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Evolutionary simulations of Z-linked suppression gene drives

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Synthetic gene drives may soon be used to suppress or eliminate populations of disease vectors, pathogens, invasive species, and pests. Recent proposals have suggested that one could use a gene drive carried on the Z chromosome to create male-biased sex ratios in species with ZW sex determination, which include Lepidopteran agricultural pests and parasitic trematodes. For example, a Z-linked 'W-shredder' might exhibit gene drive by cleaving the W chromosome and thereby causing carrier females to produce only sons. Here I use eco-evolutionary simulations to evaluate W-shredders and other hypothesised Z-linked gene drives, and to produce recommendations regarding their design and use. I conclude that W-shredders are likely to be highly effective at eradicating populations provided that resistance cannot evolve, but it may be hard to confine the drive allele to particular populations or geographic regions.

1. Introduction

Developments in genetic engineering will soon make it feasible to alter or eliminate populations of disease vectors, pathogens, agricultural pests, and invasive species using 'gene drives' [1–6]. Gene drives cause particular alleles (usually transgenes) to propagate through populations via a range of mechanisms, which include gene conversion, poison-antidote systems, segregation distortion, and genetic incompatibility [7–9]. For example, CRISPR-Cas9 gene editing can be used to create a transgenic insertion that is transmitted to almost 100% of the offspring of heterozygous individuals instead of the usual 50%; this type of gene drive functions by inducing a double-stranded DNA break at the homologous wild type locus, which is then repaired using the transgene as a template. Gene drives are often categorised into two types: replacement drives, which aim to spread a human-beneficial allele throughout a population (e.g. a mosquito allele that interferes with the transmission of malaria [1,10]), and suppression drives, which reduce the size of a population (potentially to extinction). Suppression drives typically work by using non-Mendelian inheritance to spread alleles that cause lethality or sterility [2,5,11], or skew the offspring sex ratio – typically towards males [12–16].

Recent theoretical papers have investigated the feasibility, efficacy, and potential negative consequences of various types of gene drives. For example, Noble et al. [6] used models to show that the basic version of a CRISPR-Cas9 gene drive might be highly invasive and could rapidly spread to fixation across whole species, which is often an undesirable outcome. Conversely, other models have concluded that gene drives are likely to fail if populations can evolve resistance to their effects [17,18]. The issue of resistance is compounded because the standard implementation of CRISPR-Cas9 gene drive (but perhaps not updated versions; [4,5,18,19]) tends to create its own resistance alleles, e.g. when the double-stranded break induced by Cas9 is repaired using an alternative DNA repair pathway (non-homologous end joining; NHEJ) instead of homology-directed repair [1–3,18,20]. Given the potential safety, ethical, and sociopolitical concerns surrounding gene drives, some models have focused on gene drives that would go extinct after a time [15,21,22], would stay confined to particular populations [11,22], and/or could be reversed once they have spread [23].

Here, I focus on the evolutionary dynamics of Z-linked suppression gene drives. The simulation is inspired by proposals for various types of Z-linked gene drives by Kevin Esvelt and colleagues, as well as ongoing efforts to develop these Z drives (see www.sculptingevolution.org; at the time of writing, these ideas have not been published elsewhere). Various Z-linked suppression drives proposed by Esvelt and colleagues are shown schematically in Figure 1. Depending on its design, mode of action and the biology of the target species, Z chromosomes carrying the drive allele (denoted Z^*) might enjoy a transmission advantage in Z^*W females (Figure 1B, and perhaps also 1C), and optionally also in Z^*Z males. Esvelt et al. focus on using Z drives to control the *Schistosoma* trematodes responsible for schistosomiasis, though Z drives could theoretically be used to control any organism with female-heterogametic sex determination, such as Lepidopteran agricultural pests or even invasive populations of birds.

A Z-linked gene drive could suppress populations by biasing gametogenesis in females, for example by inducing double-stranded DNA breaks in the W chromosome in order to inactivate it; such a gene drive would be a 'W-shredder', analogous to the X- and Y-shredders under development for XY species [12,13,15,16,24,25]. Females carrying the gene drive would thus produce relatively few viable W-bearing eggs, and therefore produce mainly drive-carrying sons. Esvelt et al. point out that the evolutionary dynamics of the drive will depend on the fitness of drive carriers relative to wild types, the timing of W-shredding (e.g. in germ cells, ova, or zygotes), and the ecology of the target species. For example, some W-shredder designs might allow drive females to produce roughly the same number of (mostly-male) offspring as a wild-type female provided that the W chromosome is destroyed early enough in oogenesis/development that the lost daughters can be replaced by sons (Figure 1B). Alternatively, drive-carrying females might produce half the number of offspring (or less), e.g. if the drive works by destroying all ova or

53 offspring that carry a W chromosome, and this loss is not compensated by reduced competition
54 on the surviving offspring. Esvelt et al. also proposed that one could suppress populations using
55 a Z -linked locus that caused sterility or lethality in females, either by shredding the W in somatic
56 tissues, or by spreading some other allele that harms females only. If this female-harming allele
57 were capable of gene drive in males, or were continually released into the wild, it could perhaps
58 reach high enough frequencies to suppress the population. The W -shredder could be designed
59 to also cause gene drive in males. Male gene drive could be accomplished using ‘standard’
60 CRISPR-Cas9 gene conversion, whereby the driving Z allele would convert the wild type locus
61 using homing endonuclease activity followed by homology-directed repair, causing heterozygous
62 males to produce mostly drive-carrying sperm. Esvelt et al. note that male gene drive might not
63 be necessary, since a Z -linked locus that prevents transmission of the W may already enjoy a
64 transmission advantage (Figures 1B–1C).

65 Here, I present an evolutionary simulation that can accommodate all of these hypothetical Z -
66 linked drives. I aimed to test which properties of the gene drive and the ecology of the target
67 species are critical to determining the likelihood and speed of extinction. For example, the gene
68 drive will presumably spread faster if it can bias transmission in both sexes, but perhaps a
69 simpler female-only drive would be perfectly adequate. Also, since the population will become
70 more male-biased as the gene drive invades, there will be eco-evo feedback that might affect the
71 evolutionary outcome in non-intuitive ways. For example, the altered sex ratio might intensify
72 the fitness advantage accruing to any resistant W chromosomes or autosomal modifiers that
73 prevent W -shredding (due to Fisherian selection for an even sex ratio; [26]), relative to that
74 observed in earlier models focusing on gene drives carried on autosomes [17,18]. Moreover, the
75 change in sex ratio could affect the ecology and evolution of the population, particularly if males
76 and females contribute differentially to density-dependent population growth [27,28], or have
77 different dispersal rates [29]. The model incorporates the possibility that Z -linked resistant-to-
78 drive alleles are sometimes created by NHEJ in heterozygote males, to test whether resistance is
79 just as problematic as for autosomal drives [1–3,18,20].

80 2. Methods

81 (a) Overview

82 I model a finite population of dioecious diploids with ZW sex determination, living in j discrete
83 habitat patches that are arranged linearly in a ring. The model considers the demography and
84 evolution of a population into which $n_{release}$ males carrying a Z -linked gene drive allele (Z^*) are
85 released. The drive allele causes either W -shredding or sterility in females, and optionally also
86 causes gene drive in heterozygous males (e.g. via gene conversion). Each generation proceeds
87 as follows: birth, dispersal between patches, breeding within patches, and death of the parental
88 generation. The species has 3 loci with 2–3 alleles each, some of which potentially show non-
89 Mendelian inheritance. The equilibrium population size was roughly 10,000 in all simulations
90 upon release of the gene drive, and the main outcomes of interest are the likelihood and speed of
91 extinction. The model is a stochastic individual-based simulation written in R 3.4.0; it was run on
92 the Spartan cluster at the University of Melbourne.

93 (b) Loci and alleles

94 Each male in the simulation carries one Z -linked locus and two autosomal loci, each with two
95 alleles. Each female carries a single allele at the Z -linked locus plus a W chromosome, as well as
96 two alleles at both of the autosomal loci.

97 There are three possible Z -linked alleles: a gene drive allele (Z^*), a wild-type allele (Z^+) that
98 is vulnerable to gene drive in Z^*Z^+ males, and a resistant allele (Z^r) that is immune to gene
99 drive in Z^*Z^r males. Similarly, there are two possible types of W chromosomes: a wild-type W

100 chromosome (W^+) that is vulnerable to gene drive by the Z^* allele, and a resistant W chromosome
 101 (W^r) that is immune to gene drive.

102 The two autosomal loci, denoted A/a and B/b , control immunity to W -shredding and gene
 103 conversion respectively. A/a and B/b are ‘trans-acting’ resistance loci, since they are at a different
 104 locus (indeed, a different chromosome) to the gene drive allele, in contrast to the ‘cis-acting’
 105 resistance conferred by the Z^r and W^r alleles. The A allele is dominant and confers immunity to
 106 Z -linked gene drive (e.g. W -shredding) in females. The B allele is dominant and confers immunity to
 107 to Z -linked gene drive (e.g. gene conversion) in males.

108 (c) Calculating fitness

109 Individuals with no Z^* alleles have an intrinsic fitness of $w = 1$, while other genotypes have
 110 $0 \leq w \leq 1$. The fecundity of females carrying Z^* is reduced by a factor $1 - c_f$. Small c_f implies
 111 minimal costs (e.g. because mothers replace lost gametes/offspring and/or sib-sib competition
 112 is intense), $c_f = 0.5$ could represent the case where all daughters die and are not replaced, and
 113 $c_f = 1$ means that females carrying Z^* are completely sterile. Setting $c_f = 1$ allows simulation
 114 of a female-sterilising Z -linked drive. Similarly, the fitness of males carrying Z^* is reduced by a
 115 factor $1 - c_m$; male fitness determines mating success (see below). For simplicity, I assume that
 116 the resistance alleles W^r , Z^r , A and B are cost-free. Also, the costs of Z^* to males were assumed
 117 to be dominant, such that Z^*Z^+ males and Z^*Z^* males had equal fitness.

118 (d) Gamete production and gene drive

119 I assume that the A/a and B/b loci segregate independently during meiosis and display standard
 120 Mendelian inheritance. Inheritance of the sex chromosomes is also Mendelian except for certain
 121 genotypes carrying one Z^* allele.

122 Firstly, Z^*W^+aaBB , Z^*W^+aaBb , and Z^*W^+aabb females produce a fraction $\frac{1}{2}(1 + p_{shred})$ of Z -
 123 bearing gametes and $\frac{1}{2}(1 - p_{shred})$ W -bearing gametes. Therefore, these three female genotypes
 124 produce >50% sons when $p_{shred} > 0$, due to the shortage of W chromosomes in their gametes.
 125 The gamete frequencies of Z^*W^r females, or of females carrying at least one A allele, conform to
 126 the standard Mendelian expectations due to resistance.

127 Secondly, Z^*Z^+AAbb , Z^*Z^+Aabb , and Z^*Z^+aabb males produce a fraction $\frac{1}{2}(1 + p_{conv} -$
 128 $p_{conv}p_{nhej})$ of gametes carrying the Z^* allele, $\frac{1}{2}(1 - p_{conv})$ gametes carrying the Z^+ allele, and
 129 $\frac{1}{2}(p_{conv}p_{nhej})$ gametes carrying the Z^r allele. Thus, gene conversion occurs in males if $p_{conv} > 0$,
 130 meaning that the Z^* allele is over-represented in the gametes of these three male genotypes. The
 131 parameter p_{nhej} represents the creation of resistance alleles via non-homologous end joining, in
 132 which the gene drive fails to copy itself to the homologous chromosome, and instead induces an
 133 indel mutation that creates a resistant allele. The gamete frequencies of Z^*Z^r males, or of males
 134 carrying at least one B allele, conform to the standard Mendelian expectations due to resistance.

135 (e) Calculating female fecundity

136 In the breeding phase of the lifecycle, the simulation first determines the number of offspring
 137 produced by each female. The expected fecundity of female i (F_i) is affected by three factors:
 138 the female’s genotype, the density of males and females in the local patch and/or in the full
 139 population, and some global parameters in the model, as follows:

$$F_i = (1 + w_i r(1 - (D_i/K)^\alpha)) \quad (1)$$

140 where D_i is the ‘density’ experienced by female i , w_i is her fitness, K is the carrying capacity,
 141 and r and α are constants that control the maximum possible fecundity and the shape of density-
 142 dependence respectively (function from [30]).

To ensure that the simulation captures various possible types of life history and ecology, I calculated density D_i in various ways in different simulation runs. First, I define the global density d_g , which acts equally on every female in every patch, as

$$d_g = \sum_{i=1}^{N_f} w_i + \delta N_m \quad (2)$$

where N_f and N_m are the numbers of females and males across all patches, the first term is the summed fitnesses of all these females, and δ is a constant (range: $0 - \infty$) that scales the effect of each male on d_g relative to a female with fitness $w_i = 1$. This formulation means that females with high relative fitness (i.e. fecundity) have a stronger effect on the global density than do low-fitness females. I also assume that each male contributes a fixed amount to the global density, irrespective of his genotype/fitness (since I assume that male fitness only affects male mating success; see below). The parameter δ represents sex differences in ecological niche use and behaviour. For example, we might expect $\delta < 1$ in species where males and females utilise very different environmental niches, or $\delta > 1$ in species where males are harmful to females.

Second, I define the local density d_j experienced by every female in patch j , as

$$d_j = \sum_{i=1}^{n_{f,j}} w_i + \delta n_{m,j} \quad (3)$$

where $n_{f,j}$ and $n_{m,j}$ are the numbers of females and males in patch j . As before, this formulation means that d_j depends on the summed fitnesses of the females in the patch, as well as the number of males (scaled by the constant δ).

Finally, the overall density experienced by female i in patch j (D_i) is a weighted sum of the global and local densities given by $D_i = \psi d_g + (1 - \psi)d_j$, where the parameter ψ weights the importance of global and local density to female fecundity. When $\psi = 0$, only local density matters and selection on females is entirely ‘soft’, while when $\psi = 1$ only global density matters and selection on females is completely ‘hard’ (as in [31]). Intermediate values of ψ produce a mixture of hard and soft selection on females.

After calculating the expected fecundity of each female (F_i), we generate the realised fecundity of the female by randomly sampling from a Poisson distribution with $\lambda = F_i$ (allowing for stochastic variation in fecundity between females with equal F_i). If the resulting number of offspring exceeded the global carrying capacity K , the model randomly selects K surviving offspring.

(f) Competition between males

After determining how many offspring each female produces, we determine the fathers of each of these offspring. We assume that all breeding occurs within patches, such that males only compete for matings/fertilisations with males in the same patch. If the patch contains k different male genotypes and there are n_1, n_2, \dots, n_k males of each genotype, the probability that a male of genotype k is the father of any given offspring is

$$p_j = \frac{n_k w_k}{\sum_{i=1}^k n_i w_i} \quad (4)$$

such that relatively common and/or high-fitness male genotypes are more likely to sire offspring. This formulation means that both sexes potentially reproduce with multiple partners.

(g) Reproduction, mutation and dispersal

After picking the parents, the model randomly generates each offspring’s genotype according to its parents’ expected gamete (and thus zygote) frequencies. Offspring are born in the same patch as their parents, and the parental generation is replaced by the offspring generation.

When an offspring is created, each Z^+ allele it carries has a chance μ_Z to mutate to a Z^r allele, and *vice versa* (i.e. mutation in both directions is equally probable). Similarly, each W^+ allele has a chance μ_W to mutate to a W^r allele, and *vice versa*.

Female and male offspring disperse to another patch with probabilities x_f and x_m respectively. We model two types of dispersal, in separate simulations: local dispersal, in which offspring move to one of the two neighbouring patches with equal probability (recalling that the patches are arranged in a ring), or global dispersal, in which dispersing offspring can land in any of the other patches.

(h) One compete run of the simulation

The model first initialises a population of 10,000 individuals (the carrying capacity, K) with low or zero frequencies of Z^r , W^r , A and B alleles, higher frequencies of the wild type Z^+ , W^+ , a , and b alleles, and zero Z^* gene drive alleles. It then runs 50 generations of burn-in to allow the population to reach demographic and genotypic equilibrium. Next, $n_{release}$ males with the genotype Z^*Z^*aabb are added to the population just before fathers are selected, representing the release into the wild of a laboratory-reared strain homozygous for the driving Z . In some simulations, all the Z^*Z^*aabb males were released in a single patch, while in others the $n_{release}$ males were randomly and evenly divided across all k patches. The model continued until either A) the driving Z^* allele went extinct, B) the population went extinct, C) the W^r chromosome went to fixation (making population suppression impossible), D) the Z^* allele fixed without causing extinction, or E) 1000 generations had elapsed. The model recorded which of these five outcomes occurred, as well as the allele frequencies, population size, and sex ratio at each generation.

(i) Investigating the parameter space

For each of the parameters in Table 1, I selected two or more possible parameter values (e.g. high versus low rates of W -shredding p_{shred} ; many versus few patches k). I then ran the model once for all possible combinations of these parameter values ($n = 6,000,000$ model runs). The aim was to measure the effect of each parameter across various assumptions for the other parameters, as well as to investigate all 2-way interactions between the parameters. To gauge the relative importance of the various features of the Z^* allele and the species' ecology to the extinction probability, I fit a binomial generalised linear model (GLM) with extinction as the dependent variable, and all the model parameters and their 2-way interactions as predictors. The predictors were scaled and centred before running the GLM, allowing for a meaningful ranking of the predictors by their absolute effects on extinction.

3. Results

(a) Three illustrative simulation runs

Figure 2 shows three contrasting simulation runs. In Figure 2A, the release of 20 Z^*Z^* males at generation 50 resulted in invasion of the Z^* allele, causing rapid extinction due to a lack of females. This simulation run assumed that the Z^* alleles causes perfect W -shredding ($p_{shred} = 1$), that Z^* has minimal fitness costs, and there is no resistance to W -shredding (Table S3).

In Figure 2B, Z^* invaded but failed to cause extinction, even though it was assumed that $p_{shred} = 1$ and W -shredding was not resistable. However, this simulation did assume that individuals carrying at least one Z^* allele paid heavy fitness costs ($c_f = 0.5$ and $c_m = 0.2$), and that there was no gene drive in males ($p_{conv} = 0$). The assumptions $p_{shred} = 1$ and $c_f = 0.5$ could imply that the W -bearing eggs/offspring of Z^*W^+ females are destroyed and not replaced, such that W -shredding increases the proportion but not the absolute number of offspring that inherit the Z^* allele. Essentially Z^* spreads via 'spite' [32], in that it removes W chromosomes from the local population and thereby makes room for more Z^* alleles, creating indirect fitness benefits.

228 However, the net fitness returns of the Z^* allele's 'strategy' (i.e. sacrificing 20% fitness in males in
229 order to remove W chromosomes in females) decline as females become rarer, halting the spread
230 of Z^* .

231 Lastly, Figure 2C shows a case where the invasion of Z^* was reversed by the evolution of
232 autosomal and Z-linked resistance alleles. Following the introduction of the Z^* allele, resistant
233 Z^r mutants were created via non-homologous end joining, and then Z^r spread to fixation due
234 to its immunity to gene conversion in males. The autosomal resistance allele A also spread; A
235 confers resistance to W-shredding and was initially present in the population at 5% frequency.
236 The spread of A caused the sex ratio to revert to normal, preventing extinction, and Z^* went
237 extinct due to its direct fitness costs no longer being outweighed by the benefits of W-shredding
238 and gene conversion. Incidentally, the resistant allele A was favoured over a because the male-
239 biased population sex ratio created by Z^* favours the production of daughters, and AA and Aa
240 females produce more daughters than aa females in populations where Z^* is present.

241 (b) Effects of each parameter on the evolution of a W-shredder

242 Figure 3 shows the effects of each model parameter, for models of a Z-linked W-shredder that
243 potentially also benefits from gene drive in Z^*Z males. Figure 4 shows the importance of each
244 main effect and two-way interaction term to the extinction probability, while Figure S1 shows
245 the effect of each parameter on the number of generations until extinction. Under favourable
246 assumptions, extinction occurred around 20 generations after releasing Z^* , though it often took
247 longer (Figure S1). Tables S1-S2 give the relative frequencies of the various possible outcomes
248 (e.g. extinction of the population, or loss of Z^*).

249 In Figure 3, the parameters are arranged in order of their importance to extinction probability
250 (see also Figure 4). By far the most important predictors of extinction were the efficiency of W-
251 shredding in females (p_{shred}) and the existence of resistance against W-shredding: extinction
252 never occurred unless p_{shred} was high and autosomal alleles conferring resistance to W-
253 shredding (allele A in the model) were absent. This makes sense because a W-shredder cannot
254 cause extinction unless Z^* -carrying females produce a strongly male-biased sex ratio and
255 resistance to W-shredding cannot readily evolve. Extinction also occurred more quickly when
256 p_{shred} was 1 rather than 0.95 (Figure S1), further highlighting efficient W-shredding as an
257 important design consideration.

258 The strength of gene drive in Z^*Z males (p_{conv} ; colours in Figure 3) also predicted extinction
259 probability. However, p_{conv} was less important than p_{shred} , and the W-shredder frequently
260 caused extinction even when it showed normal Mendelian inheritance in males, or if resistance
261 to male gene drive was common. The effect of male gene drive on extinction depended on other
262 factors in the model (Figures 3, 4 and S2); for example, male gene drive was at its most beneficial
263 when resistance to it could not evolve (either through pre-existing genetic variation, or the
264 creation of resistant Z^r alleles through NHEJ). Although its effects on extinction probability were
265 somewhat small, male gene drive did hasten extinction considerably (Figure S1). For example,
266 assuming perfect W-shredding, adding male gene drive with $p_{conv} = 0.95$ reduced the expected
267 time to extinction from around 75 to 22 generations.

268 The cost of the Z^* allele to female fitness also affected extinction probability, and its effect
269 interacted with the strength of gene drive in Z^*Z males. Specifically, assuming that the Z^* allele
270 halves female fitness ($c_f = 0.5$) negates the fitness benefits of segregation distortion for the
271 Z^* allele, and so extinction could only occur when $c_f = 0.5$ if there was gene drive in males.
272 Reassuringly, increasing c_f from 0.01 or 0.1 had almost no effect on the likelihood of extinction,
273 meaning that W shredders might be an effective means of population control even if females
274 carrying the gene drive suffer a 10% fitness cost. Similarly, assuming that Z^* was costly to male
275 carriers had little effect on extinction probability: extinction occurred almost as frequently when
276 the reduction in male mating success was 20% rather than 1%. Both c_f and c_m were positively
277 correlated with the time to extinction, particularly when there was no gene drive in males (Figure
278 S1).

Some of the ecological variables also affected extinction probability. Chief among these was the shape parameter of the density-dependence function, α . Setting $\alpha < 1$ causes female fecundity to decline at a decelerating rate with increasing population density, such that per-female fecundity only approaches its maximum value when the population is heavily depleted, making extinction more likely. Conversely for $\alpha > 1$, fecundity declines at an accelerating rate with increasing density, making extinction less likely due to the immediate increases in female fecundity that manifest once the population begins to shrink. Unsurprisingly, populations in which females have a higher maximum possible fecundity (r) were less likely to go extinct. Also, extinction was slightly more probable when female fecundity was determined by local density more than global density (ψ). This is because local density can remain high (and thus, per-female fecundity can remain low) even in meta-populations that are declining due to the spread of the Z^* allele in some of their sub-populations.

Extinction probability also increased with δ , the parameter that determines how male density affects female fecundity. When δ is high, female fecundity is constrained from increasing as the drive allele spreads by the ever-increasing proportion of males, contributing to extinction. Conversely, lower values of δ mean that male numbers are relatively unimportant in determining female fecundity, making extinction less likely because the shortage of females created by the gene drive alleviates competition on the remaining females. This result highlights that it is worth considering the ecology and population dynamics of target species when designing suppression drives that eliminate one sex.

Populations that are split into many semi-isolated patches were more difficult to drive extinct than those comparatively free of spatial structure, though the effect on extinction rate was small. The likely reason is that a highly-structured population creates refuges from the gene drive allele. The frequency and sex bias in dispersal was relatively unimportant to extinction probability, though there was a slight tendency for higher dispersal rates to stave off extinction, presumably because dispersal allows recolonisation of patches emptied by the gene drive. Similarly, it did not matter whether dispersal carried individuals to any patch, or only to neighbouring patches. Finally, there was no effect of the release strategy, suggesting that it may be unnecessary to release a W -shredding gene drive across the species' entire range provided that there is gene flow between patches. An additional implication of this result is that we cannot expect Z -linked gene drives to remain confined to their release sites, as previously found for autosomal drives [6].

(c) Effects of each parameter on a female-sterilising Z drive

I also used the model to examine the evolution of a Z -linked allele that causes gene drive in males and also causes total sterility in females ($c_f = 1$; Figures S3-S6). This alternative type of gene drive was also effective at causing extinction, but only under the assumption that the population has little or no resistance to gene drive in males. For example, extinction never occurred if even 1% of the progeny of Z^*Z males inherited a resistant Z' allele created by non-homologous end joining [c.f. 18]. Extinction also required that gene drive in males was strong (high p_{conv}), and that there were no autosomal resistance alleles to male gene drive. The effects of the other parameters in the model were similar as for a W -shredder, and extinction (when it occurred) took a fairly similar number of generations (around 25-30).

(d) Interactions between model parameters

Many of the model parameters interacted in their effects on extinction probability (Figures 4 and S2). For W -shredders, increasing p_{shred} only increased extinction probability provided that resistance to W -shredding was absent from the population, reaffirming the importance of resistance. Male gene drive was most beneficial when Z^*W females had half the fecundity of wild types (i.e. $c_f = 0.5$) and when p_{shred} was high, but male gene drive made little difference when $c_f \leq 0.1$ or p_{shred} was low. The demographic parameters α and r were important to extinction rate only when $p_{shred} \leq 1$; for $p_{shred} = 1$, the W -shredder was likely to cause extinction regardless

328 of the ecological assumptions. For female-sterilising Z drives, the most important interaction
329 terms underscored the importance of efficient and unresistable male gene drive (Figures S5-S6).

330 4. Discussion

331 The model shows that W-shredders are, in principle, very effective at eliminating populations,
332 especially if Z^*W females produce no daughters ($p_{shred} = 1$) and resistance to W-shredding
333 cannot evolve. The results have implications for the design of Z-linked W-shredders and
334 female-sterilising suppression drives.

335 One design consideration is whether to engineer W-shredders that are also capable of gene
336 drive in males, e.g. by including guide RNAs that target the Z as well as the W chromosome. In
337 the model, W-shredders very often caused extinction even without male gene drive (i.e. when
338 $p_{conv} = 0$), provided that females carrying the W-shredder had comparable fecundity to wild
339 type females, and that carrier females produce very few daughters (as in Figure 1B). Conversely
340 if W-shredder females had low fecundity (around half that of a wild type, or below; Figure
341 1C) or produced some daughters, male gene drive was often essential for the W-shredder to
342 cause extinction, or at least for extinction to occur rapidly enough to be useful. Although male
343 gene drive was not always essential to extinction, it did reduce the number of generations until
344 extinction occurred, sometimes substantially. Therefore, I conclude that it would almost certainly
345 be worth the effort to incorporate a male-acting gene drive if developing a W-shredder for species
346 with long generation times, such as invasive birds. Conversely, the rate of population decline
347 may be adequate even without male gene drive for species that have multiple generations per
348 year, such as Lepidoptera and *Schistosoma* parasites. Foregoing male drive could simplify the
349 design of W-shredders since they would only need to target the W chromosome (and not also the
350 Z), particularly because male-acting gene conversion drives seem more challenging to develop
351 than female-acting ones in some taxa (due to sex differences in DNA repair; [33]). Conversely,
352 strong male gene drive was always essential to extinction for female-sterilising suppression drives
353 (Figure 1D). Z-linked alleles that drive in males and cause sterility in females were effective at
354 causing extinction, but were very vulnerable to the evolution of resistance to male gene drive
355 (e.g. via drive-resistant alleles created by NHEJ; [18]).

356 Another aim when designing W-shredders should be to ensure that female carriers produce
357 as few daughters as possible (ideally none), while producing a large number of drive-carrying
358 sons (ideally as many as the total offspring produced by non-carriers). This implies that one
359 should ideally design a construct that cleaves the W chromosome early in gametogenesis or
360 development, to increase the chance that the number of surviving progeny produced by each
361 female is unaffected. Cleavage of the W should also be restricted to the female germ line, to
362 minimise fitness losses due to the loss of the W in somatic cells. For some species, this may
363 be as simple as placing the W-shredder under the control of a promoter such as *nanos* [34,35],
364 assuming that females are able to replace lost W-bearing oocytes before they are provisioned with
365 limiting resources. Even if the lost daughters are not replaced with sons, the Z^* allele might still
366 exhibit drive because the surviving Z^* sons will experience reduced competition (somewhat like
367 *Medea* [36]). In Lepidoptera, juvenile density is often strongly negatively correlated with survival,
368 and there are various maternally-transmitted endosymbionts that drive through populations
369 by killing males to lessen competition on their infected sisters (e.g. [37,38]); these observations
370 suggest that W-shredder alleles might invade Lepidopteran populations even if Z^*W females
371 produced half as many viable eggs, though male gene drive would certainly help the invasion.

372 The W-shredding mechanism should also be designed in a way that makes it difficult for W-
373 linked or *trans*-acting resistance to shredding to evolve. One way to do this would be to use a
374 single guide RNA that targets high copy number W-specific sequences, or to use multiple guide
375 RNAs that target multiple W-linked sequences [34]. This way, multiple changes to the reference
376 sequence would be required for a W chromosome to acquire resistance to cleavage by the W-
377 shredder. To ensure that the targets of cleavage do not become resistant as a result of indels
378 induced by NHEJ, one can ensure that the guide RNA's target lies within an essential gene where

379 an indel would be selectively disadvantageous, preventing resistant alleles from accumulating
380 in the population. This may not be necessary if the W-shredder targets many W-linked loci, but
381 it is an important design consideration for the male component of the gene drive, because the
382 evolution of Z-linked resistance completely nullified the usefulness of male gene drive in the
383 simulation (echoing [18]). Recent work demonstrated the feasibility of arrays containing many
384 guide RNAs separated by spacers [39], suggesting it may soon be easier to create gene drives
385 with multiple guide RNAs.

386 The model also indicated that extinction does not require the release of large numbers of
387 individuals: releasing just 20 Z^* males was often enough to eliminate a spatially-structured
388 metapopulation of 10,000 individuals in a few generations. On the one hand, this is advantageous
389 because W-shredders would be cheap and easy to deploy once they are developed, and they
390 are likely to extirpate whole metapopulations even if gene flow is weak. However, such high
391 invasiveness is not always desirable, because it makes the gene drive more difficult to restrict
392 to a particular area. This could limit the usefulness of W-shredders to control species like
393 Lepidoptera and birds, where one may wish to eradicate only invasive or agriculturally damaging
394 populations, while leaving other populations untouched. Modifications to gene drive design –
395 such as the self-limiting ‘daisy drive’ system – are being developed to address this important
396 concern [21,22].

397 The model further showed that W-shredders can fail to cause extinction if carrier individuals
398 have low fitness, although extinction was frequently observed even if these fitness costs were
399 substantial. Populations in which females can become highly fecund as the population shrinks
400 (i.e. low α and high r) were also less likely to go extinct, though extinction tended to occur
401 anyway provided $p_{shred} = 1$. The model also highlighted that W-shredders, and indeed any gene
402 drive that creates a male-biased sex ratio, are most effective in suppressing species in which
403 the density of males is an important determinant of population growth, e.g. because males use
404 resources that females need [28]. By contrast, if male density is not very important to population
405 growth (e.g. because females are limited by a resource that is not consumed by males), female
406 fecundity increases as females become rarer, slowing the decline in population size caused by the
407 W-shredder and potentially staving off extinction. Interestingly, the sexes are very different in the
408 *Schistosoma* trematodes responsible for schistosomiasis, which have been proposed as candidates
409 for control using a W-shredder by Kevin Esveld and colleagues. Female *Schistosoma* live inside the
410 body of the much larger male, who feeds on the host’s blood and passes some of it to the female.
411 Presumably, this means that the number of males (not females) is the primary determinant of
412 whether a host or habitat is saturated, making *Schistosoma* a good candidate for control with W-
413 shredders. In Lepidoptera and birds – two other ZW taxa that could potentially be controlled
414 with W-shredders – males and females generally have similar ecological niches, such that W-
415 shredders should be effective. Other ecological parameters like the patchiness of the population
416 (k), the frequency and sex bias of dispersal (x_f and x_m), and the scale of competition (ψ) had
417 relatively little effect on the probability of extinction.

418 Finally, I note that W-shredders might in general be easier to develop than X-shredders. Efforts
419 to develop an X-shredder in *Anopheles* mosquitos were initially hindered because the I-PpoI
420 protein used to cleave the X was paternally transmitted to the embryo inside sperm, causing
421 all embryos to die (not just daughters) due to loss of the maternally-inherited X. Although
422 this technical issue was later mitigated [13], such intergenerational effects would not trouble
423 a W-shredder since the W chromosome is unique to females (provided that the W-shredding
424 protein was not expressed in males and/or was not transmitted in their sperm). Additionally,
425 W-shredders might sometimes be easier to develop than gene drives that work by deleting genes
426 that are essential to female (but not male) fitness [e.g. 15]. This is because one could design a
427 prototype W-shredder based only on sequence data from the sex chromosomes, while identifying
428 genes with female-specific fitness effects requires more detailed data (e.g. expression profiling or
429 knockout studies) that are unavailable for some taxa.

430 5. Tables

431 **Table 1:** List of variables, and their corresponding parameter(s) in the model, which were varied
 432 in order to study their effects on extinction.

Variable	Parameter(s)
Strength of gene drive in females (e.g. W-shredding)	p_{shred}
Strength of gene drive in males (e.g. gene conversion)	p_{conv}
Cost of gene drive allele to female fecundity	c_f
Cost of gene drive allele to male mating success	c_m
Frequency of W-linked resistance mutations	μ_W
Frequency of Z-linked resistance mutations and NHEJ	μ_Z and p_{nhej}
Frequency of autosomal resistance alleles	μ_A and μ_B
Patchiness of the population	k
Dispersal rate of males and females	x_m and x_f
Global versus local density-dependence of female fecundity	ψ
Contribution of males relative to females in density-dependence	δ
Number of gene drive carrier males released	$n_{release}$
Release strategy: all in one patch, or global	-
Fecundity of females at low population densities	r
Shape of density dependence	α

433 6. Figures

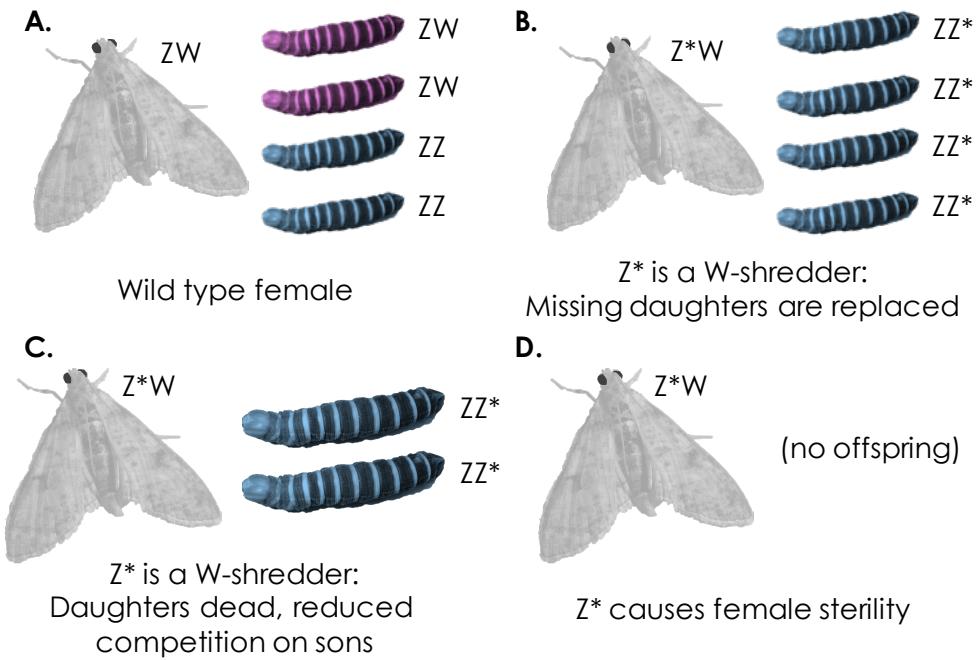


Figure 1. Some hypothetical Z -linked suppression drives considered in this study. Panel A illustrates normal inheritance of sex chromosomes in a wild type ZW female (assumed to be mated to a wild type ZZ male; not shown): the offspring sex ratio is even. In panel B, the female carries a W -shredder allele (Z^*) that kills gametes or offspring early enough that missing daughters are replaced with more Z^* -bearing sons. In panel C, the lost daughters are not replaced, though their absence increases the survival probability of the sons somewhat (shown by their larger size), causing super-Mendelian inheritance of the Z^* allele. Lastly, panel D shows a Z -linked female-sterilising allele (e.g. an allele that cleaves the W chromosome or a female-essential gene in somatic cells); since it is strongly disadvantageous in females, such an allele would go extinct unless it benefits from gene drive in heterozygous males.

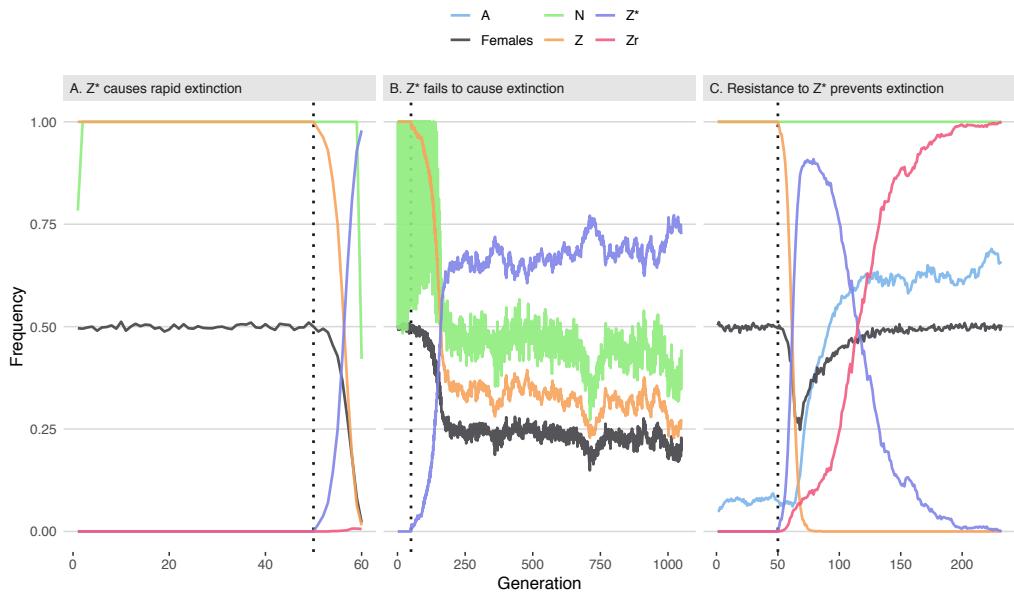


Figure 2. Three illustrative runs of the simulation, showing evolution in response to the introduction of 20 males carrying a *W*-shredder at Generation 50 (dotted line). In panel A, the driving Z^* allele fixed very quickly, causing population extinction through a shortage of females. In panel B, the Z^* allele spread until its fitness costs began to negate its transmission advantage, causing the population to persist at a reduced size. In panel C, the Z^* allele invaded, which selected for the resistance alleles A and Z^r and caused Z^* to go extinct. The population size N is shown as a fraction of its maximum value of 10,000. Table S3 gives the parameter spaces used for these three runs.

434 Data Accessibility. A website presenting all R scripts used to run the simulation and analyse the data
435 can be found at https://lukeholman.github.io/W_shredder/.

436 Authors' Contributions. LH performed the analyses and wrote the manuscript.

437 Competing Interests. The author declares no conflict of interest.

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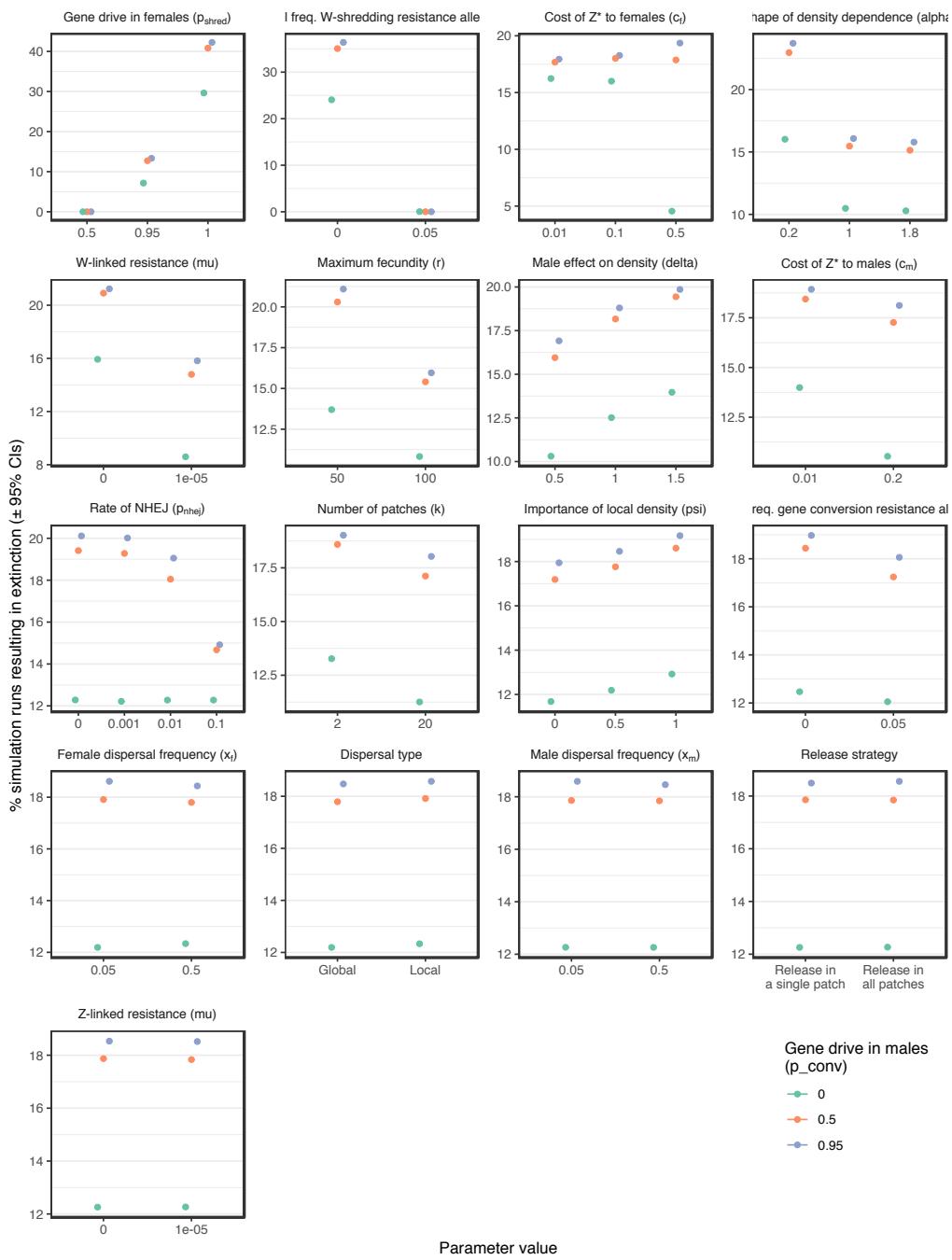


Figure 3. The percentage of simulations of a W -shredder that ended in extinction, for all runs with a particular value (shown on the x -axis) for a given parameter (shown in the panels). For example, there were no extinctions in any of the thousands of runs for which I assumed $p_{shred} = 0.5$, while 60% of runs where $p_{shred} = 1$ resulted in extinction. The panels are ordered by the range of the x -axis, which indicates the relative importance of each variable to extinction probability. Figure S3 gives a similar plot for simulations of a female-sterilising Z^* allele.

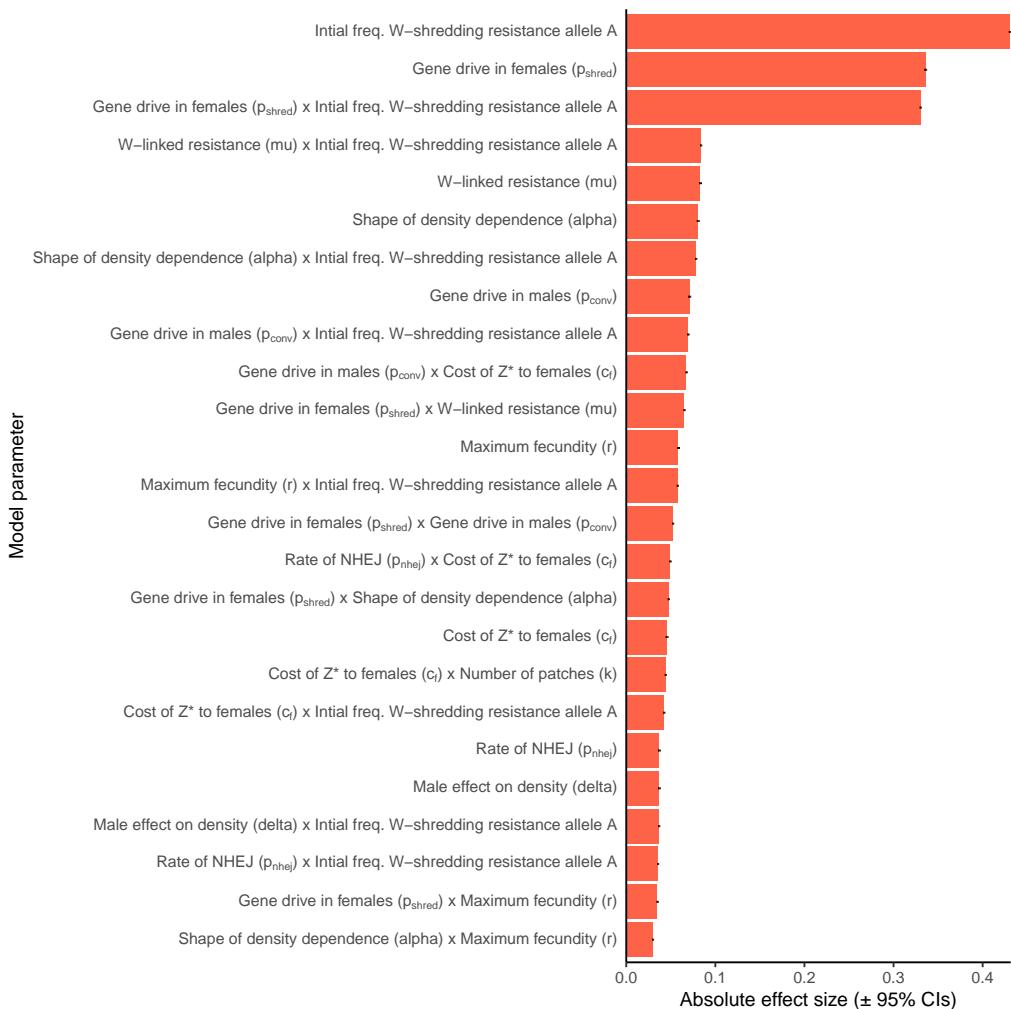


Figure 4. Relative parameter importance in the simulations of *W*-shredders, for the top 25 most important main effects or two-way interactions (from a binomial GLM that included all the main effects and all their two-way interactions). Each predictor variable was scaled before running the model, meaning that the absolute effect size indicates how important each parameter is to the extinction probability, given the range of values plotted in Figure 3. Figure S5 gives a similar plot for simulations of a female-sterilising Z^* allele.