

Gene Drive Development in Insect Targets:

A Horizon Scanning Survey

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Summary of findings up to end 2023

Screening and analysis of the scientific literature up to 31 December 2023 showed:

- Gene drives were developed or proposed in 43 insect species¹. Additionally, gene drives were proposed for 5 general taxonomic groups of insects².
- Of these 48 insect species or groups the majority are agricultural pests, 28 in total, while 17 are vectors of human disease, in particular malaria. The agricultural pests include 6 livestock pests or livestock disease vectors, which partially overlap with human disease vectors.
- The majority of gene drive proposals were based on eradication/suppression approaches. Only a very few projects were aiming to modify characteristics of insects in the wild.
- By the end of 2023 no project was close to producing a usable and proven 'product'. But some were closer to potential field trials, pending on regulation, risk assessment and further (technical) developments.
- CRISPR-based homing gene drives were shown to function with reasonable efficiency in several members of the order *Diptera* (true flies), especially within the mosquito genera *Anopheles* and *Aedes*, and within the genus *Drosophila*. However, it is notable that within another member of the *Diptera*, the mosquito *Culex quinquefasciatus*, a homing gene drive was only shown to operate at very low efficiency.
- It is unclear how applicable homing CRISPR gene drives will be in insects outside of the *Diptera*. In non-dipteran insects there was only one example of a such a gene drive showing any level of functionality: a very low efficiency system constructed in the diamondback moth (*Plutella xylostella*).

Please see Findings (pp. 2-3) and main table (pp. 5-26) for more information. Please note the table includes information up to the end of 2023.

Situation as of June 2026

We have screened the literature up to 1 June 2026, however a full analysis is still to be completed.

As of 1 June 2026 there have been few significant changes since the end of 2023. The majority of newly reported gene drive systems have been in *Anopheles* mosquitoes (e.g. Li et al. 2025, Strampelli et al. 2025), with two also developed in *Aedes* mosquitoes (Yang et al. 2025, Anderson et al. 2024). Gene drive development is also continuing in fruit fly targets: two more systems have been reported targeting spotted winged drosophila (*Drosophila suzukii* - Deng et al. 2025, Ma et al. 2024) and a gene drive has now been developed in the mediterranean fruit fly (*Ceratitis capitata* - Meccariello et al. 2024).

¹ Many experimental gene drive systems are being developed and tested in the model organism *Drosophila melanogaster*. Because we are not aware of any plans to target this organism in the wild, a survey of work in this species is not included here.

² The vast majority of the targets identified in the literature are single species. The *Lutzomyia longipalpis* (sand fly) and *Bemisia tabaci* species complexes (Silverleaf whitefly) have also been proposed as targets. Some early-stage proposals relate to broader taxonomic groups, namely the Glossina genus (Tsetse flies - row 25), the Scolytinae subfamily (Bark beetles - row 38) and the order Thysanoptera (Thrips - row 48). The *Anopheles gambiae* species complex has also been proposed as a target (see bullet point) - this has been excluded from the totals here because the survey covers many proposals to target individual species within the complex.

No releases of gene drive organisms have been reported to date, however, several gene drive mosquito projects are moving towards field-readiness, with islands stated as preferred potential release sites. São Tomé, of São Tomé and Príncipe, has been discussed by the University of California Malaria Initiative (UCMI) as a potential future field trial site (Wickramasooriya, 2026). In Tanzania, the Transmission Zero program has identified Ukerewe Island as a potential site for future pilot trials and has undertaken preparatory ecological and entomological studies (Amos 2026).

Small scale field trials of non-gene drive GM mosquitoes have taken place in Africa, in particular in Djibouti by Oxitec (Oxitec 2024) and in Burkina Faso by Target Malaria. Target Malaria's research and field trials in Burkina Faso has now been discontinued on the orders of the country's government,

Context

The emergence of gene drive technology opens-up – at least in theory - unprecedented prospects of modifying, suppressing, or even eradicating wild species to serve human purposes. The consequences of choosing to go down this path are very difficult to foresee, especially in the longer term. The assessment, regulation and international oversight of gene drive technology has thus become the subject of intensive debate, for example within the UN Convention on Biological Diversity (CBD). To help frame further discussion on this topic, we undertook a horizon scanning survey of gene drive development in insects, systematically screening the scientific literature.

We do not cover issues regarding risks, difficulties in performing robust risk assessments, or difficulties in confining, halting or reversing engineered gene drives.

Our survey gives an overview of:

- What research has taken place and where.
- Which species and taxa are 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.

Findings

Screening and analysis of the scientific literature for gene drive development in insects up to 31 December 2023 showed:

- Gene drives were under development or have been proposed for 43 insect species¹. Beyond these 43 species, an additional 5 taxonomic insect groups have been proposed as targets². A total of 48 target species or groups are thus listed in the table below (pp. 5-26, representing the orders *Diptera* (true flies), *Lepidoptera* (moths, butterflies and skippers), *Hemiptera* (true bugs), *Coleoptera* (beetles and weevils), *Hymenoptera* (sawflies, bees, wasps and ants), *Thysanoptera* (thrips). Of these 48 targets, 25 were *Diptera*, including 14 mosquito species.
- 17 of the proposed targets are vectors of human disease, in particular malaria. These are the 14 mosquito species listed in rows 1.1 to 14, sand flies and Tsetse flies in rows 24 and 25, and the kissing bug (*Rhodnius prolixus*) in row 34 of the main table (pp 5-26).
- The majority of proposed targets are agricultural pests - 28 in total. These include six livestock pests or livestock disease vectors, which partially overlap with human disease vectors. One target, the fall webworm (*Hyphantria cunea* – row 27) also impacts forestry. Gene drive targets impacting crops are detailed in rows 15-18, 21, 26-30, 31-33, 35-37, 37, 39-42, 45, 48; targets impacting livestock are listed in rows 13, 19, 20, 22, 23 and 25.
- Only five species were proposed as targets due to their wider biodiversity impacts or the combination of economic losses and biodiversity impacts (see rows 43-47). Bark beetles in row 38 were proposed as a target for forest management purposes, while *Culex quinquefasciatus* in rows 13.1-13.2 has become a target for conservation purposes – as a vector of bird malaria - and because of its role in transmitting diseases to humans and livestock.

- Some target species are part of species complexes – groups of closely related species which can in some cases inter-breed to give fertile offspring. There is a strong possibility that gene drives could spread from one species to others within a species complex. The *Anopheles gambiae* species complex contains at least nine species – some of which are not vectors of human malaria. It therefore may well be difficult or impossible to prevent gene drives impacting non vector species in this complex. In response to this situation the concept of the ‘target species complex’ has been put forward (Connolly et al. 2023), which would designate all species in the complex as targets. This proposal is controversial however – opponents have argued for example that the concept ‘risks reframing collateral impacts as intentional outcomes’ (Boete 2025).
- The majority of gene drive proposals were based on eradication/suppression approaches – for example targeting the African malaria mosquito *Anopheles gambiae* (see rows 1.1 to 1.12), or the crop pest spotted winged drosophila (*Drosophila suzukii* see rows 15.1 to 15.3). Only a few projects were aiming to modify characteristics of insects in the wild, and almost always with the intention of reducing their capacity to spread disease, for example in *Anopheles gambiae* (1.9 to 1.12), in the Asian malaria mosquito *Anopheles stephensi* (4.1 to 4.2), and in the kissing bug *Rhodnius prolixus* (34.1 to 34.2).
- By end of 2023, no projects were close to producing a usable and proven ‘product’ (and this remains the case at the date of publication). Since then, some projects have moved closer to potential field trials, pending risk assessment and regulatory approval and perhaps overcoming further technical issues (as described above).
- Among the projects that have progressed furthest towards potential field testing is the Target Malaria program developed by Imperial College London and its African partners, which aims to target *Anopheles gambiae* and related species (row 1.2). Our survey also reports examples of so-called ‘X-shredders’, a sex ratio distortion system developed by the same team (row 1.1, 2.1 and 3.1). Though not strictly gene drives, X-shredders share characteristics with certain gene drive systems – for example they rely on CRISPR/Cas and aim to remove females to eradicate populations. Releases of such X-shredder modified mosquitoes has been proposed as a preliminary step before releases of gene drive modified mosquitoes (Target Malaria, 2026).
- CRISPR-based homing gene drives have been shown to produce a high level of distorted inheritance - a ‘super-mendelian’ inheritance bias - in several members of the order *Diptera* (true flies). These include members of the mosquito genera *Anopheles* and *Aedes*, and fruit flies of the genus *Drosophila*. By contrast, in the mosquito *Culex quinquefasciatus*, another dipteran species, homing gene drives have so far only generated a very limited inheritance bias. While gene drive systems appear to be functional in a narrow sense in some dipteran species (i.e. generating non-mendelian inheritance in a laboratory trial), technical and regulatory issues remain, including the difficulties in confining or reversing gene drives.
- It remains unclear if homing CRISPR gene drives can be engineered to function in insects outside of the *Diptera*. In non-dipteran insects there is only one example of such a gene drive showing any level of functionality: a very low efficiency system constructed in the diamondback moth (*Plutella xylostella*). Unsuccessful attempts at gene drive construction have been reported in the Asian citrus psyllid (*Diaphorina citri* – row 31.1), the diamond back moth (row 26.2) and in red flour beetle (*Tribolium castaneum* (Markley et al. 2024)).
- Substantial effort has also been going towards developing gene drives in the mosquito genera *Aedes* and *Culex*, which are not vectors of malaria, but are vectors of other diseases. Both genera are vectors for viruses, including Zika, Dengue and Yellow fever in the case of *Aedes* mosquitoes, and for the nematodes that cause lymphatic filariasis (rows 11.1-14).
- Concerning crop pests, the ‘spotted winged drosophila’ (*Drosophila suzukii*) (rows 15.1-15.3) and the diamondback moth (*Plutella xylostella*) (rows 26.1-26.3) were the focus of substantial gene drive development efforts. A gene drive system targeting the mediterranean fruit fly (*Ceratitis capitata*) was reported in 2024 (Meccariello et al. 2024).

Please see main table (pp.5-26) for more details up to end of 2023.

Summary of proposed insect targets

	Taxonomic Group	Taxonomic level	Common name	Number of proposed targets	Number of proposed target groups
	CULICIDAE	family	mosquitoes	14	
	DIPTERA	order	flies - here excluding mosquitoes	9	2
	LEPIDOPTERA	order	moths, butterflies and skippers	5	
	HEMIPTERA	order	true bugs	5	1
	COLEOPTERA	order	beetles and weevils	5	1
	HYMENOPTERA	order	sawflies, bees, wasps and ants	5	
	THYSANOPTERA	order	thrips		1
	total			43	5

Concluding remarks

Undertaking a broad horizon scanning survey of gene drive development research makes the bigger picture clearer, allowing one to perceive trends, as well as obstacles and concerns. A wide-ranging ambition for gene drive technology is evident, 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 thought or hoped. Our data also show that the vast majority of proposals relate to suppressing or eradicating species or populations, as opposed to modifying them for different traits.

How might gene drive technology develop in the medium term? Our survey suggests that in the coming years gene drive development in insects will likely focus on members of the *Diptera* order (true flies), including mosquitoes and agricultural pests such as fruit flies. Fly species that impact livestock may also be targeted. Attempts will likely continue to develop gene drives in agricultural pests belonging to other insect orders, though these are likely long-term endeavours due to technical issues. Field trials of gene drive mosquitoes are now a realistic possibility – it is beyond the scope of this work to consider the ecological and other risks that such trials would bring. However, the increasing emphasis on field-readiness and potential future releases underscores the importance of precaution, robust independent risk assessment, meaningful public participation, transboundary governance arrangements, and careful consideration of potential impacts on biodiversity and ecological integrity.

Our table identifies a significant number of species where gene drives have been proposed but not yet constructed. Whilst much uncertainty remains – the possibility that gene drives could eventually be used to target a wide range of insect species, cannot be ruled out. Such an outcome scenario requires serious reflection and analysis. Questions would need to include: Who will model the deployment as a whole and analyse or assess 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?

Methodology

Please see end of document.

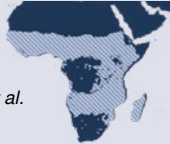
	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system												
CULICIDAE (mosquitoes) 															
1.1	<i>Anopheles gambiae</i> African malaria mosquito  (Sinka <i>et al.</i> 2012)	Reduction of transmission of malaria pathogen by this vector (to reduce morbidity and mortality from malaria in Sub-Saharan Africa)	Autosomal sex ratio distorter - 'X-shredder' (I-Ppol based) ¹	Galizi <i>et al.</i> 2014 Facchinelli <i>et al.</i> 2019 Bernardini <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	A. Crisanti Imperial College London, UK + M.Q. Benedict CDC, USA	Gates Foundation (via NIH); European Research Council
1.2			Homing CRISPR Gene drive targeting doublesex (<i>dsx</i> gene) or <i>dsxF</i> CRISPR gene drive	Kyrou <i>et al.</i> 2018 Hammond, Pollegioni, <i>et al.</i> 2021 Garrood <i>et al.</i> 2021 Taxirachi <i>et al.</i> 2021 Qureshi <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	A. Crisanti Imperial College London, UK	Gates Foundation Open Philanthropy DARPA BBSRC
1.3			Autosomal sex ratio distorter - 'X-shredder' (CRISPR based) ¹ CRISPR-Cas9 sex ratio distortion system	Galizi <i>et al.</i> 2016	1	2	3	4	5	6	7	8	9	A. Crisanti Imperial College London, UK	Gates Foundation (via NIH)
1.4			Homing CRISPR + Sex Distorter (X-shredder) (male-biased) Sex- distorter gene drive (SDGD)	Simoni <i>et al.</i> 2020 Garrood <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	A. Crisanti Imperial College London, UK	Gates Foundation

¹ Engineered sex ratio distorter systems that are NOT gene drives

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
1.5	<i>Anopheles gambiae</i> African malaria mosquito Sub-Saharan Africa  (Sinka <i>et al.</i> 2012)	Reduction of transmission of malaria pathogen by this vector Population suppression or modification	Homing gene drive using I-SceI Synthetic homing endonuclease-based gene drive system	Windbichler <i>et al.</i> 2011	1	2	3	4	5	6	7	8	9	A Crisanti Imperial College London, UK A Burt Imperial College London, UK	Foundation for National Institutes of Health NIH
1.6		Reduction of transmission of malaria pathogen by this vector Population suppression	Homing CRISPR CRISPR-Cas9 gene drive system targeting female reproduction	Hammond <i>et al.</i> 2015 Hammond <i>et al.</i> 2017 Garrood <i>et al.</i> 2021 Pescod <i>et al.</i> 2023 ²	1	2	3	4	5	6	7	8	9	A. Crisanti Imperial College London, UK	Gates Foundation (via NIH) European Research Council
1.7			Homing CRISPR CRISPR-Cas9 gene drive system targeting female reproduction	Hammond, Karlsson, <i>et al.</i> 2021 Garrood <i>et al.</i> 2021 Taxiarchi <i>et al.</i> 2021 Pescod <i>et al.</i> 2023 ²	1	2	3	4	5	6	7	8	9	A. Crisanti Imperial College London, UK	Gates Foundation
1.8		Reduction of transmission of malaria pathogen by this vector Population suppression	Homing CRISPR Adult lethal gene drive	Fuchs <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	A Crisanti Imperial College London, UK T Nolan Liverpool School of Tropical Medicine, UK	Gates Foundation Open Philanthropy

2 Pescod *et al.* (2023) carried out further work to characterise the performance of these systems in different strains of *An. gambiae* at the Liverpool School of Tropical Medicine.

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
1.9	<i>Anopheles gambiae</i> African malaria mosquito	Reduction of transmission of malaria pathogen by this vector	Homing CRISPR	Carballar-Lejarazú <i>et al.</i> 2020 Carballar-Lejarazú <i>et al.</i> 2021 Carballar-Lejarazú <i>et al.</i> 2022 Terradas <i>et al.</i> 2022 Carballar-Lejarazú <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	A. James UC Irvine, USA	Gates Foundation UC Irvine
	Sub-Saharan Africa  (Sinka <i>et al.</i> 2012)	Population modification	'Cas9/guide RNA (gRNA)-based gene- drive systems' 'autonomous gene- drive system'												
1.10		Population modification (to stop pathogen development within mosquito)	Split homing CRISPR variant (targeting CP, AP-2, and Aper-1) Integral gene drive (IGD)	Hoermann <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	N. Windbichler Imperial College London, UK	Gates Foundation
1.11		Reduction of transmission of malaria pathogen by this vector Population modification	Split homing CRISPR variants (targeting Gam1 and CP) Integral gene drive (IGD)	Hoermann <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	N. Windbichler Imperial College London, UK	Gates Foundation Wellcome Trust
1.12		Reduction of transmission of malaria pathogen by this vector Population modification	Homing CRISPR variant Describe a 'CRISPR/ Cas9 integral gene drive allele'	Ellis <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	N. Windbichler Imperial College London, UK	Gates Foundation
	<i>Anopheles gambiae</i> species complex	Connolly <i>et al.</i> (2023) have proposed designating this a 'target species complex'. This species complex includes at least nine species some of which are major malaria vectors (<i>Anopheles gambiae</i> s.s., <i>Anopheles coluzzii</i> , <i>Anopheles arabiensis</i>). Others however (<i>Anopheles quadriannulatus</i> , <i>Anopheles bwambae</i> , <i>Anopheles fontenillei</i>) are not believed to contribute to malaria transmission (Boëte 2025).													

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
2.1	<i>Anopheles arabiensis</i> Sub-Saharan Africa and a small part of Arabian peninsula  (Sinka <i>et al.</i> 2012)	Reduction of transmission of malaria pathogen by this vector (to reduce morbidity and mortality from malaria in Sub-Saharan Africa) Population suppression	Autosomal sex ratio distorter -'X-shredder' ¹ Synthetic sex ratio distortion system	Bernardini <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	A. Crisanti Imperial College London, UK	Gates Foundation
2.2		Reduction of transmission of malaria pathogen by this vector Population suppression or modification	3 approaches modelled: Homing drive targeting fertility or Y linked X-shredder (driving Y) or Homing drive for population replacement NA – preliminary study	Eckhoff <i>et al.</i> 2017	1	2	3	4	5	6	7	8	9	A. Burt Imperial College London, UK	Global Good Fund Gates Foundation
3.1	<i>Anopheles coluzzii</i>	Reduction of transmission of malaria pathogen by this vector (to reduce morbidity and mortality from malaria in Sub-Saharan Africa) Population suppression	Autosomal sex ratio distorter -'X-shredder' (I-Ppol based) 'synthetic sex ratio distortion transgene'	Pollegioni <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	P. Pollegioni National Research Council, Terni, Italy [A Crisanti - also an author now at University of Padova, Italy]	Gates Foundation Open Philanthropy

1 Engineered sex ratio distorter systems that are NOT gene drives

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
3.2	<i>Anopheles coluzzii</i>	Reduction of transmission of malaria pathogen by this vector	Homing CRISPR	Carballar-Lejarazú <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	A. A. James UC Irvine, USA	Gates UC Irvine
		Population modification	'Cas9/guide RNA (gRNA)-based gene- drive systems' 'autonomous gene- drive system'												
3.3		Population modification	Homing CRISPR variant, with toxin antidote element	Green <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	E Marois University of Strasbourg, France	Agence Nationale de la Recherche Deutsche Forschungsge- meinschaft
		Reduction of transmission of malaria pathogen by this vector	Saglin based gene drive												
4.1	<i>Anopheles stephensi</i> Asian malaria mosquito	Reduction of transmission of malaria pathogen by this vector (to reduce morbidity and mortality from malaria in India and surrounding regions)	Homing CRISPR	Gantz <i>et al.</i> 2015 Pham <i>et al.</i> 2019 Carballar-Lejarazú <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	E. Bier & A. James UC San Diego, USA UC Irvine, USA	NIH Sarah Sandell and Michael Marshall W. M. Keck Foundation TATA Institute Gates Foundation UC Irvine
	Indian subcontinent and parts of middle east - see map  (Sinka <i>et al.</i> 2012)	Population modification to 'interrupt parasite transmission'	Cas9 mediated gene drive system for population modification												

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
4.2		Reduction of transmission of malaria pathogen by this vector	Homing CRISPR	Adolfi <i>et al.</i> 2020 Carballar-Lejarazú <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	A. James UC Irvine, USA	NIH TATA Institute UC Irvine DARPA
		Population modification – proof of principle	HDR based autonomous gene drive rescue system (HDR = homology directed repair)	Terradas <i>et al.</i> 2022											
5.1		Reduction of transmission of malaria pathogen by this vector	Unspecified CRISPR based gene drive	Li <i>et al.</i> 2018	1	2	3	4	5	6	7	8	9	B J White University of California San Diego, USA Liverpool School of Tropical Medicine, UK	NIH DARPA
		Population suppression	NA -preliminary study												
5.2		Reduction of transmission of malaria pathogen by this vector	Unspecified – probably would be derived from systems developed by Gates Foundation in <i>An. gambiae</i>	Ogola <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	D.P. Tchousassi International Centre of Insect Physiology and Ecology, Kenya	Gates Foundation (via NIH) DFID Sida SDC Kenyan Govt
		Unspecified	NA – preliminary study only												
5.3		Reduction of transmission of malaria pathogen by this vector	Not stated	Djuicy <i>et al.</i> 2020	1	2	3	4	5	6	7	8	9	C S Wondji Centre for Research in Infectious Diseases (CRID), Cameroon Liverpool School of Tropical Medicine, UK	Gates Foundation Wellcome Trust
		Population suppression	NA -preliminary study												
5.4		Reduction of transmission of malaria pathogen by this vector	Probably homing CRISPR – cites these drives as showing ‘the most promise’	Quinn <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	T. Nolan Liverpool School of Tropical Medicine, UK	BBSRC
		Not specified but does talk about ‘control’ of this vector	NA – preliminary study only												

[illegible]

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?										Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9			
11.2		Reduction in transmission of arboviruses (e.g. yellow fever, chikungunya, dengue, and Zika) by this vector.	Homing CRISPR	Reid <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	A. W. E. Franz University of Missouri, USA	NIH	
		Population modification/replacement	Single locus autonomous CRISPR/Cas9 gene drive													
11.3		Presumably to reduce impacts on human health from Yellow fever and dengue transmission by this vector species, however the authors do not make this explicit	Split homing CRISPR	Anderson <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	L. Alphey Pirbright Institute, UK	DARPA Wellcome Trust BBSRC	
		NA - Technology development	'Split drive' / 'Split homing-drive'													
11.4		Reduction of disease-transmission by this vector species	Homing CRISPR	Chae <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	Z. N. Adelman Texas A&M University, USA	NIH-NIAID Texas A&M USDA	
		Population suppression	'homing-based gene drive' - preliminary research													
12	<i>Aedes albopictus</i>	Reduction in transmission of arboviruses (e.g. yellow fever, chikungunya, dengue, and Zika) by this vector.	Homing CRISPR	Zhao <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	X.-G. Chen Southern Medical University, China A. James University of California Irvine, USA	National Natural Science Foundation of China National Key Research and Development Program of China NIH	
		Population suppression	CRISPR/Cas9 gene-drive system													

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
13.1	<i>Culex quinquefasciatus</i> Southern house mosquito  (Samy <i>et al.</i> 2016)	Reduction of transmission of vector borne diseases in humans, mammals and birds (e.g. avian malaria)	Split homing CRISPR	DARPA 2017 Anderson <i>et al.</i> 2019 Anderson <i>et al.</i> 2020 Purusothaman <i>et al.</i> 2021 Feng <i>et al.</i> 2021 Harvey-Samuel <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	L. Alphey Pirbright Institute, UK [+ K. Esvelt MIT, USA On DARPA grant award]	DARPA; BBSRC; Wellcome Trust UCSD NIH TATA
13.2			Unspecified - CRISPR based NA – preliminary study only	Li, Li, <i>et al.</i> 2020	1	2	3	4	5	6	7	8	9	O. Akbari UC San Diego, USA	In part: UC San Diego Start Up Funds
14	<i>Culex tarsalis</i> Western Encephalitis Mosquito	Population suppression Reduction in transmission of arboviruses (e.g. West Nile virus) in humans and horses by this vector	Unspecified gene drive + sex ratio distorter 'gene-drive-based sex ratio distorter'	Main <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	C. M. Barker University of California, Davis	NIH U.S. Centers for Disease Control and Prevention Gordon and Betty Moore Foundation

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system												
DIPTERA (flies)  here excluding mosquitoes (see above)															
15.1	<i>Drosophila suzukii</i>³ Spotted wing drosophila (SWD) Bangladesh, Korea, Thailand. Spread into: Japan, Brazil, Argentina, Chile, Mexico, United States (esp. California), Canada, and Europe (esp. France)  (Polo <i>et al.</i> 2016) (EPPO 2022)	Reduction of damage to soft fruit crops (e.g. cherries) caused by this species Here providing proof of concept for MEDEA in <i>D. suzukii</i> for population suppression/replacement	MEDEA Synthetic <i>Medea</i> gene drive system	Buchman <i>et al.</i> 2018	1	2	3	4	5	6	7	8	9	O. Akbari UC San Diego, USA	California Cherry Board
15.2		Reduction of damage to soft fruit crops (e.g. cherries) caused by this species Population suppression	Split homing CRISPR 'CRISPR/Cas9-based split homing gene drive targeting doublesex'	Yadav <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	M. J. Scott North Carolina State University, USA	NIH
15.3		Reduction of economic costs caused by consumption of fruit crops by this species. Population suppression	NA - Stakeholder engagement study NA- Stakeholder engagement study	Kokotovich <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	A.E. Kokotovich North Carolina State University, USA	USDA

3 Wolf *et al.* (2023) published an experimental study investigating the potential for *D. suzukii* to hybridise with closely related species. The aim was to establish strategies for assessing the risk of gene drive elements impacting non-target species via hybridisation.

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
16.1	<i>Ceratitis capitata</i> Mediterranean fruit fly (medfly)	Reduction of damage to fruit crops caused by this species	Autosomal sex ratio distorter - 'X-shredder'	Meccariello <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	N. Windbichler Imperial College London, UK	BBSRC BARD
	Africa, Mediterranean area Australasia, North and South America (FAO/IAEA 2017)	Population suppression	CRISPR based sex distortion												
16.2			Homing CRISPR gene drive	KaramiNejadRanjbar <i>et al.</i> 2018	1	2	3	4	5	6	7	8	9	E. Wimmer University of Gottingen, Germany	DAAD Excellence Foundation for the Promotion of the Max Planck Society IGI UC Berkeley DARPA
			Cas9 based sex conversion suppression gene drive (note no constructs yet tested in <i>C. capitata</i>)												
16.3			Preliminary study only, but development of CRISPR methods in this species points towards CRISPR based gene drive design	Sim <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	S.M. Geib Daniel K. Inouye US Pacific Basin Agricultural Research Center, USA	USDA
			NA – preliminary study only												
17	<i>Anastrepha ludens</i> Mexican fruit fly	Reduction of damage to fruit crops caused by this species	Preliminary study only, but development of CRISPR methods in this species points towards CRISPR based gene drive design	Sim <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	S.M. Geib Daniel K. Inouye US Pacific Basin Agricultural Research Center, USA	USDA
	Mexico, Central America and parts of US (CABI 2022)	Population suppression	NA – preliminary study only												

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
18.1	<i>Bactrocera dorsalis</i> Oriental fruit fly  (CABI 2022)	Reduction of damage to vegetable, fruit and nut crops caused by this species Population suppression	Preliminary study only, but development of CRISPR methods in this species points towards CRISPR based gene drive design NA – preliminary study only	Sim <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	S.M. Geib Daniel K. Inouye US Pacific Basin Agricultural Research Center, USA	USDA
18.2			Some form of CRISPR based gene drive NA – preliminary study only	Zhao <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	R. Yan Hainan University, China	
18.3			Homing CRISPR CRISPR/Cas9-based ‘female-specific lethal gene drive’	Zheng <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	H. Zhang Huazhong Agricultural University, China	National Key R & D Program of China National Natural Science Foundation of China International Atomic Energy Agency's
18.4			Unspecified gene drive NA – preliminary work	Wishard <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	A. Rai ICAR - Indian Agricultural Statistics Research Institute, India	ICAR GOI-DST

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
19	<i>Cochliomyia hominivorax</i> New world screwworm	Reduction of disease and death of livestock caused by this species in in Uruguay, and more widely in South America and the Caribbean	Split homing CRISPR	Paulo <i>et al.</i> 2019 Scott <i>et al.</i> 2020 Fresia <i>et al.</i> 2021 Menchacha 2021	1	2	3	4	5	6	7	8	9	M.J. Scott North Carolina State University, USA A. Menchacha Institut Pasteur Montevideo, Uruguay National Institute of Agricultural Research (INIA), Uruguay	NCSU FAPESP USDA-ARS COPEG STRI Institut Pasteur de Montevideo IADB INIA
	 (CABI 2022)	Population suppression	CRISPR/Cas9-based split homing gene drive targeting doublesex	Novas <i>et al.</i> 2023 Tsanni 2024											
20	<i>Lucilla cuprina</i> Australian sheep blowfly	Reduction of disease and death of livestock caused by this species in Australia and New Zealand	Probably homing CRISPR (in line with proposals for <i>C. hominivorax</i>)	Paulo <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	M.J. Scott North Carolina State University, USA	FAPESP USDA-ARS COPEG STRI
	Throughout the world (needs warmer weather conditions)	Population suppression	NA – preliminary study only												
21	<i>Bactrocera oleae</i> Olive fruit fly	Reduction of harm to olive harvests caused by this species	Homing CRISPR	Koidou <i>et al.</i> 2020	1	2	3	4	5	6	7	8	9	J. Vontas Foundation for Research & Technology, Hellas, Greece	
	 (CABI 2022)	Population suppression	NA – preliminary study only												
22	<i>Lucilla sericata</i> Green bottle fly	Reduction of disease and death of livestock caused by this species	Propose Homing CRISPR	Davis <i>et al.</i> 2021	1	2	3	4	5	6	7	8	9	M.J. Scott North Carolina State University, USA	DARPA
	Throughout the world	Population suppression	NA – preliminary study only												

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
23	Wohlfahrtia magnifica Spotted flesh fly (or screw worm fly)	To reduce impacts on livestock health from myiasis caused by this parasitic fly species	Homing CRISPR	Jia <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	P. A. Burger University of Veterinary Medicine Vienna, Austria	Chinese Scholarship Council (CSC) National Natural Science Foundation of China Austrian Science Funds (FWF)
		Population suppression	Cas9-based homing gene drive system												
24	Lutzomyia longipalpis species complex Sand Fly	Reduction in transmission of <i>Leishmania infantum</i> by this vector (to reduce occurrence of visceral leishmaniasis disease)	Propose homing CRISPR	Wellcome 2017	1	2	3	4	5	6	7	8	9	M. Yeo London School of Hygiene and Tropical Medicine, UK	Wellcome
	Primarily central and South America (Sosa- Estani and Leonor Segura 2015)	Population modification	NA – preliminary study only												
25	Glossina genus Tsetse flies	Reduction in transmission of trypanosome parasites by this vector (to reduce occurrence of sleeping sickness in humans and livestock, esp. European cattle breeds)	NA – proposal only	Bier 2022	1	2	3	4	5	6	7	8	9	E. Bier UC San Diego, USA	NIH Allan Frontiers Group Gates Foundation; TATA trusts
	 (FAO in Kariithi <i>et al.</i> 2013)	Not stated – proposal only	NA – proposal only												

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system												
LEPIDOPTERA (moths, butterflies and skippers)  															
26.1	<i>Plutella xylostella</i> Diamond back moth  (Zalucki <i>et al.</i> 2012) Top – year round range Bottom – seasonal range	Demonstration of a functional homing CRISPR gene drive system in this species, to allow development of systems for 'genetic control of globally-distributed pest <i>P. xylostella</i> ' Proof of principal for either population modification or suppression (ultimate aim appears to be population suppression)	Homing CRISPR CRISPR/Cas9-based gene drive (CCGD)	Asad <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	G. Yuang Fujian Agriculture and Forestry University, China	National Natural Science Foundation of China Special Key Project of Fujian Province "111" program
26.2		Reduction of damage to cruciferous crops by this species Not stated	Split homing CRISPR CRISPR-Cas9 based gene drive in the diamondback moth	Xu <i>et al.</i> 2022 Xu <i>et al.</i> 2020 Huang <i>et al.</i> 2017	1	2	3	4	5	6	7	8	9	M.S. You Fujian Agriculture and Forestry University, China + L. Alphey Pirbright Institute, UK	BBSRC EU Chinese government National Natural Science Foundation of China
26.3		Reduction of damage to cruciferous crops by this species Population suppression	Drive type not specified in detail Proposed system is termed 'RIDL-with-Drive' (RIDL - Release of Insects carrying Dominant Lethal)	Harvey-Samuel <i>et al.</i> 2019	1	2	3	4	5	6	7	8	9	L. Alphey Pirbright Institute, UK	EU BBSRC

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
27	<i>Hyphantria cunea</i> Fall webworm	Population suppression	Unspecified gene drive	Li, Liu <i>et al.</i> 2020	1	2	3	4	5	6	7	8	9	Y Huang Institute of Plant Physiology and Ecology, H Chen A&F University	Special Fund for Forest Scientific Research in Public Welfare Chinese Academy of Sciences National Science Foundation of China National Key Research and Development Programme of China
		Reduction of damage to forests and fruit trees China	NA – preliminary study only												
28	<i>Helicoverpa armigera</i> Cotton bollworm	Population suppression	Unspecified 'local' gene drive	Medina 2017	1	2	3	4	5	6	7	8	9	R F Medina Texas A&M University, USA	Not stated
		Reduction of damage to corn crops caused by this species in USA	NA – proposal only												
29	<i>Ostrinia nubilalis</i> European corn borer	Population suppression	Unspecified 'local' gene drive	Medina 2017	1	2	3	4	5	6	7	8	9	R F Medina Texas A&M University, USA	Not stated
		Reduction of damage to maize crops caused by this species in USA	NA – proposal only												
30	<i>Plodia interpunctella</i> Indian meal moth	Reduction of damage to dry food stores (e.g. cereals) caused by this species	NA – proposal only	Goldsmith <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	C. Goldsmith Texas A&M University, USA	USDA
	Present on all continents except Antarctica (CABI 2022)	Not stated – proposal only	NA – proposal only												

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?										Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system													
HEMIPTERA (true bugs) 																
31.1	<i>Diaphorina citri</i> Asian citrus psyllid	Reduction in transmission of citrus greening disease, and resulting harm to citrus fruit. This species acts as a vector for <i>Candidatus Liberibacter</i> spp. bacteria which cause the disease.	Not stated – no details of design published	Described by Jones <i>et al.</i> 2019 and Turpen 2017 (Report to USDA)	1	2	3	4	x	x	x	x	x		T. Turpen Citrus Research and Development Foundation, Florida, USA	USDA
	Central and South America, India, South East Asia and Saudi Arabia (Grafton-Cardwell <i>et al.</i> 2005)	Population replacement or modification	Not stated – no details of design published													
31.2		As above	Propose homing CRISPR	Wheatley and Yang 2021	1	2	3	4	5	6	7	8	9		Y. Yang Pennsylvania State University, USA	USDA Hatch appropriations
		Population modification or suppression proposed	NA – proposal only													
32	<i>Lygus hesperus</i> Western tarnished plant bug	Reduction in damage to cotton and other crops caused by this species	Probably CRISPR based – various forms of CRISPR drive cited	Heu <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9		J. Fabrick U.S. Arid Land Agricultural Research Center, USA	Cotton Incorporated
	Mainly western US, also reported in US state of Georgia (CABI 2022)	Population suppression	NA – preliminary study													
33	<i>Riptortus pedestris</i> Bean bug	Population suppression	Homing CRISPR	Wang <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9		J. C. Zhuo Ningbo University, China	Zhejiang Provincial Natural Science Foundation of China National Natural Science Foundation of China Ningbo Natural Science Foundation
		Reduction of damage to soya bean crops caused by this species	Not stated													

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
34.1	<i>Rhodnius prolixus</i> Kissing bug	Reduction in transmission of the parasite <i>Trypanosoma cruzi</i> by this vector (to reduce occurrence of Chagas disease)	Propose homing CRISPR	Wellcome 2017	1	2	3	4	5	6	7	8	9	M. Yeo London School of Hygiene and Tropical Medicine, UK	Wellcome
	Venezuela, Columbia and parts of Central America (Sosa-Estani and Leonor Segura 2015)	Population modification	NA – no research published yet												
34.2		Reduction in transmission of the parasite <i>Trypanosoma cruzi</i> by this vector (to reduce occurrence of Chagas disease)	Probably homing CRISPR	Berni <i>et al.</i> 2020	1	2	3	4	5	6	7	8	9	H. Araujo Federal University of Rio de Janeiro, Brazil	Not stated
		Population modification or suppression	NA – unpublished preliminary study only												
35.1	<i>Bemisia tabaci</i> species complex Silverleaf whitefly	Reduction of damage to crops caused by transmission of begomoviruses by this vector species	Homing CRISPR	Li, Aidlin Harari, <i>et al.</i> 2020	1	2	3	4	5	6	7	8	9	B.E. Tabashnik University of Arizona, USA	United States— Israel Binational Agricultural Research and Development Fund
	 (Kriticos <i>et al.</i> 2020)	Population modification	NA – preliminary theoretical study												
35.2	<i>Bemisia tabaci</i>	Reduction of damage to crops via feeding or transmission of viruses (especially begomoviruses)	Probably homing CRISPR	Mahmood <i>et al.</i> 2022 Mubarik <i>et al.</i> 2020 Scott <i>et al.</i> 2018	1	2	3	4	5	6	7	8	9	Various institutions	Various funders
		Population modification/ replacement OR Population suppression/ eradication	'CRISPR based gene drive'	These papers make similar proposals so have been combined in one entry											

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
36	<i>Trioza eryteae</i> African citrus psyllid (vector of citrus greening disease)  (CABI 2022)	Reduction in transmission of citrus greening disease, and resulting harm to citrus fruit. This species acts as a vector for <i>Candidatus liberibacter</i> spp. bacteria which cause the disease.	Propose homing CRISPR	Wheatley and Yang 2021	1									Y. Yang Pennsylvania State University, USA	USDA Hatch appropriations
		Population modification or suppression proposed	NA – proposal only												
COLEOPTERA (Beetles and weevils)  															
37	<i>Tribolium castaneum</i> Red flour beetle Present on all continents except Antarctica (IRAC 2026)	Reduction of spoilage of stored grains caused by this species Population suppression	Homing CRISPR NA – preliminary theoretical study	Drury <i>et al.</i> 2017	1	2	3	4	5	6	7	8	9	M.J. Wade University of Wisconsin, USA	NIH Indiana University start- up funds
38	<i>Scolytinae subfamily</i> Bark beetles NA - No single species named as a target yet	Reduction of damage to timber crops caused by this species Population suppression	Homing CRISPR NA – preliminary theoretical study	Liu and Champer 2022 (Note that Li, Aidlin Harari, <i>et al.</i> 2020 also imply these species could be a target)	1	2	3	4	5	6	7	8	9	J. Champer Peking University, China	Peking University SLS-Qidong Innovation Fund
39	<i>Diabrotica virgifera</i> Western corn rootworm	Population suppression Reduction of damage to corn crops caused by this species in Europe	Unspecified 'local' gene drive NA – proposal only	Medina 2017	1	2	3	4	5	6	7	8	9	R F Medina Texas A&M University, USA	Not stated

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
40	<i>Listronotus bonariensis</i> Argentine stem weevil	Reduction of damage to pasture grass caused by this species	Not stated – proposal only	Dearden <i>et al.</i> 2018	1	2	3	4	5	6	7	8	9	P. Dearden University of Otago, NZ	Not stated
	Indigenous to South America, it has spread to Australia and New Zealand  (EPPO 2022)	Population suppression	NA – proposal only												
41	<i>Sitona lepidus</i> (synonym – <i>S. obsoletus</i>) clover root weevil	Reduction of damage to clover caused by this species (in agricultural contexts)	Not stated – proposal only	Dearden <i>et al.</i> 2018	1	2	3	4	5	6	7	8	9	P. Dearden University of Otago, NZ	Not stated
	 (CABI 2022)	Population suppression	NA – proposal only												
42	<i>Anthonomus grandis</i> Mexican cotton boll weevil	Reduction of damage to cotton crops caused by this species	Not stated – proposal only	Goldsmith <i>et al.</i> 2022	1	2	3	4	5	6	7	8	9	C. Goldsmith Texas A&M University, USA	USDA
	Indigenous to Central America, has spread to USA, Caribbean, Brazil and other South American countries (CABI 2022)	Not stated – proposal only	NA – proposal only												

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system												
HYMENOPTERA (sawflies, bees, wasps and ants)    															
43	<i>Vespula vulgaris</i> Common wasp	Reduction of ecological effects of invasive populations of this species in New Zealand and elsewhere (e.g. Australia)	Homing CRISPR	Dearden <i>et al.</i> 2018 Lester <i>et al.</i> 2020 Lester <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	P. Dearden University of Otago, NZ + P.J. Lester Victoria University of Wellington, NZ	New Zealand Ministry of Business Innovation and Employment Victoria University of Wellington
	Paleartic species native to Eurasia, invasive in parts of South America, Australia, New Zealand and Hawaii	Population suppression	NA – preliminary theoretical study												
44	<i>Vespula germanica</i> German wasp	Reduction of ecological effects of invasive populations of this species in New Zealand and elsewhere (e.g. Australia)	Homing CRISPR	Dearden <i>et al.</i> 2018 Lester <i>et al.</i> 2020	1	2	3	4	5	6	7	8	9		
	Predicted distribution - suitable and marginal areas  (de Villiers, Kriticos, and Veldtman 2017)	Population suppression	NA – preliminary theoretical study												
45	<i>Solenopsis invicta</i> Red imported fire ant	Reduction of impacts on agriculture, biodiversity and infrastructure caused by this invasive species	Homing CRISPR	Liu and Champer 2022	1	2	3	4	5	6	7	8	9	J. Champer Peking University, China	Peking University SLS-Qidong Innovation Fund
	Native to South America. Imported populations in United States, China, Australia, New Zealand and some other SE Asian and Carribean countries (Chen <i>et al.</i> 2020)	Population suppression	NA – preliminary theoretical study												

	Species	Intended use	Type of gene drive (our categories)	Publications (where research is described)	How close is strain/system to <i>experimental</i> releases in the wild?									Project leader (corresponding author on publications) Institution	Funders
	Geographic range (of target species)	Intended direct effect (of gene drive)	Developer's name for gene drive system		1	2	3	4	5	6	7	8	9		
46	<i>Vespa velutina nigrithorax</i> Yellow legged hornet or Asian Hornet	Reduce impacts from predation of commercial honey bees (and potentially wild pollinators)	Homing CRISPR	Meiborg <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	A. B. Meiborg Roslin Institute, University of Edinburgh, UK	EMBL Wageningen University USDA BBSRC
		Population suppression	' <i>homing gene drive</i> ' targeting a ' <i>haplosufficient female fertility gene</i> ' [model other variants, but state this is most likely to be effective]												
47	<i>Polistes dominula</i> European paper wasp	Presumably to reduce biodiversity impacts of invasive populations of this species, however the authors do not make this explicit.	Homing CRISPR	Meiborg <i>et al.</i> 2023	1	2	3	4	5	6	7	8	9	A. B. Meiborg Roslin Institute, University of Edinburgh, UK	EMBL Wageningen University USDA BBSRC
		Population suppression	' <i>homing gene drive</i> ' targeting a ' <i>haplosufficient female fertility gene</i> ' [model other variants, but state this is the only candidate likely to be effective]												
THYSANOPTERA (Thrips) 															
48	<i>Thysanoptera</i> order Thrips	Reduction of damage to crops caused by thrips	Homing CRISPR	Liu and Champer 2022	1	2	3	4	5	6	7	8	9	J. Champer Peking University, China	Peking University SLS-Qidong Innovation Fund
	NA - No single species named as a target yet	Population suppression	NA – proposal only												

Abbreviations for funders and other organisations

BBSRC	UK Biotechnology and Biological Sciences Research Council
BARD	United States –Israel Binational Agricultural Research and Development Fund
CDC	Centers for Disease Control and Prevention (Atlanta, US)
COPEG	Panama-United States Commission for the Eradication and Prevention of Screwworm
DAAD	German Academic Exchange Service
DARPA	US Defense Advanced Research Projects Agency
DFID	UK Department for International Development
FAPESP	São Paulo Research Foundation
Gates Foundation	The Bill and Melinda Gates Foundation
GoI-DST	Government of India Department of Science and Technology
IADB	Inter-American Development Bank
ICAR	Indian Agricultural Research Institute
IGI UC Berkeley	Innovative Genomics Institute, University of California, Berkeley
INIA	Instituto Nacional de Investigación Agropecuaria
NIH US	National Institutes of Health
NCSU	North Carolina State University
PAF	Philanthropy Advisory Fellowship
SDC	Swiss Agency for Development and Cooperation
STRI	Smithsonian Tropical Research Institute
Sida	Swedish International Development Cooperation Agency
TATA	TATA trusts
UC	University of California
USDA	US Department of Agriculture

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 theoretical work, or preliminary laboratory work funded:** a proposal has been made in the scientific literature supported by theoretical or modelling work, or preliminary laboratory work has been funded but has not yet been published
- 3 **Preliminary laboratory work:** laboratory research relevant to gene drive construction published (e.g. developing molecular biology methods) with possibility or intention to construct gene drive stated
- 4 **Active research on gene drive construction:** 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 small cage trials
- 7 **Large cage trials:** Data published on trials in large cages, offering a more accurate simulation of conditions in natural environment.
- 8 **Potential further contained trials:** After large cage 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

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Methodology

Literature searches

Literature searches of English language publications from 2004 through to the 1 June 2026 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 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, novel applications, or indicate wide interest in a particular target species.

We also report on certain sex ratio distorters that are relevant in the context of gene drive research.

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 up to 31 December of 2023. 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.