015). It will be important to assess any candidate effector gene against a diverse array of pathogen genotypes, and incorporate the results into models before release.

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