



The Role of CRISPR/Cas9 for Genetic Advancement of Soybean: A Review

**Muhammad Naveed ^{a*}, Jazib Javed ^a, Usama Waheed ^a, Maham Sajid ^a,
Mehrab Ijaz ^a, Areeba Sehar ^a, Mazhar Attique ^a, Mahnoor ^a
and Salman Javed ^a**

^a *Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/93311>

Review Article

Received 07 September 2022

Accepted 13 November 2022

Published 17 November 2022

ABSTRACT

Soybean is a crucial legume crop that is mainly grown for extracting oil and protein content Which can be used as a food source for human beings as well as livestock. We can also use the protein obtained from soybean for the extraction of biofuel. There is a dire need to increase genetic research on soybean for improvement and enhanced production. One big reason for genetic research on soybean is to make its resilience to the change in the climate. In modern days CRISPR/Cas9 has evolved as an emerging technique that allows us to manipulate the gene of selected traits in most crops including soybean. Advanced tools of biotechnology are widely utilized for the enhancement of crop production, improving quality and yield, introducing disease and insect resistance, and being environmentally friendly. This review gives a glimpse of how the mechanism of CRISPR/Cas9 performs its functions and a brief discussion of CRISPR/Cas9 which has increased the scope of study in the genetic advancement of soybean. It also illustrates some phenomena in which we can use CRISPR/Cas9 for the betterment of soybean.

Keywords: *CRISPR/Cas9; genetic improvement; soybean; gene editing.*

1. INTRODUCTION

Soybean (*Glycine max*) belonging to the Fabaceae family originated in China. About 23,000 different varieties of soybean were first domesticated in Asia, in China, and were then transferred to the USA and Brazil [1]. Due to their high protein content, soybeans are a highly significant legume that is eaten all over the world. They are most frequently utilized in dishes from Japan, Korea, and Indonesia. Typically, soybeans are fermented to create unique ethnic dishes or culinary components or sprouted for use in salads. When soybeans are cooked for around five minutes in Japan, they are frequently eaten as a snack with beer. Tofu is a protein-rich meat alternative that is produced from soybeans in several East Asian nations. Soybean is fermented with a food-grade fungal disease of the *Rhizopus* organisms in Indonesia to make tempeh, a protein-rich meat alternative [2]. Additionally, soybeans are a valuable commodity in the food, fuel, and fisheries industries due to their high protein content. Soybean is a major commodity crop, used for both food and fuel. Its oil content (18-22%) is second only to peanuts among edible legumes, and its protein content (40-42%) is the highest of any food crop [3]. Pests, diseases, and weeds all negatively impact soybean crop output, with weeds being the primary culprit. Each year, microorganisms including fungi, viruses, bacteria, oomycetes, and nematodes economic loss. Pests that affect soybeans include aphids, beetles, mites, and stinkbugs attack the plant as a whole. The production and quality of soybean crops are both reduced as a result of pathogen infection. Soybean rust, bacterial blight, and soybean mosaic are the most significant diseases, affecting the majority of crop output, on the list of main diseases in soybean caused by numerous pests and pathogens. [4]. Abiotic stressors are the numerous environmental challenges that plants constantly face and can significantly lower their output. Complex and involving many physiological, molecular, and cellular adaptations, plant responses to these challenges are difficult to comprehend. Different issues severe salinity or drought, excessive heat, and flooding, toxic metals/metalloids, ozone, UV radiation, bright light, etc. are some of the main abiotic stressors. The growth of plants is retarded by the stress due to osmotic pressure in the saline type of soil while the stress of drought which results due to climate change is very dangerous for plant growth. This creates an alarming situation for researchers and farmers as

well. Plants are frightened by the harmful consequences of high-temperature stressors as a result of global warming. Some major consequences of high temperature are denaturation of protein, deactivation of enzymes in many reactions, oxygen reactivity is increased in oxygen species, destruction of membrane structure, and harms in the form of ultra-structural cellular components. Another significant environmental element that frequently impacts plant development and agricultural productivity, again resulting in significant crop losses, is low temperature or cold stress [2]. To combat these stresses and increase the yield advanced technology CRISPR-Cas9 is used. The CRISPR/Cas9 method for gene editing, based on site-specific nucleases, has made strides in the effective targeted alteration of various crops for improved yield and resistance to diseases and other challenges. To create diversity and hasten breeding efforts, CRISPR-Cas9 has proved to be a powerful editing tool for the accurate editing of genome sequences in all types of crops. In this context, the review emphasizes the many functions and uses of the CRISPR/Cas9 system as potent technologies to raise agricultural yields and increase tolerance to environmental stress in agronomically significant soybean, regarding this, the review illustrates the high-efficiency use of CRISPR/Cas9 to boost yield, developing resistance of environmental and biotic stresses [5].

2. GENOME EDITING USING CRISPR/CAS9

CRISPR/Cas9 consists of the immune system of prokaryotes (those organisms which don't have prominent Nuclei). It works upon the guidelines of RNA while genome editing on a specific site. This system is widely used to cure human genetic diseases. This is a very effective system but at the back end, it has some drawbacks like off-target effects [6]. Long before the discovery of CRISPR/Cas9, it was very difficult to edit the genes. The two most important techniques (i) Zinc finger nucleases (ZFN) and (ii) Transcription activator-like effector nucleases (TALENs) was very popular for editing target DNA. But their drawback was high cost and they were more time-consuming than CRISPR/Cas9 [7]. As there are many types of stresses in the plant they can be biotic or abiotic. Researchers always want to edit the genome of plants for the genetic improvement of different traits. CRISPR/Cas system is used for improvement in nutrition, biotic and abiotic stress resistance, metabolic

engineering, etc. It has a wide range of applications [8]. CRISPR/Cas9 is a simple system that is very easy to use for the fast and efficient editing of genes [9]. It is most recent technique is genome engineering [10]. CRISPR/Cas9 system is categorized into 2 classes according to the function of the Cas protein. Class 1 has Cas protein complexes and includes type 1, 3 and 4 while Class 2 is simple and has single proteins which include types 2, 5 and 6. Cas protein and guide RNA are the most important in CRISPR/Cas9 system [7]. Efficient genome editing through this system needs a vector system, target sites, and an appropriate way of transformation. Special vectors are designed to achieve highly efficient results with accurate editing [2]. So CRISPR/Cas9 is a potential tool for genome editing. The complete process of CRISPR/Cas9 is consist of just 3 steps. First of all (i) Recognition, then (ii) Cleavage, and at the last (iii) Repair. Single-guided RNA must be present for the working of Cas protein. sgRNA signals the Cas protein to recognize the targeted DNA sequence. It then cut the sequence at specific sites. Then there are two mechanism of repairs for Double-Stranded break for homologous and non-homologous ends [7]. There are two setbacks of this efficient systems, one is that there is specific PAM sequence for ortholog of each Cas9 while other is there is danger of mutation which is not needed at all. [11].

3. IMPLEMENTATION OF CRISPR/CAS9 IN SOYABEAN

In 2015, CRISPR/Cas9 was used first time [12]. After the successful execution of initial attempts, many researchers started to use this technique for the manipulation of genes of soybean for research and development and made remarkable progress. This technique has great potential to improve the soybean by targeting mutagenesis and its qualitative and quantitative traits also.

3.1 Steps Involved in the Application

First of all selection of a plant and the selection of the targeted site for mutagenesis and PAM sequence is recognized. In the second step, sgRNA was designed and then CAS9 and sgRNA were assembled in a suitable vector. In the next step, the vector is transformed into the selected soybean plant and transformants are identified. Finally detection of mutation by sequencing or PCR/Re assay. By following the above mention procedure CRISPR/CAS9 system

was utilized for genome editing in soybean for improving its various traits by targeting its genes. By knockout of genes (SPL9a, SPL9b, SPL9c, SPL9d) and (GmLHY1a, GmLHY1b, GmLHY2a, GmLHY2b) plant architecture features influences and by targeting (GmAP1, Gmpr37, GmE1, GmFT2a) flowering period is affected which increases the crop yield. In the same way by knocking out different genes various traits in soybean such as crop nutrition and quality, and nodulation were improved, and tolerance to biotic and abiotic stresses is achieved.

3.2 Improvement of Yield

The prime objective of many researchers is to bounce the yield. Yield is the result of different factors like gene and their interaction with the environment and many abiotic and biotic factors which affects the crop in vegetative and developmental growth stages. It is the most crucial trait which is measured by different aspects like the number of pods, the number of grains, seed weight some other factors which affect yield indirectly such as plant height, node number, leaf length, width, and shape, as well as branch count, are all intermodal [13]. The four crucial genes, "GmSPL9a, GmSPL9b, GmSPL9c, and GmSPL9d, from the SPL9 family," were swapped out using CRISPR/Cas9. Soybean plant architecture was studied after mutations were induced in four genes [13]. It was concluded from research that the mutant spl9a/spl9b from T2 double homozygous has a small plastochoron value. From the experiment, it was found that the T2 double homozygous mutant spl9a/spl9b had a shorter plastochron length. This led to the uplift of trifoliolate leaves, nodes, and branches of the soybean plant [14]. These characteristics like more branches, more node number, and an increase in dry weight show a positive response in correlation with yield [13]. Height is also a yield determinant factor as a long plant means longer inter-nodal distance and stem which results in lodging. Thus yield is ultimately decreased due to grain loss [15, 16]. Another effect that was observed was due to lodging is the reduction of seed, seed loss, and unhealthy and less vigorous seed [17]. Many steps are practiced with time for the reduction of plant height in numerous staple crops [18]. In Soybeans, the CRISPR/Cas9 was used to target four major genes which are responsible for the Late Elongated Hypocotyl (LHY) family of genes to explain their potential regarding plant height and inter-nodal distance. There is a significant role of quadruple mutants in soybean for the

reduction of plant height along with inter-nodal distance for improving crop yield in comparison to wild-type plants. It is also an observation that the experimental mutant soybean has less amount of gibberellic acid while the wild type has a great quantity. Gibberellic acid acts as a role in developmental stages and improves plant height, elongation, and leaf expansion also. So gibberellic acid content also altered through this.

3.3 Altering Plant Architecture

Exemplarily Plant structure is very necessary for better production Ideotype is a necessary character for good yielding and its character is under the control of the growth habitat of soybean cultivar. So in this way genes such as GmLHY linked by gibberellic acid are altered through editing [13].

3.4 Improving Quality

CRISPR has an inevitable role in case of quality improvement in soybean which is discussed as under.

3.4.1 Improving seed sugar content

Soluble sugar contents, amino acids, and mineral nutrition are very important for the quality of seed. GmSWEET10a and GmSWEET10b assess the size of the seed, quality of oil, and protein contents at the same time in soybean. These two genes also check the allocation of sugar for the seed coat and embryo [19]. Soybean has a much larger seed as compared to Arabidopsis and it requires much more sugar. Therefore, minor changes in their sugar content will create a strong effect on seed development [20].

3.4.2 Decreasing the unpleasant seed beany taste

Soybean possesses a huge quantity of protein content. It also has a characteristic of special taste like soy flavor which inhibits the acceptance of soybean and its products for humans on the big canvas. There are three Lipoxygenases in soybean which are under the supervision or control of the *Lox1*, *Lox2*, and *Lox3* genes. This lipoxygenase plays a vital role in the oxidation of linoleic acid and linolenic acid. As a result, they produce a grassy and beany taste in soybean and its byproducts. For getting Lipoxygenase-free soybean lines, the CRISPR/Cas9 system was applied to cause a mutation in *GmLox1*,

GmLox2, and *GmLox3* genes. They could be used for the reduction of beany flavor in soybean [21].

3.4.3 Production of the hypoallergenic soybean crop

As an immunodominant protein, Gly m Bd 30 K (P34) has already been identified. To develop hypoallergenic soybeans for human consumption was also attempted to replicate low-P34 soybean germplasm [22]. Fifteen different proteins have been isolated from the serum of people who are allergic to soybeans. Important allergenic proteins in soybeans were identified as Gly m Bd 60 K, Gly m Bd 30 K, and Gly m Bd 28 K. CRISPR/Cas9 technology was utilized to alter the Gly m Bd 30 K and Gly m Bd 28 K genes in soybean plants to make them hypoallergenic. Mutant soybean plants did not store high levels of either allergen in their seeds. Identified immunodominant protein in mutant soybean seeds [21].

3.5 Regulation of Flowering Time

Soybeans' flowering time is a key agronomic factor that affects their productivity and adaptability. Yet, it is still unclear what factors at the genetic level make soybeans able to thrive in a wide range of latitudes. It's a fundamental biological process that guarantees successful plant reproduction. For flowers to bloom at the right time of year, a complex regulatory network of genes must be tightly regulated. Soybeans, an important legume, are typical short-day dicotyledons that only flower when the day length drops below a certain threshold. Her growth is limited by an inherent sensitivity to day length. Therefore, increasing the area under cultivation of this plant to low and/or elevated concentrations necessitates the creation of soybean genotypes that are not impacted by day length [23]. Exploring the various roles that CRISPR-Cas (a form of genome editing) plays in flowering and flower advancement, as well as its potential biotechnological applications in this area, is the primary goal of this research. To thrive in ever-shifting environments, plants must undergo a wide range of physiological and morphological transformations. A plant's normal flowering time is largely determined by environmental cues like low temperature and light. When deciding on a blooming period, the temperature is also an important factor to think about. Therefore, plant reactions to seasonal temperature changes are not universal. Some

plants, known as vernalizes, need to be exposed to cold temperatures for an extended period before they will flower when the weather warms up [24]. Flowering is an essential productivity feature in soybeans that are affected by seasonal changes in day duration. Several circadian clock-associated genes have been found in recent research that have a role in controlling flowering time in response to changing light phases. In soybean, twelve maturation sites (E1 through E11 and J) that influence blooming and maturity time have been found and described phenotypically and genetically [25-34]. Dominant alleles for genes E1, E2, E3, E4, E7, E8, and E10 suppress flowering, while dominant alleles for genes E6, E9, E11, and J stimulate it. E1, E3, E4, E7, and E8 mediate photoperiod sensitivity to varying light quality, especially in artificially generated LDs [35]. The E1 locus is responsible for the greatest variation in flowering time, and its associated protein contains a B3-like domain [36]. E2 is the GIGANTEA (GI) homolog in the plant species *Arabidopsis thaliana* [37], Her PHYTOCHROME A (PHYA2) and PHYA3 genetic traits have counterparts in *Arabidopsis thaliana*, designated as E3 and E4, respectively [38,39]. Soybean FT2a and FT5a, her two Flower initiation LOCUS T (FT) homogeneity, are florigen coding variables that regulate flowering time [12, 40]. Soybeans' genomes can be edited in a straightforward, effective, and highly specific way using the CRISPR/Cas9 (clustered regularly interspaced short palindromic repetition) system [41,42]. Recent effective gene manipulation has led to the discovery of genes involved and germplasm in soybean [13,18,40,43,44]. He used his CRISPR/Cas9 technique to create homozygous quadruple mutations of the LNK2 gene in soybean, which have functional homologs of *AtLNK2*. The triple mutant blossomed quickly in the bright sunlight. The results raise the possibility that fresh genes in the LNK2 family influence soybean blooming time, which could lead to improved soybean breeding [45]. The flowering roles of GmFT2a and GmFT5a, two FT homogeneity, are similar. Early flowering in soybean was induced by the upregulation of these two genes in reaction to prolonged daylight [46]. CRISPR/Cas9-mediated T2 soybean mutant ft2a was CRISPR/Cas9-mediated and bloomed under both long-day and short-day conditions [40]. Extensive examination of ft2a, ft5a, and ft2a-ft5a mutants under short- and long-day circumstances [47]. In short-day settings, GmFT2a was found to be superior to GmFT5a, while in long-day settings, GmFT5a proved superior. Soybean acclimatization to high

temperatures also depends on GmFT5a. Base-edited mutants showed the ability to fine-tune flowering time using a variety of CRISPR/Cas9-based methods, despite the fact that they flowered later than knockout mutants.

3.6 Improving Oil Contents

Scientists are investigating methods of continuing to increase the seed oil yield of oilseeds to meet the rising demand for vegetable oils. To achieve these results, scientists have used both conventional breeding and transgenic methods. However, the polyploid essence of many soybeans and the associated time constraints significantly reduce the success of conventional breeding methods. Because of this, CRISPR/Cas genetic modification has emerged as a potentially revolutionary breeding technique that could lay the groundwork for meeting rising demand and reducing regulatory burden. Our study uncovered several candidate genes for genome editing in this context and uncovered novel CRISPR-related technologies with the potential for future use in oilseed crops [48]. Genome editing strategies based on clustered regularly interspaced short palindromic repeats [CRISPR/Cas] have been developed to lower the bar without sacrificing efficiency. Because of its high mutagenicity, it has garnered a great deal of attention over the past decade. Specific DNA regions have been identified [49]. Genetic engineering techniques include the over-expression of native or foreign genes and the back of intrinsic gene expression to speed up advancements in seed oil production and quality [50]. Initial reports on oilseed living things like canola, camel, and soybean reveal a wide range of CRISPR/Cas-mediated editorial rates, from 0% to 100% [51]. This wide range of variation could be the result of alterations to factors such as target sites, sgRNA type, transformation processes, organizers used to enhance Cas and sgRNA production, and background vectors [52, 53]. Evidence from previous work on improving seed oil through gene hit utilizing CRISPR/Cas-mediated genetic modifications indicates that altering fatty acid content is feasible due to the fundamental genetically based of these features. However, due to the intricate nature of lipid accumulation and our limited knowledge of the biochemical pathways involved, increasing seed oil content by this method is expected to be difficult [54,55]. Only slight gains in seed oil content have been achieved despite the application of transgenic methods that involve genetic variants and/or concentrate on specific

tissue. Additional intriguing gene objectives that have been shown to increase seed oil yield when the bottom or changed through genome editing will almost certainly be studied in future advancements in this field. Furthermore, there are a variety of small and unique mutations that lead to increased enzymatic activity that are being uncovered by studies employing directed progression to alter numerous genes associated in lipid biosynthesis [56,57]. In this way, researchers may be able to use base- or prime-editing to improve the function of a gene of interest instead of just knocking it out entirely. As in tomato, CRISPR/Cas has been shown to control gene expression by eliminating a repressor factor from the promoter of a specific gene [58]. Since genome editing does not allow us to restrict genetic changes to specific tissue types, we must exercise caution when silencing or repairing genes; doing so could have unintended consequences that have a profound effect on a crop's agronomic performance. By targeting cis factors, researchers in other plant species have been able to fine-tune gene dosage and mitigate these effects by inducing a wide range of alleles with varying expression levels. using CRISPR/Cas9, which is a technique with great potential for improving oil-related characteristics [59].

3.7 Regulation of Nodules Formation

The symbiotic relationship between legumes and rhizobia is extremely successful and plays an important role in sustainable agriculture. It can help to increase crop productivity, resulting in high-yielding fertilizers, and it can help to reduce the usage of nitrogenous fertilizer since this collaboration can fix nitrogen from the air [60]. Soybean approximately fixed about 16.4 (Teragram) of Nitrogen which is almost 77% of the Nitrogen fixed by all legumes with the help of symbiotic relationship between legumes and Rhizomes in an entire year [61]. Many genes participate as a host in legumes and perform their roles in the SNF (a symbiotic nitrogen Fixation) process for example identification of rhizobia, and determining the nature of Positive or negative regulation based on the number of nodules, signal transmission in nodules, and development [62]. CRISPR/Cas9 technology was used to investigate the gene that controls the production of nodules in soybean. Unfortunately, a significant number of nodule formations cause plant development to be slowed due to excessive photosynthesis during the nodule formation process. The soybean (*Glycine max*) Rhizobia-

Induced Nodule Number Control 1 and 2 (*GmRIC1* and *GmRIC2*) paralogous genes contribute to auto-regulation for the signal of nodule development, number of nodules, and size of nodules formation [62]. CRISPR/Cas9 targeted and selectively edited *GmRIC1* and *GmRIC2* to increase nodule formation and size in soybean (Bai et al., 2020). In addition, the root-determined nodulation1 (*GmRDN1*) triple mutants *GmRDN1-1*, *GmRDN1-2*, and *GmRDN1-3* have fewer nodules and abnormal vegetative growth which illustrates the need for *GmRDN* for normal vegetative growth and nodule formation [63]. Another research showed that the genes that direct Root Hair like (*GmRDH3a/GmRDH3b*) along with hairy genes of the meristem (*GmHAM4a/GmHAM4b*) and leucine-rich add which repeats in soybean (*GmLRX5*) has a negative correlation with nodule formation [64]. Rhizobia produces (tRNAs) derived components, which are employed as a positive regulator of nodule production and as a suppressor of root nodulation in soybean. The elimination of suppressor genes When compared to controls, CRISPR/Cas9 resulted in the formation of more nodules in soybean [64].

3.8 Abiotic Stresses

Abiotic conditions such as salt, drought, temperature, floods, or insufficient water supply have also influenced soybean productivity [65]. According to estimates, soybean growers and farmers lose 57 million USD worth of crops each year owing to salt and drought can cause yields to drop by more than 50% [65]. As a result, scientists have been striving to uncover essential genes involved in the abiotic stress response system to overcome the existing constraint. To improve drought and salt tolerance, soybean researchers have used CRISPR/Cas9 to analyze the function of stress-related genes.

3.8.1 Drought tolerance

Severe abiotic stress and drought has reduced annual global output by half. Soybean yield and quality are significantly impacted by drought conditions, making this a major global food security concern [66]. Stomatal closure, total biomass, generate, and other important characteristics all decrease during drought [67]. Reactive oxygen species (ROS) trigger oxidation in crops and disrupt many processes [68] which are then accumulated in huge quantities [69] protein degradation, enzyme inactivation, and genetic damage are all possible outcomes [70].

High levels of reactive oxygen species (ROS) cause cell damage, which in turn affects a variety of processes, including soybean plant growth and development. [71]. Stress from drought reduces photosynthetic activity and disrupts the absorbed supply chain, resulting in a lower soybean growth ratio during grain filling. Seed germination may be reduced by 9-35% under moderate to severe drought stress, according to previous studies [72]. After seven days of drought stress, soybean seed sugar content decreased by 9% [73]. Soybeans are often made drought-resistant through molecular methods. The AtMYB44 gene from *Arabidopsis thaliana* was transferred directly into a soybean genotype using the *Agrobacterium*-mediated gene transfer method, leading to increased yield and quality under arid conditions [74]. Soybean engineering for drought stress acceptance will benefit from advances in *Agrobacterium*-mediated transgenes technology and tissue culture renewal of soybean cultivars [75]. CRISPR/Cas9, a revolutionary gene-editing tool, has produced promising results for improving soybean drought tolerance [76]. The use of CRISPR/Cas9 for gene editing has proven to be an efficient strategy for crop improvement. GmNAC8, a representative of the NAC gene family, functions as a regulatory element in the soybean plant during periods of drought [77]. By making changes to the gene with CRISPR/Cas9 technology in soybean, its function was verified. Tolerance to drought was decreased in GmNAC8 takedown lines versus control plants and increased in GmNAC8 upregulation lines. Soybean drought resistance is significantly aided by the connection between GmNAC8 and the drought-induced protein GmDi19-3 [77].

3.8.2 Salt tolerance

Salt tolerance is another abiotic factor that prevents healthy soybean production. One of the most significant environmental stresses affecting agricultural output, soil salinity affects millions of hectares of land around the world and results in enormous annual economic losses. Roughly 62 million acres (about 15 million square kilometers) are currently threatened by high salt concentration. Just 20% of farmland receives water for growing food. It is predicted that by 2050, more than half of all farmable land will have become salt-affected [78,79]. Soybean's complete genome sequence has aided in our comprehension of the underlying mechanisms of gene expression and control as they pertain to salinity [40] Several genes have been identified

in soybeans that increase their tolerance to salt stress [80]. Salt stress tolerance is improved by GmFLD19, which decreases Na ion and malondialdehyde densities, boosts antioxidant enzymatic activity, and decreases chlorophyll content [81]. Soybeans' sensitivity to salt stress is enhanced by GmNARK's promotion of ABA biosynthesis. Utilizing the CRISPR/Cas9 system, they demonstrated that GmNAC06 upregulation in soybean hairy roots functions as a regulatory element of salt tolerance. Soybean salt tolerance is facilitated by the sodium/hydrogen exchanger GmNHX5, the functional mechanism of which has been the subject of another study [81]. Soybean plants' salt tolerance was diminished after being modified using CRISPR/Cas9 technology. Soybean hairy root yield was improved by GmNHX5 overexpression by keeping the K⁺/Na⁺ ratio stable to avoid organelle damage [81]. To improve plant abiotic stress tolerance, AITRs are a promising group of candidate genes for CRISPR/Cas9 genome editing [82,83] Salt tolerance increased in the Gmaitr mutant seedlings, and their roots and stems grew longer. Since this occurs, it is possible that GmAITR gene editing can improve soybean salt tolerance [84].

3.9 Development of Herbicide Resistant Plant

Plant biotechnology relies heavily on herbicide resistance for weed management and as a diagnostic biomarker for transformation-based genetic engineering, which in turn helps farmers boost output. Recent years have seen the use of CRISPR/Cas9 to develop herbicide-resistant crops like rice [85], *Arabidopsis* [86], watermelon [87], and oilseed rapeseed [88]. Here we discuss the most recent advances in the development of weed killer plants utilizing CRISPR/Cas9-mediated gene editing technology, with a special emphasis on the targeted modification of endogenous genes such as acetoacetate biosynthetic pathway (ALS), possibly resulting synthase (EPSPS), cellulose key enzyme A subunit 3 (CESA3), and splicing factor 3B subunit 1. (SF3B1). More precise and effective genome editing tools are required because CRISPR/Cas-based genome engineering strategies are already being used extensively to develop crops with extra features like herbicide tolerance. This review will focus on the generation of HR plants through CRISPR/Cas9-mediated gene editing, as well as candidate genes for the generation of HR plants through loss-of-function mutations [66].

3.10 Disease Resistance

Soybean production and quality have been severely impacted by plant diseases. [89]. Soybean cyst nematode and charcoal rot have caused 33% of economic losses in soybean crops per hectare on average [90]. The CRISPR/Cas9 method has provided fresh insights into the development of disease-resistant soybean. This approach has produced several effective outcomes in a variety of crops [91-93]. The genome of plants is targeted in this strategy to generate resistance to certain diseases [89]. or the host has responsibility for creating plant pathogen defenses [94]. Although little is known about pathogen improvements in soybean using CRISPR/Cas9, the technique can modulate pathogen resistance in soybean [95] [96].

3.10.1 Viral resistance

The deadly disease Soybean Mosaic Virus has severely harmed soybean output (SMV) [97]. Soybean root hair and plants were treated with CRISPR/Cas9 to concurrently target three isoflavonoids synthesize genes (GmFNSII-1, GmF3H2, and GmF3H1), which resulted in an increase in isoflavone concentration in the seeds and leaves of mutant soybean plants [98]. High isoflavone content soybean plants have shown serious opposition to soybean mosaic virus strain SC7 [98]. After infection with strain SC7, the amount of SMV coat protein was lower in triple mutants.

3.10.2 Nematode resistance

Genes belonging to the nucleotide-binding-site leucine-rich repeat (NBS-LRR) family are responsible for effector-triggered immunity, which occurs in response to extremely specialized pathogenic effectors. In plants, NBDLRR is tandemly duplicated sequences that can undergo recombination to create novel disease resistance [93,99]. They were able to prevent *Phakopsora pachyrhizi* from infecting soybean [19,100] and *Phytophthora sojae* [95,101] contributes to the spread of soybean rust To identify novel resistance genes, the technique was used to generate rearrangements via targeted chromosomal cleavage [96]. Soybean NBS-LRR families Rpp1L and Rps1 were selected, and double-stranded break (DSB) and fixing with CRISPR/Cas9 were used to generate specific adjustments in the Rpp1L and Rps1 clusters. New disease-fighting properties may emerge from this unusual pairing [96].

3.11 Male Sterile Line Development

Heterosis breeding is a very efficient way for the genetic improvement of crops [102]. Heterosis (hybrid vigor) is a phenomenon in which one or more traits of heterozygous progeny are superior than both of its homozygous parents [21]. For hybrid seed production, male sterility is very important [21] For the first time in the history of soybeans male sterile lines were developed using AMS homologs, and targeted mutagenesis. The GmAMS1 mutation resulted in male sterile soybeans. This gene stimulates soybean pollen production. Researchers employed the CRISPR/Cas9 technology to successfully modify the MS1 gene to create soybean male sterile lines. Out-crossing soybean population is developed by using these male sterile lines [103].

4. FUTURE PROSPECTS

The genome system of soybean is paleopolyploid. The complete sequence of the soybean genome is done with the help of the whole genome shot gun method [104]. Among the major issues regarding the breeding of soybean is the complex structure of the genome and along with that Genome size is 1.1 GB in length while consisting of 46, 430 genes for the coding of protein. 75% of the genome is multiple copies of genes. We are unaware of the function of many known genes. This CRISPR/Cas9 is a reliable tool for estimating gene function because this system provides us the facility of both Single-gene knockout along with multiple gene editing [105,106]. Effective transformation is considered a keynote for the improvement of advanced breeding lines in the case of soybean [107]. The commonly used method of gene transformation is *Agrobacterium* with just 5% efficiency in soybean which is very low as compared to rice which is around about 90% [107]. So viral vectors were used to introduce CRISPR/Cas9 in plants [89] by using particle bombardment [108] Cas9-sgRNA Ribonucleoproteins (RNPs) [109] and nanoparticles also proposed alternative ways. When the two genes which are regulating start to overexpress *Baby boom (Bbm)* and *Wuschel2 (Wus2)*, has increased the efficiency of transformation in various types of genotypes and species [110]. Forgoing the need for tissue culture, CRISPR/Cas9 genome-edited dicots plants were produced through de novo induction in the meristem. The CRISPR/Cas9- mediated genome editing system was used successfully in soybean for creating roots with hair and a stable and smooth transgenic plant along with somatic

embryos from its first use in 2015 [111]. At this stage the progress of CRISPR/Cas9 with its new modern techniques. At the moment, the revolution in CRISPR/Cas9 with new emerging techniques and tools and different variations in Cas can update soybean complex gene scenario, which is within the scope of current research. spCas9-NG, peak editing, xCas9, Cpf1 (Cas12a), Cas1,3, and Cas different versions are just some of the cutting-edge CRISPR/Cas tools used in the genome editing system [112]. As per our information, the method which is described above never been utilized efficiently for genome editing in soybean. A has been noted in recent research that the 3-variants of Cas9 enzyme , xCas9, SpCas9-NG, and XNG-Cas9 (an xCas9 and the Cas9-NG hybrid) has introduced the desired mutation and results in soybean crop [113]. Even Cas9 is the popular and largely functional variant of CRISPR, yet there is a potential in different alternatives variants for enhancement in targeted selection and genome editing of soybean in efficient way in researches. The tag of (GMO) abbreviated as genetically modified crops is also main concern for the breeders as it is considered by socio-economic concerns along with scientific proofs [114]. The rules and regulation for the genetically modified plant has made a standard for the improvement of traits and its sales and marketing but this made it too much expensive and time consuming. If GE crops got exempted from these protocols in regulation process it will boost the improvement pathway of crops [115] In monitoring sense GE crops has a benefit over GMO crop. After completing the editing in a particular gene, it is very easy to remove CRISPR/Cas9 reactants and mutation free transgenic organism is attained [116]. Genetically edited soybean oil with higher concentration of oleic acid and less linolenic acid content are introduced in USA by Calyxt and TALEN on commercial level. However the action required for regulation and evaluation has been dropped on drought resistance soybean by the agriculture department in (USDA) [117]. Globally harmonization of this regulatory instruction for GE crops is very important to eliminate specific restrictions using genome editing technology for the betterment and improvement of crops.

5. CONCLUSION

CRISPR-based technologies, for example, have emerged to give excellent tools for soybean improvement. Various reports on the effective usage of CRISPR/Cas9 have been given. With

the progress of CRISPR/Cas9 and the advent of tools and Cas variations, research on complicated gene activity in soybeans may expand. Soybean quality, yield, and resistance to biotic and abiotic stressors have all been improved using this method. Recent TALENs-based high oleic soybean field trials have proven the crop's potential.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. McCue P, Shetty K. Health benefits of soy isoflavonoids and strategies for enhancement: a review. *Critical Reviews in Food Science and Nutrition*. 2004;44(5): 361-367.
2. Singh G, Dukariya G, Kumar A. Distribution, importance and diseases of soybean and common bean: A review. *Biotechnol. J. Int*. 2020;24(6):86-98.
3. Pagano MC, Miransari M. The importance of soybean production worldwide, in Abiotic and biotic stresses in soybean production. Elsevier. 2016;1-26.
4. Hasanuzzaman M, et al. Soybean production and environmental stresses, in Environmental stresses in soybean production. Elsevier. 2016;61-102.
5. Rajput M, et al. RNA interference and CRISPR/Cas gene editing for crop improvement: A paradigm shift towards sustainable agriculture. *Plants*. 2021; 10(9):1914.
6. Wu X, Kriz AJ, Sharp PA. Target specificity of the CRISPR-Cas9 system. *Quantitative Biology*. 2014;2(2):59-70.
7. Asmamaw M, Zawdie B. Mechanism and applications of CRISPR/Cas-9-mediated genome editing. *Biologics: Targets & Therapy*. 2021;15:353.
8. Arora L, Narula A. Gene editing and crop improvement using CRISPR-Cas9 system. *Frontiers in Plant Science*. 2017;8: 1932.
9. Gupta D, et al. CRISPR-Cas9 system: A new-fangled dawn in gene editing. *Life Sciences*. 2019;232:116636.
10. Mahfouz MM, Piatek A, Stewart Jr CN. Genome engineering via TALENs and CRISPR/Cas9 systems: challenges and perspectives. *Plant Biotechnology Journal*. 2014;12(8):1006-1014.

11. Ran F, et al. Genome engineering using the CRISPR-Cas9 system. *Nature Protocols*. 2013;8(11):2281-2308.
12. Cai Y, et al. CRISPR/Cas9-mediated genome editing in soybean hairy roots. *PLoS One*. 2015;10(8):e0136064.
13. Bao, A, et al. CRISPR/Cas9-mediated targeted mutagenesis of GmSPL9 genes alters plant architecture in soybean. *BMC Plant Biology*. 2019;19(1):1-12.
14. Sun, Z, et al. Genetic improvement of the shoot architecture and yield in soya bean plants via the manipulation of GmmiR156b. *Plant Biotechnology Journal*. 2019;17(1): 50-62.
15. Li, M, et al. Identification of traits contributing to high and stable yields in different soybean varieties across three Chinese latitudes. *Frontiers in Plant Science*. 2020;10:1642.
16. Yang X, et al. Overexpression of GmGAMYB accelerates the transition to flowering and increases plant height in soybean. *Frontiers in Plant Science*. 2021;12:667242.
17. Hwang S, Lee TG. Integration of lodging resistance QTL in soybean. *Scientific reports*, 2019;9(1):1-11.
18. Cheng Q, et al. CRISPR/Cas9-mediated targeted mutagenesis of GmLHY genes alters plant height and internode length in soybean. *BMC Plant Biology*. 2019. 19(1):1-11.
19. Zhang, M, et al.,. Progress in soybean functional genomics over the past decade. *Plant Biotechnology Journal*. 2022; 20(2):256.
20. Lu S, et al. Current overview on the genetic basis of key genes involved in soybean domestication. *Abiotech*. 2022:1-14.
21. Kara SR, Choudhuryb S, Chakrabortyc A. CRISPR/Cas9 for soybean improvement: A review.
22. Herman EM, et al. Genetic modification removes an immunodominant allergen from soybean. *Plant Physiology*. 2003; 132(1):36-43.
23. Sedivy EJ, Wu F, Hanzawa Y. Soybean domestication: the origin, genetic architecture and molecular bases. *New Phytologist*. 2017;214(2):539-553.
24. Chouard P. Vernalization and its relations to dormancy. *Annual Review of Plant Physiology*. 1960;11(1):191-238.
25. Buzzell R. Inheritance of a soybean flowering response to fluorescent-daylength conditions. *Canadian Journal of Genetics and Cytology*. 1971;13(4):703-707.
26. McBlain B, Bernard R. A new gene affecting the time of flowering and maturity in soybeans. *Journal of Heredity*. 1987;78(3):160-162.
27. Ray JD, et al. Genetic control of a long-juvenile trait in soybean. *Crop Science*. 1995; 35(4):1001-1006.
28. Bonato ER, Vello NA. E6, a dominant gene conditioning early flowering and maturity in soybeans. *Genetics and Molecular Biology*. 1999; 22:229-232.
29. Cober ER, Voldeng HD. A new soybean maturity and photoperiod-sensitivity locus linked to E1 and T. *Crop Science*. 2001;41(3):698-701.
30. Cober ER, Morrison MJ. Regulation of seed yield and agronomic characters by photoperiod sensitivity and growth habit genes in soybean. *Theoretical and Applied Genetics*. 2010; 120(5):1005-1012.
31. Kong F, et al. A new dominant gene E9 conditions early flowering and maturity in soybean. *Crop Science*. 2014;54(6):2529-2535.
32. Lu, S, et al. Natural variation at the soybean J locus improves adaptation to the tropics and enhances yield. *Nature Genetics*. 2017;49(5):773-779.
33. Yue Y, et al. A single nucleotide deletion in J encoding GmELF3 confers long juvenility and is associated with adaption of tropic soybean. *Molecular Plant*. 2017;10(4):656-658.
34. Wang F, et al. A new dominant locus, E11, controls early flowering time and maturity in soybean. *Molecular Breeding*. 2019;39(5):1-13.
35. Xia Z, et al. Positional cloning and characterization reveal the molecular basis for soybean maturity locus E1 that regulates photoperiodic flowering. *Proceedings of the National Academy of Sciences*. 2012;109(32):E2155-E2164.
36. Watanabe S, et al. A map-based cloning strategy employing a residual heterozygous line reveals that the GIGANTEA gene is involved in soybean maturity and flowering. *Genetics*. 2011; 188(2):395-407.
37. Liu, B, et al. Genetic redundancy in soybean photoresponses associated with duplication of the phytochrome A gene. *Genetics*. 2008;180(2):995-1007.

38. Watanabe S, et al. Map-based cloning of the gene associated with the soybean maturity locus E3. *Genetics*. 2009;182(4): 1251-1262.
39. Kong, F, et al. Two coordinately regulated homologs of FLOWERING LOCUS T are involved in the control of photoperiodic flowering in soybean. *Plant Physiology*. 2010;154(3):1220-1231.
40. Cai Y, et al. CRISPR/Cas9-mediated targeted mutagenesis of GmFT2a delays flowering time in soya bean. *Plant Biotechnology Journal*. 2018;16(1):176-185.
41. Jacobs TB, et al. Targeted genome modifications in soybean with CRISPR/Cas9. *BMC Biotechnology*. 2015; 15(1):1-10.
42. Li Z, et al. Cas9-guide RNA directed genome editing in soybean. *Plant Physiology*. 2015. 169(2):960-970.
43. Kanazashi Y, et al. Simultaneous site-directed mutagenesis of duplicated loci in soybean using a single guide RNA. *Plant Cell Reports*. 2018;37(3):553-563.
44. Do PT, et al. Demonstration of highly efficient dual gRNA CRISPR/Cas9 editing of the homeologous GmFAD2-1A and GmFAD2-1B genes to yield a high oleic, low linoleic and α -linolenic acid phenotype in soybean. *BMC Plant Biology*. 2019;19(1):1-14.
45. Li, Z, et al. Multiplex CRISPR/Cas9-mediated knockout of soybean LNK2 advances flowering time. *The Crop Journal*. 2021;9(4):767-776.
46. Nan H, et al. GmFT2a and GmFT5a redundantly and differentially regulate flowering through interaction with and upregulation of the bZIP transcription factor GmFDL19 in soybean. *PLoS one*. 2014;9(5):e97669.
47. Cai Y, et al. Mutagenesis of GmFT2a and GmFT5a mediated by CRISPR/Cas9 contributes to expanding the regional adaptability of soybean. *Plant Biotechnology Journal*. 2020;18(1):298-309.
48. Subedi U, et al. The potential of genome editing for improving seed oil content and fatty acid composition in oilseed crops. *Lipids*. 2020;55(5):495-512.
49. Bortesi L, Fischer R. The CRISPR/Cas9 system for plant genome editing and beyond. *Biotechnology Advances*. 2015; 33(1):41-52.
50. Villanueva-Mejia, D. and J.C. Alvarez, Genetic improvement of oilseed crops using modern biotechnology. *Adv. Seed Biol*, 2017:295-317.
51. Al Amin, N, et al. CRISPR-Cas9 mediated targeted disruption of FAD2-2 microsomal omega-6 desaturases in soybean (*Glycine max.* L). *BMC Biotechnology*. 2019;19(1):1-10.
52. Ma X, et al. A robust CRISPR/Cas9 system for convenient, high-efficiency multiplex genome editing in monocot and dicot plants. *Molecular Plant*. 2015;8(8): 1274-1284.
53. Mikami M, Toki S, Endo M. Comparison of CRISPR/Cas9 expression constructs for efficient targeted mutagenesis in rice. *Plant Molecular Biology*. 2015;88(6):561-572.
54. Singer SD, et al. Genetic engineering of lipid biosynthesis in seeds, in *Biotechnology of crucifers*. Springer. 2013;111-149.
55. Singer SD, Weselake RJ, Rahman H. Development and characterization of low α -linolenic acid Brassica oleracea lines bearing a novel mutation in a 'class a' FATTY ACID DESATURASE 3 gene. *BMC Genetics*. 2014;15(1):1-11.
56. Roesler K, et al. An improved variant of soybean type 1 diacylglycerol acyltransferase increases the oil content and decreases the soluble carbohydrate content of soybeans. *Plant Physiology*. 2016;171(2):878-893.
57. Chen G, et al. High-performance variants of plant diacylglycerol acyltransferase 1 generated by directed evolution provide insights into structure-function. *The Plant Journal*. 2017;92(2):167-177.
58. Rodríguez-Leal D, et al. Engineering quantitative trait variation for crop improvement by genome editing. *Cell*. 2017;171(2):470-480. e8.
59. Wolter F, Schindele P, Puchta H. Plant breeding at the speed of light: the power of CRISPR/Cas to generate directed genetic diversity at multiple sites. *BMC Plant Biology*. 2019; 19(1):1-8.
60. Fan Y, et al. The soybean Rfg1 gene restricts nodulation by *Sinorhizobium fredii* USDA193. *Frontiers in Plant Science*. 2017;8:1548.
61. Herridge DF, Peoples MB, Boddey RM. Global inputs of biological nitrogen fixation in agricultural systems. *Plant and Soil*. 2008;311(1):1-18.

62. Wang L, et al. Use of CRISPR/Cas9 for symbiotic nitrogen fixation research in legumes. *Progress in Molecular Biology and Translational Science*. 2017;149:187-213.
63. Bai M, et al. Generation of a multiplex mutagenesis population via pooled CRISPR-Cas9 in soya bean. *Plant Biotechnology Journal*. 2020;18(3):721-731.
64. Ren B, et al. Rhizobial tRNA-derived small RNAs are signal molecules regulating plant nodulation. *Science*. 2019;365(6456):919-922.
65. Li M, et al. GmNAC06, a NAC domain transcription factor enhances salt stress tolerance in soybean. *Plant Molecular Biology*. 2021;105(3):333-345.
66. Wei Y, et al. Quantitative response of soybean development and yield to drought stress during different growth stages in the Huaibei Plain, China. *Agronomy*. 2018;8(7):97.
67. Xiong R, et al. Root system architecture, physiological and transcriptional traits of soybean (*Glycine max* L.) in response to water deficit: A review. *Physiologia Plantarum*. 2021; 172(2):405-418.
68. Imran M, et al. Exogenous melatonin induces drought stress tolerance by promoting plant growth and antioxidant defense system of soybean plants. *AoB Plants*. 2021;13(4):plab026.
69. Sharma M, et al. Proteomics unravel the regulating role of salicylic acid in soybean under yield limiting drought stress. *Plant Physiology and Biochemistry*. 2018;130:529-541.
70. Mahajan S, Tuteja N. Cold, salinity, and drought stresses an overview. *Archives of Biochemistry and Biophysics*. 2005;444(2):139-158.
71. Dowling DK, Simmons LW. Reactive oxygen species as universal constraints in life-history evolution. *Proceedings of the Royal Society B: Biological Sciences*. 2009;276(1663):1737-1745.
72. Nakagawa A, et al. Drought stress during soybean seed filling affects storage compounds through regulation of lipid and protein metabolism. *Acta Physiologiae Plantarum*. 2018;40(6):1-8.
73. Egli D, Bruening W. Water stress, photosynthesis, seed sucrose levels and seed growth in soybean. *The Journal of Agricultural Science*. 2004;142(1):1-8.
74. Seo JS, et al. Expression of the Arabidopsis AtMYB44 gene confers drought/salt-stress tolerance in transgenic soybean. *Molecular Breeding*. 2012; 29(3):601-608.
75. Raza G, Singh MB, Bhalla PL. Somatic embryogenesis and plant regeneration from commercial soybean cultivars. *Plants*. 2019;9(1):38.
76. Yuan L, et al. GmLCLs negatively regulates ABA perception and signalling genes in soybean leaf dehydration response. *Plant, Cell & Environment*. 2021; 44(2):412-424.
77. Yang C, et al. GmNAC8 acts as a positive regulator in soybean drought stress. *Plant Science*. 2020;293:110442.
78. Jamil A, et al. Gene expression profiling of plants under salt stress. *Critical Reviews in Plant Sciences*. 2011;30(5):435-458.
79. Hamayun M, et al. Exogenous gibberellic acid reprograms soybean to higher growth and salt stress tolerance. *Journal of Agricultural and Food Chemistry*. 2010; 58(12):7226-7232.
80. Rasheed A, et al. Molecular tools and their applications in developing salt-tolerant soybean (*Glycine max* L.) cultivars. *Bioengineering*. 2022;9(10):495.
81. Sun T, et al. A golgi-localized sodium/hydrogen exchanger positively regulates salt tolerance by maintaining higher K⁺/Na⁺ ratio in soybean. *Frontiers in Plant Science*. 2021;12:638340.
82. Li X, et al. CRISPR/Cas9 technique for temperature, drought, and salinity stress responses. *Current Issues in Molecular Biology*. 2022;44(6):2664-2682.
83. Song JH, et al. Mutation of GmIPK1 gene using CRISPR/Cas9 reduced phytic acid content in soybean seeds. *International Journal of Molecular Sciences*. 2022; 23(18):10583.
84. Baek D, Chun HJ, Kim MC. Genome editing provides a valuable biological toolkit for soybean improvement. *Plant Biotechnology Reports*. 2022;1-12.
85. Sun Y, et al. Engineering herbicide-resistant rice plants through CRISPR/Cas9-mediated homologous recombination of acetolactate synthase. *Molecular Plant*. 2016;9(4):628-631.
86. Chen Y, et al. CRISPR/Cas9-mediated base-editing system efficiently generates gain-of-function mutations in Arabidopsis. *Sci China Life Sci*. 2017;60(5):520-523.

87. Tian S, et al. Engineering herbicide-resistant watermelon variety through CRISPR/Cas9-mediated base-editing. *Plant Cell Reports*. 2018;37(9):1353-1356.
88. Wu J, et al. Engineering herbicide-resistant oilseed rape by CRISPR/Cas9-mediated cytosine base-editing. *Plant Biotechnology Journal*. 2020;18(9):1857.
89. Ali Z, et al. Efficient virus-mediated genome editing in plants using the CRISPR/Cas9 system. *Molecular Plant*. 2015;8(8):1288-1291.
90. Bandara AY, et al. Dissecting the economic impact of soybean diseases in the United States over two decades. *PLoS one*. 2020;15(4):e0231141.
91. Pompili V, et al. Reduced fire blight susceptibility in apple cultivars using a high-efficiency CRISPR/Cas9-FLP/FRT-based gene editing system. *Plant Biotechnology Journal*. 2020; 18(3):845-858.
92. Pyott DE, Sheehan E, Molnar A. Engineering of CRISPR/Cas9-mediated potyvirus resistance in transgene-free Arabidopsis plants. *Molecular Plant Pathology*. 2016;17(8):1276-1288.
93. Ramakrishna W, et al. Structural analysis of the maize Rp1 complex reveals numerous sites and unexpected mechanisms of local rearrangement. *The Plant Cell*. 2002;14(12):3213-3223.
94. Wang, F, et al. Enhanced rice blast resistance by CRISPR/Cas9-targeted mutagenesis of the ERF transcription factor gene OsERF922. *PLoS one*. 2016; 11(4):e0154027.
95. Zhang P, et al. Multiplex CRISPR/Cas9-mediated metabolic engineering increases soya bean isoflavone content and resistance to soya bean mosaic virus. *Plant Biotechnology Journal*. 2020;18(6):1384-1395.
96. Nagy, E.D, et al, Novel disease resistance gene paralogs created by CRISPR/Cas9 in soy. *Plant Cell Reports*. 2021;40(6):1047-1058.
97. Liu JZ, Fang Y, Pang H. The current status of the soybean-soybean mosaic virus (SMV) pathosystem. *Frontiers in Microbiology*. 2016;7:1906.
98. Luo Y, et al. Development of a Csy4-processed guide RNA delivery system with soybean-infecting virus ALSV for genome editing. *BMC Plant Biology*. 2021;21(1):1-12.
99. Smith SM, Pryor AJ, Hulbert SH. Allelic and haplotypic diversity at the rp1 rust resistance locus of maize. *Genetics*. 2004;167(4):1939-1947.
100. Pivonia S, Yang X. Assessment of the potential year-round establishment of soybean rust throughout the world. *Plant Disease*. 2004;88(5):523-529.
101. Gao H, et al. Two classes of highly similar coiled coil-nucleotide binding-leucine rich repeat genes isolated from the Rps1-k locus encode Phytophthora resistance in soybean. *Molecular Plant-microbe interactions*. 2005;18(10):1035-1045.
102. Chen X, et al. Generation of male-sterile soybean lines with the CRISPR/Cas9 system. *The Crop Journal*. 2021;9(6):1270-1277.
103. Jianing G, et al. CRISPR/Cas9 applications for improvement of soybeans, current scenarios, and future perspectives. *Notulae Botanicae Horti Agrobotanici Cluj-Napoca*. 2022;50(2):12678-12678.
104. Schmutz J, et al. Genome sequence of the palaeopolyploid soybean. *Nature*. 2010; 463(7278):178-183.
105. Fister AS, et al. Transient expression of CRISPR/Cas9 machinery targeting TcNPR3 enhances defense response in *Theobroma cacao*. *Frontiers in Plant Science*. 2018;9:268.
106. Holubová K, et al. Modification of barley plant productivity through regulation of cytokinin content by reverse-genetics approaches. *Frontiers in Plant Science*. 2018;9:1676.
107. Chen L, et al. Improvement of soybean *Agrobacterium*-mediated transformation efficiency by adding glutamine and asparagine into the culture media. *International Journal of Molecular Sciences*. 2018;19(10):3039.
108. Svitashv S, et al. Genome editing in maize directed by CRISPR–Cas9 ribonucleoprotein complexes. *Nature Communications*. 2016;7(1):1-7.
109. Foster AJ, et al. CRISPR-Cas9 ribonucleoprotein-mediated co-editing and counterselection in the rice blast fungus. *Scientific Reports*. 2018;8(1):1-12.
110. Lowe K, et al. Morphogenic regulators Baby boom and Wuschel improve monocot transformation. *The Plant Cell*. 2016;28(9):1998-2015.
111. Campbell BW, et al. Functional analysis and development of a CRISPR/Cas9 allelic series for a CPR5 ortholog necessary for

- proper growth of soybean trichomes. Scientific Reports. 2019; 9(1):1-11.
112. Bao A, et al. Genome editing technology and application in soybean improvement. Oil Crop Science. 2020;5(1):31-40.
113. He R, et al. Expanding the range of CRISPR/Cas9-directed genome editing in soybean. aBIOTECH. 2022;3(2):89-98.
114. Biden S, Smyth SJ, Hudson D. The economic and environmental cost of delayed GM crop adoption: The case of Australia's GM canola moratorium. GM Crops & Food. 2018;9(1):13-20.
115. Xu H, et al. Progresses, challenges, and prospects of genome editing in soybean (*Glycine max*). Frontiers in Plant Science. 2020;11:571138.
116. Curtin SJ, et al. Crispr/cas9 and talen s generate heritable mutations for genes involved in small rna processing of glycine max and medicago truncatula. Plant Biotechnology Journal. 2018. 16(6):1125-1137.
117. Waltz E. With a free pass, CRISPR-edited plants reach market in record time. Nature Biotechnology. 2018;36(1):6-8.

© 2022 Naveed et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/93311>