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Seed dormancy shapes gene drive dynamics in plants

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Supplementary Text

1 Experimental parameterization of CAIN and ClvR

We obtained the male germline cleavage rate, female germline cleavage rate, and penetrance rate of CAIN directly from Liu et al. [1]. Since these rates were not explicitly reported for the ClvR drive, we inferred them from the experimental data, summary statistics, and interpretations provided by the authors.

We focused on the ClvR-ubq7 construct as this was the most efficient construct tested. We first estimated the male ($p_{d,m}$) and female ($p_{d,f}$) ClvR drive inheritance rates by calculating the sample size-weighted averages from crosses reported in Figures 2 and 3 of Oberhofer et al. [2]. Specifically, $p_{d,m}$ was derived from crosses of drive-heterozygous males with wild-type females, and $p_{d,f}$ from crosses of drive-heterozygous females with wild-type males.

The drive inheritance rates through males ($p_{d,m}$) and females ($p_{d,f}$) are calculated as:

$$\begin{aligned}
p_{d,m} &= \frac{\text{number of seeds with drive allele}}{\text{total number of seeds}},\\
&= \frac{1 \times 357 + 0.988 \times 482 + 0.988 \times 497 + 0.971 \times 513 + 0.993 \times 583 + 0.992 \times 488 + 0.984 \times 685}{357 + 482 + 497 + 513 + 583 + 488 + 685},\\
&= 0.987.
\end{aligned}$$

$$\begin{aligned}
p_{d,f} &= \frac{\text{number of seeds with drive allele}}{\text{total number of seeds}},\\
&= \frac{0.798 \times 257 + 0.858 \times 302 + 0.920 \times 250 + 0.927 \times 303 + 0.789 \times 375 + 0.773 \times 335 + 0.740 \times 407}{257 + 302 + 250 + 303 + 375 + 335 + 407},\\
&= 0.821.
\end{aligned}$$

We assume a high germline cleavage rate, such that the drive heterozygotes involved in Figures 2 and 3 of Oberhofer et al. [2] inherited a disrupted target allele from their drive-carrying parent. Thus, these individuals are heterozygous at the target locus, carrying one disrupted and one intact (non-disrupted) allele.

The authors attributed failed drive inheritance through males to a lack of germline cleavage. They also assumed full penetrance of the *YKT61* target gene, such that pollen carrying a disrupted target allele but no drive allele are always nonviable. Under these assumptions, we can derive the male germline cleavage rate (c_m). A drive-heterozygous male produces gametes of which half inherit the drive allele, remaining viable. The other half inherit the wild-type allele, with equal probabilities of inheriting either the disrupted or intact target allele. The non-disrupted target allele is cleaved with probability c_m, and cleavage is assumed to always produce a disrupted allele, resulting in gamete nonviability. Thus, the expected male drive inheritance rate ($p_{d,m}$) is given by:

$$\begin{aligned}
p_{d,m} &= \frac{\text{fraction of gametes with the drive}}{\text{fraction of viable gametes}},\\
&= \frac{\frac{1}{2}}{\frac{1}{2} + \frac{1}{2} \times \frac{1}{2} \times (1 - c_m)},\\
&= \frac{2}{3 - c_m}.
\end{aligned}$$

Using our estimated $p_{d,m} = 0.987$, we solve for c_m to obtain a male germline cleavage rate of 0.974.

The authors attributed the lower drive inheritance rates observed through females to maternal carryover rescue: drive-heterozygous females may deposit sufficient rescue protein into their ovules so that an ovule carrying a disrupted target allele but no drive allele remains viable. We denote the maternal carryover rate by m_r and the female germline cleavage rate by c_f. A drive-heterozygous female produces gametes as follows: half inherit the drive allele and are always viable, while the other half inherit a wild-type allele. Among the remaining wild-type gametes, half inherit the disrupted target allele, of which a fraction m_r remain viable. The other half inherit a non-disrupted target allele, subject to germline cleavage at rate c_f, which, if cleaved, are viable at rate m_r. Thus, the expected female drive inheritance rate ($p_{d,f}$)

is:

$$\begin{aligned}p_{d,f} &= \frac{\text{fraction of gametes with the drive}}{\text{fraction of viable gametes}},\\ &= \frac{\frac{1}{2}}{\frac{1}{2}+\frac{1}{2}\times\frac{1}{2}\times m_r+\frac{1}{2}\times\frac{1}{2}\times(1-c_f)+\frac{1}{2}\times\frac{1}{2}\times c_f\times m_r},\\ &= \frac{2}{3-c_f+m_r(1+c_f)}.\end{aligned}$$

Assuming equal germline cleavage rates ($c_f = c_m = 0.974$), we use our observed female drive inheritance rate ($p_{d,f} = 0.821$) to solve for m_r, obtaining a maternal carryover rate of 0.207.

2 Effect of drive parameters on modification and suppression drive performance

To elucidate the key parameters underlying the differences in CAIN and ClvR's performance, we conducted a systematic analysis of each drive parameter's effect on drive outcomes across a range of baseline germination rates (b) and age-dependence germination parameter (m). Details are provided in the "Gene drive parameter scan" section of the Methods in the main text. Modification drives reached fixation across all b and m tested, while the success rate of suppression drives varied with seedbank parameters. Thus, for modification drives, we compared average times to fixation across all b and two values of m: $m = 0$, at which germination rates are independent of age, and $m = 2$, at which germination rates strongly decline with age. For suppression drives, we compared population elimination rates across all b and m.

We started our analysis with the target gene penetrance rate, which controls how essential the target gene is in gametes. This parameter had only a minimal impact on modification drive performance (Supplementary Fig. 5a). For a given drive, differences in average times to fixation were negligible. When CAIN and ClvR were set to the same seedbank parameters and target gene penetrance rates, ClvR always reached fixation faster than CAIN, due to ClvR's ability to bias inheritance through both sexes. For suppression drives, however, the target gene penetrance rate was a key factor in drive success (Supplementary Fig. 12). For the ClvR male suppression drive, a penetrance rate of at least 98% allowed the drive to eliminate the population across all seedbank parameters. For the CAIN male suppression drive, target gene penetrance rate had to be higher, at around 100%, to eliminate the population across all b and m. The ClvR female suppression drive could eliminate the population across a broader range of b and m as the penetrance rate increased; however, the default 20.7% maternal carryover rate was likely too high for the drive to impose sufficient genetic load for population elimination, regardless of target gene penetrance.

We next focused on the effect of sex-specific germline cleavage rates—which determine the degree of target gene disruption in the ovule or pollen pool—on drive success. Like the target gene penetrance rate, the male germline cleavage rate and female germline cleavage rate both had no noticeable impacts on modification drive performance (Supplementary Fig. 5b,c). For a given drive parameterization and seedbank parameters, ClvR continued to outperform CAIN. For suppression drives, however, the effect of the germline cleavage rate varied by drive (Supplementary Figs. 13 and 14). The male germline cleavage rate had a large impact on the success of male-targeting drives (ClvR male suppression and CAIN male suppression) and little impact on the success of the female-targeting drive (ClvR female suppression). When the male germline cleavage rate was 100% (with the target gene penetrance rate at its default 100%), both male suppression drives eliminated the population across all seedbank parameters tested (Supplementary Fig. 13d,l). When the rate was lowered to 95%, however, these drives could eliminate the population at low enough total germination probabilities (γ; Supplementary Fig. 13b,j) but at higher γ, often reached a high equilibrium drive frequency just below that of the required genetic load (λ^*; Supplementary Fig. 13c,g). At low average seedbank durations (τ), the drive could sometimes stochastically exceed λ^* and cause population collapse if the seedbank lacked sufficient older seeds to quickly replenish the population. The female germline cleavage rate did not have a noticeable impact on either male or female suppression drive success (Supplementary Fig. 14), though we would expect the female germline cleavage rate to affect female suppression drives in the same manner that the male germline cleavage rates affected the male suppression drives, if the default maternal carryover rate were lowered.

For ClvR drives, we focused on the maternal carryover rate. The ClvR modification drive reached fixation more quickly when the maternal carryover rate was lowered (Supplementary Fig. 5d), since the drive could then spread through the female gamete pool more easily. The success of the ClvR female suppression drive was also strongly affected by the maternal carryover rate (Supplementary Fig. 15e–h), eliminating the population across all b and m once maternal carryover was set to zero, such that all ovules with a disrupted target allele had to be "rescued" from nonviability through co-inheriting a drive allele. The maternal carryover rate did not affect the ability of the ClvR male suppression drive to eliminate the population (Supplementary Fig. 15a–d), however, since this drive relies on creating enough sterile drive-homozygous males for suppression, and drive inheritance through the pollen pool plays a greater role. When the ClvR male and female suppression drives both lacked maternal carryover, the female suppression drive often eliminated the population more quickly than the male suppression drive (Supplementary Fig. 16). This is because there are far fewer effective ovules in the population than effective pollen (baseline mean effective ovule count $n_{bo} <$ baseline mean effective pollen count n_{bp} at equilibrium), so the required genetic load of female suppression drives is lower than that of male suppression drives for the same γ (Eq. 4 in the main text). Thus, when the drive can spread equally well through females as through males, it can reach λ^* more quickly as a female suppression drive than a male suppression drive.

Supplementary Tables

Supplementary Table 1 | Parameters for the CAIN and ClvR gene drives. Default drive parameters were obtained directly from CAIN's experimental study [1] and estimated from ClvR's experimental results [2] (Supplementary Text 1). The maternal carryover rate is only applicable to the ClvR drive, since CAIN's target gene only affects pollen. Unless stated otherwise, simulations assume a dioecious population, no fitness costs ($s_g = s_s = 0$), an initial drive frequency p_0 of 0.1 in plants, and male germline cleavage, female germline cleavage, target gene penetrance, and maternal carryover rates fixed at their default values. In Supplementary Text 2, these parameters are systematically varied over the ranges shown in the "Note" column. Fitness costs reducing gamete viability (s_g) or seed survival (s_s) were also systematically varied for threshold-dependent drives, as they affect drive introduction thresholds. To assess the invasion threshold under these fitness costs ($s_g > 0$ or $s_s > 0$), we explored the introduction frequency p_0. The baseline invasion threshold ($\hat{p}$) is defined as the minimum introduction frequency required for successful drive invasion in populations without a seedbank, and the effective invasion threshold ($\hat{p}_e$) as the analogous threshold in populations with a seedbank. Entries marked with "–" indicate variables without default values because they were either systematically varied or estimated directly from simulations.

Description	Default Value	Note
CAIN [1]		
Male germline cleavage rate	0.984	Varied across $\{0.9, 0.95, 1.0\}$
Female germline cleavage rate	0.941	Varied across $\{0.9, 0.95, 1.0\}$
Target gene penetrance rate	0.960	Varied across $\{0.96, 0.98, 1.0\}$
ClvR [2]		
Male germline cleavage rate	0.974	Varied across $\{0.9, 0.95, 1.0\}$
Female germline cleavage rate	0.974	Varied across $\{0.9, 0.95, 1.0\}$
Target gene penetrance rate	1	Varied across $\{0.96, 0.98, 1.0\}$
Maternal carryover rate	0.207	Varied across $\{0.0, 0.207, 0.5, 1.0\}$
Threshold-dependent drives		
Drive fitness cost reducing gamete viability (s_g)	–	Varied across $\{0, 0.05, 0.1, 0.25\}$
Drive fitness cost reducing seed survival (s_s)	–	Varied across $\{0, 0.05, 0.1, 0.25\}$
Introduction frequency (p_0)	–	Modification drive: varied $[0, 1]$ (step 0.01) Suppression drive: varied $[0, 0.5]$ (step 0.01)
Baseline invasion threshold ($\hat{p}$) Effective invasion threshold ($\hat{p}_e$)	–	Estimated directly from simulations

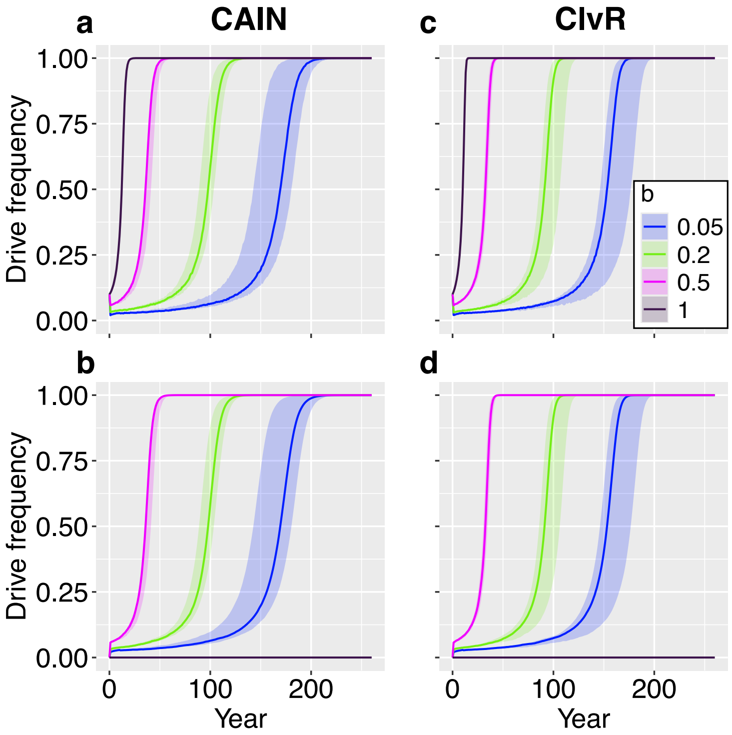
Supplementary Table 2 | Parameters, time-dependent state variables, and derived population metrics in the plant life-cycle model. Default parameter values are listed along with the ranges explored in simulations. Seedbank parameters characterize seed survival and germination dynamics; demographic parameters define population reproductive potential under two fecundity scenarios (the default fecundity setting and the low fecundity setting). Time-dependent variables track the dynamic state of the population composition and drive-induced genetic load throughout simulations. Population metrics were derived analytically from the seedbank and demographic parameters and describe key ecological and genetic features of the modeled population. Entries marked with "–" indicate variables calculated dynamically or parameters without default values because they were systematically varied. Note that m was systematically varied in heatmaps but was set to 0 for trajectory plots exploring only b.

	Description	Default Value	Note
	Seedbank parameters		
L	Maximum seed age	10	Fixed
b	Baseline germination rate	–	Varied $[0.05, 1]$ (step 0.05); drive parameter scans & selfing: step 0.1
m	Age-dependence germination parameter	0	Varied $[0, 2]$ (step 0.1); drive parameter scans & selfing: step 0.2
d	Baseline survival rate	1.0	Fixed
q	Age-dependence survival parameter	0.1	Fixed
	Demographic parameters		
K	Carrying capacity	10000	Fixed
n_{bo}	Baseline mean effective ovule count per female	60	20 for low fecundity setting
n_{bp}	Baseline mean effective pollen count per male at wild-type equilibrium	180	60 for low fecundity setting
	Time-dependent variables		
$N_{\text{sdl}}(t)$	Number of seedlings at time t	–	
$N_f(t)$	Number of fertile female plants at time t		
$N_m(t)$	Number of fertile male plants at time t		
$N_p^{\text{tot}}(t)$	Total number of effective pollen grains at time t		
$n_p(t)$	Mean number of effective pollen grains per male at time t		$n_p(t) = n_{bp} \times \dfrac{N_f(t)}{K/2}$
$c(t)$	Seedling survival rate at time t		$c(t) = \min\left(\dfrac{K}{N_{\text{sdl}}(t)}, 1\right)$
$\lambda(t)$	Genetic load imposed by the drive at time t		Eq. 3
	Population metrics		
g_a	Probability of germinating at age a	–	$g_a = \dfrac{d}{a^q} \dfrac{b}{a^m} \prod_{k=1}^{a-1} \left[\dfrac{d}{k^q}\left(1 - \dfrac{b}{k^m}\right)\right]$
γ	Total germination probability		Eq. 1
τ	Average seedbank duration		Eq. 2
$n_{\min}$	Minimum number of seeds per male or female to maintain carrying capacity		$n_{\min} = 2/\gamma$
β	Low-density growth rate of the population		$\beta_m = n_{bp}\gamma/2$ (male); $\beta_f = n_{bo}\gamma/2$ (female)
λ^*	Required genetic load to eliminate the population		Eq. 4

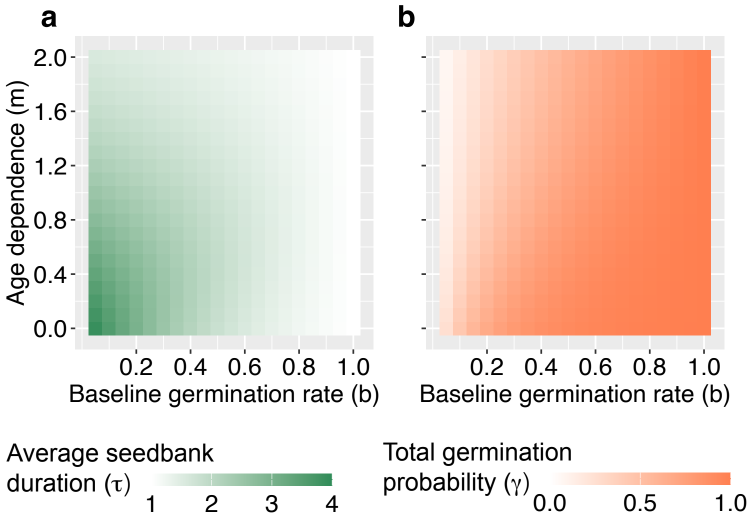
Supplementary Table 3 | Additional parameters used in the hermaphrodite model or the seed release. Variables are listed along with their default values (where applicable) and the range explored. Variables repeated from Supplementary Table 2 are included when their definitions differ in the model specified by the sub-table. Entries marked with "–" denote variables computed from other parameters or ones systematically varied (no default). Note that the seed release was performed only in the dioecious model; the hermaphrodite model used a plant release, not a seed release. All other parameters for these models appear in Supplementary Table 1 or 2.

	Description	Default Value	Note
Hermaphrodite model			
σ	Selfing rate	–	Modification: varied $[0, 1.0]$ (step 0.05); Suppression: varied $\{0, 0.03, 0.05, 0.08, 0.1\}$
n_{bo}	Baseline mean ovule count per individual	30	
n_{bp}	Baseline mean pollen count per individual	90	
$N_{\text{recv}}(t)$	Number of individuals capable of receiving pollen at time t	–	
$N_{\text{self}}(t)$	Number of individuals capable of selfing at time t	–	
$n_{\min}$	Minimum number of seeds per individual to maintain carrying capacity	–	$n_{\min} = 1/\gamma$
β_m	Low-density growth rate for male suppression drives	–	Eq. 5
β_f	Low-density growth rate for female suppression drives	–	Eq. 6
λ_m^*	Required genetic load for male suppression drives to eliminate the population	–	Eq. 7
λ_f^*	Required genetic load for female suppression drives to eliminate the population	–	Eq. 8
Seed release			
p_s	Drive introduction frequency in age-0 seeds	0.1	Threshold-dependent drives: varied, $[0, 0.96]$ (step 0.02)
S	Expected seed output each year	–	$S = n_{bo} \times \frac{K}{2}$
S_d	Expected number of drive-carrying age-0 seeds in a seed drop	–	Eq. 9 (drive heterozygote drop); Eq. 10 (drive homozygote drop)
S_0	Expected total number of age-0 seeds during drive release year	–	$S_0 = S + S_d$ (seed drop); $S_0 = S$ (seed replacement)
p_0	Expected initial drive frequency in plants after seed release	–	Eq. 11 (seed drop); Eq. 12 (seed replacement)

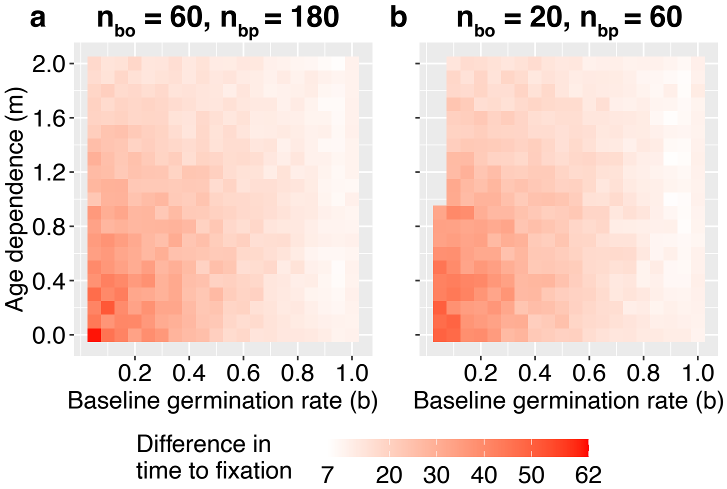
Supplementary Figures



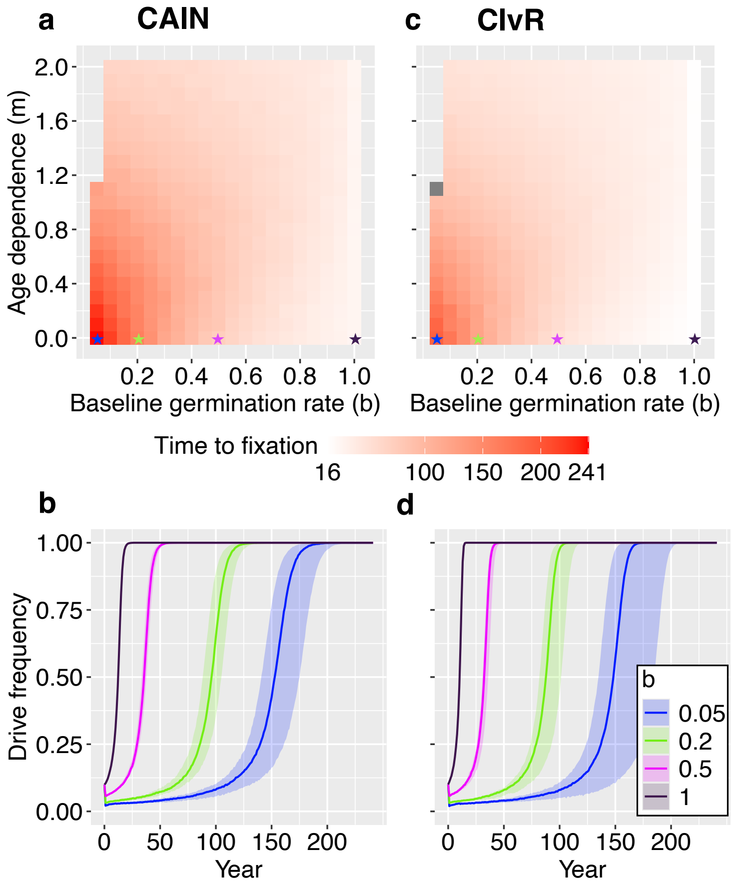
Supplementary Fig. 1 | Frequency trajectories of CAIN and ClvR modification drives in plants and seeds. **a,** Frequency trajectories of the CAIN drive in plants under four baseline germination rates (*b*), with other parameters set to default values (Supplementary Table 2). Solid lines represent median trajectories, and shaded regions indicate the observed range (minimum–maximum) across 10 replicates. **b,** Same as **a** but in seeds. **c–d,** Same as **a–b** but for ClvR drives.



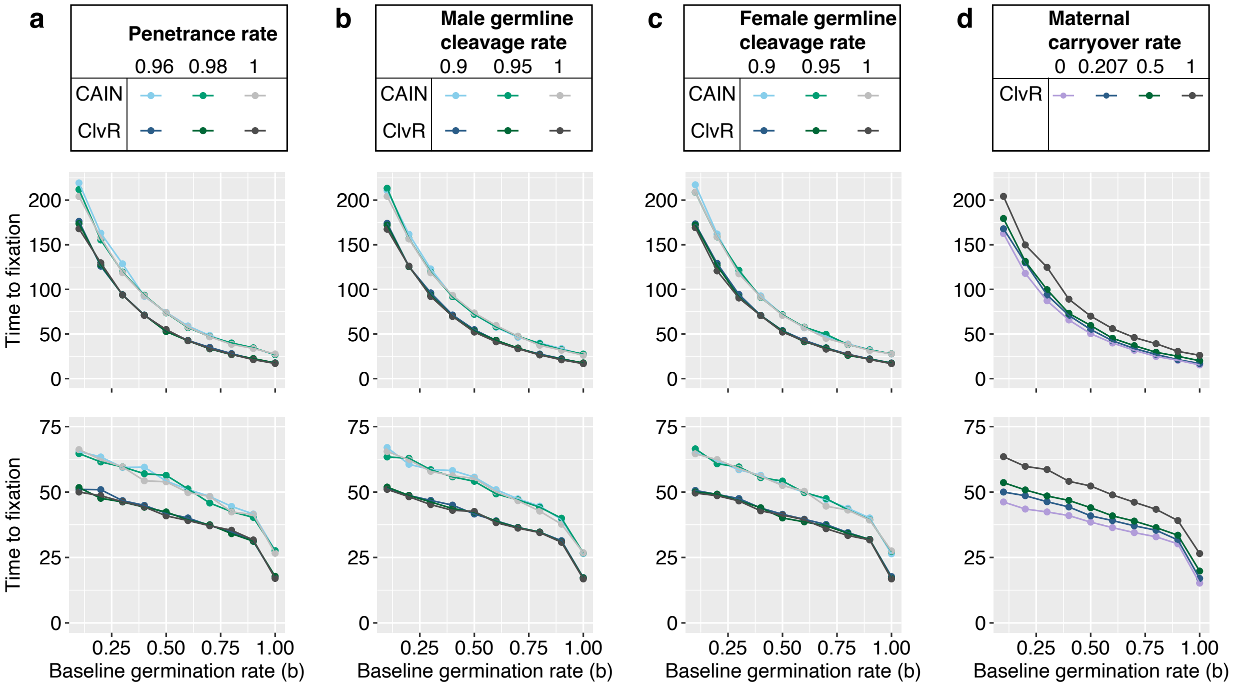
Supplementary Fig. 2 | Average seedbank duration and total germination probability. a, Average seedbank duration (τ; Eq. 2) across varying baseline germination rates (b) and age-dependent germination parameters (m). **b,** Total germination probability (γ; Eq. 1) across varying baseline germination rates (b) and age-dependent germination parameters (m). All other parameters were set to default values (Supplementary Table 2).



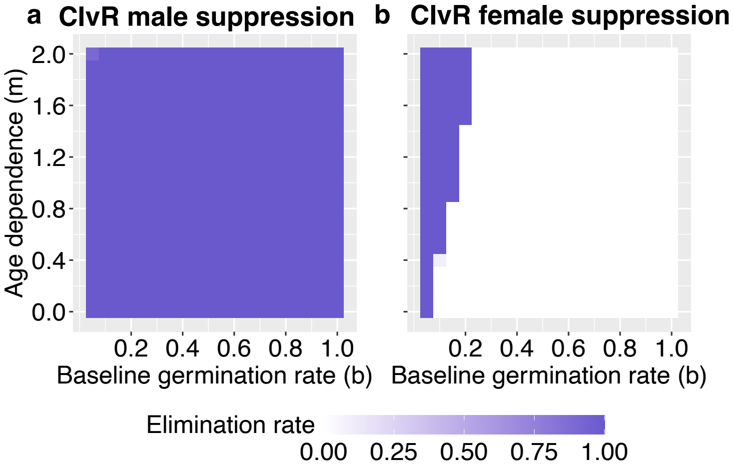
Supplementary Fig. 3 | The difference in fixation time for CAIN and ClvR modification drives. a, Difference between the average fixation time of CAIN and that of ClvR (across 10 replicates), calculated as CAIN minus ClvR, under varying baseline germination rates (b) and age-dependent germination parameters (m). All other parameters were set to their default values in Supplementary Table 2. Fixation is defined as reaching a 100% drive frequency in both plants and seeds. **b,** Same as **a** but under reduced fecundity conditions, where wild-type females at equilibrium produce an average of 20 effective ovules (n_{bo}) and wild-type males produce an average of 60 effective pollen grains (n_{bp}). Results in the upper-left region of **b** are omitted because low total germination probability (γ) and seed production lead to an insufficient number of germinated seeds within this parameter space, resulting in population collapse. For fixation times of CAIN and ClvR across this parameter range, see Supplementary Fig. 4.



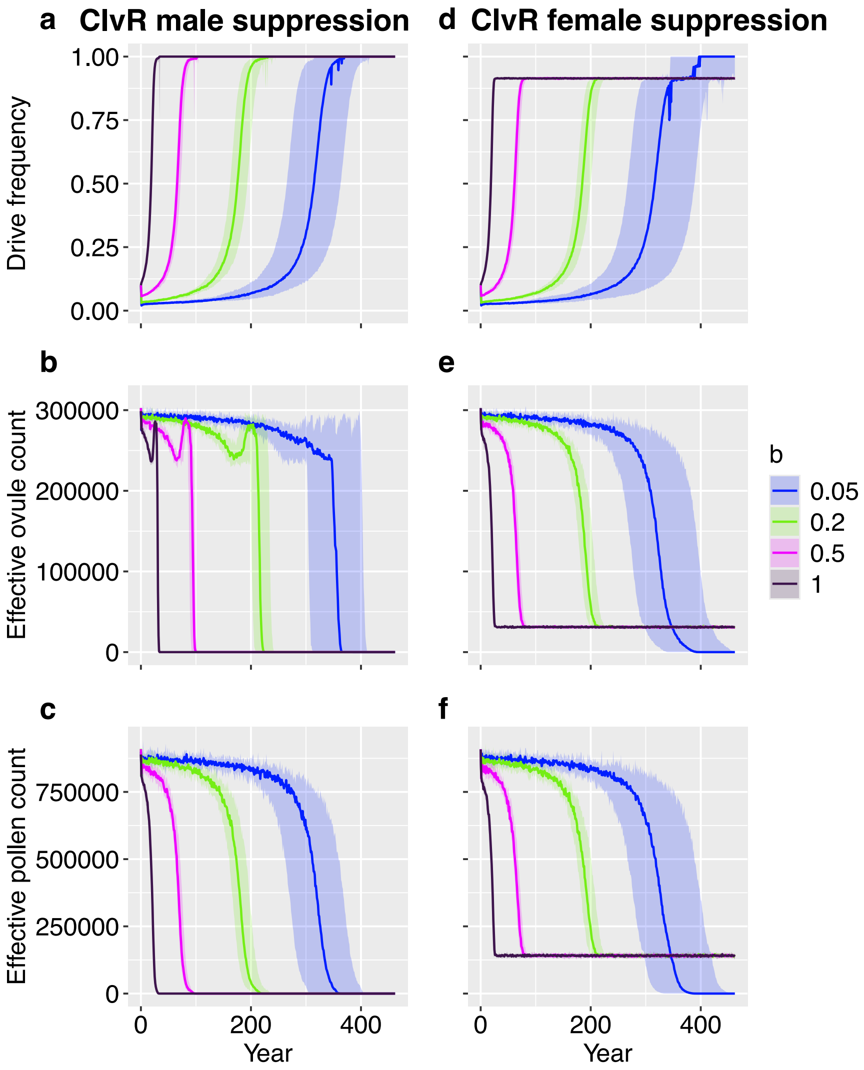
Supplementary Fig. 4 | Spread of CAIN and ClvR modification drives under varying seedbank parameters with reduced fecundity. Figure design follows Fig. 3, except with reduced fecundity: at wild-type equilibrium, females produce an average of 20 effective ovules (n_{bo}) and males produce an average of 60 effective pollen grains (n_{bp}). Results in the upper-left regions of panels **a** and **c** are omitted because low total germination probabilities (γ) combined with reduced seed production lead to an insufficient number of germinated seeds, resulting in population collapse before drive introduction.



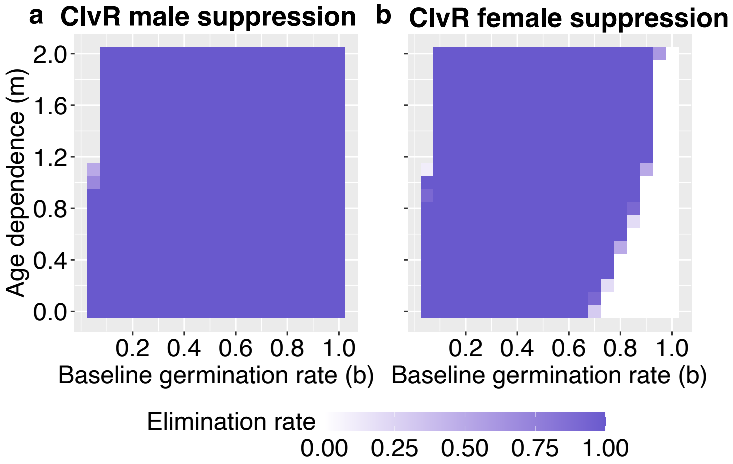
Supplementary Fig. 5 | Effect of drive performance parameters on the speed of CAIN and ClvR modification drives. Each column represents a different drive parameter varied across a range of baseline germination rates (b). Top panels show no age-dependent decline in germination rates ($m = 0$), and bottom panels show strong age-dependent decline in germination rates ($m = 2$). Points are colored by drive (lighter, CAIN; darker, ClvR) and by parameter level and represent the average time to fixation for each parameter combination across 10 replicates. Both drives reached fixation across all combinations tested. **a,** Effect of target gene penetrance rate, varied from 0.96 to 1. **b,** Effect of male germline cleavage rate, varied from 0.9 to 1. **c,** Effect of female germline cleavage rate, varied from 0.9 to 1. **d,** Effect of maternal carryover rescue rate (ClvR drive only), varied from 0 to 1.



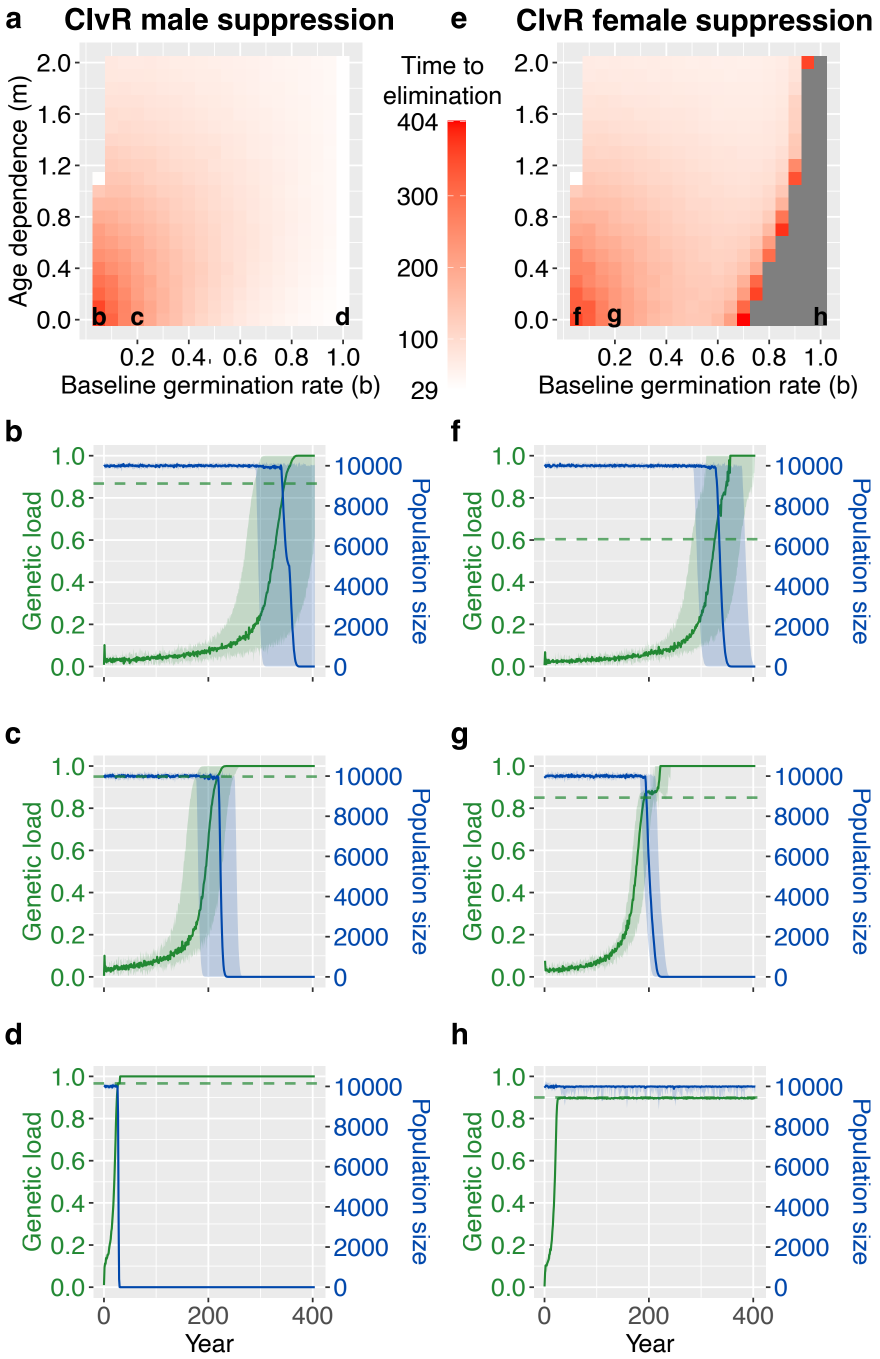
Supplementary Fig. 6 | Population elimination rate of ClvR suppression drives. a, Fraction of replicates (out of 10) in which the ClvR male suppression drive successfully eliminated the population, across varying baseline germination rates (b) and age-dependence germination parameters (m). All other parameters were kept at their default values (Supplementary Table 2). **b,** Same as **a** but for the ClvR female suppression drive.



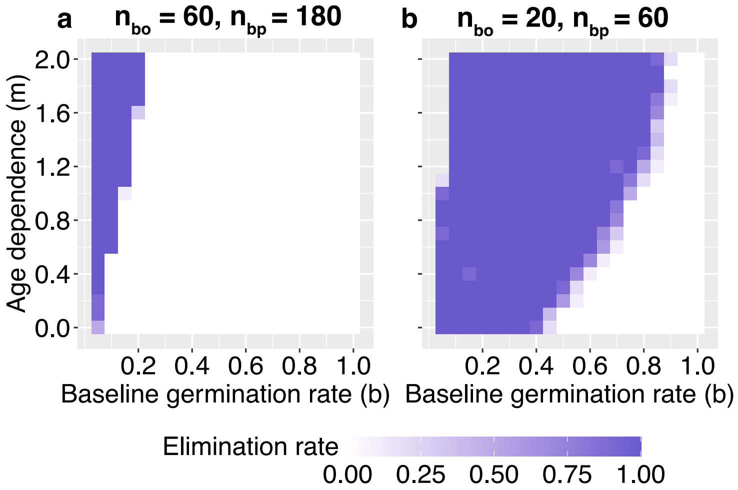
Supplementary Fig. 7 | Trajectories of drive frequency and effective gamete counts for ClvR suppression drives. a, Trajectory of the ClvR male suppression drive frequency in plants under four different baseline germination rates (*b*), with all other parameters set to their default values (Supplementary Table 2). Solid lines represent median trajectories, and shaded regions correspond to the observed range (minimum–maximum) across 10 replicates. **b,** Same as **a** but showing the total number of effective ovules in the population. **c,** Same as **a** but showing the total number of effective pollen grains in the population. **d–f,** Same as **a–c** but for the ClvR female suppression drive.



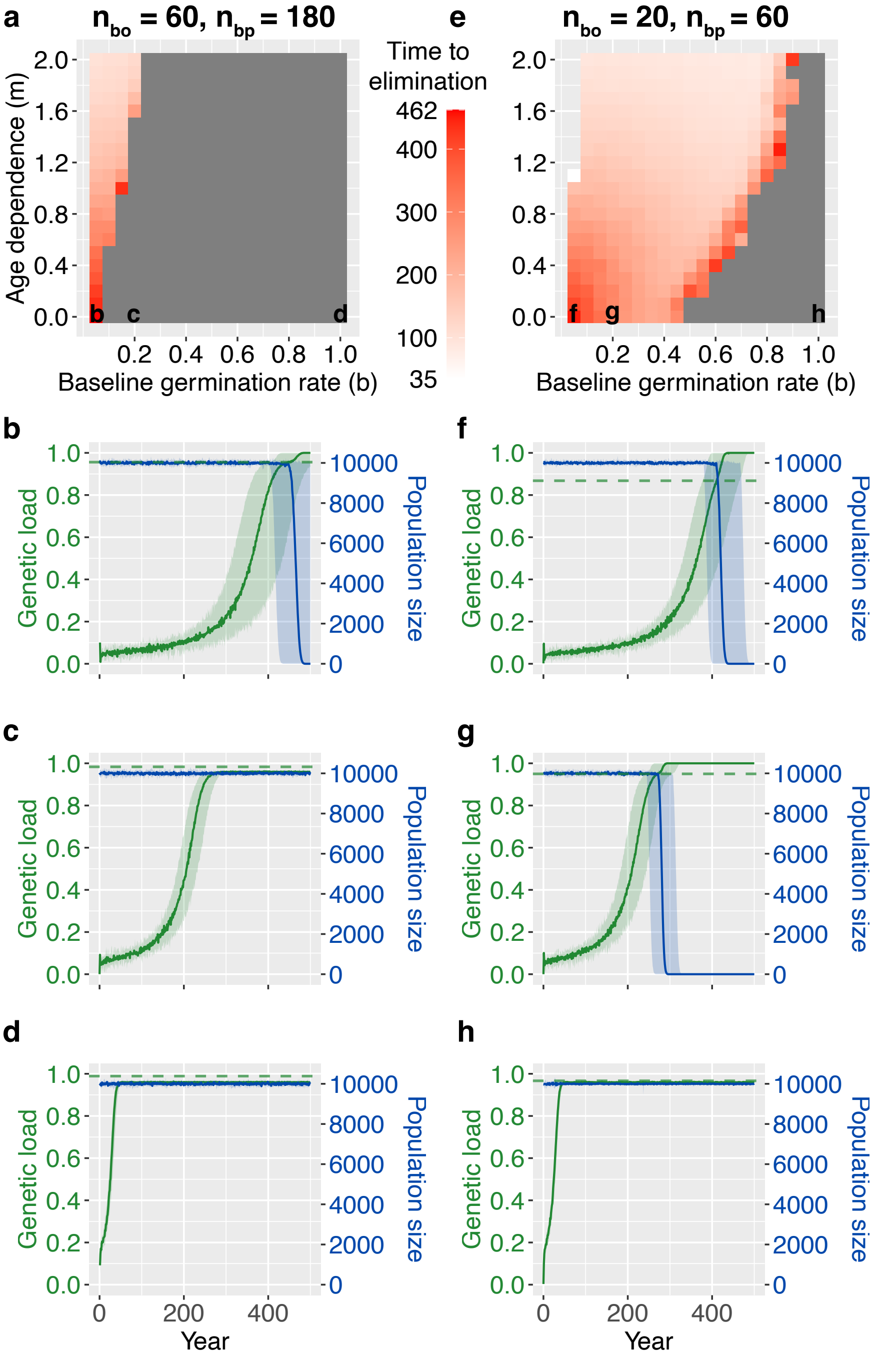
Supplementary Fig. 8 | Population elimination rate of ClvR suppression drives under reduced fecundity. **a,** ClvR male suppression. **b,** ClvR female suppression. Figure design follows Supplementary Fig. 6 but with reduced population fecundity: females produce an average of 20 effective ovules (n_{bo}), and males produce an average of 60 effective pollen grains at wild-type equilibrium (n_{bp}). Results in the upper-left regions of the heatmaps are omitted because, within this parameter space, total germination probability (γ) and seed production are insufficient to maintain the population.



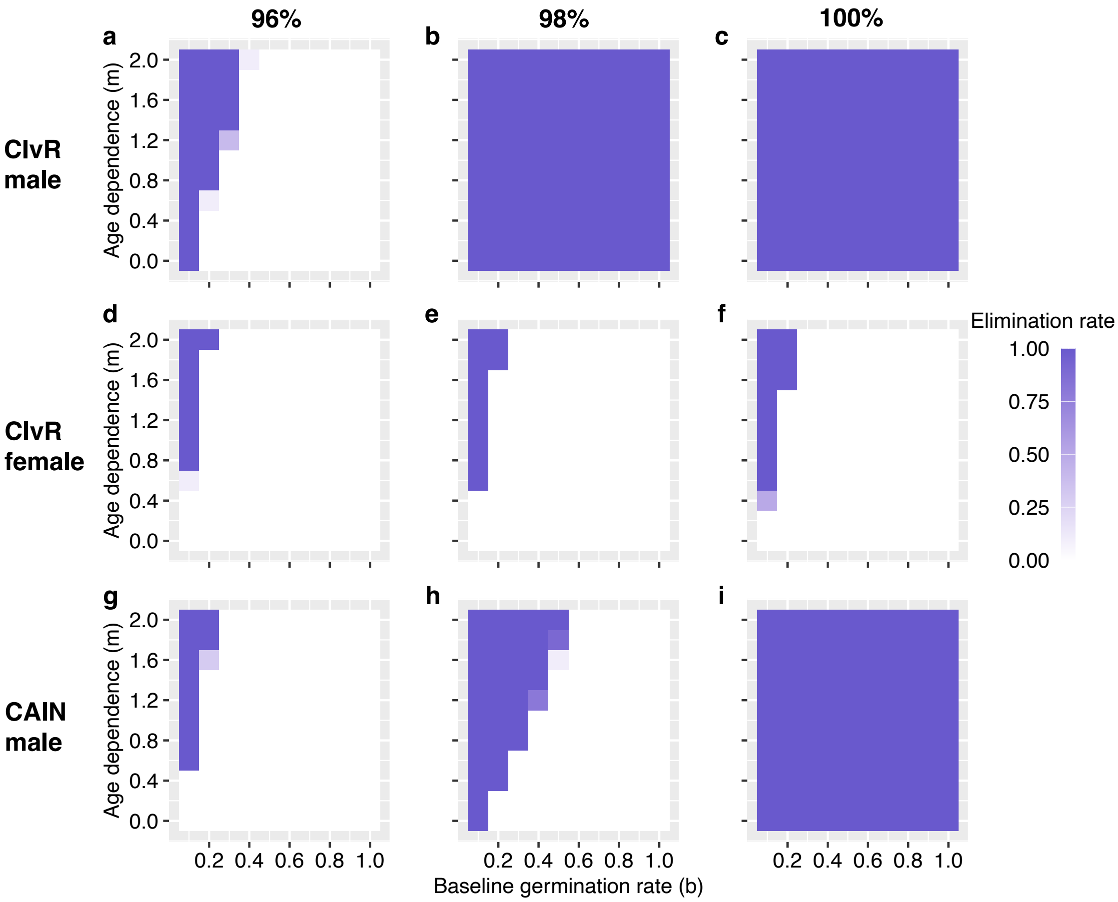
Supplementary Fig. 9 | Dynamics of ClvR suppression drives under varying seedbank parameters and with reduced population fecundity. Figure design follows Fig. 5, except population fecundity was reduced so that wild-type females at equilibrium produce an average of 20 effective ovules (n_{bo}), and males produce an average of 60 effective pollen grains (n_{bp}). Results in the upper-left regions of panels **a** and **e** are omitted because the combination of low total germination probability (γ) and low seed production in this range results in an insufficient number of germinated seeds, leading to population collapse before drive introduction.



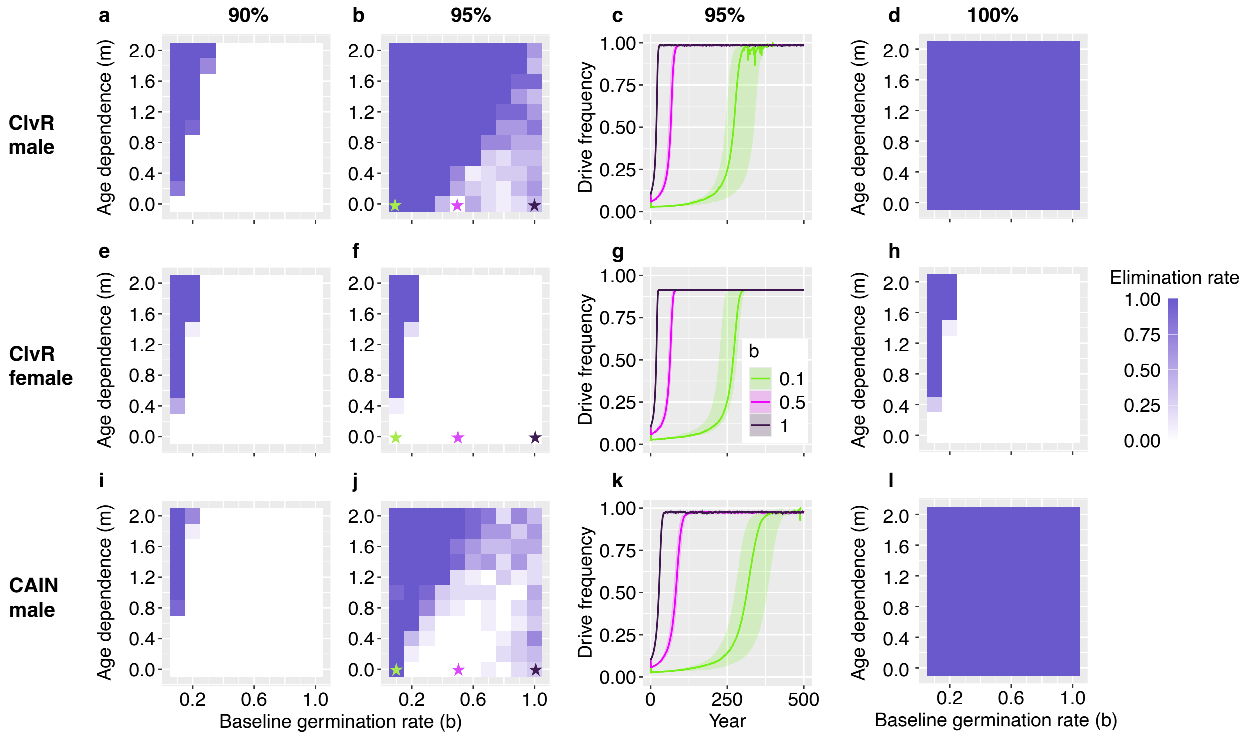
Supplementary Fig. 10 | Population elimination rate of CAIN male suppression under different population fecundity regimes. Figure design follows Supplementary Fig. 6, except here, only CAIN male suppression drive is considered under varying population fecundity. **a,** Elimination rates under the default fecundity, where wild-type individuals produce 60 effective ovules per female (n_{bo}) and 180 effective pollen grains per male at equilibrium (n_{bp}). **b,** As in **a**, but with low fecundity: 20 effective ovules per female and 60 effective pollen grains per male. Blank cells in the upper-left region of **b** indicate scenarios in which low total germination probability (γ), combined with reduced seed production, caused population collapse before drive introduction.



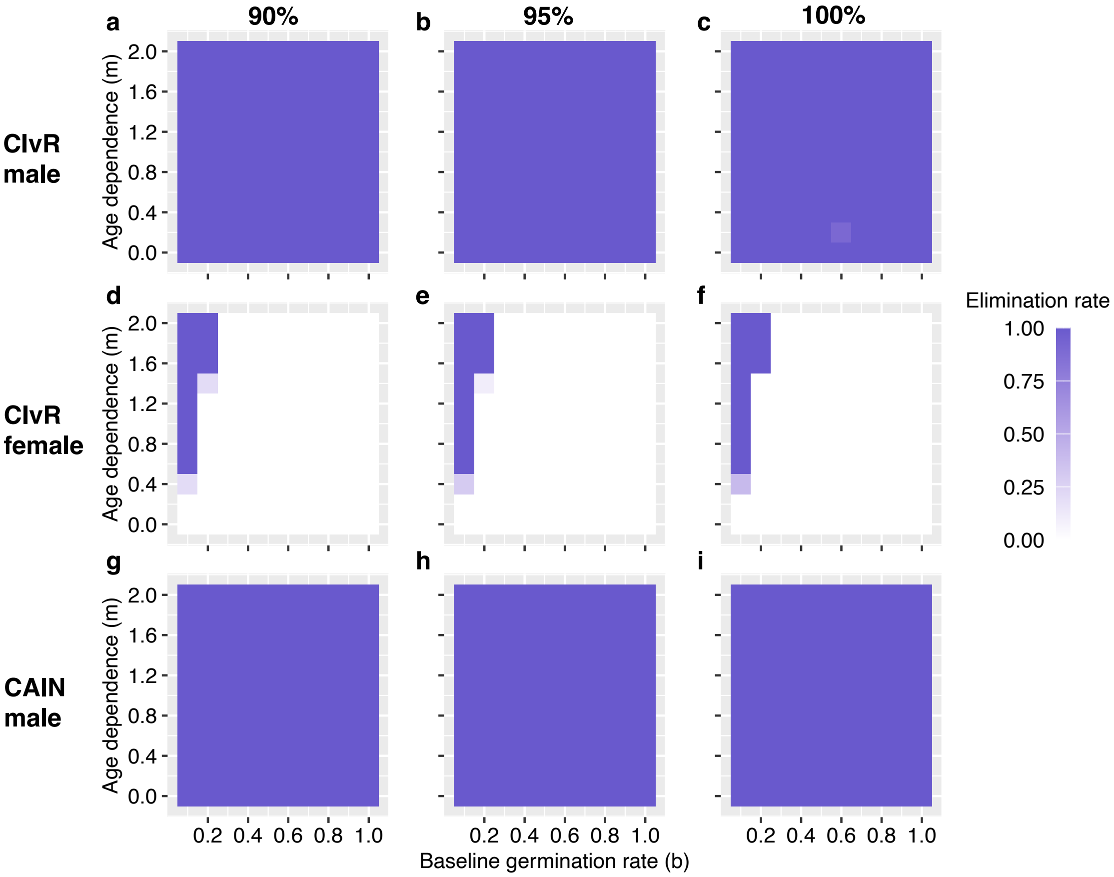
Supplementary Fig. 11 | Dynamics of CAIN male suppression drives under varying seedbank parameters and population fecundity regimes. Figure design follows Fig. 5, except in this figure, only CAIN male suppression is considered under varying fecundity. **a,** Mean time to elimination for CAIN male suppression at default fecundity (wild-type equilibrium: $n_{bo} = 60$ effective ovules per female and $n_{bp} = 180$ effective pollen grains per male), computed over replicates in which elimination occurred. **b–d,** Genetic load imposed by the drive and resulting population size over time at default fecundity, with $m = 0$ and $b = 0.05, 0.2, 1,$ respectively. **e,** As in **a**, but at low fecundity (wild-type equilibrium: $n_{bo} = 20$ effective ovules per female and $n_{bp} = 60$ effective pollen grains per male). Blank cells in the upper-left arise when low total germination probability (γ) and reduced seed production cause population collapse before drive introduction. **f–h,** As in **b–d**, but at low fecundity.



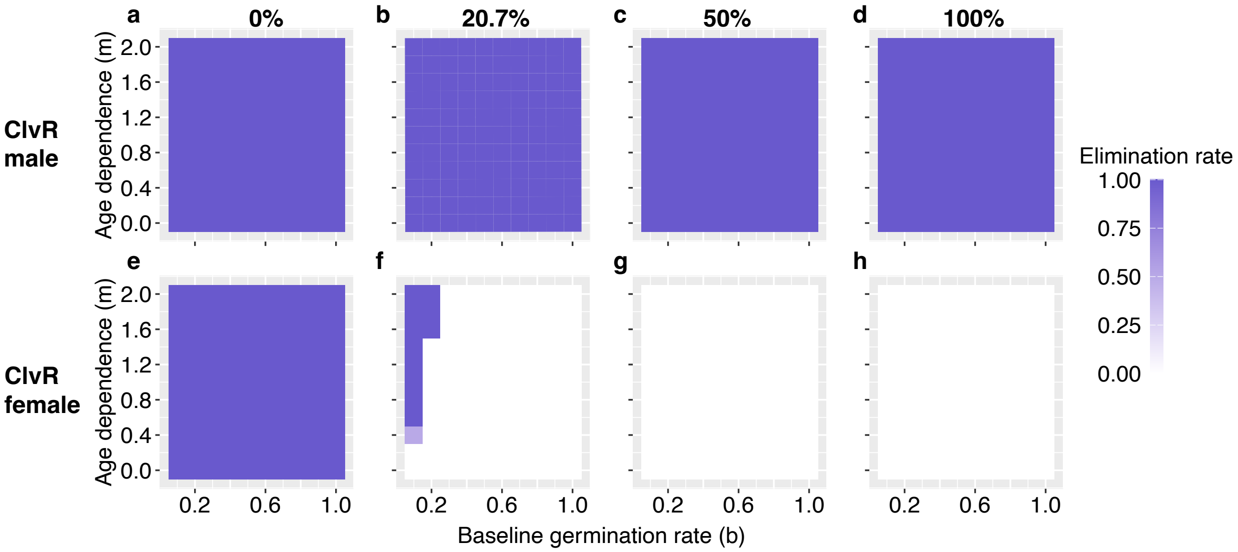
Supplementary Fig. 12 | Impact of target gene penetrance rate on the success of ClvR and CAIN suppression drives. The target gene penetrance rate was varied from 96% to 100%, while holding the male and female germline cleavage rates at 97% and the maternal carryover rate of the ClvR drive at 20.7%. Each panel shows the fraction of replicates (out of 10 total) resulting in population elimination across a range of baseline germination rates (b) and age dependence in germination rates (m). **a–c,** ClvR male suppression: elimination rate at 96%, 98%, and 100% target gene penetrance, respectively. **d–f,** ClvR female suppression: as in **a–c**. **g–i,** CAIN male suppression: as in **a–c**.



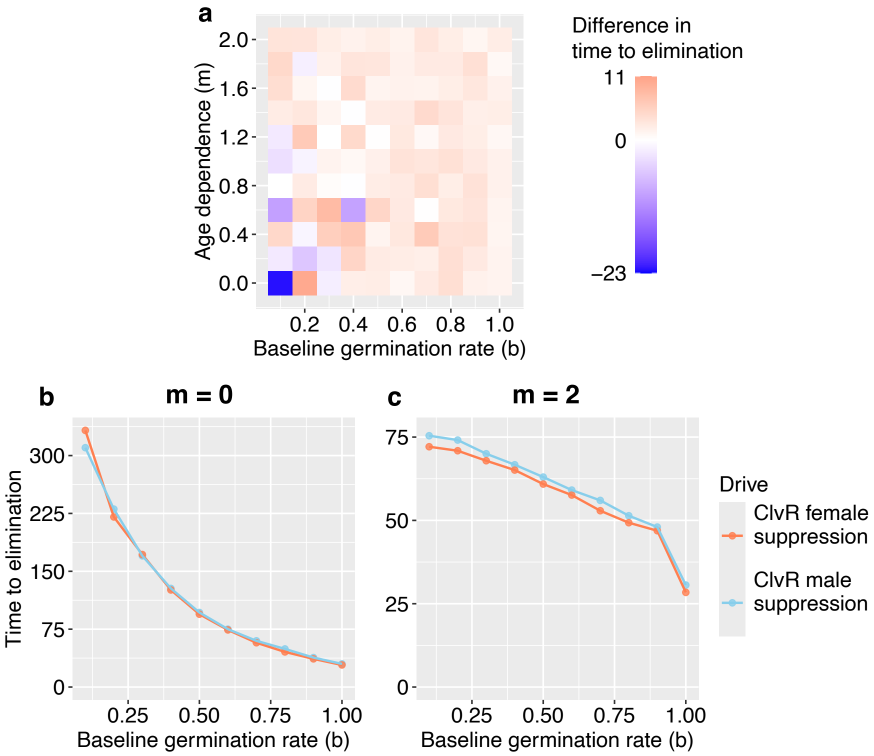
Supplementary Fig. 13 | Impact of the male germline cleavage rate on the success of ClvR and CAIN suppression drives. The male germline cleavage rate was varied from 90% to 100%, while holding the female germline cleavage rate at 97%, the target gene penetrance rate at 100%, and the maternal carryover rate of the ClvR drive at 20.7%. Each panel shows the fraction of replicates (out of 10 total) resulting in population elimination across a range of baseline germination rates (b) and age dependence in germination rates (m). **a–b,** Population elimination rate of the ClvR male suppression drive at 90% and 95% male germline cleavage rate, respectively. **c,** Median drive frequency trajectory for the ClvR male suppression drive with a male germline cleavage rate of 95%, no age-dependence in germination ($m = 0$), and $b \in \{0.1, 0.5, 1\}$ (colors match the starred cells in **b**). **d,** The ClvR male suppression drive's rate of population elimination at 100% male germline cleavage rate. **e–h,** As in **a–d**, for ClvR female suppression. **i–l,** As in **a–d**, for CAIN male suppression.



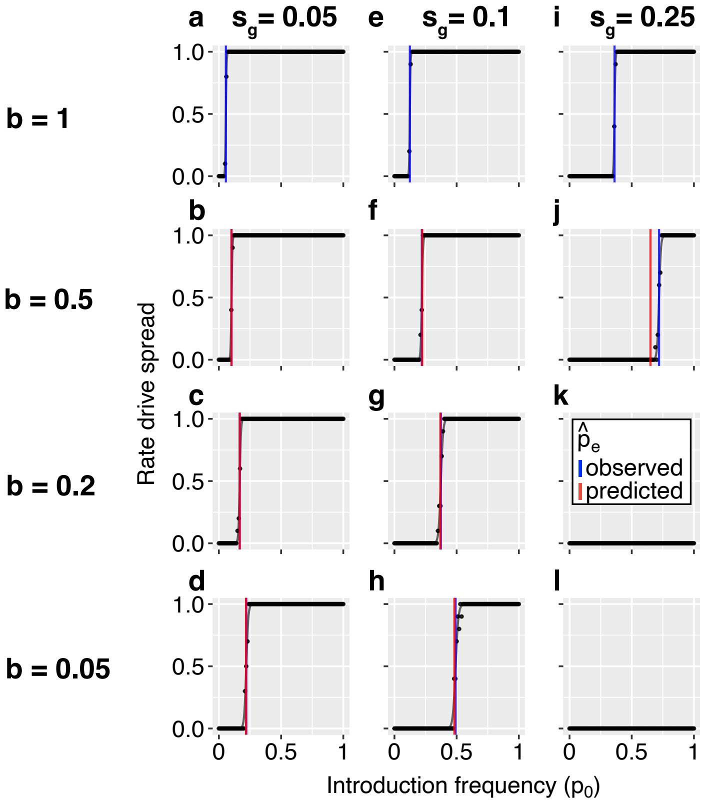
Supplementary Fig. 14 | Impact of the female germline cleavage rate on the success of ClvR and CAIN suppression drives. Figure design follows Supplementary Fig. 12, except the female germline cleavage rate was varied across 90%, 95%, and 100%, while holding the male germline cleavage rate at 97%, the target gene penetrance rate at 100%, and the maternal carryover rate of the ClvR drive at 20.7%.



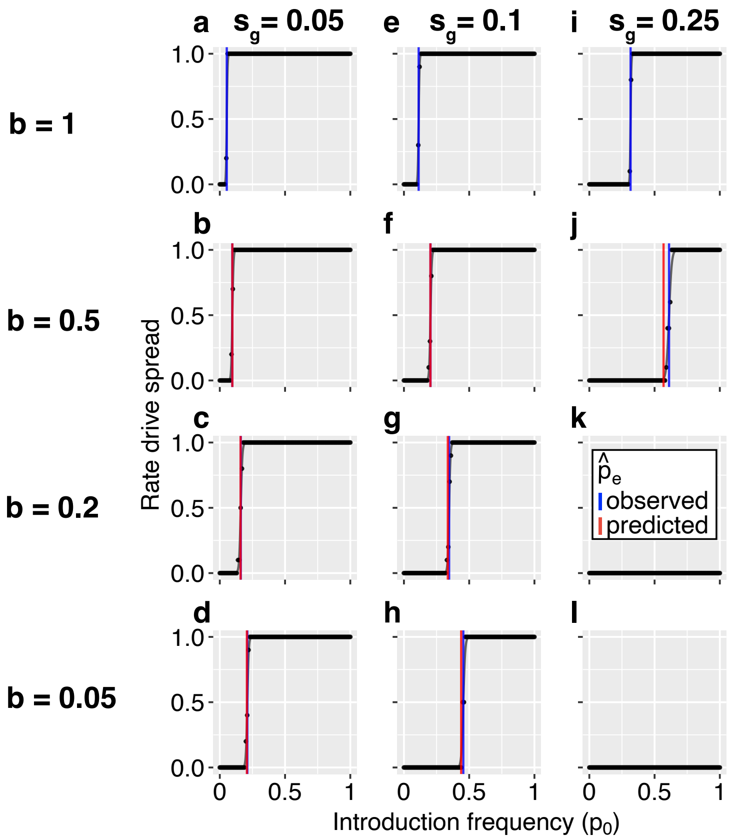
Supplementary Fig. 15 | Impact of the maternal carryover rate on the success of ClvR suppression drives. Figure design follows Supplementary Fig. 12, except the maternal carryover rate for ClvR male and female suppression drives was varied across 0%, 20.7%, 50%, and 100%, while holding target gene penetrance rate at 100% and male and female germline cleavage rates at 97%.



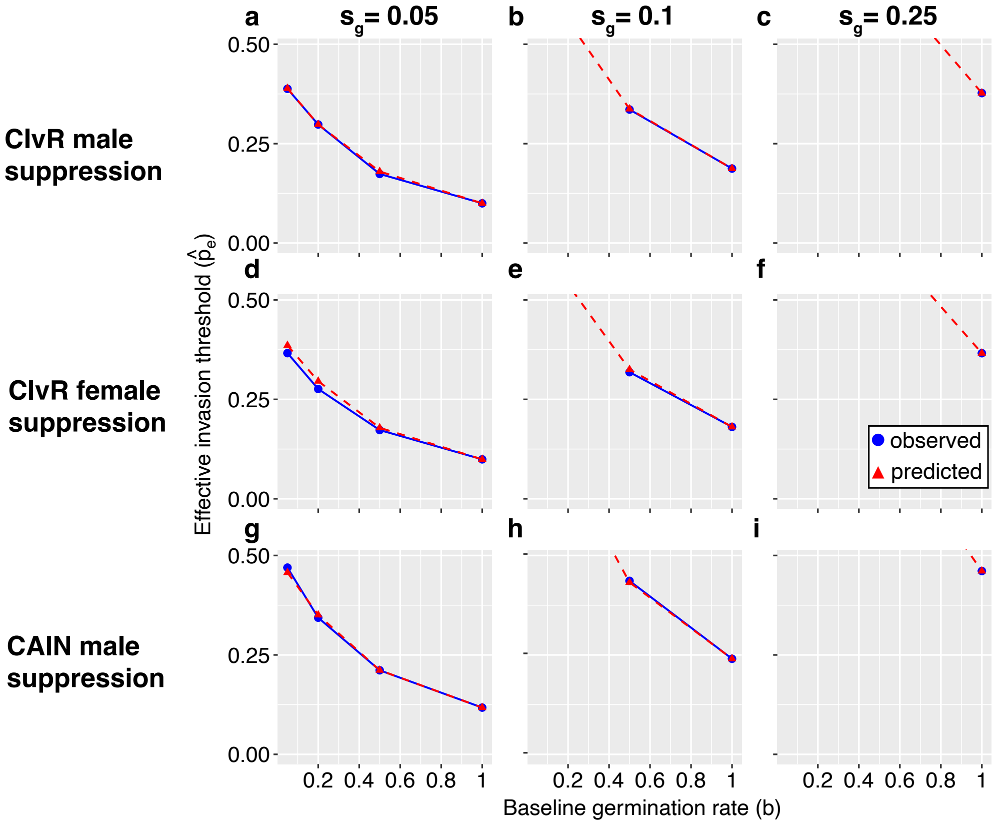
Supplementary Fig. 16 | The spread of ClvR male versus female suppression drives when maternal carryover is eliminated. a, With maternal carryover set to 0, both drives eliminated the population across all baseline germination rates (b) and age-dependence parameters (m) tested (Supplementary Fig. 15a,e). Panel **a** shows the difference in average time to elimination (ClvR male suppression minus ClvR female suppression). **b,** Average time to population elimination for both suppression drives across all b with $m = 0$ (no age-dependent decline; bottom row of **a**). **c,** As in **b** with $m = 2$ (strong age-dependent decline; top row of **a**).



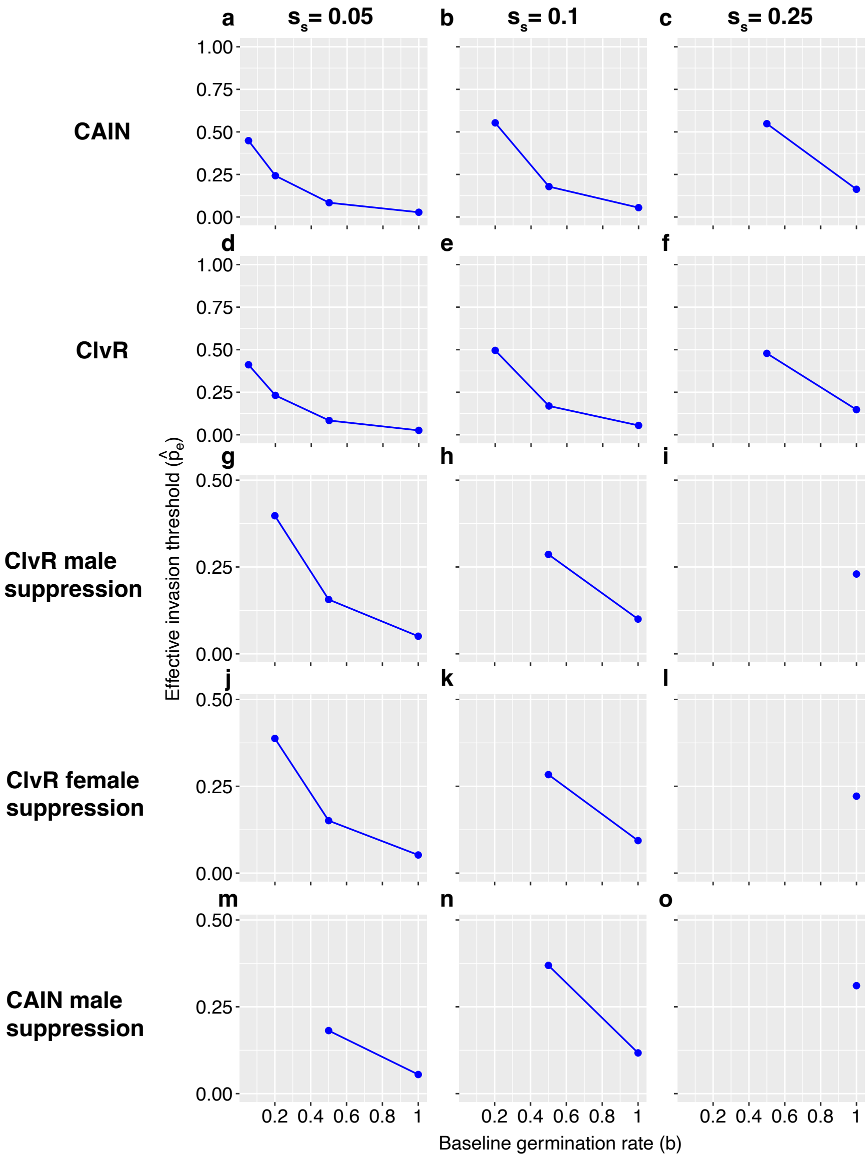
Supplementary Fig. 17 | Invasion ability of the CAIN modification drive under varying gamete viability fitness costs and baseline germination rates. For a given baseline germination rate (b) and drive fitness cost reducing gamete viability (s_g, defined as the probability that a drive-carrying gamete is nonviable), the drive was introduced by replacing a fraction p_0 of plants with drive homozygotes. All other parameters were kept at their default values (Supplementary Table 2). Each point represents the fraction of replicates (out of 10 total) in which CAIN spread successfully from a given introduction frequency (p_0). Drive spread is defined as reaching a final drive frequency that exceeds p_0. Logistic curves (blue) were fit to replicate outcomes using the `drc` R package [3], with the effective invasion threshold (blue vertical line) corresponding to the introduction frequency at which CAIN spreads in 50% of replicates (i.e., where the logistic curve intersects with $y = 0.5$). Predicted effective invasion thresholds (red vertical line) were calculated as $\hat{p}_e \approx \hat{p} \times \tau$; values exceeding 1 are not shown. **a–d,** $s_g = 0.05$ and $b = 0.05, 0.2, 0.5, 1$. **e–h,** $s_g = 0.1$ and $b = 0.05, 0.2, 0.5, 1$. **i–l,** $s_g = 0.25$ and $b = 0.05, 0.2, 0.5, 1$.



Supplementary Fig. 18 | Invasion ability of the ClvR modification drive under varying gamete viability fitness costs and baseline germination rates. Figure design follows Supplementary Fig. 17 but shows results for the ClvR drive.



Supplementary Fig. 19 | Effective invasion thresholds of CAIN and ClvR suppression drives under gamete viability fitness costs. Figure design follows Fig. 6, except results are shown for suppression drives. For male suppression drives (ClvR in **a–c**, CAIN in **g–i**), the drive was introduced by replacing a fraction p_0 of female plants with drive homozygotes, as male homozygotes for these drives are sterile. Conversely, for the ClvR female suppression drive (**d–f**), the drive was introduced by replacing a fraction p_0 of male plants with drive homozygotes, as female homozygotes for this drive are sterile. Given an equal sex ratio, the maximum drive introduction frequency was 0.5. Absence of a point at $b = 0.05, 0.2, 0.5$, or 1 indicates either drive failure to spread (if blue) or a predicted effective invasion threshold exceeding 0.5 (if red).



Supplementary Fig. 20 | Effective invasion thresholds of CAIN and ClvR modification and suppression drives under seed survival fitness costs. Baseline germination rate (b) and drive fitness cost on seed survival (s_s) were varied, with all other parameters set to default values (Supplementary Table 2). The fitness cost s_s acts to reduce the baseline survival rate (d) of drive-carrying seeds and is assumed to be codominant, such that drive-homozygous seeds have a baseline survival rate $d - s_s$ and drive-heterozygous seeds have a baseline survival rate $d - s_s/2$. Blue points show the observed effective invasion threshold, defined as the minimum introduction frequency above which the drive spreads in more than 50% of replicates (out of 10 replicates total), based on the same logistic fitting protocol as shown in Supplementary Fig. 17. For modification drives (**a–f**), the drive was introduced by replacing a fraction of plants with drive homozygotes. For male suppression drives (**g–i and m–o**), drive releases were female-specific, since males homozygous for this drive are sterile. Conversely, for the ClvR female suppression drive (**j–l**), drive releases were male-specific, since female homozygous for this drive are sterile. Given sex-specific releases and an equal sex ratio, the maximum introduction frequency was 50% for suppression drives, compared to 100% for modification drives. **a–c,** CAIN: observed effective invasion thresholds at $s_s \in \{0.05, 0.1, 0.25\}$ and $b \in \{0.05, 0.2, 0.5, 1\}$. Absence of a point at a given b indicates consistent failure to spread. **d–f,** ClvR: same settings as **a–c**. **g–i,** ClvR male suppression: same settings as **a–c**. **j–l,** ClvR female suppression: same settings as **a–c**. **m–o,** CAIN male suppression: same settings as **a–c**.

References

1. Liu Y, Jiao B, Champer J, Qian W, 2024. Overriding Mendelian inheritance in *Arabidopsis* with a CRISPR toxin–antidote gene drive that impairs pollen germination. *Nature Plants*, 10(6):910–922.

2. Oberhofer G, Johnson ML, Ivy T, Antoshechkin I, Hay BA, 2024. *Cleave and Rescue* gamete killers create conditions for gene drive in plants. *Nature Plants*, 10(6):936–953.

3. Ritz C, Baty F, Streibig JC, Gerhard D, 2015. Dose-response analysis using R. *PLOS One*, 10(12):e0146021.