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# Gene Drive Development in Non-Insect Targets – including Vertebrates, Snails, Fungi and Plants

## A Horizon Scanning Survey up to end 2023

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## Summary of findings:

Screening and analysis of the scientific literature for gene drive development in non-insect targets up to 31 December 2023,[1] showed:

- There are 46 current or proposed non-insect targets[2].
- Proposals span a wide range of species and taxonomic groups: from mammals and fish to snails, arachnids, fungi and plants (see Table 1).
- In the vast majority of cases the aim is to suppress or eradicate the target.
- Compared to gene drive systems in insects, the systems in other taxonomic groups are further away from releases into the environment.
- A significant amount of research has focussed on developing gene drives in mice, so far with limited success, though efforts are ongoing.
- Development of gene drives in mice is seen by many as a pathway to applying the technology in other mammals.
- There appear to be significant obstacles in applying homing CRISPR gene drive technology in new species and taxonomic groups.

## Context

In 2016, the National Academy of Sciences Engineering and Medicine (NASEM) published their report 'Gene Drives on the Horizon'. This was two years after Esvelt and colleagues first published their conceptual paper on utilising the then new CRISPR/Cas system to build a functional gene drive for the modification or eradication of wild populations (Esvelt *et al*. 2014). At the same time both publications highlighted the dangers and risks of this approach.

Within a year the first proof of concept was published, at that time in the fruit fly *Drosophila melanogaster*, a major model organism for insects (Gantz & Bier 2015). Other proofs of concept followed.

Where is research and development of gene drives now? What is on the horizon? What are the trends? Where has research advanced and where has it hit obstacles? Which species are being focused on and why? And which gene drive systems are being proposed and for which purposes?

To answer these questions, we have undertaken a survey of the scientific literature up until 31 December 2023. Whilst there was a slow steady stream of publications related to "gene drives" in the 10 years up to 2015, a steep rise occurred in 2016 and 2017 (see Figure 1). This started to plateau by 2018, with an average of 120 publications per year since, covering a wide range of disciplines, also including ethics, social sciences, and regulatory issues.

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[1] A preliminary version of this survey was published in November 2023.

[2] The vast majority of the targets identified in the literature are single species, however some early stage proposals relate to broader taxonomic groups, the *Cervid* family (entry 11), the *Tetranycahidae* (20), snail genera hosting schistosome parasites (22.1 -22.3), two species from the *Schistosoma* genus (24) and the *Myrtaceae* family (32).

This survey focuses on non-insect targets only. A separate horizon scanning survey for insect targets was published in November 2023 (Wells and Steinbrecher 2023).

This survey does not cover issues regarding risks, difficulties in performing robust risk assessments, or the lack of proven methods to confine, halt or reverse engineered gene drives.

This survey gives an overview of:

- What research has taken place or is ongoing.
- Which species and taxa are current or proposed targets for gene drive development, and which types of gene drives are being put forward.
- How far developments have progressed and what the next stages of experimentation might be.

| KINGDOM | PHYLUM or SUB-PHYLUM | CLASS or SUPERCLASS or INFRAPHYLUM | ORDER | | Entry number(s) |
|---|---|---|---|---|---|
| **Animals** | | | | | |
| | Vertebrates | Mammals | *Rodentia* (Rodents) | House mice | 1.1.1 - 1.9 |
| | | | | Other rodents | 2.1 - 6.2 |
| | | | *Carnivora* (cats, dogs and related mammals) | | 7.1 - 9 |
| | | | *Diprotodontia* (Possums and related marsupials) | | 10 |
| | | | *Artiodactyla* (Deer, pigs and related mammals) | | 11-12 |
| | | | *Lagomorpha* (Rabbits and hares) | | 13.1-13.4 |
| | | Birds | | | 14 |
| | | Amphibians | | | 15.1-16 |
| | | Bony fish | | | 17-18 |
| | | Jawless fish | | | 19.1-19.2 |
| | Arthropods | Arachnids | | | 20-21 |
| | | Insects | | | See separate table |
| | Molluscs | | | | 22.1-22.3 |
| | Nematodes | | | | 23 |
| | Flatworms | | | | 24 |
| **Fungi** | | | | | 25-28 |
| **Plants** | | | | | 29-32 |

**Table 1: Overview of current gene drive targets.**

Overview of gene drive survey data in taxonomic order. Entry numbers correspond to rows in the main data table.

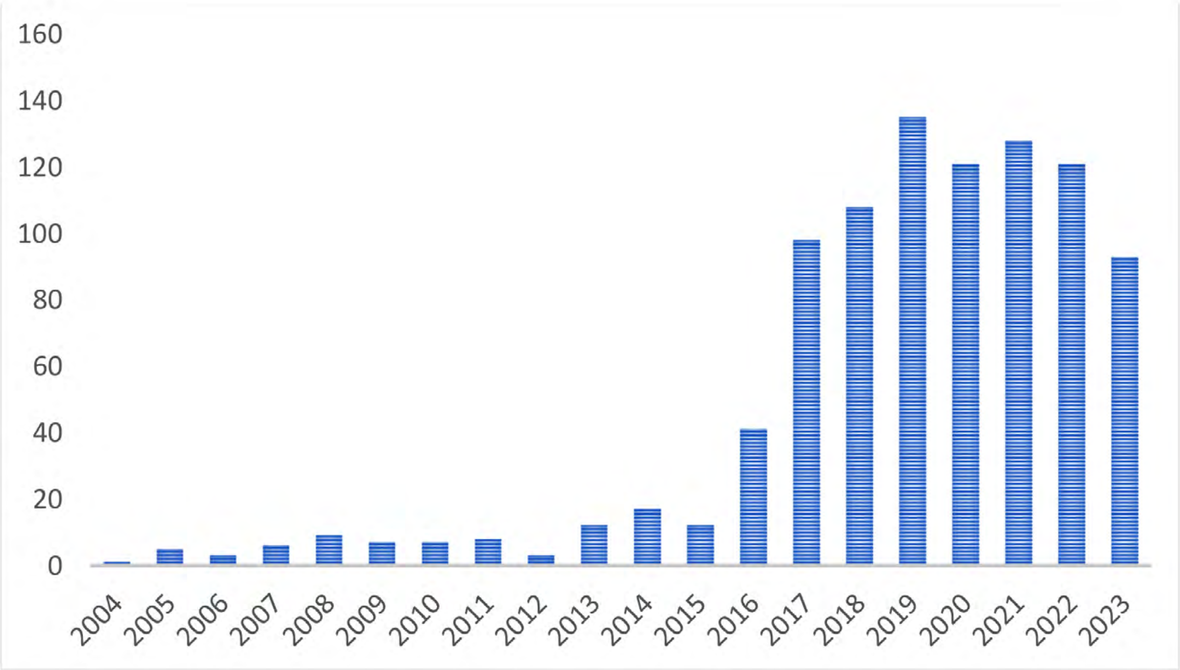

Figure 1: Number of publications per year related to gene drives

## Findings

1. **There are proposals in a wide range of species and taxonomic groups:** showing there is momentum and ambition that goes far beyond mosquitoes and mice.
2. **In the vast majority of cases the aim is to suppress or eradicate the target**[2] (36 out of 41 target species or groups[3]), in some cases by modifying the target to render it susceptible to suppression.[4]
3. **Compared to gene drive systems in insects, the systems in other taxonomic groups are further away from releases in the environment.** The two most advanced systems - where there is an intention to target the organism in the wild - are both being developed in house mice (entries 1.1.1 and 1.7 in table). Neither of these systems have yet reached full proof of concept in the laboratory.
4. **A significant amount of research has focussed on developing gene drives in mice, so far with limited success, though efforts are ongoing.**
5. **Development of gene drives in mice is seen as a pathway to applying the technology in other mammals.** While this intention is often stated in general terms, an example that names a specific eventual target is the study from Castle *et al.* (2022) who use mice as a model organism with the ultimate aim of modifying deer (entries 1.6 and 11 in table).
6. **No functional gene drive system has been constructed in plants** up to December 2023. A homing CRISPR gene drive was reported in Arabidopsis (29) but the publication was later retracted. A 'gene drive like' system has been reported in Nicotiana tabacum (30), however the functionality of this system is limited, namely to produce point mutations in the mitochondrial genome. *Please note that subsequent to the cut-off date for this survey, two groups have reported laboratory proof of concept for gene drives in plants (Oberhofer et al. 2024 and Liu et al. 2024), both of which use toxin-antidote based designs rather than homing CRISPR.*

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[3] Five species that are model organisms where there is no intention to apply the technology in the wild are excluded from this total - these are entries 23 and 27-30 in the table

[4] Targets where aim is suppression/eradication: 1, 3-10, 12-22, 24 (this entry comprises two species), 31 (this entry encompasses 14 invasive plant species). Targets where the aim is modification: 2, 11, 15, 22 (but suppression also proposed for *B. marinus* and *B. glabrata*), 25, 32. In one case - 26- the intention has not yet been specified.

7. **There appear to be significant obstacles in applying homing CRISPR gene drive technology in new species and taxonomic groups.** While homing CRISPR gene drives appear to be functional in laboratory settings in dipteran insects (i.e. flies and mosquitoes)[5] and some fungi (*S. cerevisiae* and *C. albicans*: 27.1-28), the technology is so far only partially functional in mice (1.1.1 – 1.6). Despite efforts to apply this technology more widely, it is not yet functional in plants (29), nematodes (23), flatworms (24) or in the fungi *Fusarium graminearum* (25.2).
8. **It is possible that gene drive designs not based on homing CRISPR technology may be more effective in some species and taxonomic groups.** Development of designs based on the T-haplotype in mice (1.7) and Spok1 in *F. graminearum* (25.1), appears to have made some progress in the laboratory.
9. **Seventeen of the vertebrate targets relate to controlling or eliminating invasive species for conservation purposes, especially mammals.**
10. **While many proposals relate to eliminating invasive mammals on islands, there is ambition to apply gene drive technology for eradications at continental scale in Australia** (e.g. see Birand, Cassey, Ross, Thomas, *et al*. (2022)). There is ongoing interest in Australia in a number of mammalian targets including house mice, black rats, rabbits, cats, and foxes, with a body of work published from 2017 through to the present day relating to some or all of these species.
11. **A number of target species are integral and important species within ecosystems in their native range**, for example the red fox, the possum or the rabbit. Other targets are able to cross-breed with endangered species, such as feral house cats with the European wild cat. Significantly Thresher (2022) argues that employing a gene drive that carries the risk of causing complete global extinction of the European rabbit would be justifiable because '….the species seriously threatens agriculture, and native flora and fauna in almost all it's extensive invasive ranges, and its loss, however serious, would still in turn damage only a limited ecosystem and set of economies.'
12. Genetic modification systems described as 'gene drives' have been developed in bacteria (Valderrama *et al*. 2019) and in viruses (Walter and Verdin, 2020). While these systems share some features with homing gene drives, for example employing CRISPR-Cas9, we do not include such systems in this survey because neither bacteria or viruses reproduce sexually, and they therefore do not meet the established definition of a gene drive.

**Please see main table (pp.6-29) for details of findings.**

## Concluding remarks

Undertaking a broad survey of the research in this field makes the bigger picture clearer, allowing one to perceive trends, as well as obstacles. The wide-ranging ambition for gene drive technology is remarkable, and yet the survey also reveals that homing CRISPR gene drives may not be as broadly applicable across different species and taxonomic groups as originally hoped. A prevalence of proposals to suppress and potentially eradicate species or populations, as opposed to modifying them, is evident. While the reasons for this are not completely clear - it is possible that gene drives are starting to be perceived as a form of species-specific pesticide.

A key outcome of the survey is to raise questions: How might deployment of gene drive technology develop in the medium and long term? Is it going to become the go-to technology to tackle invasive species and 'pests'? From vertebrates to insects to plants, be it for agriculture, conservation, or forestry, will gene drives be used as pesticides have been in the past? If the technology develops on this trajectory – and we observe that many agencies and academics do appear to view it this way – then serious reflection and analysis will be required. Who will model the deployment as a whole and analyse or asses the consequences, especially with regards to cumulative effects? What would this mean for biodiversity, and what for risk assessment, regulation, and governance, especially on an international and global level?  And could the technology be used for purposes other than those currently discussed in the literature?

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[5] Wells and Steinbrecher 2023

# Methodology

Please see end of document.

## Key to technology levels

**1** **Gene drive proposed**
**2** **Gene drive proposed with supporting modelling work, or preliminary laboratory work funded**
**3** **Preliminary laboratory work published**
**4** **Research on gene drive construction funded**
**5** **Limited proof of concept**
**6** **Laboratory proof of concept**
**7** **Non-insects- scaled up trials**
**Insects - large cage trials**
**8** **Potential further contained trials**
**9** **Experimental releases in natural environment**
**X** **Abandoned project**

Please see page 26 for a complete explanation of the technology levels

## Colouring/symbols for progress of technology

| | |
|---|---|
| ■ | Evidence shows this approach doesn't work |
| 🟦 | System is not intended for release |
| 🟨 | No publications in three years up to December 2023 |
| ? ? ? | Uncertain if research has progressed to this stage |
| **M** | Modelling work has been done |
| **G** | Genome sequenced (with intention/possibility of constructing gene drive stated) |

## Key to geographic distribution maps

| | |
|---|---|
| ■ | Species is not present |
| ▨ | Species native range |
| ▨ | Species invasive range |

| | Species<br>Geographic range | Intended direct effect<br>Intended use (as stated by authors) | Type of gene drive (our categories)<br>Developer's name for gene drive system | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? | Project leader(s)<br>Institution | Funders |
|---|---|---|---|---|---|---|---|
| Kingdom: ANIMALS | Subphylum: Vertebrates | Class: Mammals | Order: (*Rodentia*) Rodents | Species: House mice | | | |
| 1.1 | *Mus musculus* **Homing CRISPR – proof of concept only** | | | | | | |
| 1.1.1 | ***Mus musculus***<br>House mouse<br><br>After Musser *et al.* 2021 | NA – intention is proof of concept of homing CRISPR gene drive in mammals<br>Initial aims:<br>1) using gene drive technology to create lab mouse strains carrying multiple modifications (with otherwise impractical genotypes) for laboratory studies<br>2) finding a way to eliminate invasive rodent species or addressing rodent-borne diseases | Homing CRISPR<br>CRISPR-Cas9 mediated gene drive | Grunwald *et al.* 2019<br>Weitzel *et al.* 2021<br>Grunwald, Weitzel and Cooper 2022 | 1 2 3 4 5 6 7 8 9 | K.L. Cooper<br>University of California San Diego, USA | Kinship<br>Pew<br>Packard<br>NIH<br>Allen<br>TATA<br>UCSD |
| 1.1.2 | | Population suppression<br>Suppressing/eradicating invasive rodents on islands, and reducing impacts of rodents on agriculture | Split homing CRISPR<br>CRISPR-Cas9 based gene drive (test both 'zygotic' and 'germline' forms) | Pfitzner *et al.* 2020 | 1 2 3 4 5 6 7 8 9 | P.Q. Thomas<br>University of Adelaide, Australia | DARPA |
| 1.2 | *Mus musculus* **Homing CRISPR – targetting female fertility** | | | | | | |
| 1.2.1 | | Population suppression<br>The 2017 press release says the aim is to improve pest control methods | Homing CRISPR (targeting 'haplosufficient female fertility gene')<br>'Homing gene drive targeting female fertility'<br>(2018 paper)<br>'CRISPR-Cas9 split gene drive which disrupts an essential female fertility gene'<br>(2019 poster) | RoslinInstitute 2017<br>McFarlane, Whitelaw, and Lillico 2018 – theoretical explanation of proposed GD designs<br>McFarlane *et al.* 2020 – poster abstract<br>**No results published except poster abstract** | 1 2 3 4 5 6 7 8 9 | C.B.A. Whitelaw<br>S.G. Lillico<br>Roslin Institute, University of Edinburgh, UK | CSC<br>BBSRC |

|  | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** |  |  |  |  |  |  |  |  | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** |  |  |  |  |  |  |  |  |  |  | **Institution** |  |
| 1.2.2 |  | Population suppression | Homing CRISPR (targeting 'haplosufficient female fertility gene') | Brown 2021 - press release<br>Birand, Cassey, Ross, Russell, *et al.* 2022<br>Birand, Cassey, Ross, Thomas, *et al.* 2022 | ■ 1 | ■ 2<br>M | ■ 3 | ■ 4 | 5 | 6 | 7 | 8 | 9 | T.A.A. Prowse<br>P.Q. Thomas<br>University of Adelaide, Australia | ARC<br>New South Wales Government<br>South Australia Government |
|  |  | 'eradicating mice from islands' or at continental scale [presumably Australia] to address their impacts on biodiversity | Homing gene drive |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.2.3 |  | Population suppression | Homing CRISPR<br>(targeting locally[1] fixed alleles of female fertility genes) | Sudweeks *et al.* 2019<br>Oh *et al.* 2021 | ■ 1 | ■ 2<br>M | ■ 3<br>G | 4 | 5 | 6 | 7 | 8 | 9 | A.L. Lloyd<br>North Carolina State University, USA<br>+<br>A.J. Piaggio<br>USDA APHIS Wildlife Services, USA | DARPA |
|  |  | 'Suppressing' invasive rodents on islands to reduce impacts on biodiversity, agriculture and human health | Localized synthetic gene drive |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.2.4 |  | Population suppression | Homing CRISPR – four[2] designs modelled | Prowse *et al.* 2017<br>(see also entries 1.3.3 and 1.5) | ▨ 1 | ▨ 2<br>M | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.A. Prowse<br>University of Adelaide, Australia | University of Adelaide |
|  |  | 'eradication of alien rodents on islands' to address impacts on bio-diversity<br>The impacts of rodents on agriculture are also noted as a driver | 'CRISPR gene drive'<br>'Homozygotic XX sterility' |  |  |  |  |  |  |  |  |  |  |  |  |

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[1] Locally fixed alleles refers to alleles found in specific geographic locations - sometimes also referred to as 'private alleles'

[2] The designs modelled in this publication are covered in entries 1.2.4, 1.3.3 and 1.5

|  | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** |  |  |  |  |  |  |  |  | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** |  |  |  |  |  |  |  |  |  |  | **Institution** |  |
| 1.3 | *Mus musculus* **Homing CRISPR sex ratio distorter – Sox9 cargo**[3] |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.3.1 |  | Population suppression | CRISPR based gene drive involving *Sox9* – probably a homing CRISPR drive with *Sox9* cargo | Campbell *et al.* 2019<br>**No results published despite substantial funding**<br>(the work described in entry 1.3.3 may have informed this project) | 1 | 2 | 3 | 4<br>?<br>?<br>? | 5 | 6 | 7 | 8 | 9 | Probably P.Q. Thomas<br>University of Adelaide, Australia | DARPA |
|  |  | 'eradicating invasive rodent populations on islands' to address impacts on biodiversity | Paper describes development of 'CRISPR/Cas9 and CRISPR/Cpf1[4] gene drives with *Sox9* and Y-shredder' |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.3.2 |  | Population suppression | Homing CRISPR (with *Sox9* cargo) | Brown, Eikenbary, and Landis 2022 | 1 | 2<br>M | 3 | 4 | 5 | 6 | 7 | 8 | 9 | W.G. Landis<br>Western Washington University, USA | Funders not stated |
|  |  | Eradicating invasive mouse populations on islands to address biodiversity impacts - with the Southeast Farallon island used as a case study | '*sox9* CRISPR cas9 gene drive' |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.3.3 |  | Population suppression | Homing CRISPR - four designs modelled[2] | Prowse *et al.* 2017<br>(see also entries 1.2.4 and 1.5) | 1 | 2<br>M | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P.Q. Thomas<br>University of Adelaide, Australia | University of Adelaide |
|  |  | 'eradication of alien rodents on islands' to address impacts on bio-diversity<br>Aim ultimately is also to address impacts of alien rodents (esp. mice and rabbits) on agricultural production | 'CRISPR gene drive'<br>Variants named:<br>'Heterozygotic XX sterility'<br>'Heterozygotic XX sex reversal' |  |  |  |  |  |  |  |  |  |  |  |  |

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[3] *Sox9* is an autosomal gene that codes for a developmental transcription factor crucial for sex determination.

[4] Cpf1 is the old term for what is now named Cas12a

|  | **Species**<br>**Geographic range** | **Intended direct effect**<br>**Intended use** (as stated by authors) | **Type of gene drive** (our categories)<br>**Developer's name for gene drive system** | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** |  |  |  |  |  |  |  |  | **Project leader(s)**<br>**Institution** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.4 | *Mus musculus* **Homing CRISPR sex ratio distorter – 'Y-shredder' cargo** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.4 |  | Population suppression<br>'Suppression or eradication' of rodent populations to reduce impacts on biodiversity and agriculture | Homing CRISPR<br>(with 'Y shredder' cargo)<br>Y chromosome shredding gene drive (Campbell *et al.* 2019)<br>'Y-Chromosome deletion using Orthogonal Programmable Endonucleases (Y-CHOPE)'<br>(Prowse *et al.* 2019) | Prowse *et al.* 2019<br>Campbell *et al.* 2019<br>**No results regarding gene drive construction published** | 1 | 2<br>**M** | 3 | 4<br>**?**<br>**?**<br>**?** | 5 | 6 | 7 | 8 | 9 | J.V. Ross<br>University of Adelaide, Australia | DARPA |
| 1.5 | *Mus musculus* **Homing CRISPR causing recessive emrbyonic lethality** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.5 |  | Population suppression<br>'eradication of alien rodents on islands' to address impacts on bio-diversity<br>The impacts of rodents on agriculture are also noted as a driver | Homing CRISPR – four designs modelled[2]<br>'CRISPR gene drive'<br>'Homozygotic embryonic non-viability' | Prowse *et al.* 2017<br>(see also entries 1.2.4 and 1.3.3) | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P.Q. Thomas<br>University of Adelaide, Australia | University of Adelaide |
| 1.6 | *Mus musculus* **Feasibility study for homing CRISPR for population modification in deer (see entry number 11)** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 1.6 |  | Population modification<br>To demonstrate feasibility of a gene drive rendering wild deer immune to chronic wasting disease [by spreading *PRNP* null alleles] | Homing CRISPR<br>CRISPR/Cas9 gene drive | Castle *et al.* 2022 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | D. Westaway<br>University of Alberta, Canada | Alberta Prion Research Institute<br>CFI<br>University of Alberta |

| | **Species**<br>**Geographic range** | **Intended direct effect**<br>**Intended use** (as stated by authors) | **Type of gene drive** (our categories)<br>**Developer's name for gene drive system** | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | **Project leader(s)**<br>**Institution** | **Funders** |
|---|---|---|---|---|---|---|---|
| 1.7 | *Mus musculus* **T-haplotype[5] targetting female fertility** | | | | | | |
| 1.7 | | Population suppression | Split drive:<br>a) *T*-haplotype element with gRNA cargo targeting 'haplosufficient female fertility gene' *(Prl)*<br>b) Cas9 expressed separately (in male germline) | Gierus *et al.* 2022 | **1** **2 M** **3** **4** **5** 6 7 8 9 | P.Q. Thomas<br>University of Adelaide, Australia | Funders not stated in pre-print publication |
| | | Aim is to explore the potential of an engineered form of the *T*-haplotype for 'mouse population suppression or even eradication on islands' | tCRISPR split drive | | | | |
| 1.8 | *Mus musculus* **T-haplotype sex ratio distorter -Sry[6] cargo (T-Sry)** | | | | | | |
| 1.8.1 | | Population suppression | *T*-haplotype sex ratio distorter (carrying *Sry* cargo) | Leitschuh *et al.* 2018<br>Campbell *et al.* 2019<br>**No results published despite substantial funding** | **1** **2** **3** **4** 5 6 7 8 9 | J. Godwin<br>North Carolina State University, USA | NSF<br>DARPA |
| | | Eradicating invasive populations on islands to address biodiversity impacts | *T*-complex drive | | | | |
| 1.8.2 | | | *T*-haplotype sex ratio distorter (carrying SRY cargo) | Backus and Gross 2016 | **1** **2 M** 3 4 5 6 7 8 9 | K. Gross<br>North Carolina State University, USA | North Carolina State University<br>NSF |
| | | | *t-Sry* | | | | |

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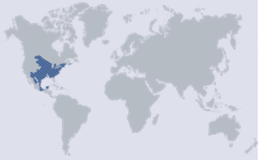
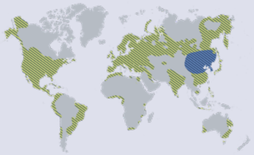
[5] *T*-haplotype or t-complex is a selfish genetic element functioning as a meiotic drive and sex-ratio distorter that naturally occurs in mice, though does not spread widely. It is a form of a toxin-antidote system and allows for the insertion of 'cargo' genes into the t-complex, for example female infertility genes such as *Sry*. The *t*-haplotype is linked to the occurrence of taillessness (gene symbol T), which gave it its name.

[6] *Sry* is a Y-chromosomal gene responsible for sex determination (**s**ex-determining **r**egion **Y**) and is required for initiating male development. It is also described as the *male phenotype control gene*. In females it will result in infertility due to partial male development.

| | **Species**<br>**Geographic range** | **Intended direct effect**<br>**Intended use** (as stated by authors) | **Type of gene drive** (our categories)<br>**Developer's name for gene drive system** | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)**<br>**Institution** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.8.3 | | | T-haplotype sex ratio distorter (carrying *Sry* cargo)<br>synthetic sperm-killing gene drive:<br>'t-Sry' | Manser *et al.* 2019 | **1** | **2 M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.R. Price<br>University of Liverpool, UK | SNSF<br>NERC |
| 1.9 | *Mus musculus* **Y linked 'X-shredder' gene drive** | | | | | | | | | | | | | | |
| 1.9 | | Population suppression<br>'eradicating mice from islands' or at continental scale [presumably Australia] to address their impacts on biodiversity | CRISPR based X-shredder gene drive ('driving Y')<br>X chromosome shredding gene drive | Brown 2021<br>Birand, Cassey, Ross, Russell, *et al.* 2022<br>Birand, Cassey, Ross, Thomas, *et al.* 2022 | **1** | **2 M** | **3** | **4** | 5 | 6 | 7 | 8 | 9 | T.A.A. Prowse<br>P.Q. Thomas<br>University of Adelaide, Australia | ARC<br>New South Wales Government<br>South Australia Government |
| Kingdom:<br>ANIMALS | Class:<br>Mammals | Order:<br>(*Rodentia*) Rodents | Species:<br>Other rodents | | | | | | | | | | | | |
| 2.1 | ***Peromyscus leucopus***<br>White footed mouse<br><br>After Cassola *et al.* 2016 | Population modification<br>To modify wild populations of this species to render them resistant to the bacteria causing Lyme's disease, and thus reduce spread of this disease to humans | Not specified<br>Not specified | Long *et al.* 2019 | **1** | **2** | **3 G** | 4 | 5 | 6 | 7 | 8 | 9 | A.G. Barbour<br>University of California Irvine, USA | NIH<br>Bay Area Lyme Foundation<br>UCI<br>USC<br>DoD |
| 2.2 | | | CRISPR daisy drive<br>localized 'daisy drive' system | Buchthal *et al.* 2019 | **1** | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | K.M. Esvelt<br>MIT, USA | Greenwall<br>Rainwater<br>CDMRP - DoD<br>Sloan<br>Burroughs Wellcome Fund<br>NIH<br>MIT Media Lab |

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | **Institution** | |
| 3.1 | ***Rattus norvegicus***<br>Brown rat | Population suppression | Homing CRISPR<br>(targeting 'haplosufficient female fertility gene' or<br>'haplosufficient zygote viability gene') and<br>'Y-shredder' (located on X-chromosome) | Champer *et al.* 2021 | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P.W. Messer<br>Cornell University, USA | Predator Free NZ<br>NIH<br>Bio-heritage NZ<br>UK NERC |
| | <br>After Khlyap 2012, appended after Hulme-Beaman 2021. | Eradicating invasive rat populations on islands to address their impacts on biodiversity | Three drives modelled:<br>'homing drive' targeting either female fertility or zygote viability; and 'Y-shredder located on the X-chromosome' | | | | | | | | | | | | |
| 3.2 | | Population suppression | Homing CRISPR (targeting 'haplosufficient female fertility gene') | RoslinInstitute 2017<br>McFarlane, Whitelaw, and Lillico 2018 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | C.B.A. Whitelaw<br>S.G. Lillico<br>Roslin Institute, University of Edinburgh, UK | CSC<br>BBSRC |
| | | 'to curb pest rodent populations' | Homing gene drive targeting female fertility | | | | | | | | | | | | |
| 3.3 | | Population suppression | T-haplotype sex ratio distorter (carrying SRY cargo) | Manser *et al.* 2019 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.R. Price<br>University of Liverpool, UK | SNSF<br>UK NERC |
| | | To eradicate invasive populations on islands | synthetic sperm-killing gene drive:<br>'t-Sry' | | | | | | | | | | | | |
| 3.4 | | Population suppression | Homing CRISPR or not specified | Dearden *et al.* 2018<br>Godwin *et al.* 2019<br>**These papers make similar proposals so have been combined in one entry** | | | | | | | | | | Various institutions | Funder not stated for Dearden *et al.*<br>Godwin *et al.* funded by DARPA |
| | | To control or eradicate invasive populations in New-Zealand or on islands | NA – proposal only | | | | | | | | | | | | |

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | **Institution** | |
| 4.1 | ***Rattus rattus***<br>Common rat or black rat | Population suppression | Homing CRISPR – two variants modelled | Prowse *et al.* 2017 | 1 | 2<br>M | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P.Q. Thomas<br>University of Adelaide, Australia | University of Adelaide |
| | <br>Shiels & Veitch, 2023 [7] | 'eradication of alien rodents on islands' to address impacts on bio-diversity.<br>The impacts of rodents on agriculture are also noted as a driver. | 'CRISPR gene drive'<br>Two variants modelled:<br>'Homozygotic embryonic non-viability'<br>'Homozygotic XX sterility' | | | | | | | | | | | | |
| 4.2 | | Population suppression | Homing CRISPR (targeting 'haplosufficient female fertility gene' or 'haplosufficient zygote viability gene')<br>or<br>'Y-shredder' located on X-chromosome | Champer *et al.* 2021 | 1 | 2<br>M | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P.W. Messer<br>Cornell University, USA | Predator Free NZ<br>NIH<br>Bio-heritage NZ<br>UK NERC |
| | | Eradicating invasive rat populations on islands to address their impacts on biodiversity | Three drives modelled:<br>'homing drive' targeting either female fertility or zygote viability<br>'Y-shredder located on the X-chromosome' | | | | | | | | | | | | |
| 4.3 | | Population suppression | Homing CRISPR or<br>'Y-linked X shredder'-<br>Y-chromosome-linked X-shredder | Birand, Cassey, Ross, Thomas, *et al.* 2022 | 1 | 2<br>M | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.A. Prowse<br>University of Adelaide, Australia | ARC<br>New South Wales Government<br>South Australia Government |
| | | Eradication of this species at continental scale, presumably in Australia, to address impacts on biodiversity | 'CRISPR homing drive targeting female fertility'<br>or<br>shredding drive ('driving-Y') | | | | | | | | | | | | |

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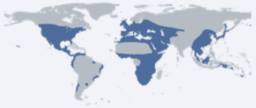
[7] This map shows countries and regions where this species is present, and so does not show the true geographic range. It may be that the species is not present in the whole territory of a country, for example it is probably absent from Arctic areas of Canada.

|  | **Species**<br>**Geographic range** | **Intended direct effect**<br>**Intended use** (as stated by authors) | **Type of gene drive** (our categories)<br>**Developer's name for gene drive system** | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** |  |  |  |  |  |  |  |  | **Project leader(s)**<br>**Institution** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 4.4 |  | Population suppression<br>To eradicate invasive populations on islands | T-haplotype sex ratio distorter (carrying SRY cargo)<br>synthetic sperm-killing gene drive: 't-Sry' | Manser *et al.* 2019 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.R. Price<br>University of Liverpool, UK | SNSF<br>UK NERC |
| 4.5 |  | Population suppression<br>To control or eradicate invasive populations in Australia, New-Zealand or on islands | Homing CRISPR or not specified<br>NA – proposal only | Dearden *et al.* 2018<br>Moro *et al.* 2018<br>Godwin *et al.* 2019<br>Thresher 2022<br>**These papers make similar proposals so have been combined in one entry** |  |  |  |  |  |  |  |  |  | Various institutions | Funder not stated in most cases.<br>Godwin *et al.* funded by DARPA |
| 5 | ***Sciurus carolinensis***<br>Grey squirrel | Population suppression<br>To 'control a targeted grey squirrel population' to reduce impacts on biodiversity and damage to property in the UK (where it is invasive) | Homing CRISPR + Cleave and Rescue [Toxin Antidote] CRISPR combination, with 'daisy-field'<br>HD-ClvR: 'composed of homing (H), daisyfield (D), and cleave-and-rescue (ClvR) gene drives'<br>(a highly speculative and complex drive) | Faber *et al.* 2021 | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | G. Gorjanc<br>Roslin Institute, University of Edinburgh, UK | BBSRC |
| 6.1 | ***Rattus exulans***<br>Polynesian rat<br><br>After Ruedas *et al.* 2016 | Population suppression<br>To control or eradicate invasive populations in New-Zealand or on islands | Homing CRISPR or not specified<br>NA – proposal only | Dearden *et al.* 2018<br>Godwin *et al.* 2019<br>**These papers make similar proposals so have been combined in one entry** | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | Various institutions | Funder not stated for Dearden *et al.*<br>Godwin *et al.* funded by DARPA |

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | **Institution** | |
| Kingdom: ANIMALS | Class: Mammals | Order: *Carnivora* (Cats, dogs and related mammals) | | | | | | | | | | | | | |
| 7.1 | ***Felis catus***<br>House cat & feral cat | Population suppression | Not stated | Australian Wildlife Conservancy 2022 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | Not known | AWC and/or CSIRO |
| | <br>After Bengsen *et al.* 2015 | To eradicate or control feral cats in Australia to reduce predation of native species | Not stated | | | | | | | | | | | | |
| 7.2 | <br>*Felis silvestris* (wild cat). After Yamaguchi *et al.* 2015 [8] | Population suppression | Homing CRISPR<br>or<br>'Y-linked X shredder'-<br>Y-chromosome-linked X-chromosome shredding drive | Birand, Cassey, Ross, Thomas, *et al.* 2022 | 1 | 2<br>M | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.A. Prowse<br>University of Adelaide, Australia | ARC<br>New South Wales Government<br>South Australia Government |
| | | Eradication at continental scale, presumably in Australia, to address impacts on biodiversity | 'CRISPR homing drive targeting female fertility'<br>or<br>('driving-Y') | | | | | | | | | | | | |
| 7.3 | | Population suppression | Homing CRISPR | Moro *et al.* 2018 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | M. Tizard<br>Australian Animal Health Laboratory, Australia | No specific funder acknowledged<br>All authors appear to be Australian Government employees |
| | | Eradication or control of feral cats in Australia to address their impact on biodiversity, i.e. native fauna. | RNA-guided gene drive | | | | | | | | | | | | |

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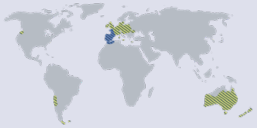
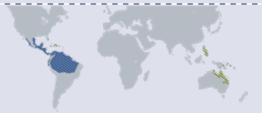
[8] We have included the range of the wild cat, *Felis silvestris*, which can readily hybridise with the domestic cat, *Felis catus*.

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)**<br>**Institution** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | | |
| 8.1 | ***Vulpes vulpes***<br>European red fox | Population suppression | Homing CRISPR<br>or<br>'Y-linked X shredder'<br>Y-chromosome-linked X-chromosome-shredding drive | Birand, Cassey, Ross, Thomas, *et al.* 2022 | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.A. Prowse<br>University of Adelaide, Australia | ARC<br>New South Wales Government<br>South Australia Government |
| | <br>After Hoffman & Sillero-Zubri, 2021 | Eradication at continental scale, presumably in Australia, to address impacts on biodiversity | 'CRISPR homing drive targeting female fertility'<br>or<br>'driving-Y' | | | | | | | | | | | | |
| 8.2 | | Population suppression | Homing CRISPR | Moro *et al.* 2018 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | M. Tizard<br>Australian Animal Health Laboratory, Australia | No specific funder acknowledged<br>All authors appear to be Australian Government employees |
| | | Suppression/eradication to address decline in 'Australia's terrestrial mammal fauna' caused by predation by foxes. The paper also states '...foxes are a serious agricultural pest'. | RNA-guided gene drive | | | | | | | | | | | | |
| 9 | ***Mustela erminea***<br>Stoats | Population suppression | Homing CRISPR | Dearden *et al.* 2018 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | D.R. Penman<br>Lincoln University, New Zealand | Funder not stated |
| | | To control or eradicate this invasive species in New Zealand to reduce predation of native birds including kiwis | NA – proposal only | | | | | | | | | | | | |

| | Species | Intended direct effect | Type of gene drive (our categories) | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? | | | | | | | | | Project leader(s) | Funders |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Geographic range | Intended use (as stated by authors) | Developer's name for gene drive system | | | | | | | | | | | Institution | |
| Kingdom: ANIMALS | Class: Mammals | Order: *Diprotodontia* (Possums and related marsupials) | | | | | | | | | | | | | |
| 10 | ***Trichosurus vulpecula***<br>Brushtail possum | Population suppression | Homing CRISPR | Dearden *et al.* 2018 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | D.R. Penman<br>Lincoln University, New Zealand | Funder not stated |
| | | To control or eradicate this invasive species in New Zealand to reduce damage to native trees and the spread of bovine tuberculosis | NA – proposal only | | | | | | | | | | | | |
| Kingdom: ANIMALS | Class: Mammals | Order: *Artiodactyla* (Deer, Pigs and related mammals) | | | | | | | | | | | | | |
| 11 | ***Cervid family***<br>Deer | Population suppression | Homing CRISPR | Castle *et al.* 2022 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | D. Westaway<br>University of Alberta, Canada | Alberta Prion Research Institute<br>CFI<br>University of Alberta |
| | | To render the wild population immune to chronic wasting disease [by spreading *PRNP* null alleles]<br>> see entry 1.6 | CRISPR/Cas9 gene drive<br>initial work on rabbit and mouse cell lines only | | | | | | | | | | | | |
| 12 | ***Sus scrofa***<br>Feral pigs | Population suppression | Not specified | Carter *et al.* 2022 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T Strive<br>Centre for Invasive Species Solutions,<br>Australia | Not stated<br>Probably CSIRO |
| | | To address the 'social, economic and environmental burden' of this non-native species in Australia | NA – proposal only | | | | | | | | | | | | |

| | **Species**<br>**Geographic range** | **Intended direct effect**<br>**Intended use** (as stated by authors) | **Type of gene drive** (our categories)<br>**Developer's name for gene drive system** | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)**<br>**Institution** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Kingdom:<br>ANIMALS | Class:<br>Mammals | Order:<br>*Lagomorpha* (Rabbits and hares) | | | | | | | | | | | | | **Theoretical studies only** |
| 13.1 | ***Oryctolagus cuniculus***<br>European rabbit | Population suppression | Homing CRISPR – two variants modelled | Prowse *et al.* 2017 | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P.Q. Thomas<br>University of Adelaide, Australia | University of Adelaide |
| | <br>After Tablado *et al.* 2009 | Eradication of invasive rabbit populations on islands to address biodiversity impacts<br>Impacts of rabbits on agriculture are also noted | CRISPR gene drive<br>Two variants modelled:<br>'Homozygotic embryonic non-viability'<br>'Homozygotic XX sterility' | | | | | | | | | | | | |
| 13.2 | | Population suppression | Homing CRISPR<br>or<br>'Y-linked X shredder'-<br>Y-chromosome-linked X-chromosome shredding drive | Birand, Cassey, Ross, Thomas, *et al.* 2022 | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T.A.A. Prowse<br>University of Adelaide, Australia | ARC<br>New South Wales Government<br>South Australia Government |
| | | Eradication at continental scale, presumably in Australia, to address impacts on biodiversity | 'CRISPR homing drive targeting female fertility'<br>or<br>'driving-Y' | | | | | | | | | | | | |
| 13.3 | | Population suppression | Homing CRISPR or not specified | Moro *et al.* 2018<br>Thresher 2022<br>**These papers make similar proposals so have been combined in one entry** | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | Various institutions | Funder not stated in both cases. |
| | | To control or eradicate invasive populations in Australia or New-Zealand | NA – proposal only | | | | | | | | | | | | |

|  | Species<br>Geographic range | Intended direct effect<br>Intended use (as stated by authors) | Type of gene drive (our categories)<br>Developer's name for gene drive system | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? |  |  |  |  |  |  |  |  | Project leader(s)<br>Institution | Funders |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Kingdom: ANIMALS | Class: Birds |  |  |  |  |  |  |  |  |  |  |  |  |  | Theoretical studies only |
| 14 | ***Sturnus vulgaris***<br>Common starling | Population suppression<br>Suppression to address 'impacts to biodiversity and agriculture', however this species is noted for the damage it causes to crops so this is likely the primary driver | Homing CRISPR<br>RNA-guided gene drive | Moro *et al.* 2018 | **1** | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | M. Tizard<br>Australian Animal Health Laboratory, Australia | No specific funder acknowledged<br>All authors appear to be Australian Government employees |
| Kingdom: ANIMALS | Class: Amphibians |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 15.1 | ***Bufo marinus* or *Rhinella marina***<br>Cane toad<br><br>After Solís *et al*, 2009 | Population modification<br>To 'detoxify' toads in Australia to address impacts on native species which are poisoned by eating them. | Homing CRISPR<br>NA – proposal only | Tingley *et al.* 2017 | **1** | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | R Shine<br>University of Sydney, Australia | Not stated |
| 15.2 |  | Population suppression<br>Suppression to address impacts on native species in Australia, which are either predated by toads or poisoned by eating them. | Homing CRISPR<br>RNA-guided gene drive | Moro *et al.* 2018<br>Cooper *et al.* 2020 – conference abstract | **1** | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | M. Tizard<br>Australian Animal Health Laboratory, Australia | No specific funder acknowledged<br>All authors appear to be Australian Government employees |
| 15.3 |  | Population suppression<br>Suppressing 'invasive populations of cane toads' | Z linked W-shredder, with variable parameters<br>*(to control species with ZW sex determination)*<br>Z linked 'W-shredder'<br>(analogue to Y linked X-shredder) | Holman 2019 | **1** | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | L. Holman<br>University of Melbourne, Australia | ESEB<br>SNSF |

| | Species | Intended direct effect | Type of gene drive (our categories) | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? | | | | | | | | | Project leader(s) | Funders |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Geographic range | Intended use (as stated by authors) | Developer's name for gene drive system | | | | | | | | | | | Institution | |
| 16 | ***Eleuthero-dactylus coqui***<br>Caribbean tree frog | Population suppression | Homing CRISPR | Thresher 2022<br>Feasibility study | **1** | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | A.C. Thresher<br>University of California San Diego, USA | Funder not stated |
| | | Eradication or suppression of this species, (accepting risk of global extinction), to address biodiversity impacts of invasive populations | 'CRISPR/Cas suppression-drive' | | | | | | | | | | | | |
| Kingdom: ANIMALS | Super-class: Bony fish | | | | | | | | | | | | | | |
| 17 | ***Cyprinus carpio***<br>European carp [9] | Population suppression | Not specified | Minnesota Aquatic Invasive Species Research Centre 2022 | **1** | **2** | **3** | 4<br>?<br>? | 5 | 6 | 7 | 8 | 9 | M. Smanski<br>University of Minnesota, USA | ENRTF |
| | | Control of invasive populations of this species | Not specified | | | | | | | | | | | | |
| 18 | ***Pterois volitans***<br>Red lionfish | Population suppression | Homing CRISPR | Vacura *et al.* 2018 | **1** | **2** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P. Venturelli<br>Ball State University, USA | Funder not stated |
| | | To control or eradicate this invasive species to address damaging impacts to native reef communities in Caribbean and Western Atlantic | NA -preliminary theoretical study | | | | | | | | | | | | |

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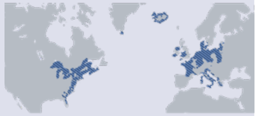
[9] Kopf *et al.* 2019 raised the possibility of using a gene drive to suppress invasive populations of carp but do not recommend this approach.

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | **Institution** | |
| Kingdom: ANIMALS | Infraphylum: Jawless fish | | | | | | | | | | | | | | **Theoretical studies only** |
| 19.1 | ***Petromyzon marinus***<br>Sea lamprey | Population suppression<br>or population modification to enable suppression | Options proposed include:<br>Split homing CRISPR<br>'Y-Linked X-shredder'<br>Homing CRISPR<br>Toxin Antidote | Ferreira-Martins *et al.* 2021 | ▨ 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | M.S. Docker | Funders not stated |
| | <br>After NatureServe, 2013[10] | Suppression or eradication of the lamprey from the North American Great Lakes to prevent this parasitic species damaging fish stocks | Options proposed include:<br>'Split gene drive'<br>'Driving y'<br>'Homing suppression gene drive'<br>'Toxin-antidote gene drive' | | ▨ | | | | | | | | | University of Manitoba, Canada | |
| 19.2 | | Population suppression | Homing CRISPR or not specified | York, Thresher, and McCauley 2021<br>Lampman *et al.* 2019<br>**These papers make similar proposals so have been combined in one entry** | ▨ | | | | | | | | | Various institutions | Funders not stated |
| | | Suppression or eradication of the lamprey from the North American Great Lakes to prevent this parasitic species damaging fish stocks | NA - proposal only | | ▨ | | | | | | | | | | |
| Kingdom: ANIMALS | Phylum: Arthropods | Class: Arachnids | | | | | | | | | | | | | |
| 20 | ***Tetranychidae family***<br>Spider mites | Propose population replacement (to render them more susceptible to insecticides) | Homing CRISPR | Li *et al.* 2020 | ▨ 1 | ▨ 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | B.E. Tabashnik | BARD |
| | | Reduction of damage to agricultural and horticultural crops | NA -preliminary theoretical study | | ▨ | ▨ | | | | | | | | University of Arizona, USA | |

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[10] This map shows only the inland range for this species, that is watersheds and freshwater lakes where it is present. The species lives part of its life in saltwater and its native range also 'includes the Atlantic coast of North America from Newfoundland to northern Florida, the Atlantic coast of Europe, and the Baltic, western Mediterranean and Adriatic seas.' (Government of Ontario, 2018). In the great lakes, where it is invasive, it has adapted to live entirely in freshwater conditions (Government of Ontario, 2018).

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | **Institution** | |
| 21 | ***Varroa destructor***<br>Varroa mite | Population modification to enable suppression | Homing CRISPR | Faber *et al.* 2021 | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | B.A. Harpur | BBSRC<br>University of Edinburgh<br>Purdue University<br>Project Apis M. |
| | | Suppression or eradication of varroa mites from honeybee colonies to prevent harm to the colony and honey production | (homing) CRISPR Cas9 gene drive | | | | | | | | | | | Purdue University, USA | |
| Kingdom:<br>ANIMALS | Phylum:<br>Arthropods | Class:<br>Insects | | | | | | | | | | | | | |
| **SEE SEPARATE TABLE** | | | | | | | | | | | | | | | |
| Kingdom:<br>ANIMALS | Phylum:<br>Molluscs | Class:<br>Gastropods | | | | | | | | | | | | | |
| 22.1 | ***Biomphalaria glabrata*** | Population modification | Not specified but cites examples of homing CRISPR | Hambrook *et al.* 2020 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | P.C. Hannington | NSERC |
| | <br>After Habib *et al.* 2021[11] | The aim is to modify snail populations to increase their immunity to schistosome infection, thereby disrupting the schistosome lifecycle and reducing transmission to humans | Not specified | | | | | | | | | | | University of Alberta, Canada | |

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[11] This map show countries where this species is present and does not show the exact geographic range.

| | Species | Intended direct effect | Type of gene drive (our categories) | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? | | | | | | | | | Project leader(s) | Funders |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Geographic range | Intended use (as stated by authors) | Developer's name for gene drive system | | | | | | | | | | | Institution | |
| 22.2 | ***Biomphalaria glabrata***<br>(and other snails of *Biomphalaria, Bulinus, Oncomelania & Neotricul* genera which host schistosome parasites) | Population suppression<br>and/or<br>Population modification | Several approaches proposed | Maier *et al.* 2019 - presentation | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | M. Zamanian<br>University of Wisconsin, USA<br>J. Reinhard-Rupp<br>Global Health Institute of Merck, Switzerland | Global Health Institute of Merck |
| | All *Biomphalaria* species susceptible to *Schistosoma mansoni*. After Habib *et al.* 2021 [12]  | 'Modification of natural snail populations' to reduce 'schistosomiasis prevalence and transmission' | Several approaches proposed | | | | | | | | | | | | |
| 22.3 | ***Biomphalaria glabrata*** | Population modification | Homing CRISPR | Grewelle *et al.* 2022 | 1 | 2<br>**M** | 3 | 4 | 5 | 6 | 7 | 8 | 9 | G.A. De Leo<br>Stanford University, USA | Stanford University<br>NSF |
| | | The aim is to modify snail populations to increase their immunity to schistosome infection, thereby disrupting the schistosome lifecycle and reducing transmission to humans | CRISPR gene drive | | | | | | | | | | | | |
| Kingdom: ANIMALS | Phylum: Nematodes | | | | | | | | | | | | | | |
| 23 | ***Caenorhabditis brenneri*** | Proof of principle experiments – not intended for release | daisy-chain drive,<br>daisyfield drive,<br>daisy quorum drive | Esvelt 2017a<br>Esvelt 2017b<br>**No results have been published despite substantial funding** | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | K.M. Esvelt<br>MIT, USA | DARPA<br>This funding has now ended |
| | | to 'test and optimize daisy-chain, daisyfield, and daisy quorum drives—including for daisy restoration—in fast-reproducing laboratory populations of worms… ' | daisy-chain drive,<br>daisyfield drive,<br>daisy quorum drive | | | | | | | | | | | | |

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12 This maps show countries where these species are present, and does not show the exact geographic range.

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | **Institution** | |
| Kingdom: ANIMALS | Phylum: Flatworms | | | | | | | | | | | | | | |
| 24 | ***Schistosoma mansoni (Schistosoma haematobium*** **also proposed)**<br>Blood flukes | Population suppression | Z linked W-shredder, with variable parameters<br>(as described by Holman, 2019) | AAAS 2016<br>Iordanskiy *et al.* 2017 - conference abstract<br>Holman 2019<br>**No results have been published** | ▨ 1 | ▨ 2 | ▨ 3 | ▨ 4 | 5 | 6 | 7 | 8 | 9 | K.M. Esvelt<br>MIT, USA<br>P. Brindley<br>George Washington University, USA | MaxMind and probably others<br>This funding has likely ended |
| | | To suppress schistosome parasites to thereby reduce human morbidity and mortality from schistomiasis | One proposal would be a Z linked 'W-shredder'<br>(as described by Holman, 2019)<br>'all of the offspring will be born either female or male.' (AAAS 2016) | | | | | | | | | | | | |
| Kingdom: FUNGI | | | | | | | | | | | | | | | |
| 25.1 | ***Fusarium graminearum*** | Population modification | Engineered gene drive employing *Spok1* (spore killer meiotic drive from *Podospora* spp.) | Gardiner *et al.* 2020<br>Urquhart and Gardiner, 2022[13] | ■ 1 | ■ 2 | ■ 3 | ■ 4 | ■ 5 | 6<br>?<br>?<br>? | 7 | 8 | 9 | K. Kazan<br>CSIRO, Queensland, Australia<br>D. M. Gardiner<br>CSIRO, Queensland, Australia | CSIRO<br>ARC<br>Australian Goverment |
| | | To modify populations of *F. graminearum* to disrupt virulence factors in this species, and so reduce head blight in wheat and barley | *Spok1* | | | | | | | | | | | | |
| 25.2 | | Population modification | Split homing CRISPR | Gardiner *et al.* 2020 | ■ 1 | ■ 2 | ■ 3 | ■ 4 | 5 | 6 | 7 | 8 | 9 | K. Kazan<br>Agriculture and Food, CSIRO, Australia | CSIRO |
| | | To modify populations of the *F. graminearum* (presumably for same reasons as in 25) | Do not use any particular term – but give detailed description of design | | | | | | | | | | | | |

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[13] Urquhart and Gardiner (2022) report further experimental work to characterise *Spok1* using the model organisms *S. cerevisiae* and *E. coli.* The 'genetic control of plant-pathogenic fungi' is mentioned as a possible future goal, with *F. graminearum* mentioned specifically.

| | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** | | | | | | | | | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** | | | | | | | | | | | **Institution** | |
| 26 | ***Fusarium verticillioides*** | To control this plant pathogen which causes 'ear and stalk rot of maize' and which can 'contaminate maize kernels with fumonisin mycotoxins' | Engineered gene drive employing Spore Killer Candidate-1 *(SKC1)* from *F. verticillioides* | Lohmar, Rhoades, Hammond, *et al.* 2022<br>Lohmar, Rhoades, Patel, *et al.* 2022 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | T. M. Hammond<br>University of Illinois, USA<br>Daren W Brown<br>USDA, Agricultural research service, Illinois, USA | NSF<br>USDA |
| | | Not specified | 'SKC1 based control practices' [which would 'require modifications to SKC1'] | | | | | | | | | | | | |
| 27.1 | ***Saccharomyces cerevisiae***<br>brewer's or baker's yeast | Population modification | Split homing CRISPR | DiCarlo *et al.* 2015 | 1 | 2 | 3 | 4 | 5 | 6<br>**?**<br>**?**<br>**?** | 7 | 8 | 9 | G.M. Church<br>Harvard Medical School, USA | DOE<br>NCI<br>NIDDK<br>Wyss Institute |
| | | Proof of principle of population modification via a split homing gene drive in this model organism | 'split CRISPR-Cas9 gene drive' | | | | | | | | | | | | |
| 27.2 | | Population modification | Split homing CRISPR | Roggenkamp *et al.* 2017 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | GC Finnigan<br>Kansas State University, USA | NIH<br>Kansas State University |
| | | To generate homozygous diploid states in modified yeast | Cas9 gene drive system | | | | | | | | | | | | |
| 27.3 | | Population modification | Probably homing CRISPR (as team had used this technology in other work) | Aguilera 2017 - press release<br>**No results published** | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | S. Kryazhimsky<br>J. Meyer<br>University of California San Diego, USA | DARPA |
| | | To study gene drives over many generations to understand the emergence of resistance | NA – no publications | | | | | | | | | | | | |
| 27.4 | | Population modification | Split homing CRISPR | Roggenkamp *et al.* 2018<br>Basgall *et al.* 2018<br>Goeckel *et al.* 2019 | 1 | 2 | 3 | 4 | 5 | 6<br>**?**<br>**?**<br>**?** | 7 | 8 | 9 | G.C. Finnigan<br>Kansas State University, USA | NIH<br>USDA<br>Kansas State University |
| | | To test various methods to modulate gene drive activity, e.g. Cas9 expression level (Roggenkamp *et al.* 2018), expression of anti-CRISPR proteins (Basgall *et al.* 2018) and Cas9 nuclear localisation (Goeckel *et al.* 2019). | CRISPR-Cas9 gene drive / CRISPR gene drive | | | | | | | | | | | | |

| | Species | Intended direct effect | Type of gene drive (our categories) | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? | | | | | | | | | Project leader(s) | Funders |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Geographic range | Intended use (as stated by authors) | Developer's name for gene drive system | | | | | | | | | | | Institution | |
| 27.5 | | Population modification | Multi-locus split homing CRISPR | Yan and Finnigan 2018 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | G.C. Finnigan | NIH<br>USDA |
| | | To test a split gene drive system to simultaneously propagate gene drives at three different loci | multi-locus CRISPR gene drive | | | | | | | ?<br>?<br>? | | | | Kansas State University, USA | |
| 27.6 | | Population modification | Split homing CRISPR employing Cas12a | Lewis, Yan, and Finnigan 2021 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | G.C. Finnigan | Kansas State University<br>USDA |
| | | Proof of principle of population modification via a split homing gene drive based on Cas12a | 'Cas12a-based gene-drive system' | | | | | | | ?<br>?<br>? | | | | Kansas State University, USA | |
| 27.7 | | Population modification | Split homing CRISPR | Bakerlee *et al.* 2022 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | M.M. Desai | DoD<br>NSERC Canada<br>NIH<br>NSF |
| | | To generate a library of 'all combinations of 10 missense mutations from across the genome' to study interactions between these mutations (epistasis) | 'hierarchical' CRISPR gene drive | | | | | | | ?<br>?<br>? | | | | Harvard University, USA | |
| 27.8 | | Population modification | Homing CRISPR variant | Abdullah *et al.* 2023 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | A H Kachroo | NSERC Canada<br>CFI<br>Québec Ministère de l'Économie, de la Science et de l'Innovation<br>Concordia University<br>Welch Foundation<br>Army Research Office<br>NIH |
| | | '[T]o readily combine genetically engineered loci' in yeast | marker-less enrichment and recombination of genetically engineered loci (MERGE) | | | | | | | | | | | Concordia University, Montreal, Canada | |

| | Species<br>Geographic range | Intended direct effect<br>Intended use (as stated by authors) | Type of gene drive (our categories)<br>Developer's name for gene drive system | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? | | | | | | | | | Project leader(s)<br>Institution | Funders |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 28 | ***Candida albicans*** | Population modification | Split homing CRISPR | Shapiro *et al.* 2018<br>Halder *et al.* 2019 | 1 | 2 | 3 | 4 | 5 | 6<br>?<br>?<br>? | 7 | 8 | 9 | J. Collins<br>MIT & Harvard University, USA<br>R.S. Shapiro<br>University of Guelph, Canada | Allen<br>CIHR<br>NIH<br>Wyss Institute<br>NSERC Canada<br>Banting<br>Burroughs Wellcome Fund |
| | | To create single and double deletion mutants in this species for laboratory studies | CRISPR-Cas9 based gene drive | | | | | | | | | | | | |
| Kingdom: PLANTS | | | | | | | | | | | | | | | |
| 29 | ***Arabidopsis thaliana***<br>Thale cress | Population modification | Homing CRISPR | Zhang, Mudgett, *et al.* 2021<br>Zhang *et al.* 2022<br>**paper WITHDRAWN after a year** | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | Y. Zhao<br>University of California San Diego, USA | TIGS UCSD<br>NIH |
| | | The intention was to demonstrate a gene drive system in a plant model species. The authors state this technology could 'accelerate crop breeding' | CRISPR/Cas9-based gene drive | | | | | | | | | | | | |
| 30 | ***Nicotiana tabacum***<br>Tobacco | Population modification | TALEN gene-drive mutagenesis | Forner *et al.* 2022 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | R. Bock<br>Max Planck Institute for Molecular Plant Physiology, Germany | Max Planck Society<br>ERC |
| | | The aim is to demonstrate a technology for modifying the plant mitochondrial genome for laboratory experiments and to 'enable the exploitation of mitochondria in biotechnology and synthetic biology' | transcription activator-like effector nuclease (TALEN) gene-drive mutagenesis (GDM), or TALEN-GDM | | | | | | | | | | | | |

|  | **Species** | **Intended direct effect** | **Type of gene drive** (our categories) | **Publication(s) where research is described** | **How close is strain/system to experimental releases in the wild?** |  |  |  |  |  |  |  |  | **Project leader(s)** | **Funders** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | **Geographic range** | **Intended use** (as stated by authors) | **Developer's name for gene drive system** |  |  |  |  |  |  |  |  |  |  | **Institution** |  |
| PLANTS |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 31 | **Various weed and invasive species:** | Population modification to enable suppression | Homing CRISPR is most common proposed technology | Neve 2018<br>Chen *et al.* 2019<br>Kumaran *et al.* 2020<br>Perotti *et al.* 2020<br>Tek and Budak 2022<br>Wong *et al.* 2022<br>Croghan *et al.* 2023<br>Kumam *et al.* 2023<br>**All the above papers make similar proposals so have been combined into one entry**<br>Mitchell and Bartsch (2020) suggest common ragweed as a target | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | Proposals from several funded CSIRO researchers including at the University of Queensland, Australia, and researchers at Rothamsted Research UK | Various funders including BBSRC and CSIRO |
|  | ***Alopecurus mysuroides*** Black grass[14]<br>***Amaranthus palmeri*** Palmer amaranth[14]<br>***Amaranthus Tuberculatus*** Rough fruited water hemp[14]<br>***Ambrosia artemisiifolia*** Common ragweed[14]<br>***Cynodon dactylon*** Bermuda grass[14]<br>***Cyperus rotundus*** Purple nut sedge[14]<br>***Eichhornia crassipes*** Water hyacinth<br>***Kochia scoparia*** Kochia[14]<br>***Lantana camara*** Common lantana[14]<br>***Lolium rigidum*** Rigid rye grass[14]<br>***Lupinus arboreus*** Yellow bush lupin/tree lupin<br>***Lychnis coronia 'Alba'*** Rose campion<br>***Tanacetum vulgare*** Common tansy[14]<br>***Setaria glauca*** Yellow foxtail[14] | To reduce the presence and impact of weed species on agricultural production by modifying them, potentially to render them less competitive, or more sensitive to herbicide.<br>The technology might also be used to tackle other invasive plant species. | NA - Proposals only |  |  |  |  |  |  |  |  |  |  |  |  |

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[14] Agricultural weed

| | Species | Intended direct effect | Type of gene drive (our categories) | Publication(s) where research is described | How close is strain/system to experimental releases in the wild? | | | | | | | | | Project leader(s) | Funders |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Geographic range | Intended use (as stated by authors) | Developer's name for gene drive system | | | | | | | | | | | Institution | |
| 32 | ***Myrtaceae* family** (including ***Eucalyptus* spp.**) | Population modification | NA | Barrett *et al.* 2019 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | D.M. Gardiner | CSIRO |
| | | To modify wild populations in Australia to render them resistant to the fungal pathogen *Puccinia psidii* | The proposals do not focus on any particular type of gene drive | | | | | | | | | | | CSIRO Agriculture and Food, Australia | |

## Key to technology levels

1 **Gene drive proposed:** a proposal has been put forward in the scientific literature or from another academic source (e.g. funding body)

2 **Gene drive proposed with supporting modelling work, or preliminary laboratory work funded:** a proposal has been made in the scientific literature supported by modelling work, or preliminary laboratory work has been funded but has not yet been published

3 **Preliminary laboratory work published**: laboratory research relevant to gene drive construction published (e.g. developing molecular biology methods) with possibility or intention to construct gene drive stated

4 **Research on gene drive construction funded:** research on gene drive construction has been funded, but no results yet published OR results published showing non-functional gene drives, or similar very limited progress

5 **Limited proof of concept:** Published results show a gene drive is to some extent functional, however there are outstanding technical issues such as resistance or low efficiency

6 **Laboratory proof of concept:** Taking published results at face value, the system works effectively in the laboratory

7 **Scaled up trials:** Data published from scaled up trials in contained environments, offering a more accurate simulation of conditions in natural environment

8 **Potential further contained trials:** After large cage trials (or other scaled up trials), it is not currently clear what further trials may take place prior to experimental releases. One possibility is trials in outdoor cages

9 **Experimental releases in natural environment:** Field trials are underway with releases in the natural environment. This does not indicate that the technology has been shown to be effective or safe

X **Abandoned project:** Research to construct a gene drive has been carried out, but has been unsuccessful and to our knowledge is no longer active

# Abbreviations for funders and other organisations

| | |
|---|---|
| Allen | Allen Frontiers Group |
| ARC | Australian Research Council |
| AWC | Australian Wildlife Conservancy |
| Banting | Banting Research Foundation |
| BARD | United States—Israel Binational Agricultural Research and Development Fund |
| BBSRC | UK Biotechnology and Biological Sciences Research Council |
| Bioheritage NZ | New Zealand Bio-heritage National Science Challenge |
| CDMRP - DoD | Congressionally Directed Medical Research Programs Department of Defense |
| CFI | Canada Foundation for Innovation |
| CIHR | Canadian Institutes of Health Research |
| CSC | Commonwealth Scholarship Commission |
| CSIRO | Commonwealth Scientific and Industrial Research Organisation |
| DARPA | US Defense Advanced Research Projects Agency |
| DoD | US Department of Defense |
| DOE | US Department of Energy |
| ERC | European Research Council |
| ESEB | European Society for Evolutionary Biology |
| Greenwall | Greenwall foundation |
| Kinship | Kinship foundation |
| NCI | US National Cancer Institute |
| NERC | UK Natural Environment Research Council |
| NIDDK | US National Institute of Diabetes and Digestive and Kidney Diseases |
| NIH | US National Institutes of Health |
| NSERC Canada | Natural Sciences and Engineering Research Council of Canada |
| NSF | US National Science Foundation |
| Packard | David and Lucile Packard Foundation |
| Pew | Pew Charitable Trust |
| Predator Free NZ | New Zealand Predator Free Program |
| Rainwater | Rainwater Foundation |
| Sloan | Sloan Foundation |
| SNSF | Swiss National Science Foundation |
| TATA | TATA trusts |
| TIGS UCSD | Tata Institute for Genetics and Society University of California San Diego |
| UCI | University of California Irvine |
| UCSD | University of Califronia San Diego |
| USC | University of South Carolina |
| USDA | US Department of Agriculture |
| Wyss Institute | Wyss Institute for Biologically Inspired Engineering |

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# Methodology

## Literature searches

Literature searches for 2004 through to the 31 December 2023 were carried out using the advanced search function in the Web of Science Core Collection database, with the search term TS= (“gene drive” or “gene drives”). Relevant journal articles were identified by systematically screening titles and abstracts from the search outputs. Press releases from academic institutions and other relevant materials on the web were identified using appropriate web searches (e.g. searching for the names of group leaders, target species, and the term ‘gene drive’). We recognise that all relevant material on the web may not have been identified.

## Criteria for inclusion

Laboratory research and modelling on gene drives in non-insect species as reported in the academic literature and other sources such as press releases from funders and universities, has been included. This includes ‘preliminary research’ – i.e. research that states it could potentially support gene drive construction – for example genome sequencing or identification of target genes.

Proposals for gene drives which do not include any modelling or laboratory research are included if they are the first such proposal, and if no more advanced work has taken place for this target.  Additional proposals are included at our discretion, for example if they contain novel ideas for gene drive technology (e.g. the Z-linked W-shredder), novel applications, or indicate wide interest in a particular target species.

## Basis for generating entries in table

Broadly, each entry in the table describes development of a particular gene drive concept in a specific target species or group, as described in the relevant literature. In some cases where multiple options are considered in a single publication, multiple proposed gene drives are described in a single row (generally these are early-stage proposals or modelling studies). Where similar proposals to target a particular species have been made in different publications without any supporting modelling or laboratory work, these are also combined into one entry. The ‘project leader’ is identified as the last author on the publications describing the research or proposals.

Citation: Wells M. A. and Steinbrecher R. A. (2026) Gene Drive Development in Non-Insect Targets - including Vertebrates, Snails, Fungi and Plants: A Horizon Scanning Survey up to end 2023. Gene Drive Monitor. https://genedrivemonitor.org/publications