Integrative
Plant Biotechnology
ISSN: 3007-2735 (Online), 3007-2727 (Print)

Check for updates

ROOTS PRESS

Review Article

Gene Drive Technologies for the Control of Invasive Species

Amna Saghir Aasi[1], Laiba Ashfaq[1], Aleena Jaffar[1], Muhammad Moazzam Bin Rasheed[1], Waqar Ahmad Khan[2], Rao Sohail Ahmad Khan[1]*

[1]*Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture, Faisalabad, Pakistan.*
[2]*Institute of Molecular Biology and Biotechnology, Bahauddin Zakariya University, Multan, Pakistan.*

ABSTRACT

Pests and disease cause a loss in agronomic output every year, making it more difficult to eradicate hunger and poverty. The arrival of invasive animals has been associated with the disappearances of local wildlife and with major losses in agriculture. Controlling invasive species today usually involves high levels of effort and authority for many years and often the control does not last. New and creative ideas are needed now. Experts are now suggesting that gene drives based on CRISPR/Cas9 and guided by RNA could help wildlife managers decrease the numbers of pest animals without harming them. Though strong control and social agreement are crucial, we have a chance now to recognize where there are not enough scientific studies or understanding for some key invasive species. We identify the areas in pest knowledge where gene drives could have a helpful impact. Applying an ecological risk framework within a gene drive context, we outline what must be achieved before working on seven invasion species in Australia. It enables assessing the value of different research ideas related to invasive species by considering gene drives and risks. We use the available biological, genetic and ecological information for the house mouse, European red fox, Feral cat, European rabbit, black rat and European starling to find out what we don't yet understand and identify suitable species for additional study. We explain these findings in relation to what other research topics could be studied before gene drives are formally assessed for containing these and other invasive species.

Keywords: Invasive species, Gene drive, Biosphere, Transposable elements, CRISPR-Cas 9, Selfish genes

OPEN ACCESS

***Correspondence**
Rao Sohail Ahmad Khan
srao@uaf.edu.pk

Article History
Received: April 23, 2025
Accepted: June 19, 2025
Published Online: June 29, 2025

Cite this article
Aasi, A. S., Ashfaq, L., Jaffar, A., Rasheed, M. M. B., Khan, W. A., & Khan, R.S. A. (2025). Gene Drive Technologies for the Control of Invasive Species. Integrative Plant Biotechnology, 3, 145–152.

INTRODUCTION

Each year, crops are faced with a variety of serious challenges, such as insect pests and diseases, which not only harm the crops themselves but also hinder progress in the global fight against hunger and poverty. To address this, one promising approach is to breed crops that are naturally resistant to both pests and diseases, which aligns with environmentally conscious farming practices. However, a significant hurdle exists: the lack of sufficient genetic diversity in the available gene pool, which limits the development of stronger, more resilient crop varieties (Moro *et al.*, 2018). Without the necessary genetic resistance, farmers often have to rely on chemical pesticides and other harmful treatments to protect their crops. Unfortunately, these solutions are not only costly but also have devastating effects on the environment, threatening ecosystems and wildlife. In light of the growing concerns about ecological degradation and the impacts of global climate change, there is an urgent need to focus on cultivating plants that are naturally resistant to pests and diseases (Ricroch and Hénard-Damave, 2016).

Fortunately, recent advances in biological research are providing new tools and systems that offer exciting possibilities. These breakthroughs allow scientists to explore innovative ways to understand the intricate relationships between plants and the organisms that threaten them. By better understanding these biological interactions, researchers are now able to find new strategies for strengthening the natural defenses of plants by reducing the reliance on harmful chemicals and helping ensure more sustainable agricultural practices in the future.

INVASIVE SPECIES

Invasive species are ones that are introduced outside of their natural environment. These infections often infect a larger area and sometimes bring serious side effects to the environment. Across the world, people understand the effect invasive animals and plants have on both biodiversity and agriculture (Bellard *et al.*, 2016). Islands and similar places in fact experience these effects even more strongly. Australia and New Zealand are cases where the introduction of species that became invasive has led to localized. Many local species are losing their habitats and numerous financial losses are being caused (Doherty *et al.*, 2017). New Zealand is now making a strong effort to remove several alien predators that put their native animals in danger (Russell *et al.*, 2015). Because Australia is an island nation, it wants to keep invasive species from affecting its native animals. Guiding both conservation and the production of agriculture. For example, both feral cats and the European red fox have both contributed to have been recognized as massive contributors to Australia's terrestrial mammal population decline (Woinarski *et al.*, 2015). Best stated, invasive species are those strange classes that, when familiarized, get recognized and damage social and ecological morals (Fleming *et al.*, 2017).

On the other hand, there are various innate types that, when the circumstances are altered, damage those identical ethics. In Cuba, the presence of *Dichrostachys cinerea* (L.) Wight & Arn., *Mimosa pigra* (L.) and *Vachellia farnesiana* (L.) seriously affects the country's ecosystem. Marabú is a common case of the widespread damage that affect tropical areas caused by foreign species (Valero-Jorge *et al.*, 2024). Koalas were brought to Kangaroo Island around the 1920s to protect them. The population grew so fast that many habitats have been damaged. It is the presence of preferred food species (rough-barked manna gum, South Australian blue gum and red gum) along waterways that accounts for high numbers of koalas. For instance, Phascolarctos cinereous, the iconic koala, has aggressive influences on flora in Kangaroo Island (Whisson *et al.*, 2012). Species that can be damaging in some situations are still considered useful, for example, flowers that reappear after things like erosion, flood and fire happen (Harvey-Samuel *et al.*, 2019).

EMERGENCE

Biodiversity loss is mainly caused by invasive species. It is known to be a major cause of the destruction of many vertebrate species. The number of invasive species has steadily increased worldwide, including an obvious rise during the years 1970 to 2014. We knew at the time that further invasions were being predicted in the near future. Invasive types are changing the normal atmosphere found in the biosphere (Baron, 2008). Many more than half a million new classes are given in terrestrial habitats as a result of social factors (Pimentel *et al*., 2005). If invading species are detected soon after forming or if only a small area is affected, removal is possible. If a pest spreads quickly and over large areas, the proper solution is classic genetic control and putting out sterile male plants. As civilization has advanced, it has also made some invasive species appear. The habit of getting mates from afar grew which made it more possible for invasive species to enter (Barrett *et al.*, 2019).

GENE DRIVE

Gene drive is a genetic engineering technology that is achieved through number of mechanisms. Gene drive works to increase how likely a specific gene is to be passed to the next generation which makes it possible for that gene to quickly affect large numbers of individuals, even when it doesn't offer a real advantage. With the help of tools like CRISPR-Cas9, scientists can influence the inheritance of certain traits(Heitman *et al.*, 2016). These are capable of being inherited at higher rates within the progeny, ultimately spreading quickly over through different populations (Figure 1). It is the method of passing on inherited traits from one generation to the next, which allows some inheritable traits to spread rapidly among people even if they do not contribute to or reduce the existence and imitation of organisms (Thresher *et al.*, 2014). Genetic features that can be dispersed by drive method includes transposable elements, zygotic and gametic killers, chromosomes and meiotic drivers. The element that method of the gene drive design can results in the dispersal of characters marks it a striking process to deliberate the improvement to control the disease routes and various other pests (Burt and Crisanti, 2018). The RNA directed gene drives skilled at scattering the genomic modifications made in the test animals over uninhabited populations in a transmissible manner might be

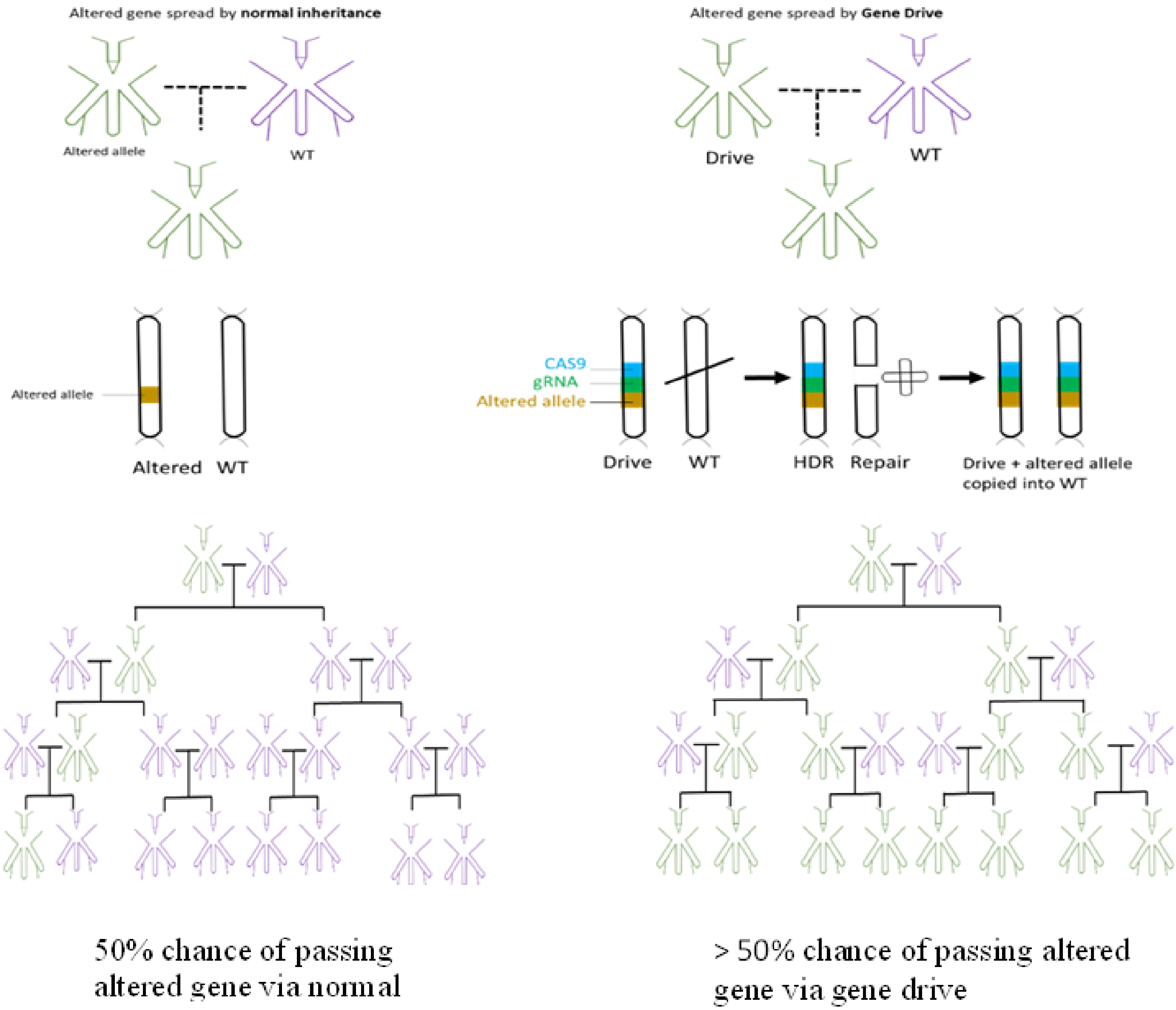

Figure 1. Comparison of gene spread between normal inheritance and gene drive.

applied to control the populations of animals that could be a source of community health complications. Nonetheless, the probability of unplanned genome excision through the emission of toxins from laboratories, requires carefulness (DiCarlo *et al.*, 2015).

SELFISH GENES

Selfish genes are basically those genes that can replicate themselves within a population. This replication might or might not interfere with the machinery of the organism carrying those genes. The term selfish genes were first coined in 1976 by Richard Dawkins. These genes can enhance their transmissions within the genome because these genes have control over their transmission. Hence, the rules change. The Self duplicating gene drives coding the homing endonucleases might possibly elucidate many persistent conservational glitches, as in the management of vector-borne illnesses (Beaghton *et al.*, 2017), the elimination of the IAS, also termed as invasive alien species as well as the problem regarding herbicide plus pesticide confrontation now in agricultural science. The gene drives are labelled 'selfish' since they are able to cross their personal heritage by self-duplication across the chromosomes, and as a result disperse over various populations even though they transmit at suitability rate (Champer *et al.*, 2016). For this reason, the idea of selfish genes could offer an answer to pest suppression (Monaco, 2022).

GENE DRIVE METHODS

Transcriptional gene silencing

Gene silencing may happen when methylation at the promoter site causes RNA synthesis to decrease. Transcriptional Gene Silencing occurs similarly to the stopping of a gene's transcription. It mainly comes from knowing that transcription is prevented at the nucleus-level in many diseases (El-Sappah *et al.*, 2021). Researchers show that these sites are included in the genome but are absent from the extra-chromosomal DNA. Alternatively, it is affirmed that adding methyl groups to DNA in the plant compartments is not observed with methylation-target free agents. This suggests that just adding methylation to sense structure can be enough to stop expression. TGS of combined systems is divided into six main modules according to the kind of gene silencing used (Rajeevkumar *et al.*, 2015) . It can begin working inside Trans or outside of it. Some pieces of the system that modify cells' function may be included inside the hetero-chromatin, placed right by the artificially introduced gene, formed from adding Methyl groups to nearby DNA or as modifications caused by several replications of the transferred gene. Possible ways the trans-acting components connect are by having ectopic or alleic homologous loci and sharing their epigenetic form using straight DNA-DNA bonding or support from proteins (Matzke *et al.*, 2015).

Post-transcriptional gene silencing (PTGS)

Post-transcriptional gene silencing takes place only in the cytoplasm and serves to break down mRNA copies of identified genes. Three main ones are RNA interference (RNAi), clustered regularly interspaced short palindromic repeats (CRISPR/Cas9) and NMD (Zebec *et al.*, 2016). Some recent experiments have tested RNAi, VIGS and CRISPR/Cas9 to strengthen plants against pathogens, drought and genes involved in the formation of lignin and cellulose (Abbas *et al.*, 2019). In plants, small RNAs known as microRNA (miRNA) and small-interfering RNA (siRNA) are important in their defenses against pathogens (Axtell, 2013). Gene silencing lowers the amount of mRNA or protein produced from the gene temporarily. Genes that are silenced by gene expression mechanisms are responsible for regulating when or where development-related processes in plant metabolism, for example genome stability, waste detoxification and allergens occur (Ito, 2013).

PTGS by sense and antisense transgenes

There was still a small noncoding RNA of directed ribonucleic acid observed in the PTG Silenced leaves. However, their exact function in the PTGS remains largely unidentified yet. In particular, some ribonucleic acid particles may carry PTGS from a graft where viruses are controlled by PTG Muzzled, all the way to a graft without PTG Muzzling or ribonucleic acid may spread from plants with controlled PTGS due to viruses on their leaves alongside unprotected plants (Sabbione *et al.*, 2019). Another approach used genes in codes or no code mentioning sections of viral genomes that failed to function properly, so that they reliably induced resistance toward the PVY disease in tobacco. Though the genes were still not clear, the virus did not contaminate the floras. The essayists went on to say that Double-stranded RNA is mandatory before PTGS can be activated and afterward, the RdRp could get stuck when moving on to the next step (Zheng *et al.*, 2018).

PTGS by DNA and RNA viruses

Certainly, in plants, post transcriptional gene silencing is carried out with the help of various viruses. Just like the artificially introduced genes, viruses could exist as the basis, objective, or may be both basis and objective of muzzling. Viruses can serve themselves as the target for the PTGS machinery. Post Transcriptional Gene Silencing assisted by the viruses could happen with the DNA infections as well, which duplicates inside the nucleus, plus through the RNA viruses, which duplicates inside the cytoplasm(Sun *et al.*, 2015). These infections could be immunised inside the plant parts at a particular phase during their growth, or else could remain articulated among the plant parts during the course of growth by firmly combined virus articulating transgenes. It serves as a versatile tool for the functional analysis of various genes in many crops particularly those which are associated with the stress situations. What basically happens is, these viruses interfere with the original host machinery, and introduce the particular viral symptoms (Borges and Martienssen, 2015).

CRISPR-CAS 9 AND GENE DRIVE

CRISPR-Cas9 arrangement remains an RNA directed endonuclease enzyme which wounds DNA next to an objective order documented by the RNA director (Figure 2). The gene drives based on the CRISPR, contain an enzyme called Cas9, which is basically an altered gene along with many guide RNAs. Talking about their transmission, these altered genes do not get transmitted solely, but also the gene drive machinery is transmitted along it (Marshall *et al.*, 2017). Significantly, the gene initiative component remains introduced next to the chromosomal position which is directed through the endonuclease, allowing directed cutting of isolated DNA arrangement taking place inside the chromosome

(Bisht *et al.*, 2019). Additionally, the scheme could be planned so that endonuclease is articulated inside the germline earlier to the meiosis. There are various concerns that the use of gene drives based on CRISPR may cause some adverse effects on the environment, different control mechanisms are being designed by the researchers.

GENOME EDITING MEDIATED BY CRISPR/CAS9

CRISPR organization remains an adaptable defense machinery existent inside the bacteria which defends them from attacking plasmids and bacterial viruses (Jinek *et al.*, 2012). It naturally serves as a defense system for the bacteria and protects them against various undesired attackers. DNA piece from the attacking plasmids and phages are combined into the mass CRISPR location as insertion between crRNA echoes (Marshall *et al.*, 2017). CAS9 protein that works as a molecular scissor, chopping DNA in selected places. DNA that is stored in the nucleus of a cell as the genetic code. The target DNA in green is formed like the matching double helix sequence. The focus sequence in this study was East-West. DNA with this sequence is what the CAS9 system is meant to recognize and cut. An RNA sequence of a few nucleotides operates as a guide for the CAS9 protein to the specific area. There are two parts to it: crRNA: This guide RNA matches the sequence of the DNA you want to change. tracrRNA: A molecule that holds the crRNA to the CAS9 protein. PAM short section of DNA called the protospacer adjacent motif is required for CAS9 to bind and cut the DNA. All in all, guide RNA leads the CAS9 protein to look for the target site on the genomic DNA. Once in the cell, CAS9 performs the needed cuts to allow the editing of a specific gene. (Figure 3). In non-appearance of the original strand, the disruptions are fixed by NHEJ which frequently leads to transmissible alteration changing the prearranged characteristic (Symington and Gautier, 2011). Being a modest two section system, it is effortlessly applicable for changing particular genomic objectives. In plants, there are numerous instances where modified gRNA Cas9 compound has applied to object cautiously significant characters (Yin *et al.*, 2017). Multiple types of genomic modifications are being supported by CRISPR. It could either induce deletions, insertions or replacements in an already existing DNA segment.

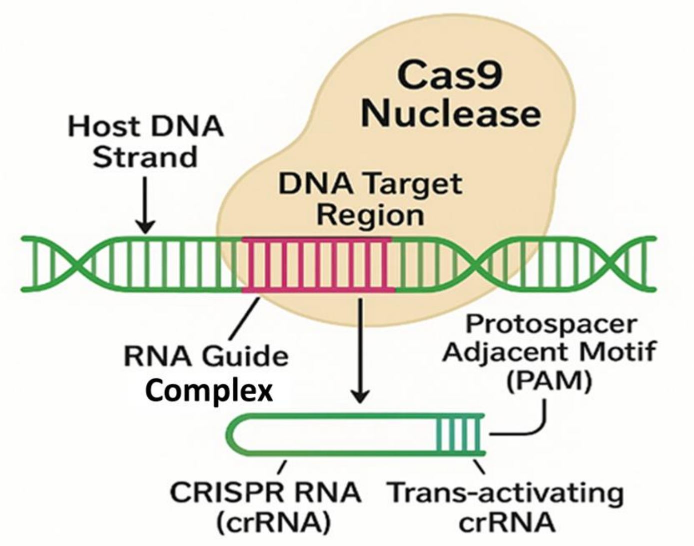

Figure 2. Main components of CRISPR-Cas9 System.

NEW CONSIDERATIONS

Gene drive resistance

The novel thoughts concerning the prospective aimed at initiative confrontation has risen after the molecular contrivances of the position particular endonucleases (Esvelt *et al.*, 2014). When these HEGs existed primary as a location particular gene initiative, it remained accepted that difference plus alteration now in the system of board position could deliver a basis of confrontation towards the drive, then again as well that planned initiative project could probably point towards the prosperous gene drive system (Hasselbeck *et al.*, 2023). The latest demonstration of bases of system differences, both obviously happening and persuaded by the drive machinery, proposes that confrontation will nearly indeed appear to a modest Cas9 based, gene drive design (Unckless *et al.*, 2017). Although diffident degrees of NHEJ remain to exist influence towards the efficiency of a gene drive approach (Unckless *et al.*, 2017). The latest studies into these recommendations deliver hopefulness that inadequacies of Cas9-based gene drives

https://doi.org/10.55627/pbiotech.003.02.1310

designs can be compensated in upcoming gene drive projects (Galizi *et al.*, 2014). Possible methods to complex Cas9-based gene drive designs have been established by means of post-transcriptional handling of numerous sgRNAs articulated from a distinct promoter (Marshall *et al.*, 2017).

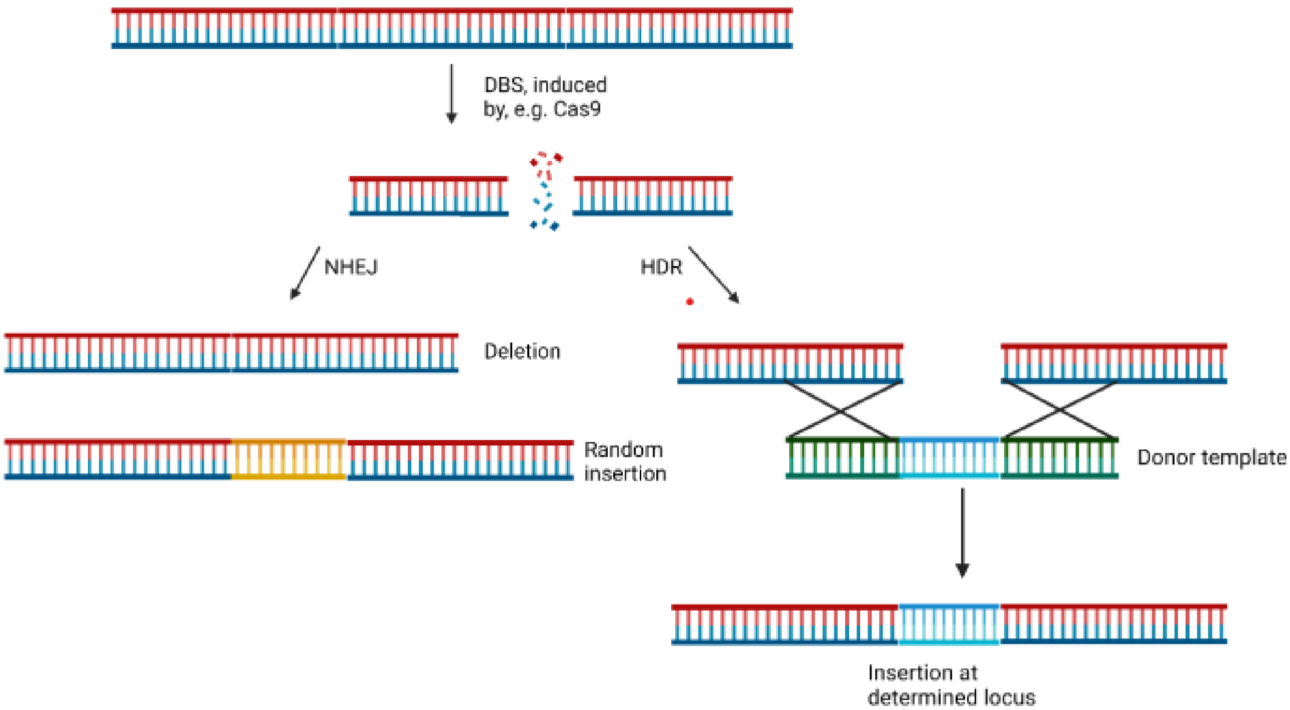

Figure 3. Possible genomic alterations through CRISPR. The figure is used with permission from Hasselbeck and Cheng (2023) given as pre-print at https://www.preprints.org/manuscript/202312.0905/v1.

Off-target special effects of Cas9

Possible off-target movement of Cas9 owing towards the homology among the sgRNAs and non-particular locations on the individual's genetics gives a remarkable test for Cas9-based gene drive designs (Macias *et al.*, 2017). In broad-spectrum, genome positions with ability aimed at off-target breakage by means of a certain sgRNA or Cas9 compound could be anticipated by means of computational procedures and then being investigated for alterations by means of PCR grounded inspects or bigger components of genomic materials can be sequenced deeply for SNPs (Cho *et al.*, 2014). But, these SNPs could be problematic to compute precisely without a vigorous dataset (Gratz *et al.*, 2014).

Enclosing an effectual gene drive

The probability that a certain gene initiative project can continue now in the atmosphere as a result of unintentional discharge inaugurating the laboratory control, an examination location has been demonstrated between diverse drive machineries and be contingent unevenly on the productivity of the design (Marshall, 2009). A great amount of precaution when functioning by means of gene drive theories has resonated over the area equally vital towards the moral improvement of CRISPR/Cas9-based machinery for total prospective uses (Esvelt *et al.*, 2014). Such schemes have remained established now in yeast and shown towards offering a vigorous plus containable gene initiative machinery (Noble *et al.*, 2019).

CONCLUSION

The practical improvements that have headed towards well-organized gene drives have resulted in an alteration of application in the discipline of biology since the tool improvement that may permit us to practice the use of genetics to fight diseases, to considerations, experimentation, and demonstrating of what it will feel like to practice these methodologies successfully. Many concerns for prosperous application of heritable gears for route mechanism are on the thoughts by environmentalists used for greater than 60 years and approximately few have risen since the particular gears which we expect in the direction of practice. The possibility for molecular machinery plus the flexibility of heritable manufacturing given by CRISPR/Cas9 and connected schemes show that we consume numerous possibilities on the way to follow the production of types which discourse the difficulties of diverse device plans in addition to that could remain incorporated through current physical, biochemical and the biocontrol gears aimed at fruitful ailment plans. Now in the necessity for distinctive sets of gears under diverse ecological, route and pathogen conditions, we should not simply assume to show advantage of the knowledge our personal collection is emerging, but in its place to deliver excellence examines of the drives of and the conditions underneath which our gears will be and will not be worthwhile, so that a communal party tallying a genetic constituent to their ailment mechanism scheme can make knowledgeable conclusions on what will have the utmost epidemiological influence.

AUTHOR CONTRIBUTIONS

Conceptualization, ASA; methodology, ASA; software, ASA; validation, ASA and RSAK; formal analysis and investigation, RSAK.; data curation, LA.; writing—original draft preparation, ASA; writing—review and editing, RSAK, LA and ASA; supervision, RSAK. All authors have read and approved the manuscript.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ACKNOWLEDGMENTS

Authors acknowledge Center of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture, Faisalabad, Pakistan for providing space and research environment.

REFERENCES

Abbas, M., Peszlen, I., Shi, R., Kim, H., Katahira, R., Kafle, K., Xiang, Z., Huang, X., Min, D., Mohamadamin, M., Yang, C., Dai, X., Yan, X., Park, S., Li, Y., Kim, S.H., Davis, M., Ralph, J., Sederoff, R.R., Chiang, V.L., & Li, Q. (2019). Involvement of CesA4, CesA7-A/B and CesA8-A/B in secondary wall formation in *Populus trichocarpa* wood. Tree Physiology, 40, 73-89.

Axtell, M. J. (2013). Classification and comparison of small RNAs from plants. Annual Review of Plant Biology, 31, 403-433.

Barrett, L. G., Legros, M., Kumaran, N., Glassop, D., Raghu, S., & Gardiner, D. M. (2019). Gene drives in plants: Opportunities and challenges for weed control and engineered resilience. Proceedings of the Royal Society B, Biological Sciences, 286, 1911-1922.

Beaghton, A., Beaghton, P. J., & Burt, A. (2017). Vector control with driving y chromosomes: Modelling the evolution of resistance. Malaria Journal, 16, 1–14.

Bellard, C., Genovesi, P., & Jeschke, J. M. (2016). Global patterns in threats to vertebrates by biological invasions. Proceedings of the Royal Society B, Biological Sciences, 283, 1823-1835.

Bisht, D. S., Bhatia, V., & Bhattacharya, R. (2019). Improving plant-resistance to insect-pests and pathogens: The new opportunities through targeted genome editing. Seminars in Cell & Developmental Biology, 96, 65–76.

Borges, F., & Martienssen, R. A. (2015). The expanding world of small RNAs in plants. Nature Reviews Molecular Cell Biology, 16, 721-741.

Burt, A., & Crisanti, A. (2018). Gene drive: Evolved and synthetic. ACS Chemical Biology, 13, 343–346.

Champer, J., Buchman, A., & Akbari, O. S. (2016). Cheating evolution: Engineering gene drives to manipulate the fate of wild populations. Nature Reviews Genetics, 17, 146–159.

Cho, S. W., Kim, S., Kim, Y., Kweon, J., Kim, H. S., Bae, S., & Kim, J. (2014). Sup2. Cold Spring Harb Lab Press, Method, 132–141.

DiCarlo, J. E., Chavez, A., Dietz, S. L., Esvelt, K. M., & Church, G. M. (2015). Safeguarding CRISPR-Cas9 gene drives in yeast. Nature Biotechnology, 33, 1250–1255.

Doherty, T. S., Dickman, C. R., Johnson, C. N., Legge, S. M., Ritchie, E. G., & Woinarski, J. C. Z. (2017). Impacts and management of feral cats *Felis catus* in Australia. Mammal Review, 47, 83-97.

El-Sappah, A. H., Yan, K., Huang, Q., Islam, M. M., Li, Q., Wang, Y., Khan, M. S., Zhao, X., Mir, R. R., Li, J., El-Tarabily, K. A., & Abbas, M. (2021). Comprehensive mechanism of gene silencing and its role in plant growth and development. Frontiers in Plant Science, 12, 78-96.

Esvelt, K. M., Smidler, A. L., Catteruccia, F., & Church, G. M. (2014). Concerning RNA-guided gene drives for the alteration of wild populations. eLife, 3, 1–21.

Fleming, P. J. S., Ballard, G., Reid, N. C. H., & Tracey, J. P. (2017). Invasive species and their impacts on agri-ecosystems: Issues and solutions for restoring ecosystem processes. The Rangeland Journal, 39, 523–535.

Galizi, R., Doyle, L. A., Menichelli, M., Bernardini, F., Deredec, A., Burt, A., Stoddard, B. L., Windbichler, N., & Crisanti, A. (2014). A synthetic sex ratio distortion system for the control of the human malaria mosquito. Nature Communications, 5, 1–8.

Gratz, S. J., Ukken, F. P., Rubinstein, C. D., Thiede, G., Donohue, L. K., Cummings, A. M., & Oconnor-Giles, K. M. (2014). Highly specific and efficient CRISPR/Cas9-catalyzed homology-directed repair in Drosophila. Genetics, 196, 961–971.

Harvey-Samuel, T., Campbell, K., Edgington, M., & Alphey, L. (2019). Trialling gene drives to control invasive species: What, where, and how? Ocassional Paper SSC, 62, 618-627.

Hasselbeck, S., Cheng, X., Molecules, G., Editing, G., & Scholar, G. (2023). Molecular marvels: Small molecules paving the way for enhanced gene therapy. Pharmaceuticals, 17, 41-52.

Heitman, E., Sawyer, K., & Collins, J. P. (2016). Gene drives on the horizon: Issues for biosafety. Applied Biosafety, 21, 580-589.

Ito, H. (2013). Small RNAs and regulation of transposons in plants. Genes & Genetic Systems, 88, 3-7.

Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J. A., & Charpentier, E. (2012). A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. Science, 337, 816–822.

Macias, V. M., Ohm, J. R., & Rasgon, J. L. (2017). Gene drive for mosquito control: Where did it come from and where are we headed? International Journal of Environmental Research and Public Health, 14, 1001-1006.

Marshall, J. M. (2009). The effect of gene drive on containment of transgenic mosquitoes. Journal of Theoretical Biology, 258, 250–265.

Marshall, J. M., Buchman, A., Sánchez, C. H. M., & Akbari, O. S. (2017). Overcoming evolved resistance to population-suppressing homing-based gene drives. Scientific Reports, 7, 1–12.

Matzke, M. A., Kanno, T., & Matzke, A. J. M. (2015). RNA-directed DNA methylation: The evolution of a complex epigenetic pathway in flowering plants. Annual Review of Plant Biology, 66, 243-267.

Monaco, A. P. (2022). The selfish environment meets the selfish gene: Coevolution and inheritance of RNA and DNA pools. BioEssays, 44, 239-248.

Moro, D., Byrne, M., Kennedy, M., Campbell, S., & Tizard, M. (2018). Identifying knowledge gaps for gene drive research to control invasive animal species: The next CRISPR step. Global Ecology and Conservation, 13, e00363.

Noble, C., Min, J., Olejarz, J., Buchthal, J., Chavez, A., Smidler, A. L., DeBenedictis, E. A., Church, G. M., Nowak, M. A., & Esvelt, K. M. (2019). Daisy-chain gene drives for the alteration of local populations. Proceedings of the National Academy of Sciences of the United States of America, 116, 8275–8282.

Rajeevkumar, S., Anunanthini, P., & Sathishkumar, R. (2015). Epigenetic silencing in transgenic plants. Frontiers in Plant Science, 6, 687-693.

Ricroch, A. E., & Hénard-Damave, M. C. (2016). Next biotech plants: New traits, crops, developers and technologies for addressing global challenges. Critical Reviews in Biotechnology, 36, 675–690.

Russell, J. C., Innes, J. G., Brown, P. H., & Byrom, A. E. (2015). Predator-free New Zealand: Conservation country. BioScience, 65, 520-525.

Sabbione, A., Daurelio, L., Vegetti, A., Talón, M., Tadeo, F., & Dotto, M. (2019). Genome-wide analysis of AGO, DCL and RDR gene families reveals RNA-directed DNA methylation is involved in fruit abscission in *Citrus sinensis*. BMC Plant Biology, 19, 1-13.

Sun, C., Feschotte, C., Wu, Z., & Mueller, R. L. (2015). DNA transposons have colonized the genome of the giant virus *Pandoravirus salinus*. BMC Plant Biology, 13, 38-41.

Symington, L. S., & Gautier, J. (2011). Double-strand break end resection and repair pathway choice. Annual Review of Genetics, 45, 247–271.

Thresher, R. E., Hayes, K., Bax, N. J., Teem, J., Benfey, T. J., & Gould, F. (2014). Genetic control of invasive fish: Technological options and its role in integrated pest management. Biological Invasions, 16, 1201–1216.

Unckless, R. L., Clark, A. G., & Messer, P. W. (2017). Evolution of resistance against CRISPR/Cas9 gene drive. Genetics, 205, 827–841.

Valero-Jorge, A., González-De Zayas, R., Matos-Pupo, F., Becerra-González, A. L., & Álvarez-Taboada, F. (2024). Mapping and monitoring of the invasive species *Dichrostachys cinerea* (Marabú) in central Cuba using Landsat imagery and machine learning (1994–2022). Remote Sensing, 16, 793-798.

Whisson, D. A., Holland, G. J., & Carlyon, K. (2012). Translocation of overabundant species: Implications for translocated individuals. The Journal of Wildlife Management, 76, 1661–1669.

Woinarski, J. C. Z., Burbidge, A. A., & Harrison, P. L. (2015). Ongoing unraveling of a continental fauna: Decline and extinction of Australian mammals since European settlement. Proceedings of the National Academy of Sciences of the United States of America, 112, 4531-4540.

Yin, K., Gao, C., & Qiu, J. L. (2017). Progress and prospects in plant genome editing. Nature Plants, 3, 1–6.

Zebec, Z., Zink, I. A., Kerou, M., & Schleper, C. (2016). Efficient CRISPR-mediated post-transcriptional gene silencing in a hyperthermophilic archaeon using multiplexed crRNA expression. G3: Genes, Genomes, Genetics, 6, 3161–3168.

Zheng, X., Yang, L., Li, Q., Ji, L., Tang, A., Zang, L., Deng, K., Zhou, J., & Zhang, Y. (2018). MIGS as a simple and efficient method for gene silencing in rice. Frontiers in Plant Science, 6, 662-667.