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# Revolutionizing Vegetable Crops: Genome Editing for Enhanced Nutrition, Quality and Stress Tolerance

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Vegetable crops are widely regarded as protective foods because of their vital role in ensuring a balanced human diet, particularly for vegetarian populations. They are rich sources of essential vitamins, minerals and dietary fiber, contributing significantly to nutritional security. However, the productivity and quality of vegetable crops are severely affected by a range of biotic and abiotic stresses. In the context of rapid population growth, climate variability and diminishing natural resources, enhancing the resilience of vegetable crops has become a major agricultural priority. Conventional breeding approaches, although effective, are often time-consuming and limited in their ability to rapidly incorporate multiple desirable traits.

In this regard, genome editing has emerged as a powerful and precise tool for crop improvement. Advanced technologies such as meganucleases, zinc finger nucleases, TALENs and the CRISPR-Cas9 system enable targeted genetic modifications, facilitating the development of stress-tolerant and high-quality vegetable varieties. Recent innovations, including base editing and prime editing, allow precise nucleotide changes without introducing double-stranded breaks or foreign DNA, thereby enhancing the efficiency and acceptability of these techniques. Furthermore, multiplex and epigenome editing approaches enable simultaneous modification of multiple genes and regulatory pathways.

Genome editing has already demonstrated promising applications in vegetables, including improved nutritional quality, enhanced stress tolerance and resistance to pests and diseases. Therefore, it represents a transformative approach for accelerating vegetable crop improvement and addressing future food and nutritional security challenges.

**Keywords:** genome-editing technology, CRISPR-cas application, vegetable crops

## Introduction

Vegetable crops play a pivotal role in global food and nutritional security, supplying essential vitamins, minerals, antioxidants and dietary fiber required for a balanced diet. According to the Food and Agriculture Organization, global vegetable production exceeded 1.1 billion tonnes in recent years, highlighting their importance in human nutrition and agricultural economies. Despite this, vegetable productivity is frequently constrained by biotic stresses such as pests and diseases, which can cause yield losses of 20–40% and abiotic stresses like drought, salinity and temperature extremes, which are further intensified by climate change. With the global population projected to reach 9.7 billion by 2050, the demand for nutrient-dense foods, particularly vegetables, is expected to increase significantly.

Traditional breeding methods have contributed to crop improvement; however, their progress is often slow due to long generation cycles and limited genetic variability. In this context, genome editing has emerged as a transformative tool for precise and efficient crop improvement. Technologies such as CRISPR-Cas systems enable targeted modification of

genes associated with stress tolerance, yield and nutritional quality. Recent advancements, including base and prime editing, further enhance precision by enabling single nucleotide changes without introducing foreign DNA. Therefore, integrating genome editing into vegetable breeding programs offers immense potential to accelerate the development of resilient, high-quality varieties suited to future agricultural challenges.

## Clustered Regularly Interspaced Short Palindromic Repeats–CRISPR-associated Protein 9 (CRISPR-Cas9)

CRISPR-Cas9 is a highly advanced genome editing tool that allows precise modification of DNA sequences, including insertion, deletion or alteration of specific genomic regions. CRISPR-Cas systems are broadly classified into three major types (I–III) based on their structure and mechanism of action for target interference. Among these, the Type II system is widely utilized due to its relatively simple effector mechanism, which relies on two nuclease domains, RuvC and HNH, to mediate DNA cleavage.

The Cas9 protein derived from *Streptococcus pyogenes* (SpCas9) is the most extensively used nuclease in CRISPR-based applications. The system operates through a single guide RNA (sgRNA) that directs the Cas9 enzyme to a specific DNA sequence. Target recognition is dependent on the presence of a protospacer adjacent motif (PAM), which is essential for Cas9 binding. Once the sgRNA-Cas9 complex binds to the target site, Cas9 introduces a double-strand break (DSB) in the DNA. This break subsequently activates the cell's natural DNA repair pathways, enabling targeted genome modifications.

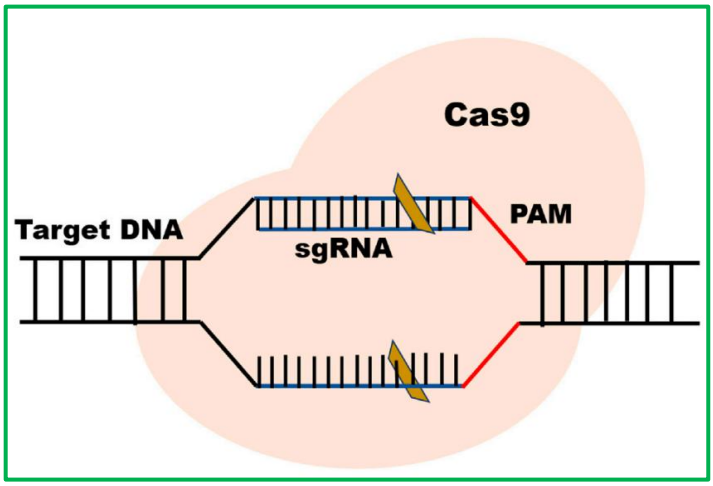


**Fig.1. Basic structure of CRISPR/Cas9 system**

## Mechanism of CRISPR-Cas9

The CRISPR-Cas9 system functions through two key components: the Cas9 enzyme and a guide RNA (gRNA). Cas9 acts as a molecular "scissor" that cleaves DNA at a specific site, while the gRNA directs the enzyme to the target sequence. The gRNA consists of two parts: CRISPR RNA (crRNA), which is complementary to the target DNA and trans-activating crRNA (tracrRNA), which facilitates binding with the Cas9 protein. Together, they form a complex that locates and binds to the specific DNA sequence. Once the target is recognized, the Cas9 enzyme introduces a double-strand break (DSB) at the precise location. This break is then repaired by the cell through two primary pathways: non-homologous end joining (NHEJ) and homology-directed repair (HDR). NHEJ is a rapid and commonly used repair mechanism that joins DNA ends without a template, often resulting in small insertions or deletions. In contrast, HDR is a more accurate process that uses a homologous DNA template to enable precise gene insertion or replacement, although it occurs less frequently.

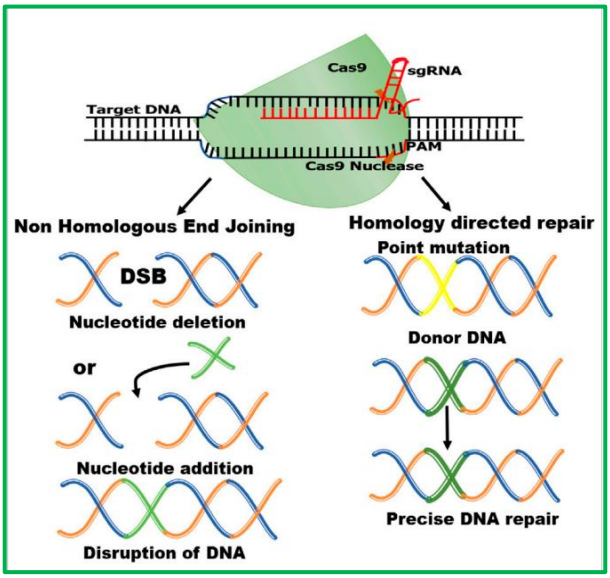


**Fig.2. Schematic diagram of CRISPR/Cas9 mechanism**

## Abiotic Stress

Vegetable crops are significantly affected by abiotic stresses such as heat, drought, salinity, chilling and UV-B radiation, which reduce growth and yield. Genome editing using CRISPR-Cas9 has emerged as an efficient tool to develop stress-resilient varieties. Heat stress induces excessive reactive oxygen species (ROS), causing cellular damage, where mitogen-activated protein kinases (MAPKs) play a crucial role in stress response. Gene modifications such as *BZR1* and *SlMAPK3* in tomato have enhanced heat tolerance by reducing ROS accumulation and improving antioxidant activity.

CRISPR-mediated knockout of *LsNCED4* in lettuce improved seed germination under high temperature (>70% at 37°C). In drought stress, *SlMAPK3* regulates stress tolerance by protecting membrane integrity and activating stress-responsive genes. Cold tolerance is governed by C-repeat binding factors (CBFs), where mutations result in increased chilling sensitivity. Additionally, editing of *SlUVR8* enhanced UV-B tolerance in tomato. Salinity tolerance has been improved through editing of genes such as *HKT1/2* and *SlHyPRP1*, leading to stable inheritance of salt-resistant traits.

## Biotic Stress

Diseases caused by pathogens significantly reduce vegetable productivity. CRISPR-Cas9 enables rapid development of disease-resistant varieties by targeted gene editing. In tomato, knockout of *DMR6* confers broad-spectrum resistance against bacterial and fungal pathogens. Similarly, mutations in *SlMlo1* provide resistance to powdery mildew. Editing *SlJAZ2* prevents bacterial colonization by restricting stomatal reopening. Virus resistance has been achieved by targeting viral genes or host susceptibility factors, such as *eIF4E* in cucumber and CRISPR targeting of viral genomes in tomato. In potato, editing genes like *StDND1* and *StDMR6-1* improves resistance to late blight and viral diseases.

## Quality Improvement

CRISPR-Cas9 has been used to enhance post-harvest quality and nutritional traits. In tomato, modification of ripening genes improves shelf life, while gene editing increases lycopene content up to fivefold and GABA levels by 7–15 times. In potato, editing starch biosynthesis genes improves starch quality, while mutation of *PPO* genes reduces enzymatic browning. Reduction of glycoalkaloids enhances tuber safety and taste. Similar browning resistance has been achieved in brinjal through knockout of PPO genes.

## Yield Improvement

CRISPR technology contributes to yield enhancement by modifying reproductive traits. In cucumber and watermelon, editing *WIP1* genes induces gynoecy (female flower production), improving hybrid seed production and yield. In tomato, mutations in *SP5G* promote early flowering and compact plant architecture, enabling early harvests and increased productivity.

**Traits Modified Using CRISPR/Cas in Vegetable Crops**

| Crop | Target Gene(s) | Trait Modification |
|---|---|---|
| **Tomato** | SlAMS | Affects pollen viability |
| | SlHyPRP1 | Salt tolerance |
| | SlPelo and SlMlo1 | Resistance to TYLCV and powdery mildew |
| | CCD8 | Host resistance |
| | HKT1;2 | Salt tolerance |
| | SlMAPK3 | Heat and drought stress tolerance |
| | BZR1 | Regulates heat stress tolerance |
| | Coat protein & Replicase (TYLCV) | Virus resistance |
| | SlMlo1 | Powdery mildew resistance |
| | PL, PG2a, TBG4 | Cell wall development, fruit color and |

| | | |
|---|---|---|
| | | weight |
| | AP2a, NOR, FUL1, FUL2 | Fruit development and ripening |
| | SlGAI | Gibberellin-responsive dwarf phenotype |
| | SBPase | Induces leaf senescence |
| | Psy1 and CrtR-b2 | Carotenoid biosynthesis |
| | lncRNA1459 | Alters ripening, lycopene, ethylene and carotenoids |
| | SGR1, BLC, LCY-E, LCY-B1, LCY-B2 | Increased lycopene content |
| | SlCBF | Reduced chilling tolerance |
| | PDS, GABA-TP1/2/3, CAT9, SSADH | Increased GABA content |
| | SlNPR1 | Reduced drought tolerance |
| | SlMYB12 | Pink fruit color |
| **Brinjal** | SmelPPO4, SmelPPO5, SmelPPO6 | Reduced flesh browning |
| **Potato** | StDND1, StCHL1, StDMR6-1 | Late blight resistance |
| | GBSS, GBSS1 | Improved starch biosynthesis |
| **Carrot** | F3H | Altered anthocyanin biosynthesis |
| | DcMYB113-like | Enhanced anthocyanin production |
| **Watermelon** | ALS | Herbicide resistance |
| **Pumpkin** | GRF12, AHA1, HAK5 | Salt stress response |
| **Lettuce** | LsNCED4 | Regulation of seed germination under high temperature |
| **Chinese Cabbage** | BraFLCs | Early flowering independent of vernalization |

## Conclusion

Genome editing, particularly CRISPR/Cas9 technology, has revolutionized vegetable crop improvement by enabling precise, efficient and targeted genetic modifications. Unlike conventional breeding methods, which are time-intensive and limited by genetic variability, CRISPR-based approaches accelerate the development of improved cultivars with desirable traits. The application of genome editing in vegetables has demonstrated significant progress in enhancing tolerance to abiotic stresses such as heat, drought, salinity and chilling, as well as improving resistance to a wide range of biotic stresses including bacterial, fungal and viral pathogens.

Furthermore, CRISPR/Cas9 has been successfully employed to improve quality traits such as nutritional content, shelf life and reduction of anti-nutritional compounds, along with yield-related characteristics like gynoecy and early flowering. Advanced techniques such as base editing, prime editing, and multiplex genome editing further expand the scope of precision breeding without introducing foreign DNA, making them more acceptable and efficient.

Despite these advancements, challenges such as off-target effects, regulatory concerns and public acceptance remain. Continued research focusing on gene function, regulatory pathways and field-level validation is essential to fully harness the potential of genome editing. Overall, CRISPR/Cas9 represents a transformative tool for sustainable vegetable production, contributing significantly to global food and nutritional security under changing climatic conditions.

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