"Genome Edited" Rice in India and the Potential for Genome Editing for Rice Weed Management

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Abstract

Innovative crop and weed management technologies are necessary to meet the food and nutrition demands of an increasingly global population while addressing other challenges. The challenges that people face worldwide include a changing climate, limited cultivable land, erratic weather patterns and the emergence of new pests, diseases and weeds with greater adaptability to a changing climate.

This paper aims to synthesise information on the recent practical applications and successes of gene editing technology in developing two multiple stress-tolerant, high-yielding rice varieties in India. We commend this new development and discuss the possibility of utilising gene editing technology to improve various components of integrated weed management in rice.

Recently, two rice varieties, viz. DRR Dhan 100 (Kamala) and Pusa DSR Rice were developed by the *Indian Council of Agricultural Research* (ICAR), India, using the CRISPR-Cas9 genome-editing technology. India is the first country in the world to develop and approve genome-edited rice varieties using gene editing technology that does not involve genetically modified organisms.

These varieties, developed under the project "Enhancing climate resilience and ensuring food security with genome editing tools," are early maturing by 20 days and have significantly improved drought and salinity tolerance, as well as nitrogen-use efficiency in rice. Simultaneously, the varieties provide higher yields while reducing methane emissions.

Other areas where gene editing technology may be utilised to enhance components of Integrated Weed Management (IWM) in rice include the development of herbicide-tolerant (HT) rice varieties through targeted genome editing and modifying the genes involved. Recent advances in gene editing, particularly 'gene drives', also offer promising tools and novel approaches that can modify weed populations, making them more susceptible to weed management tactics.

Gene technology may also help produce rice varieties that are less susceptible to competition from weeds. This would require identifying novel quantitative trait loci (QTLs) and genes/alleles related to competitive abilities in major rice weeds, as well as allelopathy traits in rice. Gene editing may then lead to the production of weed-competitive and strongly allelopathic rice varieties that can be bred more successfully. Recent research has also shown that gene editing could be used to make weedy species more visible to machine-learned robots.

This paper presents several examples of the potential applications of gene editing, highlighting the capabilities of these new genetic technologies in enhancing the components of integrated weed management. It is possible to predict that IWM in rice is changing rapidly with the novel technologies offering hope for improved management of rice weeds, leading to associated yield improvements.

Keywords: CRISPR-Cas9, Genome editing, India, Herbicide-tolerant rice, Weed management

Introduction

The current world population is expected to reach 9.8 billion in 2050 and 11.2 billion in 2100 (UN, 2017). This increase, which appears inevitable, would result in an ever-increasing demand for nutritious food. It necessitates the need for innovative technologies to combat challenges such as climate change, limited arable land, unpredictable weather patterns, and the emergence of new pests, diseases and weeds, with greater adaptability to a changing climate. Humans have used genetic modification, in varying forms, for centuries to create crop plants with desired traits.

Selective breeding and mutagenesis or mutation breeding have long been used for crop improvement (Hernández-Soto et al., 2021). However, the experience of the past six decades of plant breeding suggests that traditional breeding strategies are insufficient for the rapid development of new plant traits that improve rice productivity and production to meet the increasing demands of global food and nutrition security (ISAAA, 2019; Bacha et al., 2025).

With the advent of genetic engineering technologies, transgenic technologies, and *Clustered Regularly Interspaced Short Palindromic Repeats* (**CRISPR**) genome editing, these tools are becoming the most preferred options for rice improvement (see **Figure 1** for a schematic).

CRISPR is a technology that enables scientists to edit the genome of living organisms, including animals, plants, and even human cells. The CRISPR system relies on an enzyme called Cas9, which acts as molecular scissors and a guide RNA molecule that directs the Cas9 to a specific DNA sequence. CRISPR was initially discovered in bacteria as a defence mechanism against viruses. Bacteria utilise CRISPR arrays to store the DNA sequences of viruses. When the virus attacks again, the bacteria produce RNA that guides the Cas9 enzyme to cut the viral DNA into pieces, thereby disabling it (Westra et al., 2016; Wada et al., 2020; Li et al., 2023; Qi, 2024).

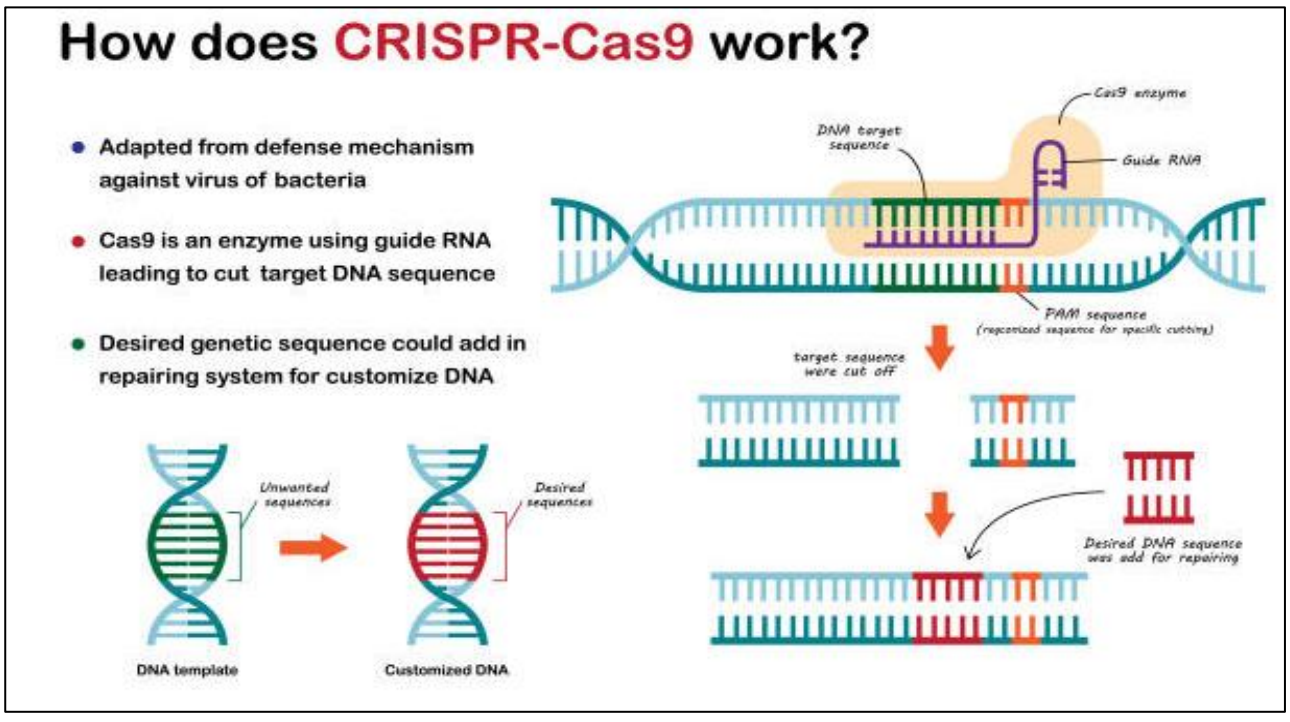


Figure 1. A schematic diagram of CRISPR technology

CRISPR/Cas9 is now the most widely used and efficient site-directed nuclease system in modern biotechnology. It consists of two main parts: (a) Guide RNA, which acts like a GPS, leading the system to the exact spot in the DNA where editing is needed. (b) The Cas9 protein, which acts like molecular scissors, cuts the DNA at that specific location.

Once the DNA is cut, the cell tries to repair the break. During this repair, scientists can either allow the gene to get disrupted or make specific changes to the gene sequence. This makes CRISPR/Cas9 an extremely valuable research tool in agriculture, medicine and the applications mentioned above.

The CRISPR/Cas9 technology is pivotal to producing the next generation of crops that are better adapted to changing climates, achieving higher yields and improved product quality. In crop improvement, the tool is now extensively employed for genetic enhancement due to its advantages, including cost-effectiveness, ease of use, and the ability to effectively and precisely edit multiple genes (IGA, 2022; Luo and Liu, 2025).

The technology has also enabled the enhancement of various traits, allowing crops to become more tolerant and better suited to withstand the challenges posed by both biotic and abiotic stresses (**Figure 2**).

As discussed by Somado, et al. (2008), Westra, et al. (2016), Char et al. (2019), Usman, et al. (2020), Liu, et al. (2020), Zhu, et al. (2020), Wada, et al. (2020), Kobayashi, et al. (2023), Li, et al. (2023), Qi (2024), Pacesa, et al. (2024) and Luo and Liu (2025) from various perspectives, these new genetic technologies also offer options for addressing global food and nutrition security challenges.

This article aims to synthesise the information on the recent practical utility successes of gene editing technology for developing multiple stress-tolerant and high-yielding rice varieties in India and to discuss the possibility of utilising gene editing technology in improving different components of Integrated Weed Management (IWM) in rice.

New Tools for Genetic Modifications

Research over the past 25 or so years has proven that CRISPR has a wide range of potential applications (Li et al., 2023; Qi, 2024), including:

- **Treating genetic diseases:** By correcting disease-causing mutations, CRISPR offers the potential to cure or prevent genetic disorders.
- **Developing new therapies**: CRISPR is being explored for the treatment of cancer, infectious diseases, and other conditions.
- **Improving crops**: CRISPR can be used to develop crops that are more resistant to pests, diseases, and harsh environmental conditions.
- **Creating disease models:** Scientists can utilise CRISPR to develop animal models of human diseases, enabling the study of the disease and testing potential treatments.

In highlighting the importance of CRISPR genome editing, coupled with advances in computing and imaging capabilities, Wang and Doudna (2023) said that it has initiated a new era in which genetic diseases and individual disease susceptibilities are both predictable and actionable. Similarly, genes responsible for specific plant traits can be identified and altered rapidly, thereby transforming the pace of agricultural research and plant breeding (**Figure 2**).

The power of CRISPR technologies is in their ability to make specific changes to individual plant genes, generating new plant genomes with targeted traits rather than relying on random DNA changes (Char et al., 2019; Usman et al., 2020; Liu et al., 2020; Zhu et al., 2020; Wada et al., 2020; Lin et al., 2020; Kobayashi et al., 2023; Pacesa et al., 2024; Luo and Liu, 2025).

Breeding precisely altered plants can quickly yield varieties that can reliably exhibit the desired trait. While CRISPR technologies offer significant promise, they also raise ethical and moral concerns, particularly regarding the editing of germline cells, such as eggs, sperm, or embryos.

Advances in genome editing technologies, particularly CRISPR/CRISPR-associated protein 9 (Cas9) (CRISPR/Cas9), have the potential to revolutionise rice varietal improvement through targeted genome modifications. There is ample and convincing evidence available to show that novel genetic technologies, such as CRISPR/Cas9, enable researchers to precisely edit genes in rice, modifying favourable traits, including biotic and abiotic stress tolerance and herbicide tolerance.

Three major types of site-directed nucleases (outlined below) have revolutionised gene-editing technologies, allowing researchers to precisely target and modify DNA sequences within living cells.

CRISPR-Cas Systems

These systems use a guide RNA (gRNA) to direct a Cas protein (such as Cas9) to a specific DNA sequence, where it can then make a targeted cut. The CRISPR-Cas system, derived from bacterial immune systems, has become a widely used tool for gene editing due to its simplicity and versatility (Westra et al., 2016; Wada et al., 2020).

Zinc Finger Nucleases (ZFNs)

ZFNs consist of a zinc finger DNA-binding domain fused to a *Fok*I nuclease domain. The zinc fingers can be engineered to recognise and bind to

a specific DNA sequence, while the *Fok*I domain creates a double-strand break (Miller et al., 2007).

*Fok*I is an unusual restriction endonuclease enzyme that recognises a specific DNA sequence and cleaves DNA at a non-specific site a short distance away from its recognition sequence. The *Fok*I protein has two distinct domains: a DNA recognition domain and a DNA cleavage domain. The recognition domain binds to the DNA sequence 5'-GGATG-3', while the cleavage domain cuts the DNA on both strands, nine base pairs away on one strand and 13 base pairs away on the other (Wah et al., 1998).

Transcription activator-like effector nucleases (TALENs)

TALENs are similar to ZFNs in that they use a DNA-binding domain (TALE) fused to a *Fok*I nuclease domain. The TALE domain can be engineered to recognise a specific DNA sequence, and the *Fok*I domain then creates a double-strand break (Christian et al., 2010).

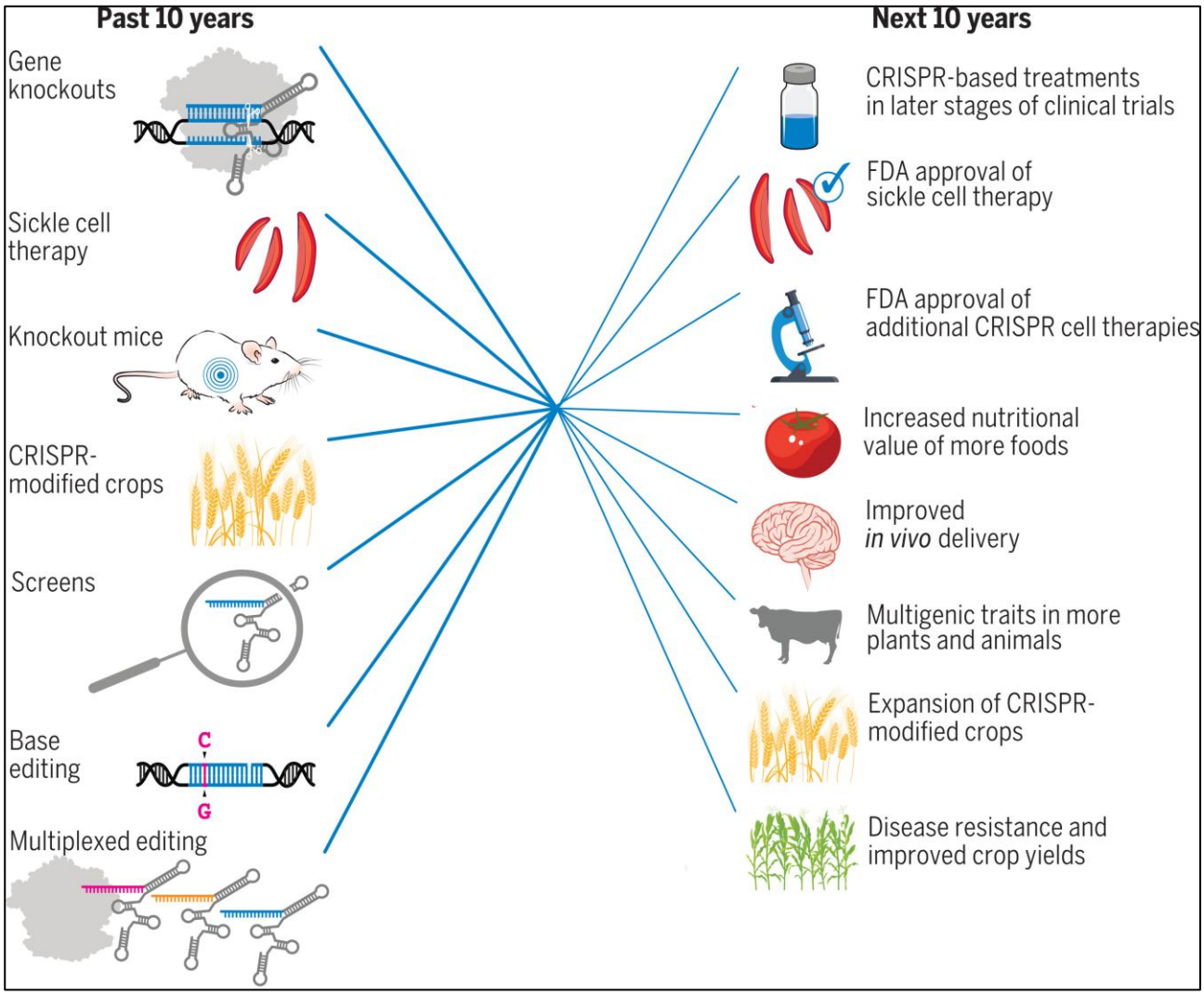


Figure 2. Source: Wang and Doudna (2023). CRISPR: past, present, and future

The past decade of CRISPR technology has focused on building platforms for generating gene knockouts, creating 'knockout mice' and other animal models, conducting genetic screening, and multiplexed editing.

CRISPR's applications in medicine and agriculture are already underway and will continue to serve as the focus for the next decade, as society's demands drive further innovation in CRISPR technology. These include improved crop varieties, resistance to pests and diseases, and herbicide resistance.

Development of New Rice Varieties using CRISPR genome editing

India needs to produce 520 million tons of food grains by 2047, which is 1.6 times the current production. Concurrently, water and nutrient use efficiency must be increased by more than 1.7-fold to address dwindling freshwater resources, deteriorating soil health, and the impacts of climate change. Thus, a quantum leap in quality yield is necessary to ensure India's food and nutritional security. Simultaneously, such a yield improvement must be achieved in line with the *Sustainable Development Goals* (SDGs) in India.

Based on our experience, it is clear that this yield increase in rice must primarily result from improved genetic gains in rice breeding and variety improvement programs, as well as technological advances in rice crop management that can combat biotic stresses, such as pests, diseases, and weeds.

Recognising the potential of genome editing to cost-effectively develop improved varieties with enhanced yield, nutritional quality, and climate resilience while reducing agrochemical inputs, the *Indian Council of Agricultural Research* (ICAR) initiated a project titled "Enhancing Climate Resilience and Ensuring Food Security with Genome Editing Tools".

In this project, ICAR successfully utilised gene editing to develop high-yielding, drought- and salt-tolerant mutants in the rice CV. **MTU1010**, which is a high-yielding mutant of *Samba Mahsuri*. The work was carried out at ICAR-Indian Agricultural Research Institute (IARI), New Delhi, and ICAR-Indian Institute of Rice Research (ICAR-IIRR), Hyderabad, respectively.

Following the development of the mutant varieties, ICAR obtained IBSC and RCGM exemption for these mutants under Rules 7-11 of the 1989 Rules. As a consequence, for the first time in the country, genome-edited mutants have been nominated for AICRIP trials in kharif 2023 (http://genetools.iari.res.in/about.html). The two rice varieties developed by ICAR are described below:

i. DRR Dhan 100 (Kamala)

The genome-edited rice variety 'Kamala' was developed by the ICAR-IIRR from the popular *Samba Mahsuri* variety. Through precise editing of the CKX2 gene, researchers achieved a 19% yield increase, early maturity by 20 days, improved drought tolerance, enhanced nitrogen-use efficiency and reduced methane emissions.

ICAR-IIRR researchers utilised a novel OsCKX2-deficient mutant allele, modified through SDN-1 genome editing, to increase cytokinin levels in rice panicle tissue. The loss of OsCKX2, a gene in rice that encodes a cytokinin oxidase enzyme involved in the degradation of cytokinin, thus boosts the growth-promoting cytokinin hormone in rice panicle tissue, resulting in higher grain yield and better productivity (Mayee and Choudhary, 2025).

The genome-edited rice variety 'Kamala' is now promoted for cultivation across all of the most critical rice-growing states of India, including Andhra Pradesh, Telangana, Karnataka, Tamil Nadu, Puducherry, Kerala, Chhattisgarh, Maharashtra, Madhya Pradesh, Odisha, Jharkhand, Bihar, Uttar Pradesh, and West Bengal (**Figure 3**).

ii. Pusa DSR Rice 1

Pusa DSR Rice 1 was developed by ICAR-IARI in the popular MTU1010 rice background by editing the DST gene using the SDN-1 technique of CRISPR-Cas9. By removing a gene responsible for suppressing stress resistance using SDN-1 technology again, scientists achieved plants with reduced stomatal density and water use, along with improved tillering, grain yield, and salt tolerance (Mayee and Choudhary 2025).

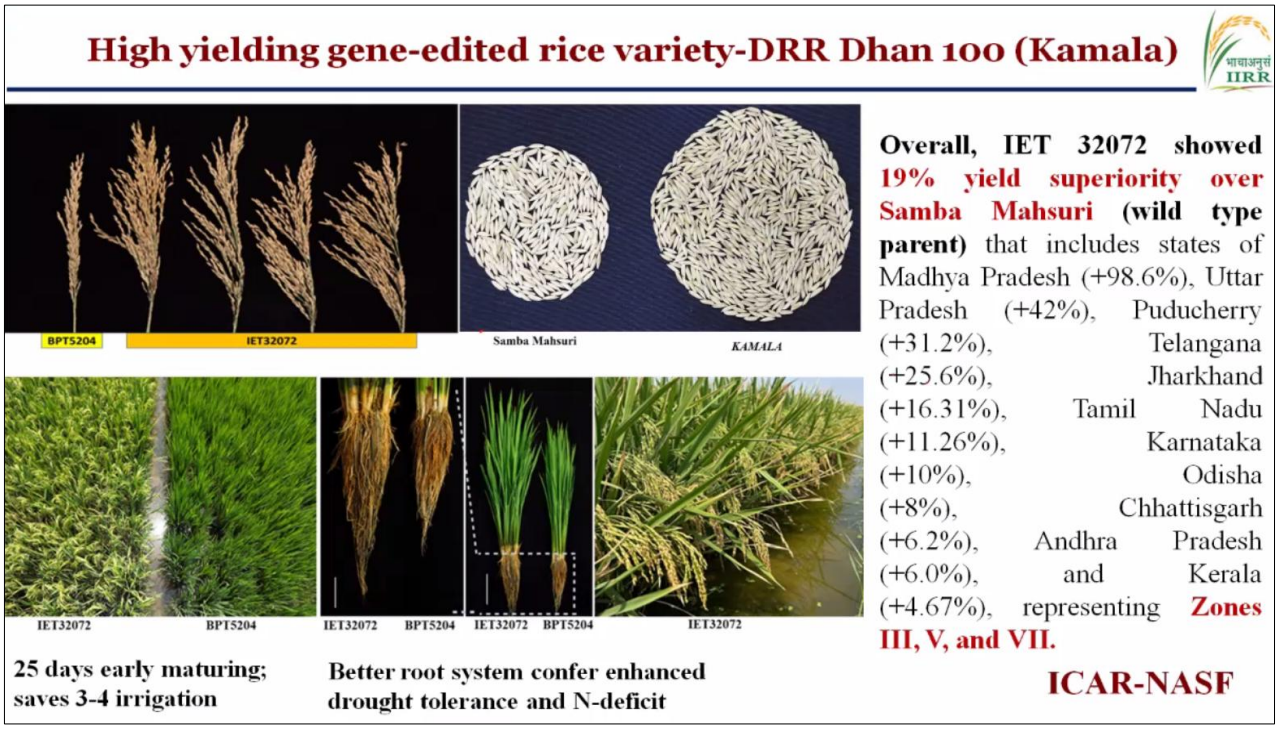
The new variety is drought- and salinity-tolerant, with yield improvements ranging from 9.66% to 30.4% in challenging soil conditions. It is also suitable for direct seeding (DSR), which helps conserve water, reduce fuel consumption, and lower greenhouse gas emissions.

The '**Pusa DST Rice 1**' is now recommended for cultivation in most of the states in which Kamala is also promoted. Cultivating these two improved varieties over five million hectares, particularly in eastern and southern India, could yield 4.5 million tonnes of additional rice. ICAR estimated that the two varieties could also save approximately 7,500 million cubic meters of irrigation water while reducing greenhouse gas emissions by 20% (**Figure 3**).

* * *

It is important to note that these varieties were developed using CRISPR/Cas9 technology, which does not introduce any foreign DNA, unlike other genetically modified (GM) crops. This distinction

placed them under the *Site-Directed Nuclease 1* (SDN-1) and *Site-Directed Nuclease 2* (SDN-2) categories of genome modifications. Both SDN-1 and SDN-2 category modifications to DNA are regulated more flexibly in India compared with other GM crops. These rice varieties, therefore, represent India's first significant success in applying CRISPR-based genome editing under the framework of New Breeding Technologies (NBTs).



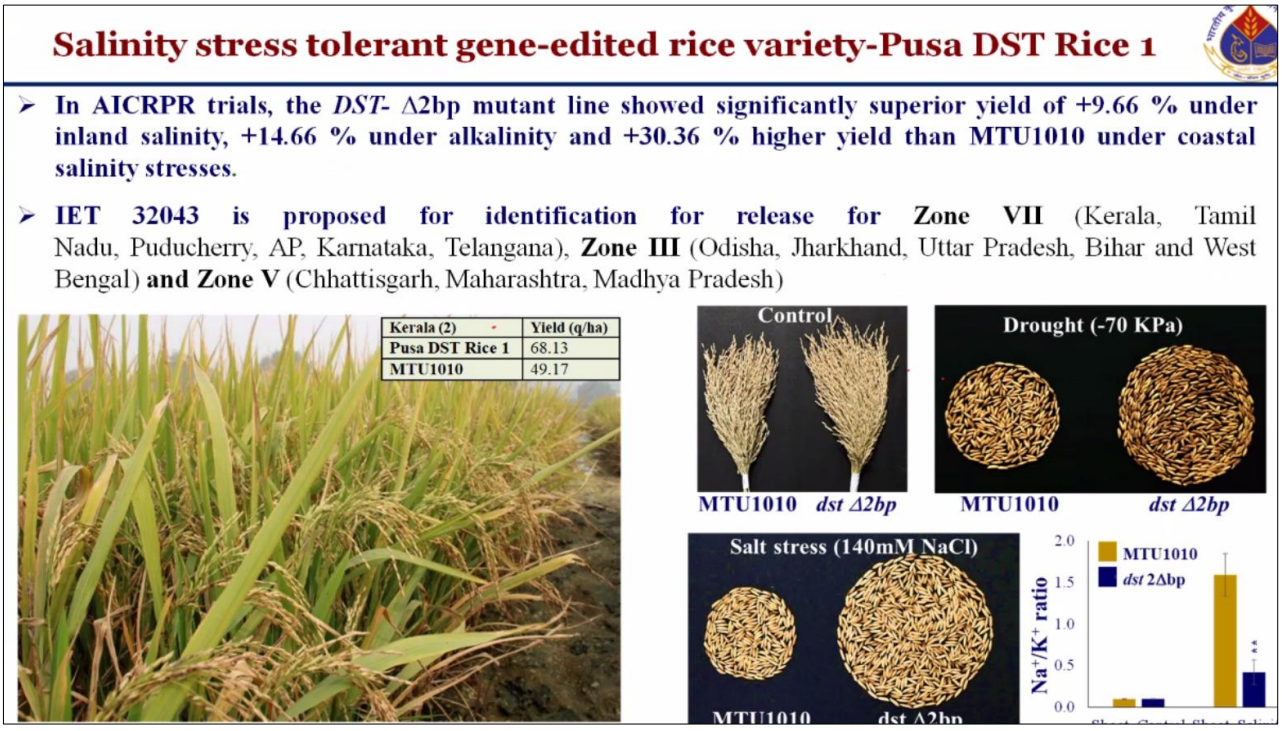


Figure 3. Genome revolution: India's trailblazing path to first edited rice varieties (Chinnusamy, 2025)

Site-directed nucleases are unique molecular tools that create targeted breaks in DNA at specific locations. To develop these two rice varieties, the SDN-1 and SDN-2 techniques were used to precisely edit specific genes without introducing any foreign DNA. In this approach, the DNA is cut at a specific site using the CRISPR/Cas9 system.

The cell then repairs the break using its natural repair system, known as the non-homologous end joining (NHEJ) process. This process may introduce minor errors such as insertions or deletions. It is known that these small changes can also disrupt a gene, preventing it from functioning correctly. No foreign DNA is added in this method. It is often used to turn off unwanted genes.

In the SDN-2 method, the DNA is also cut at a precise location. But this time, a small piece of repair DNA is also given to the cell. This repair of DNA has a few specific changes that the scientist wants to introduce. The cell employs a process called homology-directed repair (HDR) to repair the break and incorporate the small changes from the repaired DNA into its own genome. Just like SDN-1, no foreign gene is inserted. Only a few base pairs are altered with great precision.

These tools are designed to recognise and cut DNA at a specific site. Once the DNA is cut, the cell uses its natural repair mechanisms to fix the break. During this repair process, scientists can either disable a gene or introduce precise changes. This allows for highly accurate editing of the genome without affecting other parts of the DNA. This makes the process non-transgenic and different from traditional genetically modified crops.

The gene editing process in developing two varieties is precise and yields a natural outcome. These genome-edited novel crop genomes, which contain no foreign genes, have been approved by the international scientific community. With these breakthroughs, India became the first country in the world to develop and approve genome-edited rice varieties using gene editing technology that does not involve genetically modified organisms.

Although the success of the two gene-edited new varieties has been widely lauded, concerns have also been raised about safety issues and future environmental effects (Menon, 2025). Nevertheless, the ICAR proponents highlighted that SDN-1 and SDN-2 genome edits are as safe as natural mutations. In our view, after the successes of technology, the success of the developed gene-edited rice depends on creating effective awareness, educating farmers, adopting stewardship guidelines, ensuring access to seeds, and building farmer confidence through targeted campaigns.

iii. Other Gene-edited Rice Mutants

In India, there are a few varieties that are most popular and most widely cultivated. These are called ‘mega varieties’ and include ‘SWARNA’, IR 64 and MTU 1010 varieties. These varieties are known to have higher adaptability to different environments, along with desirable morphological features, favourable grain quality and high rice grain recovery. Such characteristics make them popular not only among farmers but also among consumers and exporters (Sah et al., 2024; Kar et al., 2024).

All of these varieties are presently targeted for gene editing and varietal improvement. For example, in addition to the above-mentioned gene-edited rice varieties, other gene-edited rice mutants for the genes DEB1, CKX2, and TB1 have also been developed in the rice cultivar CV MTU1010 using CRISPR technology. These genes are involved in various aspects of plant development, including grain yield, cytokinin regulation, and plant architecture. For instance, the DEB1 (OsSPL16) gene is involved in regulating the rice grain yield.

Mutations in DEB1 increase the grain yield in rice, potentially through alterations in protein expression related to pyruvate metabolism and cell division (Usman et al., 2020).

In addition, targeting the ‘Ideal Plant Architecture’ gene (IPA-1), gene-edited mutant lines of ‘SWARNA’ have been developed by the ICAR-National Rice Research Institute (NRRI) in Cuttack. The rice variety “Swarna” is highly popular in India, as it yields reasonable profits to farmers even under low-input management.

Gene editing of the SWARNA cultivar has successfully produced mutants that show favourable differences in plant architecture. These include increased plant height, the number of panicle branches, panicle length, and the number of spikelets per panicle relative to the original, traditional cultivar (Bandita et al., 2024; Sah et al., 2024). These mutants are currently under analysis to identify the presence of any exogenous DNA. Those that are free of foreign DNA are expected to enter field trials in India soon.

Gene Editing Applications for IWM in Rice

Weeds are among the most significant biotic limitations on agricultural output, posing substantial yield losses to crops alongside other pests and diseases (Zimdahl, 1980; 2007; Hernández-Soto et al., 2021; Rao, 2022a, b). Weeds compete with rice for essential resources, including space, sunlight, water, and nutrients, contributing to reduced crop productivity (Rao et al., 2017).

Furthermore, weeds can serve as hosts for various insects, bacteria and viruses that can harm crop plants, exacerbating damage in the field. Beyond agricultural impacts, weeds also adversely affect native habitats, threatening local flora and fauna and disrupting ecosystems. Addressing these challenges is critical for ensuring food security and maintaining biodiversity.

Over the decades, many weed control tactics, tools and management strategies have been developed and deployed. Combined packages of these come under the banner of *Integrated Weed Management* (IWM). Despite various successes in rice weed management, as reviewed elsewhere (Rao et al., 2007; Ramesh et al., 2017; Rao et al., 2017), a continuing need remains for the development of more sustainable and affordable methods for weed management.

Modern tools, such as gene editing, appear to offer robust options that can be incorporated as a component of future IWM in rice. Several crucial areas where gene editing technologies might be applicable to enhance IWM are discussed below.

Developing Herbicide-Tolerant (HT) rice varieties

Herbicides are widely used to manage undesirable weeds. However, one of the most significant problems associated with the continuous use of herbicides is that weeds develop resistance to these chemicals. Cultivating herbicide-tolerant (HT) crops provides farmers with alternative options for effective weed management of herbicide-resistant weeds, thereby realising increased rice productivity (Yaduraju, 2021; Dong et al., 2021; Kar et al., 2024; Luo and Liu, 2025).

Herbicide-tolerant (HT) rice refers to rice varieties that have been genetically modified or bred to withstand the application of specific herbicides. This trait allows farmers to control weeds more effectively by using herbicides that would otherwise damage or kill the rice plants. The most common method for developing HT rice is through mutagenesis of the acetolactate synthase (ALS) gene, which is a target for several herbicides (Luo and Liu, 2025).

Introducing HT crops via genetic engineering is one of the most effective strategies for controlling a broad spectrum of herbicide-resistant weeds. In recent decades, traditional breeding, combined with transgenic methods and mutagenesis, has played a pivotal role in driving the progress of herbicide-tolerant (HT) rice (Rao et al., 2007).

The genetic approaches to creating HT rice have been comprehensively reviewed recently by Luo and Liu (2025). The two central herbicide-tolerance mechanisms in rice are (a) target-site resistance (TSR; conferred by mutations or overexpression of target proteins) and (b) non-target-site resistance (NTSR, involving the sequestration, translocation, detoxification via metabolic degradation, or reduced penetration of herbicides).

The primary techniques used to create HT rice using one or the other tolerance mechanism include (a) Mutagenesis, (b) Transgenic methods, and (c) CRISPR/Cas9 gene editing.

Mutagenesis - This non-transgenic approach involves selecting naturally occurring mutations or inducing random mutations by irradiation (such as UV light, X-rays, gamma rays, or ion beams) or chemical mutagens (such as ethyl methane sulfonate). These aim to alter the responsible gene in a way that reduces its sensitivity to specific herbicides without introducing foreign genes from other organisms into the rice genome. Herbicide-resistant mutant rice genes, derived from mutagenesis breeding, are then usually transferred into other rice varieties by backcrossing.

Commercialised HT rice, developed through non-transgenic approaches, includes the *Clearfield*®, *Provisia*®, and *Jietian*® varieties. Among these, *Clearfield* is the most widely used HT variety (Chen et al., 2021; Jin et al., 2022). **Provisia** rice is resistant to ACCase inhibitors (Ile to Leu mutant) in the ACCase protein, and **Jietian** rice varieties, named from Chinese (meaning rice fields free of weeds), are resistant to ALS inhibitors carrying a mutation (Trp to Met) in the ALS gene (Jin et al., 2022). *Clearfield* rice was produced by mutagenesis of cultivated rice, via modification of a single codon (Ser to Asn) in the AHAS gene (Tan et al., 2005).

After 15 years of use, *Clearfield* rice continues to produce high yields in Brazil owing to its superior weed-control effects. Nevertheless, *Clearfield* rice is now facing challenges from herbicide-resistant barnyard grass [Echinochloa crus-galli (L.) Beauv.] and weedy rice (*Oryza sativa*) (Ulguim et al., 2021).

Transgenic Methods – Transgenesis is the process of introducing foreign genes (transgenes) into an organism's germline, allowing the transgene to be inherited by all offspring. Several examples discussed below demonstrate that this approach has been effective in creating HT rice.

The introduction of specific transgenes reduces the crop plant's sensitivity to herbicides through target-site resistance (TSR) or non-target-site resistance (NTSR) mechanisms. HT genes for this purpose can be isolated from bacteria, mutants produced by mutagenesis breeding, or herbicide-resistant weed biotypes. For example, the CP4-EPSPS gene from *Agrobacterium* sp. strain CP4 is widely used for the breeding of glyphosate-resistant 'Roundup Ready' crops that have been accepted and grown in many countries (Cuhra, 2015) [1].

However, Ouyang et al. (2021; 2024) found that mutations in the *5-enolpyruvylshikimate-3-phosphate synthase* (EPSPS) gene (i.e. TIPS-EiEPSPS) obtained from a herbicide-resistant biotype of goosegrass [*Eleusine indica* (L.) Gaertn.], which contains two mutated sites (T102I and P106S), conferred better resistance to glyphosate than CP4-EPSPS in transgenic rice (Zhonghua11).

Emerging research continues to focus on enhancing the resistance of rice to herbicides that can kill weeds by transferring well-established resistance genes from other organisms to the crop. Herbicide resistance-imparting genes have been derived from both soil bacteria and recalcitrant weeds (see recent reviews by Kobayashi et al. [2023] and Luo and Liu [2025]).

In one significant example, transgenic rice (*Nipponbare*) [2] expressing the rigid ryegrass (*Lolium rigidum* Gaud.) metabolic P450 gene CYP81A10v7 exhibited resistance to seven herbicides: diclofop-methyl (6000 g ha^{-1}), tralkoxydim (200 g ha^{-1}), chlorsulfuron (400 g ha^{-1}), Mesotrione (200 g ha^{-1}), atrazine (2000 g ha^{-1}), chlortoluron (2000 g ha^{-1}), and trifluralin (240 g ha^{-1}) (Han et al., 2021).

In a recent study, the potential effects of transgene stacking in glyphosate-tolerant rice and its wild-type parent, Zhonghua 11, were examined as a safety assessment strategy (Wang et al., 2023b). Another study analysed the genetic stability of insect- and herbicide-resistant genes in transgenic rice lines. The findings suggested that growing Bar-transgenic rice and using Basta (up to 300 mg/l) could be an effective strategy for overcoming weed damage in rice (Sun et al., 2023).

Transgenic methods offer several advantages, including the ability to utilise genes from diverse organisms, ranging from wild crop relatives to domesticated crops. They also enable gene stacking ('pyramiding') to obtain improved phenotypes or alter multiple traits simultaneously.

However, transgenic technologies have several disadvantages, including biosafety concerns and the potential for causing off-target mutations. Also, consumers and regulatory agencies have expressed concerns about the introduction of foreign DNA into food crops and the potential for adverse effects on biodiversity. Indeed, biosafety concerns about the breeding of genetically modified (GM) rice have halted their commercial cultivation in some rice-growing countries.

CRISPR/Cas9 Approach - The current, most suitable alternative to conventional genetic engineering approaches for developing HT rice is the creation of transgenic varieties through targeted genome editing using CRISPR-Cas9 (Dong et al., 2021; Akhtar et al., 2024; Luo and Liu, 2025).

Various gene editing tools are now available that could be used to develop HT rice. These tools include: target-based editing (ABEs and CBEs), CRISPR ribonucleo-protein complexes/Cas9, prime-editing-library-mediated saturation mutagenesis (PLSM), Prime editing (PE), single-nucleotide

[1] The CP4-EPSPS gene has been widely used commercially to create glyphosate-resistant crops, including soybeans, corn, cotton, and canola. These crops, often referred to as "Roundup Ready" crops, allow farmers to use glyphosate to control weeds without harming their crop.

[2] *Nipponbare* is a widely used temperate *O. sativa* var. *japonica* cultivar of rice. Its well-annotated and fully sequenced genome makes it valuable as a model organism and a research tool for genetic studies and the development of transgenic lines. Transgenic *Nipponbare* rice has been engineered for various traits, including improved tolerance to environmental stresses, such as salinity, enhanced nutritional value, and resistance to herbicides (Matsumoto et al., 2016). However, the genetically modified HT Nipponbare is yet to be commercialised.

polymorphisms (SNPs), Non-homologous end joining (NHEJ), base-editing-mediated gene evolution (BEMGE), and Homology-directed repair (HDR), along with 2 DNA targeting systems (protein-based): namely, TALENs, ZFNs—that are utilised for site-directed genome mutagenesis (Char et al., 2019; Asadullah and Shah, 2025).

As recently reviewed by Luo and Liu (2025), impressive and rapid advances have been made utilising genetic tools to develop varieties with broad-spectrum tolerance to rice herbicides (see **Figure 4**).

The precise gene editing approach provides a reliable method for developing HT rice through successive rounds of gene editing. The outputs offer efficient alternatives to traditional gene modification techniques. Research has shown that by targeting specific genes and inducing precise mutations, CRISPR/Cas9 has facilitated the development of rice that can withstand specific herbicide applications, as discussed below.

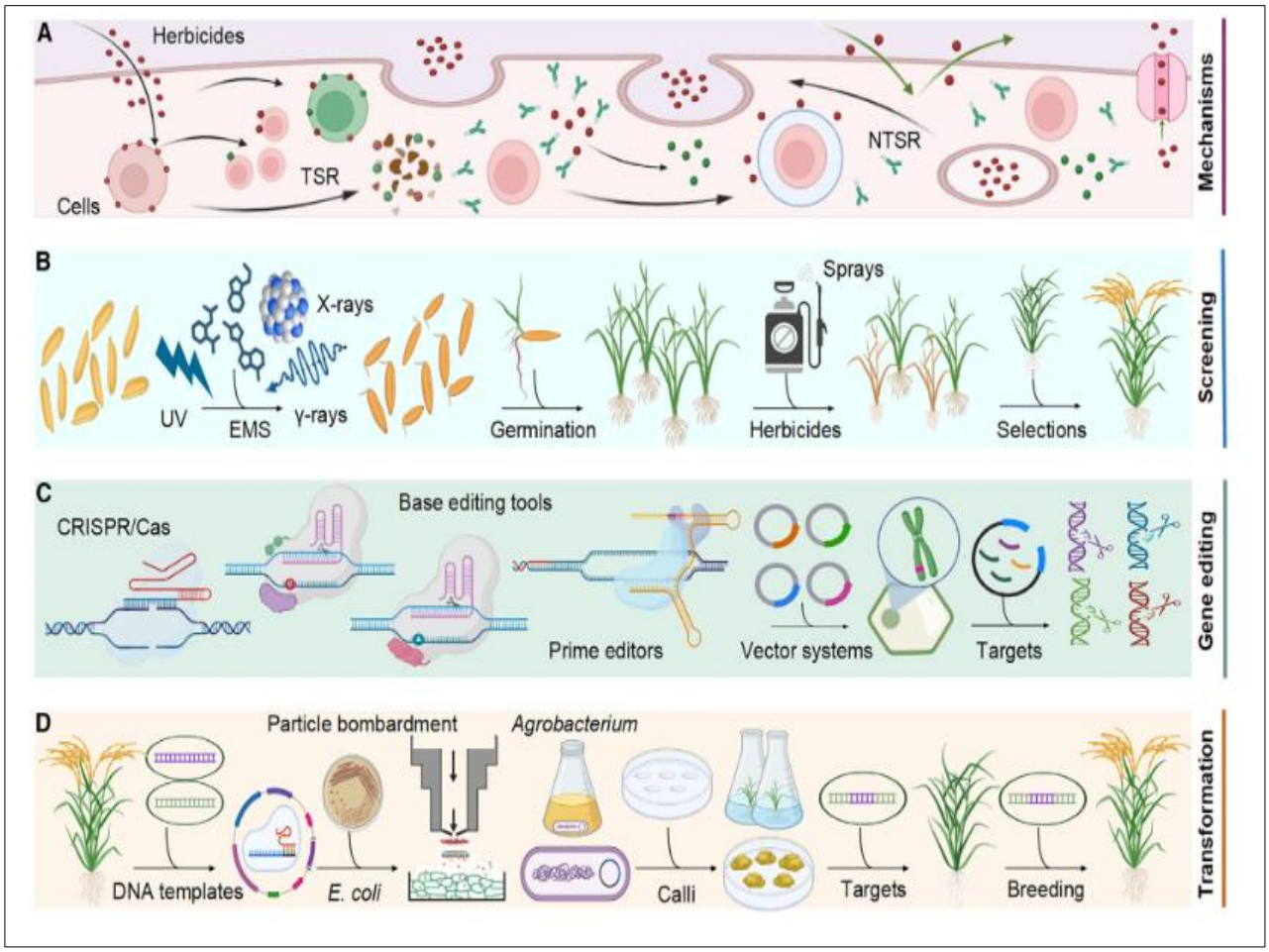


Figure 4. Source: Luo and Liu (2025). Graphical representation of the strategies used to breed herbicide-resistant rice.

(A) There are two central herbicide-resistance mechanisms in rice cells: target-site resistance (TSR; conferred by mutations or overexpression of target proteins) and non-target-site resistance (NTSR; involving the sequestration, translocation, detoxification via metabolic degradation, or reduced penetration of herbicides).

(B) Steps involved in the screening of herbicide-resistant rice mutants generated by chemical treatment or irradiation, with subsequent herbicide treatment used to impose selection pressure.

(C) The use of gene-editing tools, including gene knockout, base editing, and prime editing, in the breeding of HT rice.

(D) The two principal systems for delivery of transgenes during the breeding of herbicide-resistant rice are particle bombardment and Agrobacterium-mediated methods.

The new varieties are said to provide higher crop yields and highly sustainable rice production [see reviews by Faizal et al. (2024) and Luo and Liu (2025)]. For instance, Sun et al. (2016) had earlier described how two specific amino acid residues in the Acetolactate Synthase (ALS) gene were precisely edited and replaced to develop HT rice plants with homozygous resistance.

Following a similar approach, Wang et al. (2021) employed the base editing technique mediated by CRISPR/Cas9 to modify the OsALS gene, thereby conferring ALS herbicide resistance to rice in response to imazethapyr. Butt et al. (2020), using *Nipponbare*, also described how similar CRISPR modifications to the ALS gene provided HT rice resistant to the rice ALS-inhibiting herbicide bispyribac-sodium.

In another study, Li et al. (2016) developed gene replacement and insertion strategies targeting the non-homologous end-joining (NHEJ) pathway using CRISPR/Cas9. This strategy was successfully employed to induce local lesions in genomes and to introduce amino acid substitutions in the rice 5-enol pyruvylshikimate-3-phosphate synthase (EPSPS) gene, conferring resistance to glyphosate in rice.

Building on these studies, Sony et al. (2023) recently described the development of glyphosate-resistant rice lines through site-specific amino acid substitutions (G172A, T173I, and P177S: GATIPS-m*OsEPSPS*) and modification of the phosphoenol pyruvate-binding site in the *OsEPSPS* gene. They employed the CRISPR/Cas9 system to use the fragment knockout technique.

Interestingly, the GATIPS mutations in the *OsEPSPS* gene created not only new rice lines with high glyphosate resistance (foliar spray of 6 mL L-1) but also those with enhanced aromatic amino acids (Phenylalanine, two-fold; tryptophan, 2.5-fold; and Tyrosine, two-fold), and improved rice grain yields. The authors suggested that this gene modification would be a new strategy for higher rice productivity (Sony et al., 2023)

Herbicides that inhibit 4-hydroxyphenylpyruvate dioxygenase (HPPD), including Mesotrione (MST), block electron transport in photosynthetic systems, resulting in bleaching and plant death. Wu et al. (2023) edited the gene involved, *OsHPPD* 3′ UTR, using CRISPR-Cas9 and CRISPR-Cas12a and created new rice lines with HPPD resistance to Mesotrione (120–480 g ai ha^{-1}). Their results demonstrated that CRISPR-Cas9-mediated editing in the 3′ UTRs of elite rice genes may facilitate improvement of important plant agronomic traits.

Acetyl-CoA carboxylase (ACCase) catalyses the first step of fatty acid biosynthesis in plants. Loss-of-function mutations in ACCase are lethal to plants. As a consequence, the ACCase enzyme is the target of a large number of herbicides (e.g., ‘Fops’ and ‘Dims’). Using the CRISPR-Cas9 gene editing tool, Liu et al. (2020) modified the ACCase gene, *OsACC* (LOC_Os05g22940) of an elite *japonica* rice variety, cv. Feigeng2020. The CRISPR-mediated new rice mutants demonstrated stability in their modified genomes and showed no fitness losses, indicating that the approach could be used to confer ACCase herbicide resistance in rice (Wu et al., 2020).

The successes demonstrated by such examples reveal that CRISPR/Cas9 is an efficient method for both identifying and modifying target genes, making rice tolerant to herbicides that can suppress its major weeds. The literature on the uses of these technologies is growing rapidly, as reviewed by Luo and Liu (2025).

Their view is that key genes in HT signalling pathways could be edited to manipulate the underlying biological processes. Studying structural features of receptor proteins that bind to herbicides with different modes of action in HT mutants should accelerate the development of methods to modify genes that encode for HT target enzymes. Other potential areas for future research include the stacking of mutations in HT genes using gene editing to confer multiple herbicide resistance in rice.

The premise of this intensified research is that creating a greater number of HT rice varieties can simultaneously achieve both improved rice yields and management of herbicide resistance in weeds by modifying specific genes.

‘Gene Drive’ Systems to Modify Weed Populations

Over the last eight decades, the constant use of herbicides has led to the widespread evolution of herbicide resistance in numerous weed species (Duke, 2005; Heap, 2025). The CRISPR/Cas9 ‘gene drive’ has come as a novel genetic control strategy in managing herbicide resistance in weeds (Kumam et al., 2023).

The CRISPR tool could be used to ‘edit’ weed genomes and modulate their fitness and ‘weediness’ in the field. The introduction and proliferation of some mutations could make target weed populations more prone to subsequent weed management strategies, including herbicides (Neve, 2018).

‘Gene drives’ are genetic elements that increase the likelihood of a specific gene being inherited by offspring, causing it to spread rapidly through a population over generations. This is different from

normal Mendelian inheritance, where a gene has a 50% chance of being passed on.

It is a process that promotes a mechanism of biased inheritance of specific genes from one generation to the next. The process can be harnessed to 'drive' a desired allele throughout a population (Alphey et al., 2020). Thus, it can serve as a tool to effect specific changes in a biological population. Gene drives can be found in nature, but scientists are also developing 'synthetic gene drives' using CRISPR technology, which can be used to modify organisms and potentially control populations or combat diseases.

'Gene drives' could be designed to modify populations of weed species. One promising application is to 'knock out' a reproduction-specific gene, which could lead to the sterility of a species. Such a change could lead to a population-level decline in a highly problematic weed species.

Another application might be to modify weed populations and make them more susceptible to herbicide applications, as has been suggested (Barrett et al., 2019). Neve (2018) also suggested that gene drive technology may enable the reversal of herbicide-resistant weeds to their natural forms, making them susceptible to herbicides once again.

It appears that gene drive systems can be safely used as an approach to suppress the aggressive growth and reproductive behaviour of weeds and the targeted elimination of some problematic species. However, as these are novel approaches, their efficacy is yet to be thoroughly tested (Kumam et al., 2023). Such approaches are not currently used for the management of any species and need to be more cautiously explored.

Nevertheless, gene drives do seem to have the potential to become an effective and efficient tool for weed management. As an alternative to the excessive and unsustainable use of herbicides, gene drive poses no safety concerns regarding exposure to hazardous chemicals. The added advantages of using gene drive include fewer disturbances to the soil or environment (Myers et al., 2016), reduced long-term costs for managing weed populations, and minimal ongoing human intervention (Croghan et al., 2023).

Based on concerns about unintended consequences, we recommend applying the precautionary principle in modifying weed populations. A cautious approach is necessary when utilising novel gene drive technology to prevent unexpected gene flow and related undesirable effects that could further complicate weed management. Moreover, significant regulatory and ethical challenges exist with genetic manipulations of plant genomes. As discussed by Yaduraju (2021) and Menon (2025), these are obstacles that need to be addressed in countries like India.

Strengthening the Competitive Ability of Rice against Weeds

In most rice-growing regions of the world, considerable research effort has been made to produce high-yielding rice varieties. While high-yielding varieties are globally available, they are often less competitive against major rice weeds. As a result, if agronomic conditions and weed management strategies are not appropriately implemented, significant yield losses could occur.

For example, the New Rice for Africa (NERICA) reported that newly developed African rice (*Oryza glaberrima* Steud.) varieties can thrive in the challenging African environment. In addition to favourable growth, they also demonstrated some degree of the high-yielding potential of *O. sativa* (Somado et al., 2008). However, the new varieties lack resistance mechanisms to certain local constraints, including weeds, compared to the traditional *O. glaberrima* varieties (Mmbando, 2020).

Oryza glaberrima is recognised as a source of genes that confer resistance to various biotic stresses, including those from weedy species (Johnson et al., 1998; Dingkuhn et al., 1999; Fofana and Rauber, 2000). A cross-species hybridisation between *O. glaberrima* and *O. sativa* combined the greater competitive ability of the former and the higher yield qualities of the latter (Dingkuhn et al., 1997). The hybridisation resulted in rice lines with increased competitiveness and improved yields.

Given that *O. glaberrima* has been a potential source for improving weed competitive traits in Rice, it has been subjected to genetic analysis, especially to identify the quantitative trait loci (QTLs) associated with weed competitive traits. Nine QTL hotspots for weed competitive traits (qWCA2a, qWCA2b, qWCA2c, qWCA3, qWCA5, qWCA7, qWCA8, qWCA9, and qWCA10) were identified in BC1F2:3 population derived from weed competitive accession of *O. glaberrima* (IRGC105187) and *O. sativa* cultivar IR64, wherein several QTLs were co-localised (Bharamappanavara et al., 2020).

As demonstrated by this research, advanced molecular technologies offer significant opportunities to identify QTLs as well as specific genes and alleles associated with weed-competitive traits in rice.

A few of the rice plant characteristics associated with weed competitiveness are plant height, early canopy cover, high tiller density, vertical leaf orientation, high biomass accumulation at the early

crop stage, high leaf area index and high specific leaf area during vegetative growth, early vigour, and greater root biomass and volume (Saito et al., 2010; Ramesh et al., 2017). The gene editing tools hold great promise for identifying the specific genes involved in such plant attributes and for boosting rice's ability to compete with weeds by strengthening its competitive characteristics.

Seedling vigour, especially early seedling vigour (ESV) of seedlings less than 28 days old, is imperative for crop stand establishment and weed competitiveness (Richards, 1996; Zhao et al., 2007). The ESV is highly correlated with the ability of rice seedlings to compete with weeds, especially under aerobic conditions (Mahender et al., 2015).

Four QTL regions, qSV1a, qSV3e, qSV4c, and qSV7c, have now been identified, which delimit and harbour quantitative trait nucleotides responsible for ESV-related traits. Chen et al. (2019) recently reported favourable haplotype mining for the candidate genes within these four regions, as well as the ESV gene OsGA20ox1. These are considered highly promising developments.

The development of competitive rice cultivars requires interdisciplinary approaches. It involves screening rice germplasm to identify potential donors, as well as utilising races and other wild species that have been proven to harbour genetic heterogeneity and offer competitive advantages.

The availability of novel gene editing techniques could accelerate the development of competitive rice cultivars that can then be integrated into innovative weed management packages (Bharamappanavara et al., 2020). However, as Zhao et al. (2007) discussed, a more thorough understanding is also required of genotype-environment interactions and environmental variance concerning the development of a competitive rice phenotype using gene editing.

Developing Allelopathic Rice Cultivars Using Gene Editing Tools

Allelopathy is the ability of plants to inhibit or stimulate the growth of other plants in the neighbouring environment through the activity of exuded bioactive secondary metabolites, referred to as allelochemicals. However, as discussed by Bhowmik and Inderjit (2003) and Olofsdotter et al. (1999, 2002a, b), there are numerous challenges to utilising allelopathy for natural weed management.

Despite claims of incorporating allelopathy as a weed management tool, in our view, actual progress has been limited. This is mainly due to the complex challenge of accurately assessing allelopathic interactions in the field, where natural variability and changing environmental conditions prevail (see review by Chandrasena, 2023, pp. 202-216).

Allelopathic potential exists in many of the major world crops, including rice (Dilday et al., 2001; Olofsdotter et al., 2002a; b; Khanh et al., 2007; 2009; Yang and Kong, 2017). Key allelochemicals in rice include phenolic acids, terpenoids, and flavonoids.

While the allelopathic potential of rice was recognised decades ago, many questions remain unresolved regarding the biosynthesis, exudation, and biological activity of momilactones, phenolic acids and other bioactive chemicals exuded by rice (Kato-Noguchi and Ino, 2003; Kato-Noguchi et al., 2008; Amb and Ahluwalia, 2016; Serra et al., 2021).

Many studies have confirmed that rice roots, shoots, and leaves produce momilactones, which are diterpenoids released into the rhizosphere, inhibiting the growth of numerous plant species and exhibiting strong interactions within the rhizosphere zone. Apart from momilactones, an impressive array of other allelochemicals is also produced by rice (Khanh et al., 2007; Amb and Ahluwalia, 2016).

Specific compounds, particularly momilactone A and B, are capable of strongly inhibiting the growth of barnyard grass (Kato-Noguchi and Ino, 2003; Kato-Noguchi et al., 2008).

Their direct use of allelochemicals identified in rice and other crops as pesticides has not been successful for several reasons. These include the stability of most compounds in the natural soil environment, their selectivity and limited activity, as well as potential effects on non-target organisms.

Additionally, developing any novel allelopathic compound that could be used as a commercially viable biopesticide is known to be prohibitively expensive, thereby limiting investment opportunities. Even the isolation of allelochemicals from plants in required amounts is a tedious process. This has been the *Achilles' heel of allelopathy research,* and the reason why there are not many that have been earmarked for commercial production.

Furthermore, the genetics of allelopathic effects in crops and weeds, as well as the genes involved in producing allelochemicals, have been poorly studied. Mapping populations consisting of recombinant inbred lines (RILs) have highlighted that the allelopathic nature of rice is a quantitatively inherited trait (Olofsdotter et al., 2002a; b).

Recently, Yang and Kong (2017) investigated two rice genotypes, *Huagan-3* (an allelopathic variety) and *Liaojing-9* (non-allelopathic), for their effects on several major rice weeds, including dirty Dora (*Cyperus difformis* L.), barnyard grass, false daisy [*Eclipta prostrata* (L.) L.], red sprangletop

[*Leptochloa chinensis* (L.) Nees], and *Oryza sativa* (weedy Rice). The findings indicated that significant allelopathic inhibition occurred more at the root level (total root length, total root area, maximum root breadth, and maximum root depth) of the weedy species than at the shoot level.

Nevertheless, the identification of allelopathic genes or genomic regions (i.e. Quantitative Trait Loci, QTLs) has been a challenge in implementing specific breeding programs (Aci et al., 2022). A new approach to utilising the concept of allelopathy would be the development of transgenic allelopathic rice through gene editing technologies.

More than 20 years ago, Ebana et al. (2001) identified some quantitative trait loci (QTLs) associated with the allelopathic effect of rice exudates using restriction fragment length polymorphism (RFLP) markers. The study, using lettuce (*Lactuca sativa* L.) as the test species, identified seven QTLs on rice chromosomes 1, 3, 5, 6, 7, 11, and 12. One of the QTLs on chromosome 6 had the most significant effect on the allelopathic inhibition of lettuce, explaining 16.1% of the test plant's response. The other six QTLs explained the variation in the range from 9.4% to 15.1%.

Since then, the last 20 years have seen numerous studies on genes that produce allelochemicals and may be implicated in rice allelopathy (see reviews by Amb and Ahluwalia, 2016; Rahaman et al., 2022). Chung et al. (2020) more recently studied the occurrence of QTLs in rice using 'Sathi', an indica cultivar with high allelopathic potential, and 'Nong-an', a non-allelopathic cultivar.

As the test species, the researchers used a lettuce cultivar 'Yeolpungjeokchima', which was highly sensitive to low concentrations of allelochemicals. This study led to the identification of a QTL region on chromosome 8, a 194-kbp segment containing 31 genes, as being responsible for inhibiting the shoot length and total length of lettuce. The research showed that qISL-8 was directly implicated in the highest inhibition (20.83%) of the test species, suggesting that this region is a possible candidate for further study to clone genes for allelopathy traits (Chung et al., 2020).

A review of the literature on rice research, particularly the genetic studies conducted over the past 20 years, reveals no decline in interest in using allelopathic rice varieties for weed suppression in the field. However, in our view, the real challenge is to retain the highly favourable yield, plant architecture, and grain quality of rice varieties while conserving the crop's weed-competitive capabilities through genetic manipulations of allelopathic and non-allelopathic traits. Developing novel varieties through the rapid advancement of genetic tools may help achieve this highly desired outcome.

Gene editing for visual recognition of Rice Weeds by machine-learned robots

Weeds in rice, such as weedy rice and barnyard grasses, are strong competitors with rice. Often, most rice cultivars are unable to outcompete such aggressors (Johnson et al., 1998; Saito et al., 2010). The removal of such grasses by manual or mechanical means is difficult, as they closely resemble rice. Rice weed managers have been attempting to solve this problem for many decades (Rao et al., 2017; Rao, 2021, 2022a, b).

Hence, in rice weed management, it is also worth testing the proposal made by Pedro et al. (2024) to use gene editing techniques to introduce traits into crops, enabling visual recognition of the crops by weeding robots trained through machine learning.

Given the rapid advancements in machine learning, artificial intelligence (AI), robots and drones that can identify weeds, this possibility offers an opportunity for further development for future applications. In India, an AI-driven robotic system incorporating advanced image recognition capabilities has already demonstrated remarkable precision and speed, outperforming manual labour in weed removal (Mohanty et al., 2025).

Whether these systems can be further enhanced by slight modifications to the visual image of the crops remains to be seen.

Genome editing to manage parasitic weeds

Infestations of purple witchweed [*Striga hermonthica* (Delile) Benth.] and related parasitic plants result in substantial yield losses in many crops, including Rice. These are significant problems for agriculture in sub-Saharan Africa, Southern Europe, the Middle East and Asia, including India (Parker, 2009).

Nevertheless, recent research has been very promising in this regard. Genome editing and gene silencing-based technologies offer new opportunities to enhance crop resistance to parasitic weeds (Yildirim et al., 2024). The strategies of silencing host or parasite genes may serve as an effective strategy to obtain more sustainable and durable crop resistance to parasitic weeds. For example, CRISPR/Cas9 has been used to knock out the CCD7 gene in Rice, thereby reducing strigolactone content in the roots (Butt et al., 2018).

The reduced levels of CCD7 may help fine-tune the levels of strigolactones, leading to altered plant architecture (especially tillering to improve crop yields) and thereby lowering the risk of *Striga* infection and adverse effects. Based on these findings (see Butt et al., 2018; 2020), it is possible to predict that knowledge of whole-genome sequences and transcriptomes of parasitic plants can be utilised to enhance resistance in rice to parasitic weeds by employing molecular breeding and advanced genome editing strategies.

Conclusions

We agree with the assessments of Kobayashi et al. (2023) and Luo and Liu (20025) that genetic tools are robust options that can be deployed to safeguard food security and nutrition, which is crucial for countries to overcome hunger and malnutrition problems in many regions, including India and the broader Asian-Pacific region.

The application of new genome-editing breeding technologies has significantly expanded the possibilities for improving rice crops. In recent years, various genome-editing techniques, including CRISPR-directed evolution, CRISPR-Cas9, and base editors, have emerged as powerful tools for efficient and precise genome modifications in rice.

The suitability of rice as a model system for functional studies, its small genome size, and its close relationships with other cereal crops have further accelerated the development of novel genome-editing technologies in rice. The advances in genetic studies and their applications in rice research over the last decade are revolutionary.

As shown by the examples we highlighted, advances in biotechnology are now driving a new wave of potential increases in food production (ISAAA, 2019; Hernández-Soto et al., 2021; Bacha et al., 2025). Biotechnology is revolutionary in that it now offers novel opportunities that were previously unavailable, thereby increasing productivity and contributing to global food, feed, and fibre security.

New crops and food production approaches via biotechnology will support self-sufficiency on any nation's arable land while conserving biodiversity, reducing deforestation, and protecting the environment. They also mitigate the challenges associated with climate change and improve economic, health, and social benefits.

Public acceptance and enabling policies in the government are crucial for the agricultural, socio-economic, and environmental benefits of biotechnology crops to reach those experiencing poverty and hunger. While there are challenges to overcome – both technological and regulatory – the new generation of crops produced by genetic technologies must be viewed as crucial to meeting the food and nutrition demands of an increasingly global population.

The use of gene editing technologies in rice presents various opportunities for more strategic and enhanced integrated weed management in rice cultivation. Among the many options is the capacity to introduce modifications to the genomes of weedy species that make them less successful in rice fields and more susceptible to rice herbicides (Asadullah and Shah, 2025). Other options include identifying and utilising novel herbicide target sites of action, novel genes for improving crop competitive traits, allelopathic weed-suppressive traits, and innovative means of weed management.

In a recent review. Akhtar et al. (2024) discussed how allelopathic research may once again focus on improving weed management. We agree with them that by combining molecular, genetic, biochemical, and bioinformatic tools, research can unravel the complexities of allelopathic interactions and their potential for sustainable crop production.

The new genetic technologies, such as gene drive, transgene technologies, gene silencing, marker-assisted selection (MAS), and CRISPR-Cas9, are promising in this regard. By strengthening the competitive characteristics of rice, these tools hold great promise for boosting crops' ability to compete with weeds.

The rapid integration of AI across disciplines is now driving another transformative phase in genome editing, including the optimisation of editing systems, the prediction of editing site efficiency, and the design of editing strategies, as well as the streamlining of workflows and the enhancement of precision (Jiang et al., 2025).

While integrating classical and advanced genetic technologies and utilising novel tools for weed management, we must also necessitate a critical evaluation of the ecology and physiology of weeds using genomic technologies.

Looking forward, we can expect to see CRISPR-edited crops, including rice varieties, continue to emerge in the literature, laboratories, and even our markets over the next decade. Generally, the new crop varieties will possess favourable traits related to climate adaptation, improved consumer quality, and yield enhancement. The rapidly changing gene editing technology will go way beyond the simple "knocking out" of particular genes in favour of precise gene insertions, base-pair edits, and/or multiple types of edits carried out simultaneously. These will represent the growing use of more technically

complex gene editing techniques (Dong et al., 2021; Kobayashi et al., 2023; Luo and Liu, 2025).

The technological power of CRISPR is undeniable. However, the ultimate global impact across various fields of endeavour, including its use as a tool for improved weed management, depends on implementation. The most significant obstacles to implementation include favourable regulation, fast-tracked approval processes of gene-edited products, grower education, and public understanding and acceptance of such technologies.

We believe that it is not just technological innovation but also navigating the complex sociopolitical landscape of sustainable food systems that is crucial to determining the extent to which gene editing should be used to improve our food systems and food security.

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