

Demographic feedbacks can hamper the spatial spread of a gene drive

Léo Girardin¹ & Florence Débarre²



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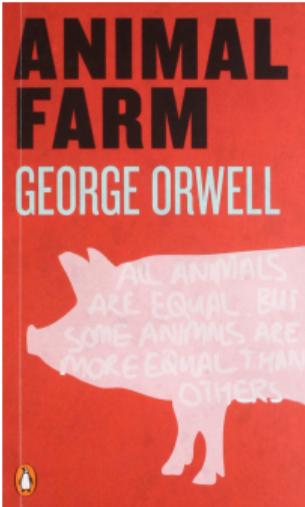


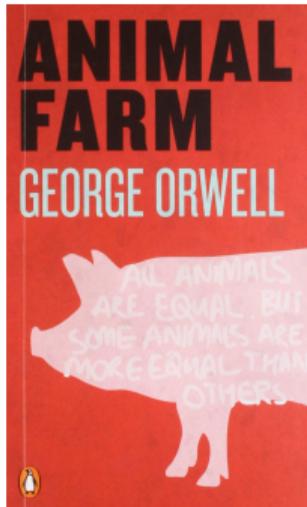
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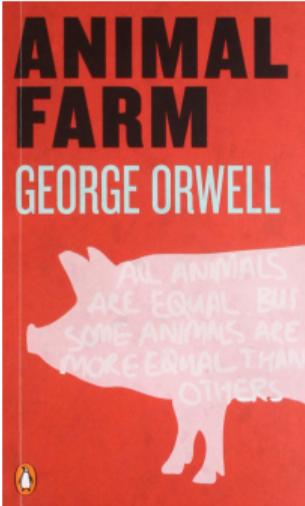
Voir <https://arxiv.org/abs/2101.11255>
pour plus de détails !

MMB

January 2021



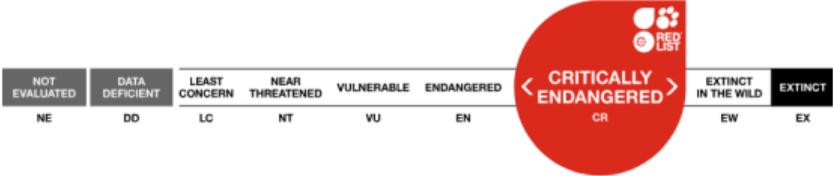




All animals are equal...



(c) Andrew Suryono, Natl Geographic



(c) IUCN

Some animals are less equal than others



(c) J. Gathany/CDC



(c) Penarc, Wikipedia



(c) J. Gathany, CDC



(c) pestworld.org



(c) C. J. Sharp, Wikimedia



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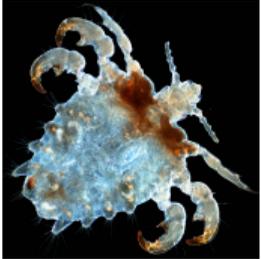
(c) Benjamint444, Wikimedia



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Pest control

Mechanical, Physical



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Chemical



(c) USDA, Wikimedia

Biological



(c) Fishbase

Pest control

Mechanical, Physical



Chemical



Biological



Genetic

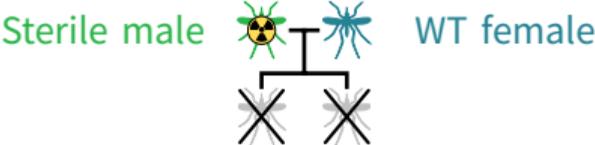


“Dissemination, by mating or inheritance, of factors that reduce pest damage”

Alphey 2014, *Ann. Rev. Entomo.*

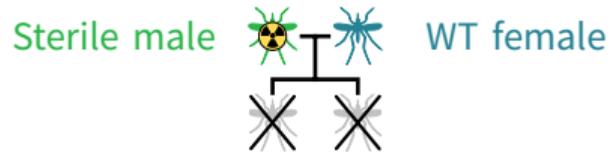
Genetic control of populations

Sterile Insect Technique

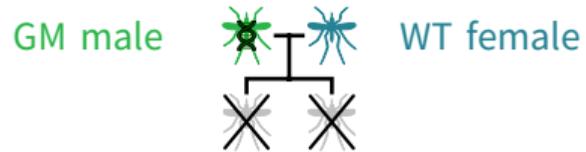


Genetic control of populations

Sterile Insect Technique

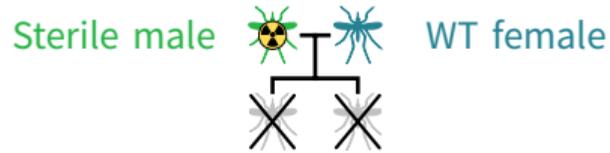


Sterile Insect Technique 2.0

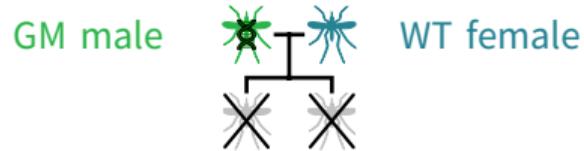


Genetic control of populations

Sterile Insect Technique



Sterile Insect Technique 2.0



Plan to release genetically modified mosquitoes in Florida gets go-ahead

- 750m insects to be released with second trial planned for Texas
- Critics say risks of 'Jurassic Park experiment' not assessed

Oliver Milman in New York

✉ @olliemilman

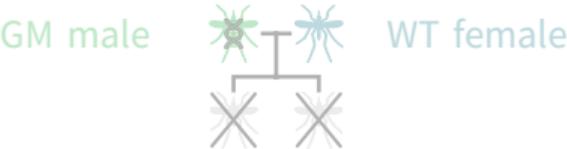
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Genetic control of populations

Sterile Insect Technique



Sterile Insect Technique 2.0

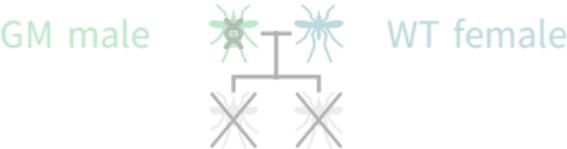


Genetic control of populations

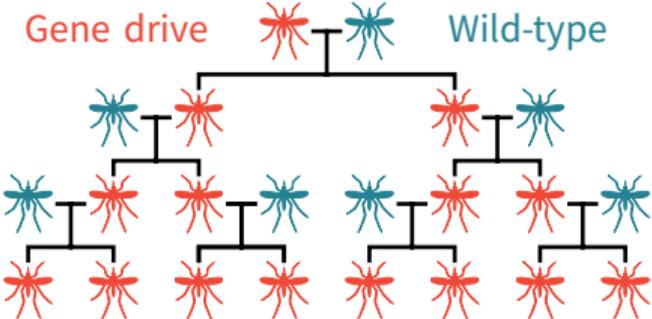
Sterile Insect Technique



Sterile Insect Technique 2.0



Gene Drive



Genetic control of populations

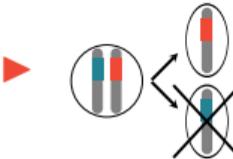
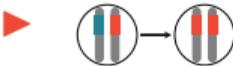
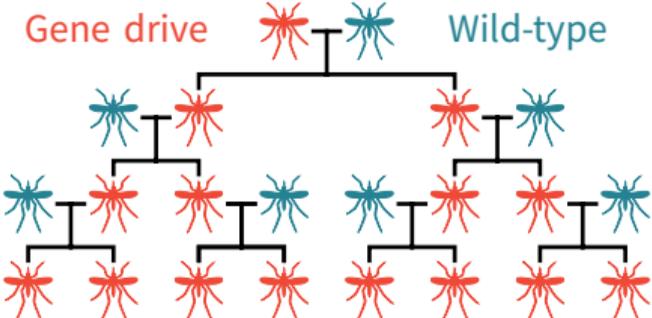
Sterile Insect Technique



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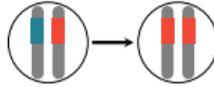


Gene Drive



Champer et al. (2016)

Homing-based gene drive



► Homing endonuclease genes (HEG)

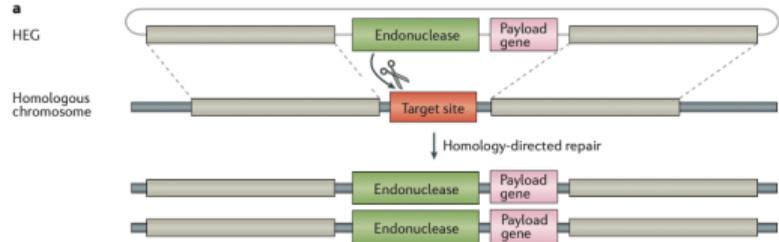


Site-specific selfish genes as tools for the control and genetic engineering of natural populations

Austin Burt

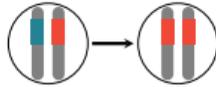
Department of Biological Sciences and Centre for Population Biology, Imperial College, Silwood Park, Ascot, Berkshire SL5 7PY, UK (a.burt@ic.ac.uk)

Received 14 October 2002
Accepted 12 December 2002
Published online 19 March 2003



(c) Champer et al. (2016)

Homing-based gene drive



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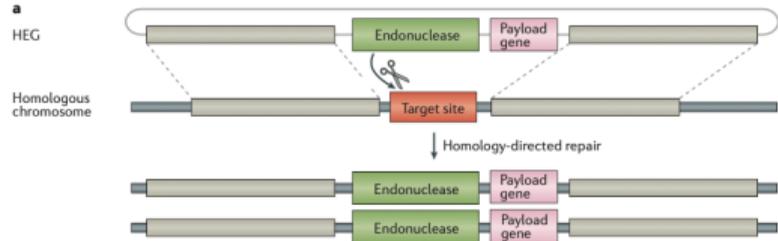


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▶ RNA-guided gene drive



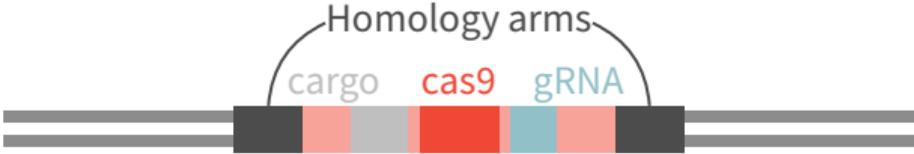
Concerning RNA-guided gene drives for the alteration of wild populations

DOI: 10.7554/eLife.03401.001

KEVIN M ESVELT*, ANDREA L SMIDLER, FLAMINIA CATTERUCCIA* AND GEORGE M CHURCH*

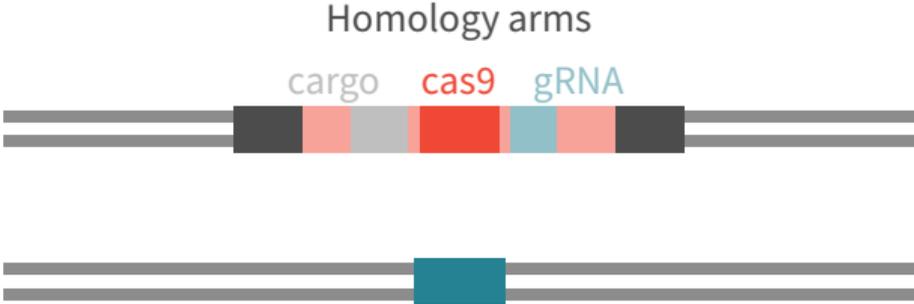
RNA-guided gene drive

Esvelt *et al.* 2014, *eLife*



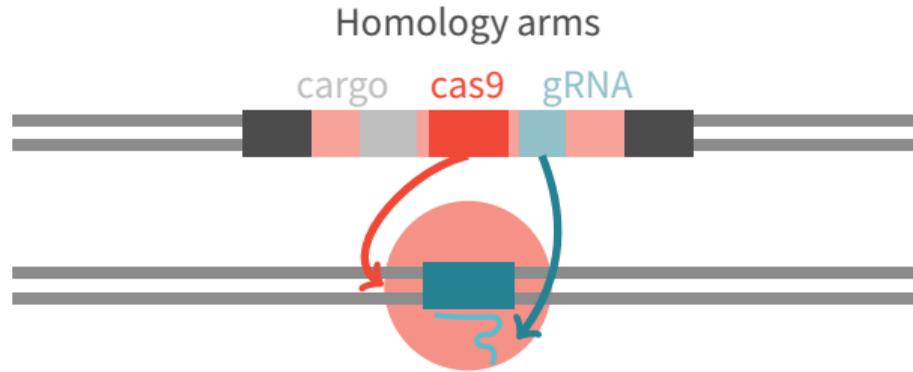
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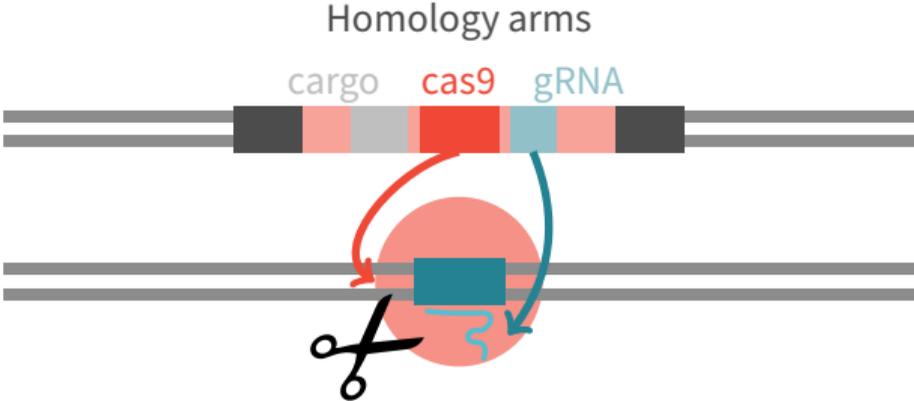
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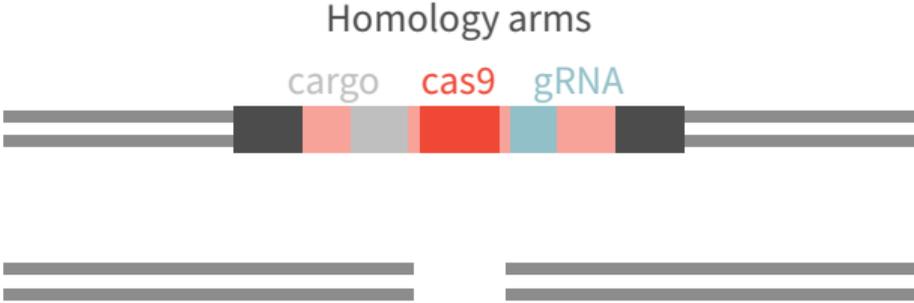
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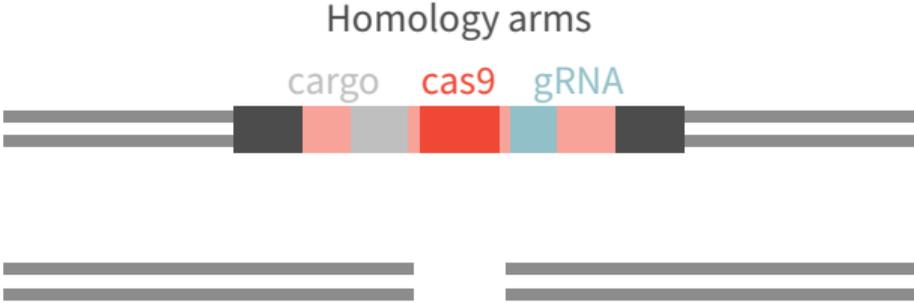
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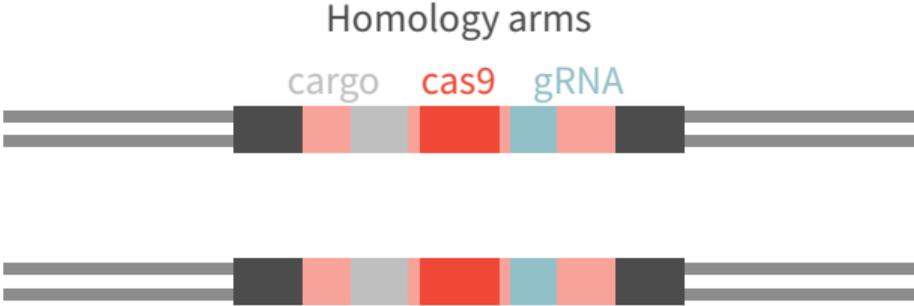
Esvelt *et al.* 2014, *eLife*



Homologous directed repair (HDR)

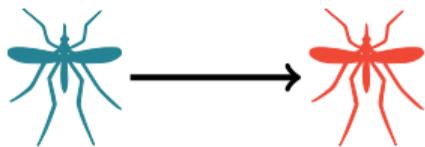
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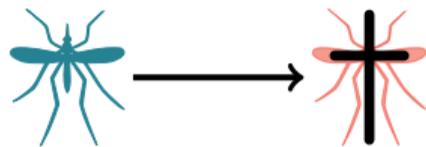


Types of drive

Modification drive



Eradication drive

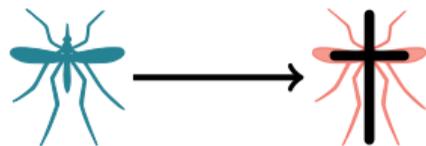


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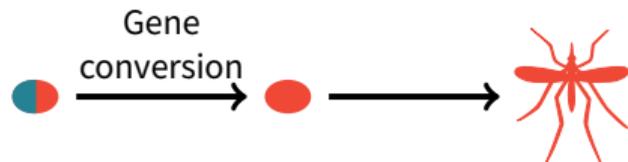


Eradication drive



Timing of gene conversion

In the zygote (Z)



In the gonads (G)



Modelling a homing-based gene drive

Deredec *et al.* (2008)

Alleles

Wild-Type W , Drive D

Modelling a homing-based gene drive

Deredec *et al.* (2008)

Alleles

Wild-Type W , Drive D

Parameters

Fitnesses			
Genotype	WW	WD	DD
Fitness	1	$1 - h_D s_D$	$1 - s_D$

c_D Conversion efficiency

Modelling a homing-based gene drive

Deredec *et al.* (2008)

Alleles

Wild-Type W , Drive D

Parameters

Fitnesses



Genotype

WW

WD

DD

Fitness

1

$1 - h_D s_D$

$1 - s_D$

c_D Conversion efficiency

Equations (Conversion in the zygote)

Allele frequencies

$$q_W = 1 - q_D,$$

$$q'_D = \frac{q_D^2(1 - s_D) + 2q_W q_D(c_D(1 - s_D) + \frac{1}{2}(1 - c_D)(1 - h_D s_D))}{1 - s_D q_D^2 - 2q_W q_D(c_D s_D + (1 - c_D)h_D s_D)}.$$

Modelling a homing-based gene drive

Deredec *et al.* (2008)

Alleles

Wild-Type W , Drive D

Parameters

Fitnesses

Genotype

Fitness



WW

1



WD

$1 - h_D s_D$



DD

$1 - s_D$

c_D Conversion efficiency

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Population size

$$N' = \min(\alpha \bar{w} N, K)$$

Modelling a homing-based gene drive

Equilibria

$q_D = 0$: drive allele is lost

$q_D = 1$: drive allele is fixed

$q_D = q_D^*$: intermediate drive frequency

→ coexistence or bistability

Modelling a homing-based gene drive

Equilibria

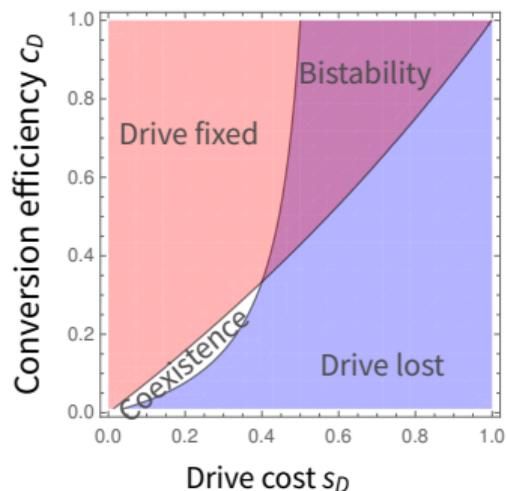
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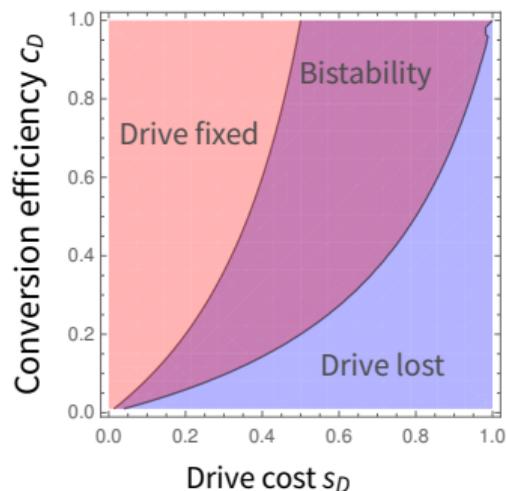
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Dominance $h_D = 0.25$



Dominance $h_D = 0.75$



Modelling a homing-based gene drive

Equilibria

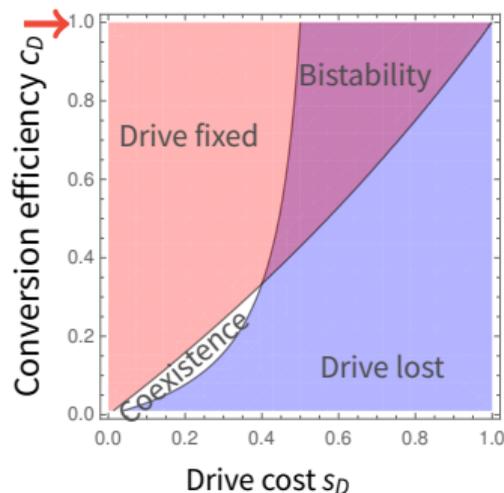
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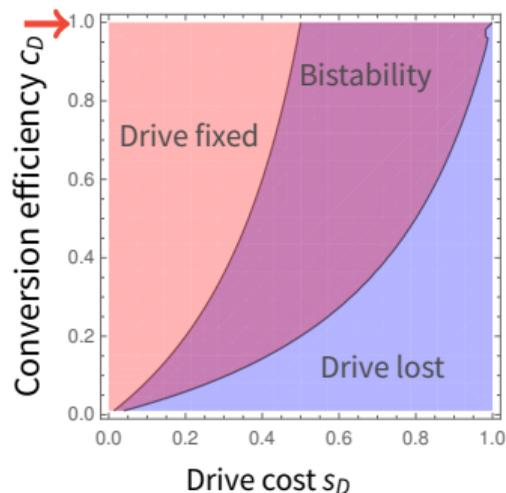
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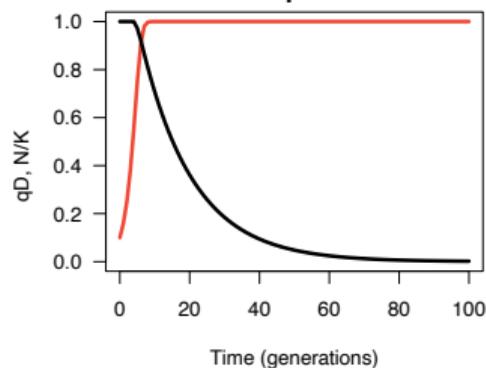
Dominance $h_D = 0.75$



Modelling a homing-based gene drive

Drive fixation

Threshold-independent drive



Legend:

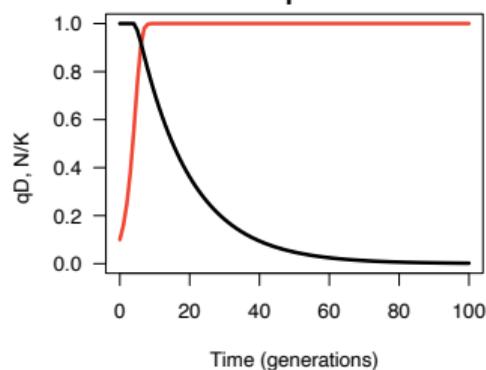
drive frequency,

population size

Modelling a homing-based gene drive

Drive fixation

Threshold-independent drive

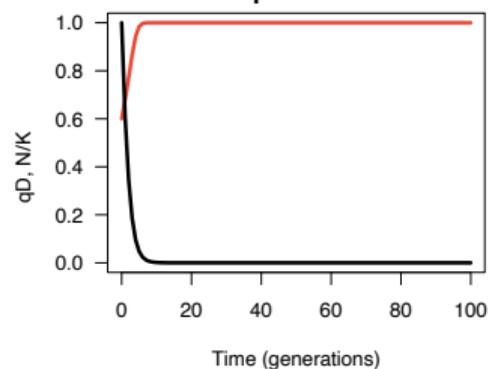


Legend:

drive frequency,
population size

Bistability

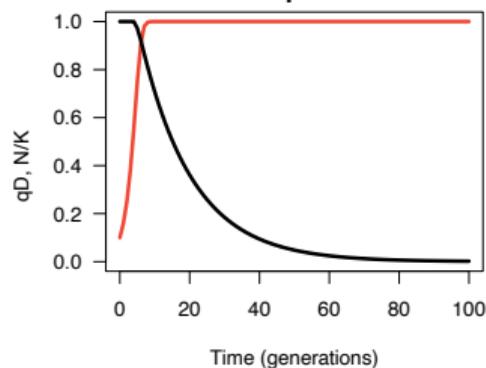
Threshold-dependent drive



Modelling a homing-based gene drive

Drive fixation

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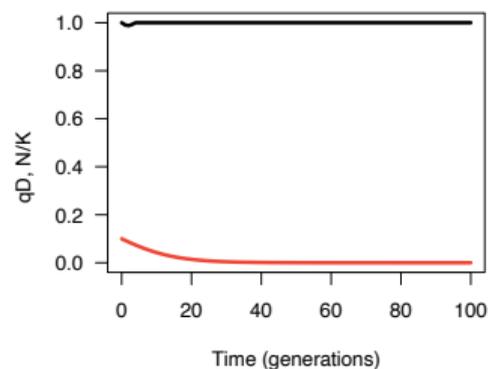
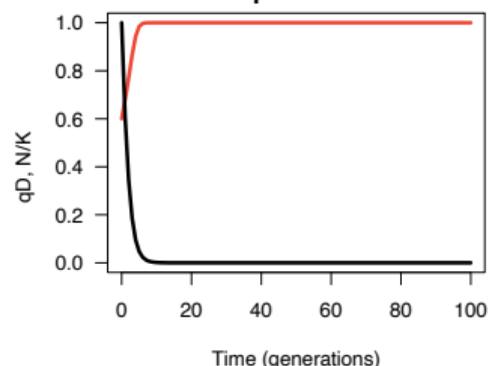


Legend:

drive frequency,
population size

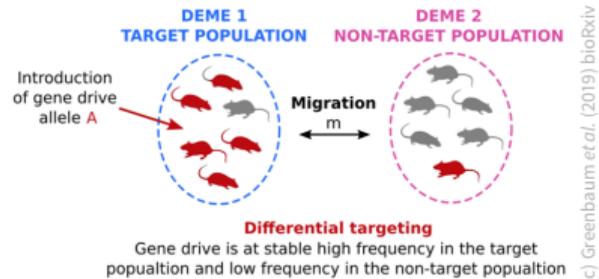
Bistability

Threshold-dependent drive



Spatial spread of threshold-dependent drives

- ▶ Potentially limited spread to non-target populations



(c) Greenbaum et al. (2019) bioRxiv

Greenbaum *et al.* 2019

- ▶ Continuous space: “pushed wave” regime

Spatial spread of a homing-based drive

Tanaka et al. 2017, PNAS

Reaction-diffusion; Assuming perfect conversion ($c_D = 1$)

$$\tau_g \frac{\partial q}{\partial t} = \tau_g D \frac{\partial^2 q}{\partial x^2} + \frac{sq(1-q)(q-q^*)}{1-sq(2-q)}, \text{ where } q^* = \frac{2s-1}{s}$$

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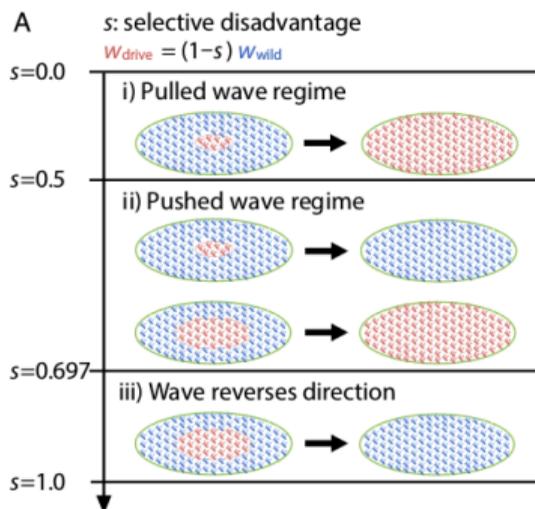
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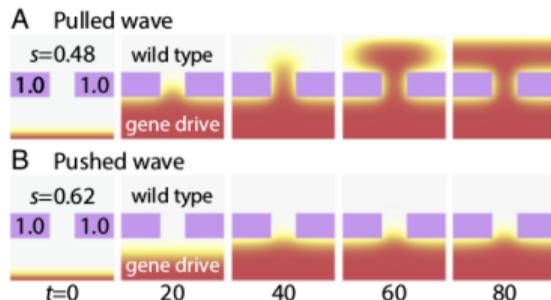
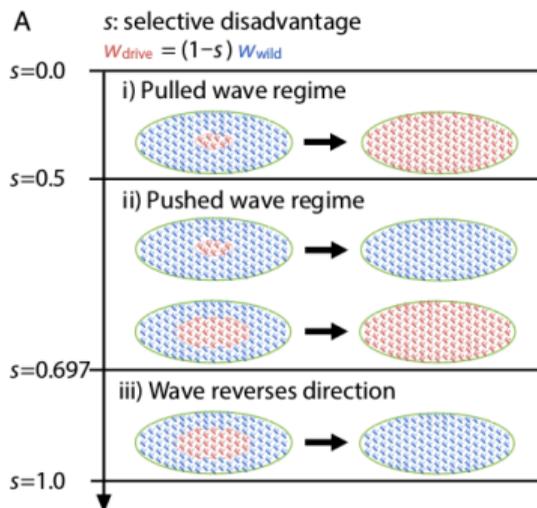
NB: $s < 0.5$ corresponds to the “Fixation” regime; $s > 0.5$ to the “Bistability” regime.

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Reaction–diffusion model

Modeling

- ▶ O, D : wild-type allele, gene drive allele
- ▶ Conversion rate $OD \rightarrow DD$: 100%
- ▶ $n_O(t, x), n_D(t, x)$: population densities for OO, DD
- ▶ OO population: unitary diffusion rate, unitary death rate, reproduction rate $1 + r(1 - n_D - n_O)$ ($\partial_t n_O - \Delta n_O = r n_O(1 - n_O)$ in the absence of D)
- ▶ Phenotypical effects of D : diffusion rate δ_D , fecundity rate β_D , juvenile survival rate ω_D , death rate μ_D

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$$\begin{cases} \partial_t n_O - \Delta n_O = \frac{n_O^2}{n_D + n_O} (1 + r(1 - n_D - n_O)) - n_O \\ \partial_t n_D - \delta_D \Delta n_D = \frac{\beta_D^2 n_D^2 + 2\beta_D n_O n_D}{n_D + n_O} \omega_D (1 + r(1 - n_D - n_O)) - \mu_D n_D \end{cases}$$

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Reaction–diffusion model

Modeling

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Assumption: selection only acts on juvenile survival

$$(\delta_D = \beta_D = \mu_D = 1, \omega_D = 1 - s)$$

Proportion–density variables

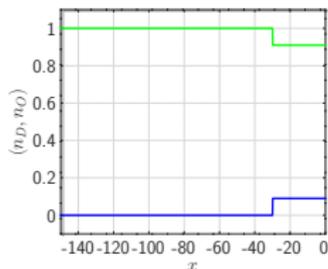
- ▶ $p(t, x)$: allelic proportion of gene drive
- ▶ $n(t, x)$: total population density
- ▶ $s \in [0, 1]$: fitness cost of the gene drive population
- ▶ $r > 0$: Malthusian growth rate of the wild-type population

$$\begin{cases} \frac{\partial p}{\partial t} - \Delta p - 2\nabla(\ln n) \cdot \nabla p = (1 + r(1 - n)) sp(1 - p) \left(p - \frac{2s - 1}{s} \right) \\ \frac{\partial n}{\partial t} - \Delta n = n \left((1 - s + s(1 - p))^2 (1 + r(1 - n)) - 1 \right) \end{cases}$$

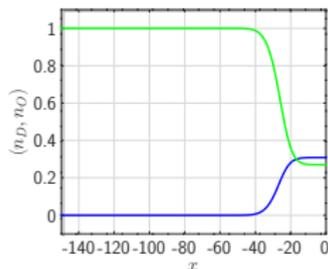
Stationary states

- ▶ $(p, n) = (0, 1)$: no gene drive
- ▶ $(p, n) = \left(1, \max \left(1 - \frac{s}{r(1-s)}, 0 \right) \right)$: fixated gene drive

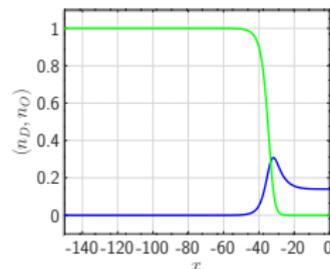
1D numerical simulations



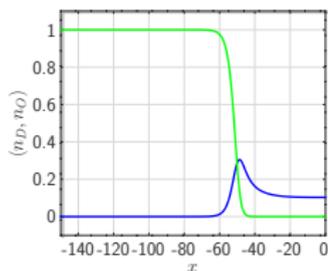
(a) $t = 0$



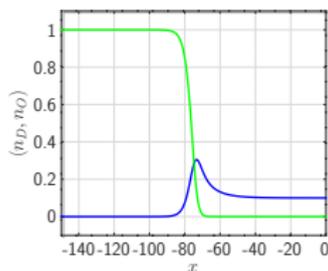
(b) $t = 20$



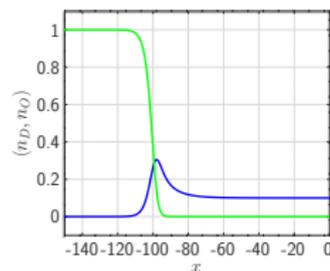
(c) $t = 40$



(d) $t = 80$



(e) $t = 140$

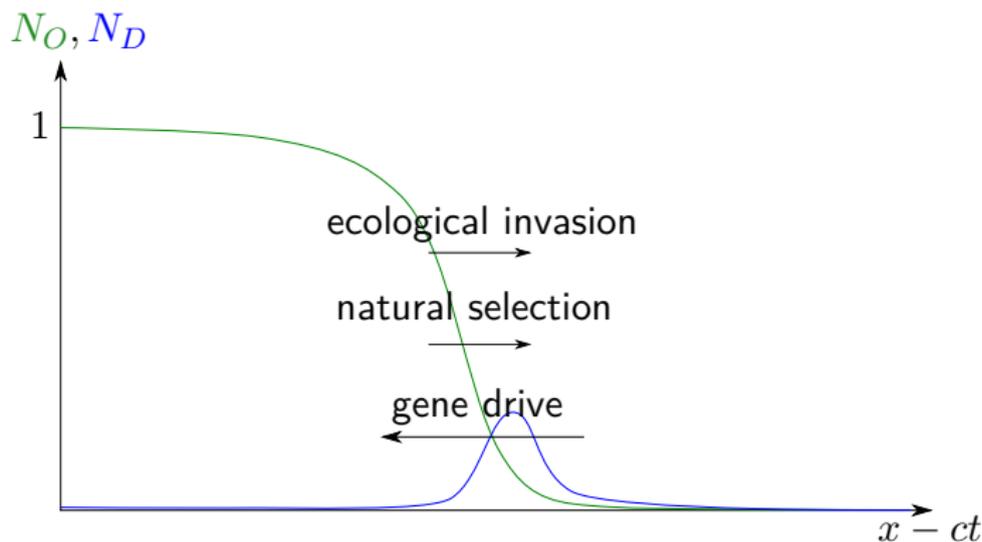


(f) $t = 200$

Figure: $n_D(t, x)$, $n_O(t, x)$, $r = 10/9$, $s = 0.5$ $(1 - \frac{s}{r(1-s)} = 0.1)$

Traveling wave with speed c

$$(n_D, n_O)(t, x) = (N_D, N_O)(x - ct) + \text{conditions at infinity}$$

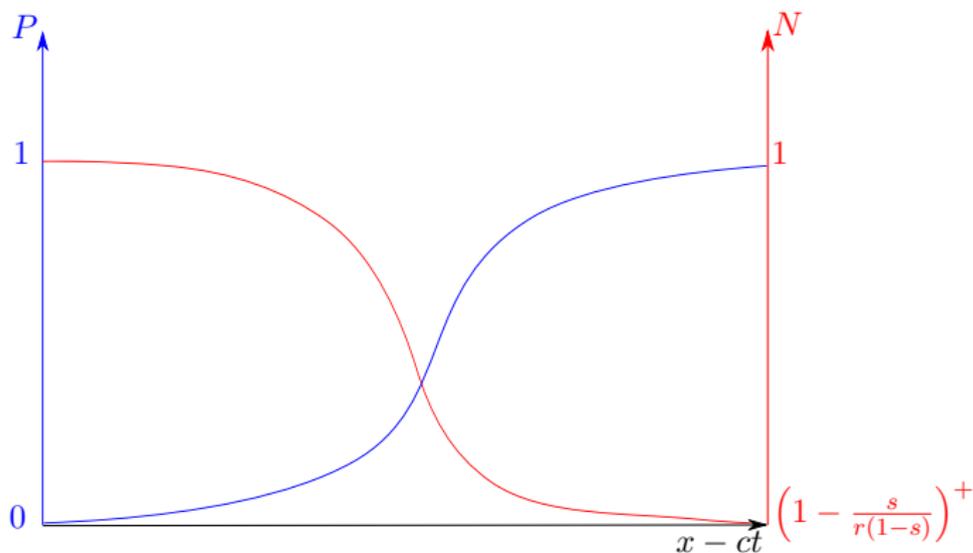


Q: sign of c as a function of r and s ?

A: numerical simulations, theoretical analysis

Traveling wave in proportion–density variables

$$(p, n)(t, x) = (P, N)(x - ct) + \text{conditions at infinity}$$



Numerical observation: monotonic P and N

Pure population replacement: assumption constant n

$$\partial_t p - \Delta p = sp(1-p) \left(p - \frac{2s-1}{s} \right)$$

- ▶ **Stability:** $p = 1$ stable ; $p = 0$ stable iff $s > 1/2$ (reversibility)
- ▶ **Sign of c :** sign of $s - 2/3$ (viable iff $s < 2/3$)
- ▶ **“Good” region:** viable and reversible iff $1/2 < s < 2/3$

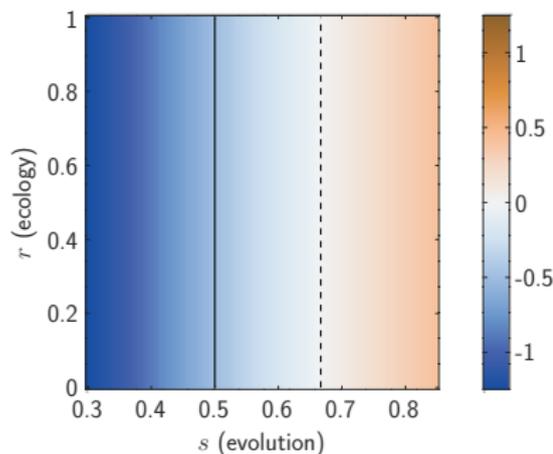


Figure: Values of $c_{s,r}$

- threshold 1-2-stability $s = 1/2$
- - level-line $\{c = 0\}$ $s = 2/3$

Partial suppression or total eradication

$$\begin{cases} \partial_t p - \Delta p - 2\nabla(\ln n) \cdot \nabla p = (r(1-n) + 1)sp(1-p) \left(p - \frac{2s-1}{s} \right) \\ \partial_t n - \Delta n = n \left((1-s + s(1-p)^2) (r(1-n) + 1) - 1 \right) \end{cases}$$

- ▶ “Good” region: reduced, larger nonviable region
- ▶ Eradication region ($1 < \frac{s}{r(1-s)}$): with a discontinuity in the nonviable region between retraction and nonexistence [num.]

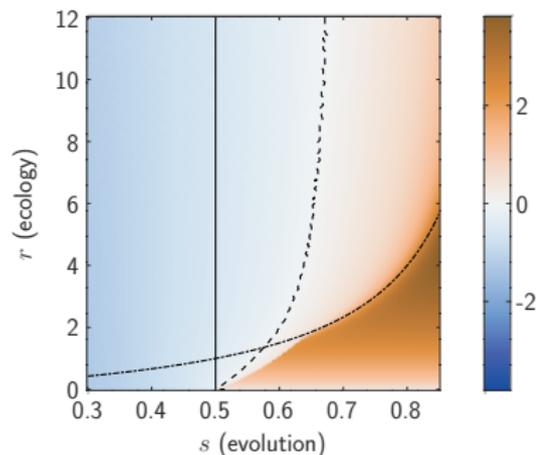


Figure: Values of $c_{s,r}$ [num.]

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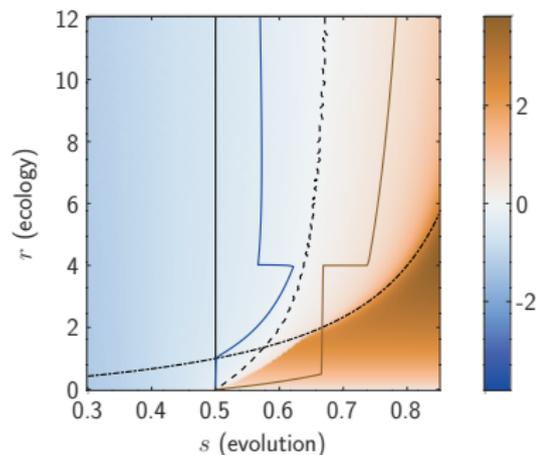


Figure: Values of $c_{s,r}$ [num.]

- threshold 1-2-stability $s = 1/2$
- - level-line $\{c = 0\}$ [num.]
- - eradication threshold $r = \frac{s}{1-s}$
- - known sign thresholds

Mathematical obstacles

$$\begin{cases} \partial_t p - \Delta p - 2\nabla(\ln n) \cdot \nabla p = (r(1-n) + 1)sp(1-p) \left(p - \frac{2s-1}{s} \right) \\ \partial_t n - \Delta n = n \left((1-s + s(1-p)^2) (r(1-n) + 1) - 1 \right) \end{cases}$$

- ▶ Reaction term without monotonicity: no comparison principle
- ▶ Singularity as $n \rightarrow 0$

Same obstacles in variables n_D - n_O

Elements of proof

Sign of c under assumption of existence and monotonicity

► Monotonicity: $N = h(P)$, $h : [0, 1] \rightarrow \left[\left(1 - \frac{s}{r(1-s)}\right)^+, 1 \right]$

► Equation on P :

$$-cP' - P'' - 2\frac{h'(P)}{h(P)}|P'|^2 = (r(1-h(P))+1)sP(1-P) \left(P - \frac{2s-1}{s}\right)$$

► Change of variable (Nadin-Strugarek-Vauchelet, *J. Math. Biol.*, 2018):

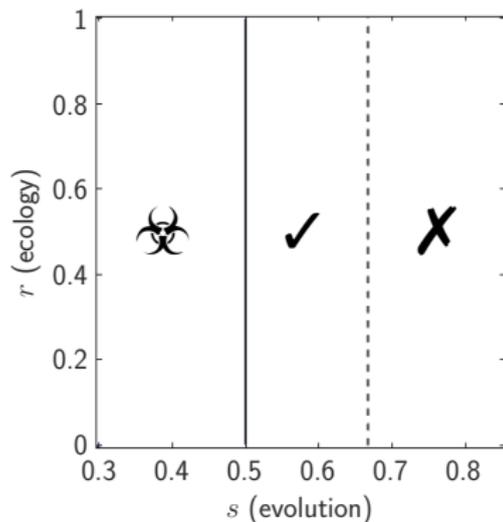
$$\operatorname{sgn}(c) = \operatorname{sgn} \left[- \int_0^1 h(\rho)^4 (r(1-h(\rho))+1)s\rho(1-\rho) \left(\rho - \frac{2s-1}{s}\right) d\rho \right]$$

► Estimates

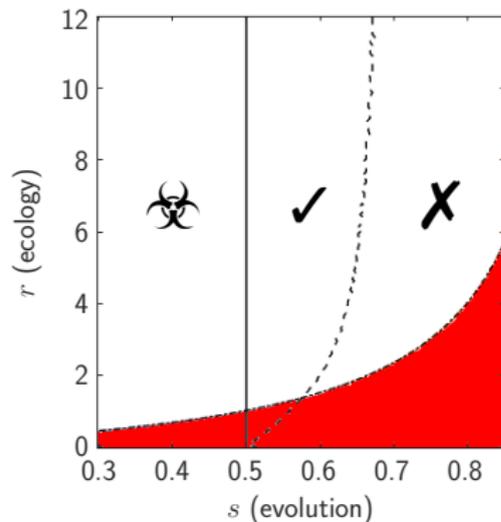
Nonexistence result: if $r \leq \frac{2s-1}{2(1-s)}$, by maximum principle

Conclusion

Summary



(a) Neglecting demography



(b) Accounting for demography

Figure: Gene drive regimes

☠: irreversible ; ✓: possible ; ✗: nonviable ; ■: eradication

Developments & perspectives

Developments not mentioned in this talk

- ▶ Sensibility analysis (parameters ω_D, β_D, μ_D)
- ▶ Density-dependent death rate
- ▶ Allee effect
- ▶ Stochasticity

Perspectives

- ▶ Existence, multiplicity, stability and monotonicity of traveling waves
- ▶ Limit $r \rightarrow +\infty$
- ▶ Better estimates of the sign of the speed
- ▶ Conversion in the germinal line instead of the egg
- ▶ Emergence and evolution of gene drive resistance (Champer *et al.*, *PLOS Genetics*, 2017 ; Unckless *et al.*, *Genetics*, 2017)

Gene drives may not work as advertised

Gene drives may not work as advertised

▶ Evolution of resistance

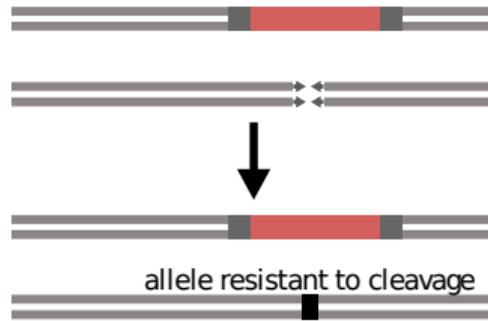
Unckless et al. 2017 Genetics, Champer et al. 2017 PLOS Genetics, KaramiNejadRanjbara et al. 2018 PNAS

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- ▶ natural variants at the target site already in the population
- ▶ generation of resistance by Non Homologous End Joining

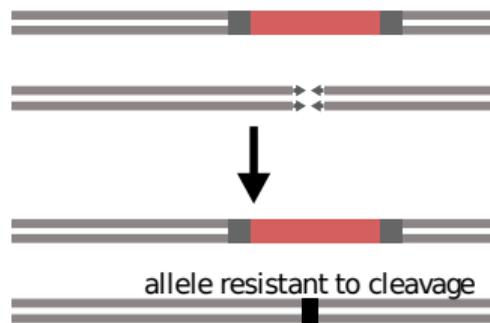


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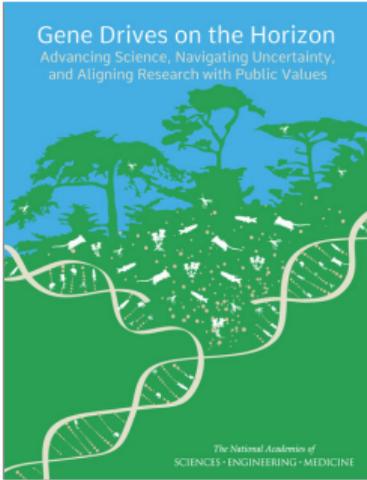


▶ Evolution of mating systems

Bull 2017, Bull et al. 2019 Evolution, Medicine and Public Health

Should gene drives be used in the first place?

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HOUSE OF LORDS
Science and Technology Select Committee
1st Report of Session 2015–16

Haut
conseil
des
biotechnologies

COMITE SCIENTIFIQUE
Avis

en réponse à la saisine du 12 octobre 2015
concernant l'utilisation de moustiques génétiquement modifiés
dans le cadre de la lutte antivectorielle¹.

Paris, le 31 mai 2017

Genetically Modified Insects

Gene-Drive – Vererbungsturbo in Medizin und Landwirtschaft

Öffentliche Tagung

Donnerstag · 26. Oktober 2017 · 11:00 bis 18:15 Uhr

Risks of gene drives

Specific to gene drive

Generic

Risks of gene drives

Specific to gene drive

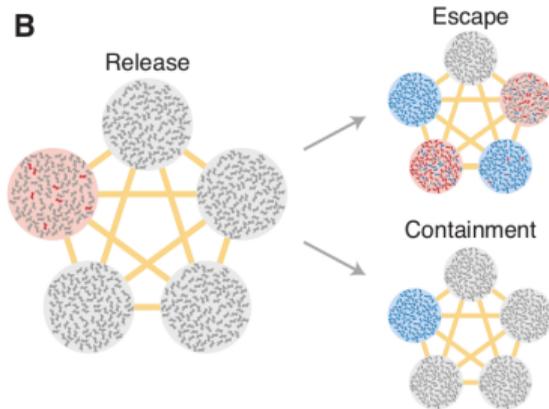
- ▶ Off-target mutations
Target sequence elsewhere in the genome

Generic

Risks of gene drives

Specific to gene drive

- ▶ Off-target mutations
Target sequence elsewhere in the genome
- ▶ Propagation to other populations



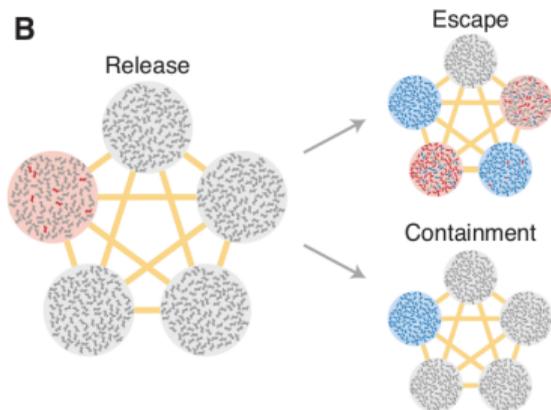
Noble et al. (2018) eLife

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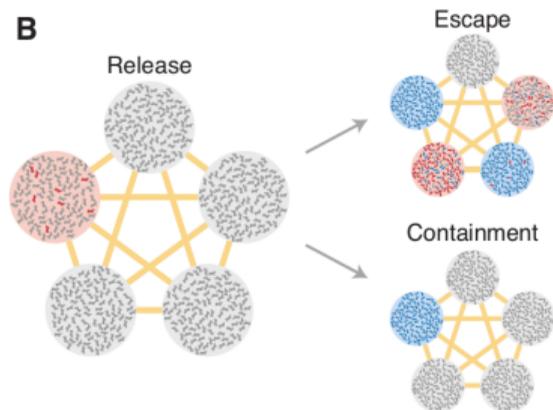
- ▶ Propagation to other species
Horizontal gene transfer

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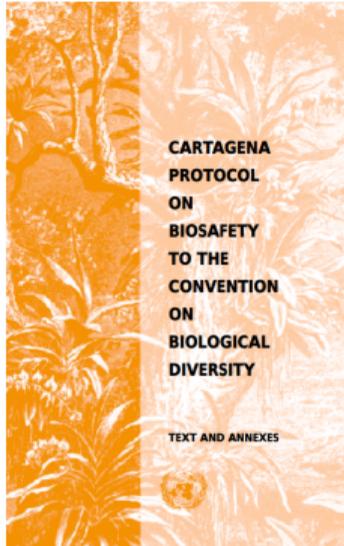
- ▶ Ecosystem consequences of population suppression

Regulatory issues

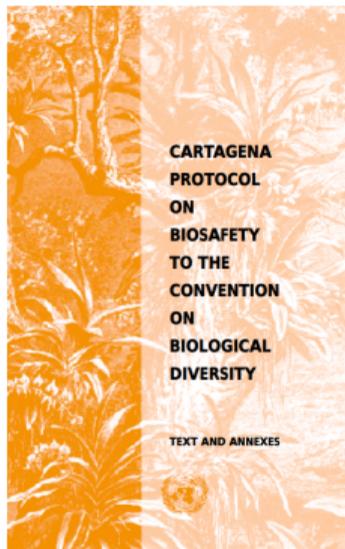
Gene drive-modified organisms are living genetically modified organisms

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Gene drive-modified organisms are living genetically modified organisms



Gene drive-modified organisms are living genetically modified organisms



Press and Information

Court of Justice of the European Union

PRESS RELEASE No 111/18

Luxembourg, 25 July 2018

Judgment in Case C-528/16

Confédération paysanne and Others v Premier ministre and Ministre de l'Agriculture, de l'Agroalimentaire et de la Forêt

Organisms obtained by mutagenesis are GMOs and are, in principle, subject to the obligations laid down by the GMO Directive

However, organisms obtained by mutagenesis techniques which have conventionally been used in a number of applications and have a long safety record are exempt from those obligations, on the understanding that the Member States are free to subject them, in compliance with EU law, to the obligations laid down by the directive or to other obligations

Funding

Main funders of gene drive research:



▶ Need for independent risk assessment

- ▶ Gene drive vs. other methods of population control

Ethics

- ▶ Gene drive vs. other methods of population control
- ▶ Are the benefits worth the risks?

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- ▶ Are the benefits worth the risks?
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- ▶ Modifying wild populations

Thanks for your attention!

<https://arxiv.org/abs/2101.11255>