Supplementary Materials

Methods

We used the individual-based and spatially explicit model framework introduced by Birand et al. (2022). In the model, individuals occupy a rectangular array of patches that form a landscape. Patches hold multiple individuals, and individuals can utilize multiple patches. Individuals are diploid and have genetically controlled autosomal traits and sex chromosomes. A breeding cycle is a single time-step with: mate search, mating, density-dependent reproduction, natal dispersal, survival, and breeding dispersal of adults. There are multiple breeding cycles (n_{c}) per year and generations are overlapping. Individuals can go through a number of breeding cycles provided that they survive until they reach a maximum age (age_{m}).

All females mate, unless there are no males present within their mate-search area determined by mate-search distance parameter D_{m}. The search starts in the central patch and covers all patches, including the diagonals within D_{m}. Females pick males randomly, which implies that some males can mate multiple times, whereas some may not mate at all. Depending on the probability of multiple mating (p_{m}), a female can mate with multiple males ($n_{\mathrm{m}} = 2$) in a single breeding cycle if there are more than one male present in her central patch. Fertility is density dependent. The number of offspring per female is drawn from a Poisson distribution with mean parameter $v = b/(1 + [(b/2) - 1][N/K])$, where b is the average number of offspring; N and K are the population size and the carrying capacity in the female's central patch, respectively (discrete-time Beverton-Holt model Kot, 2001). Under polyandrous mating, each male is assigned a probability of paternity. Y-drive carrying males' probability are reduced by sperm-disadvantage coefficient ($d_{\mathrm{s}} = 0.2$) when they are competing against wild-type males since sperm production is essentially halved in male gene-drive carriers.

All offspring are assumed to survive since the density-dependent fertility incorporates offspring mortality. Offspring can disperse to a new patch within distance D_{n} to establish a mate search area. Natal dispersal is both distance and negative density dependent, and the probability of picking a patch with distance δ is calculated as: $P(\delta) = \exp\left[(\delta/D_{\mathrm{n}} - N_{\mathrm{r}}/K_{\mathrm{r}})^2\right]$ where D_{n} is the maximum dispersal distance; N_{r} is the population size, and K_{r} is the carrying capacity summed across all the patches within distance D_{n} (Birand et al., 2022).

The negative density-dependent dispersal function ensures that individuals tend to retain the same central patch at high densities; whereas at low densities, the probability of dispersal to greater distances is larger. Density-dependent dispersal is ubiquitous in nature, and dispersal rates and distances increase with decreasing abundance in various taxa (Amarasekare, 2004; Matthysen, 2005; Travis and French, 2000; Diffendorfer, 1998), including small rodents (Ims and Andreassen, 2005; Lambin, 1994; Sandell et al., 1990; Jones et al., 1988; Russell et al., 2005; Nathan et al., 2015; MacKay et al., 2019; Moro and Morris, 2000), rabbits (Parer, 1982; Richardson et al., 2002; Ziege et al., 2020), cats (Quilodrán et al., 2019), and foxes (Trewhella et al., 1988). Random dispersal within a dispersal range is a common assumption used in theoretical models, but it is overly simplistic and fails to capture the complexity of dispersal observed in nature (Travis and French, 2000). Moreover, it can also lead to underestimation of times to eradication (Birand et al., 2022). After dispersal, survival of adults is implemented using a fixed probability of surviving ω to the next breeding cycle.

Surviving adults can establish new mate-search areas with a new central patch within distance D_{b} (Harts et al., 2016). The probability of picking a patch is calculated as natal dispersal above (for simplicity, we assume that the maximum distances for natal dispersal, breeding dispersal, and mate-search distance parameter are physiologically constrained to be equal, and determined by D).

We explored the spread of X-chromosome shredding Y-drive. The X-chromosome shredding drive is a CRISPR-based drive located on the Y chromosome, and destroys the X chromosome with probability $p_{\mathrm{x}} = 0.96$ by cleavage at X chromosome specific repeat sequences during spermatogenesis (Fig. 1A). Since most of the X-bearing sperm are inviable, and eggs are predominantly fertilized by Y-bearing sperm, causing disproportionately more male offspring. We also checked the effect of a CRISPR-based homing drive, which is located within an exon of a fertility gene, causing deactivation of the gene in the germline in both sexes. The gene is haplosufficient and is present in both sexes but required only in females (Birand et al., 2022). We assumed that the probability of Non-Homologous End Joining (NHEJ), $p_{\mathrm{N}} = 0.01$; the probability of a successful cut, $p_{\mathrm{C}} = 0.9$; and the probability of loss of gene function following NHEJ, $p_{\mathrm{L}} = 0.9999$ across all species. Reducing the survival probabilities of drive carrying individuals further by 10% had low influence ($\sim 2\%$) on the probabilities of eradication for both the drives (Birand et al., 2022) and is not considered here.

Model parameters are based on empirical data (Table 1 in the main text). For survival (ω) and probability of polyandry (p_{m}), we used a uniform distribution defined by ±0.05 of the parameter estimate; and for dispersal distance D, we used a uniform discrete distribution with range ±1 patch. We created $1,000$ unique parameter combinations for each species based on these distributions using Latin hypercube sampling (randomLHS, R software package *lhs* Carnell, 2020) and ran a single simulation for each of the parameter combinations (Prowse et al., 2016). Drive-carrying males are introduced after a burn-in period of 12 breeding cycles. After exploring various spatial release strategies in mice, we modelled a single release into 256 patches distributed systematically across the landscape, with one gene-drive carrying individual ($N_{\mathrm{i}} = 1$) released per patch. We ran simulations for a maximum of 500 breeding cycles. The model is coded using the C programming language (Dryad Digital Repository, https://doi.org/10.5061/dryad.wstqjq2p0).

We performed a global sensitivity analysis to investigate the relative influence of parameters on the time to eradication when eradication was successful. We fit Boosted Regression Tree models using the function 'dismo' (BRT; R package *dismo* Hijmans et al., 2011) with the following settings: learning rate = 0.01; bag fraction = 0.75; tree complexity = 3; 5-fold cross-validation (Elith et al., 2008). We assumed Bernoulli error distribution for the probability to eradication, and Poisson error distribution for time to eradication (Elith et al., 2008). The relative influence of parameters are presented in Table S1 below.

Table S1: Relative influence of parameters on probability of eradication and time to eradication based on sensitivity analysis results. Note that the probabilities of eradication was 1 for both black rats and rabbits with the parameter ranges simulated; therefore, relative influence of parameters could not be determined.

	Species	ω	D	p_{m}
Probability of eradication				
	Mouse	36.33	32.26	31.41
	Black rat	-	-	-
	Rabbit	-	-	-
	Cat	26.41	73.10	0.49
	Fox	64.80	29.73	5.47
	all species	50.45	46.71	2.83
Time to eradication				
	Mouse	12.43	78.72	8.85
	Black rat	89.19	2.67	8.15
	Rabbit	93.79	4.36	1.85
	Cat	12.56	87.05	0.39
	Fox	66.01	26.34	7.65
	all species	44.35	26.69	28.95

Table S2: Median time to 50% and 90% reduction, and time to eradication (100% reduction) in years across all species with Y-drive.

Species	50%	90%	100%
Mouse	6.7	9.2	17.7
Black rat	9.0	11.7	18.5
Rabbit	16.8	24.1	48.0
Cat	71.0	92.0	143.2
Fox	74.0	103.5	169.0

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