

Manuscript ID:
IJRSEAS-2025-020524



Quick Response Code:



Website: <https://eesrd.us>



Creative Commons
(CC BY-NC-SA 4.0)

DOI: 10.5281/zenodo.18595999

DOI Link:
<https://doi.org/10.5281/zenodo.18595999>

Volume: 2

Issue: 5

Pp. 129-134

Month: October

Year: 2025

E-ISSN: 3066-0637

Submitted: 10 Sept. 2025

Revised: 15 Sept. 2025

Accepted: 10 Oct. 2025

Published: 31 Oct. 2025

Address for correspondence:

Dr. Bharti Mahajan
Assistant Professor, Department of
Botany, Pradhanmantri College of
Excellence, Shri Neelkantheshwar
Government Post Graduate College,
Khandwa, Madhya Pradesh, India
Email:
bhartimahajan44@gmail.com

How to cite this article:

Mahajan, B. (2025). Enhancing
Grain Yield and Quality Traits in
Wheat through Precision Gene
Editing. *International Journal of
Research Studies on Environment,
Earth, and Allied Sciences*, 2(5),
129–134.
<https://doi.org/10.5281/zenodo.18595999>

Enhancing Grain Yield and Quality Traits in Wheat through Precision Gene Editing

Dr. Bharti Mahajan

Assistant Professor, Department of Botany, Pradhanmantri College of Excellence, Shri Neelkantheshwar Government Post Graduate College, Khandwa, Madhya Pradesh, India

Abstract

One of the most important and critical staple crops worldwide is wheat (*Triticum aestivum* L.), which serves as an important source of food security and nutrition, almost 20 per cent of human caloric and nutrition. Nonetheless, the increase in world demand, climatic change, and the decreasing arable lands require the emergence of wheat varieties with high yield and nutritional enrichment to be developed at a high rate. CRISPR/Cas system and precision gene editing has become an efficient and potent tool to target crop improvement. The technology allows introducing particular changes into the genomes of wheat to modify the primary agronomic characteristics of grain yield, grain size, spike architecture, and nutrient use efficiency. At the same time, gene editing can help to enhance grain quality properties, such as protein content, gluten content, fortification of micronutrients, and can decrease the anti-nutritional components, such as phytic acid. Latest achievements show that it is possible to successfully edit the genes like *TaGW2*, *TaGS3*, and *TaGluD-1*, which result in development of better grain weight, dough quality, and nutrient density without the use of foreign DNA. Improvement of traits in wheat by precise editing of homoeologous genes in polyploid wheat has also been possible without compromising genetic integrity. Although it has great potential, other challenges like off-target effects, regulatory issues and acceptance by the people are still there. To tackle such concerns with better editing fidelity, a clear communication and more science-based regulations is essential in order to become more widely adopted. The study explore existing approaches, the most important gene targets, case studies, and perspectives of gene editing in the improvement of wheat. It emphasizes the significance of combining gene editing with traditional breeding and genomic selection to achieve sustainable food and nutritional security in the world by producing next generation of wheat seeds.

Keywords: CRISPR/Cas9, Wheat, Productivity, Nutrition, Genetics, Crops.

Introduction

Wheat (*Triticum aestivum* L.) is a staple crop serving about 20-30 percent of daily calories all over the world. With global population growth approaching 10 billion by the year 2050, the necessity to further improve wheat yield and grain quality is becoming particularly pressing against the background of climate change and reduced arable lands, as well as new biotic and abiotic stresses (Ni et al., 2023; Yigider et al., 2023). The most notable types of precision genome editing technologies include CRISPR/Cas9 and prime editing which can provide radical solutions to enhancing wheat faster. CRISPR/Cas9 has facilitated selective knockout of adverse regulators like *TaGASR7* and *TaGW2*, which has remarkably increased the weight of the thousand kernel, grain area, length, and width (Hillary, 2019). It has also enabled the production of low-gluten wheat by disruption of gliadin genes and high-amylose wheat by *TaSBE1a* mutagenesis, which improves nutritional profile and food safety (Zhang et al., 2021; Li et al., 2021). In addition to CRISPR/Cas 9, prime editing is another more sophisticated tool of gene editing in wheat. Ni et al. (2023) developed a more efficient prime editor, ePPEplus, which enhanced editing efficiency (up to ~100-fold) and made it possible to multiplex edit up to eight genes at once in regenerated wheat plants. The changing delivery modes and streamlined editing elements drive these technological changes. Transgene free genome editing has been shown including DNA or RNA based transient delivery (TECC methodologies) and ribonucleoprotein (RNP) systems with homozygous wheat mutants without foreign DNA integration (Wang et al, 2018; Liang et al., 2017). Although wheat has a complicated allohexaploid genome and transformation is a difficult process, with the convergence of better CRISPR/Cas9 editing, prime editing, and better delivery, the future of wheat breeding is happening. Such advances bring a new avenue of tackling yield, quality, stress resilience, and nutritional characteristics that are fundamental in attaining sustainable global food and nutrition security. This paper takes a wholesome look at the latest developments in precision gene editing of wheat, with a high impact genetic target, emerging technologies, and the translational potential of these technologies to transform wheat improvement.

Precision Gene Editing Processes

Precision gene editing can use sequence-specific nucleases including Zinc Finger Nucleases (ZFNs), Transcription Activator Like Effector Nucleases (TALENs) and CRISPR/Cas. CRISPR/Cas9 is the most popular of them, as it is quite simple, cost effective, and can be multiplexed. In the field of crop improvement, especially in wheat (*Triticum aestivum* L) with its allohexaploid genome, the modern precision gene editing has resulted in a revolution in gene editing. Precision technology has provided the ability to manipulate genes that control grain yield and quality, such as the CRISPR/Cas systems, base editors, and prime editors.

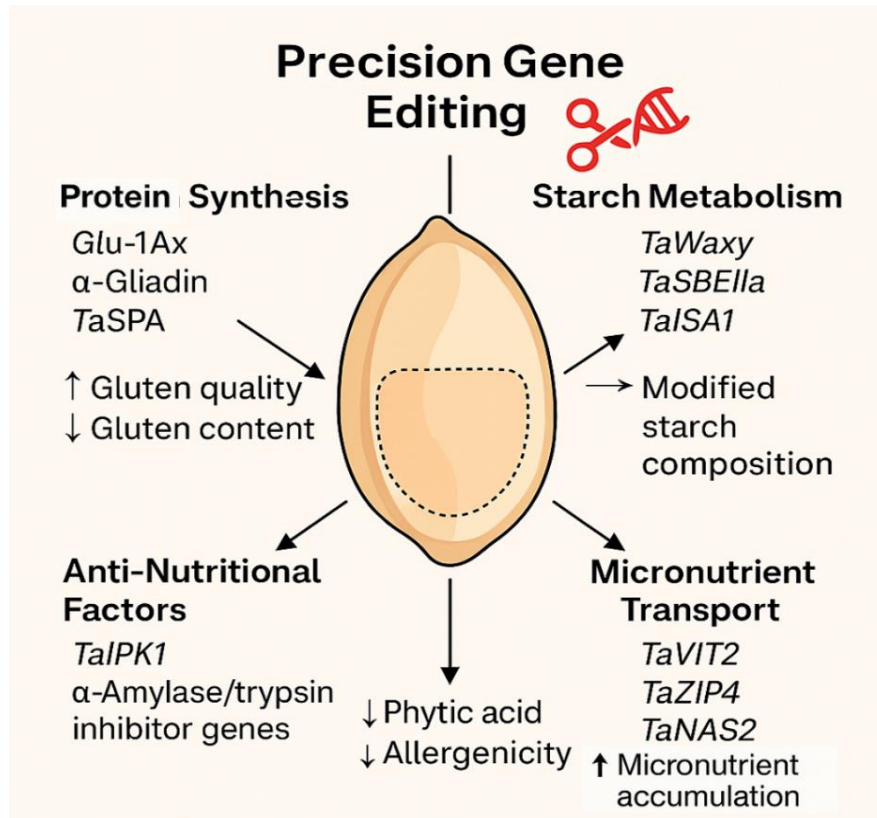


Figure 1: Precision gene editing targets multiple grain quality pathways.

1. CRISPR/Cas9 and Variants

The CRISPR/Cas9 system is broadly applied in the targeted genome editing of wheat. It has been used to knock out negative regulators like *TaGW2* and *TaGASR7* which have led to an increase in the grain weight and size. The specificity of the method is supported by studies employing transient expression systems (i.e. TECC DNA/RNA delivery) that demonstrated on-target editing in wheat without any off-target mutations of *TaGW2* and *TaGASR7*. In addition to Cas9, another targeting system and PAM preference can be provided by Cas12a (Cpf1). LbCas12a and engineered forms (e.g., LbCas12a-RVR) have been able to induce hereditary mutations into genomic regions including *TaGW7-B1* gene that induces a change in the weight and size of grains, especially in regions that are inaccessible to Cas9 (Wang et al., 2021). CRISPR/Cas9 has the potential to target the homeologous genes of the A, B, and D genomes in wheat concomitantly. This polyploid complexity was a challenge in the past but is currently, becoming an opportunity to manipulate traits with selective editing of multiple copies of the gene. More recent progress has enhanced the performance of multiplex editing, where optimized Cas9/Cas12a toolkits exhibit > 90% editing in all subgenome targets in wheat T0 plants (Lawrenson et al., 2024).

2. Base Editing

Base editors consist of cytosine (C→T) and adenine (A→G) deaminases that permit specific, transition-only base conversions without formation of double-strand breaks. These tools have the potential to change important agronomic genes but with minimal large-scale genomic disturbance though they have not been used extensively in wheat yet.

3. Prime Editing

Prime editing is a flexible innovation, which allows any base substitution, small insertions, or deletions to be introduced without donor templates. It relies on a Cas9 nickase that is fused with reverse transcriptase and relies on pegRNA to precisely target (Anzalone et al., 2019). The engineered prime editor ePPEplus (harboring a V223A RT mutation) tremendously increased the efficiency of editing in wheat (up to approximately 33-fold

more effective than earlier editors and allowed the expression of up to eight genes at once in regenerated plants with frequencies reaching 74.5 % (Ni et al., 2023).

4. **Delivery and Optimization Strategies.**

The successful transfer of gene editing aspects is essential. TECC DNA/RNA systems and RNP complexes are transgene free and provide a good integration free option of editing wheat. Moreover, guide RNA design, promoter choice, and editing enzyme and architecture engineering (e.g. pegRNA alterations in prime editing) also increase editing specificity and efficacy (Singh et al., 2025) further.

Target Traits of Yield Enhancement.

To increase the yield of wheat grain products, there should be a thorough knowledge of genetic, physiological, and environmental determinants to measure the productivity. Precision gene editing technology including CRISPR/Cas9 and TALENs has allowed the specific targeting of the enhancement of yield-related phenotypes with greater precision than ever before. The primary target characteristics of wheat to improve yield are yield potential characteristics, resource use efficiency characteristics and stress resilience characteristics (Ma et al., 2024).

Grain Size and Weight

Two of the most important factors that determine the potential yield of wheat and its prices in the market are grain size and weight. All these characteristics are more closely affected not only by genetic factors but also by environmental ones, and heritability rates indicate a lot of potential in regard to enhancements that can be made through the help of precise breeding and editing the genes (Qian et al., 2025). The complex interactions through genes which govern cell proliferation, grain filling period and assimilate partitioning control grain weight which is usually expressed in thousands of grain-weight per thousand-kernel-weight (TKW). The grain size is adversely regulated by the genes such as TaGW2, TaGS3, and TaGASR7 (Wang et al., 2025). CRISPR editing of these genes has led to an increase in the size of the grains and the thousand-kernel weight (TKW).

Spike Architecture and Tiller Number

The parameters that also play a significant role in determining wheat yield are the spike architecture and the number of tillers since they directly affect the grains per plant. The morphology of the spike such as the length of the spike, the number of spikelets and floret fertility determines the potential number of grains per spike of a plant and the number of spikes per tiller of a plant determines the total spike bearing capacity of a plant. Collectively, these characteristics combine genetic, physiological, and environmental aspects which are ultimately summed up to condition yield results (Li et al., 2022). Editing of TaTB1 and TaDEP1 two major regulators of spike development and tillering has been found to promote spikelet abundance and total biomass.

Nutrient Use Efficiency

The successful uptake, assimilation and utilization of vital nutrients especially nitrogen (N), phosphorus (P) and micronutrients like zinc (Zn) and iron (Fe) is very critical in wheat yield. Nevertheless, traditional types of wheat tend to have low NUE and, as a result, they tend to use more and more fertilizers, increasing the production cost and causing negative ecological effects. Enhancing NUE with high accuracy gene editing is a viable tool towards realizing increased yields with less input demands (Zang et al., 2021). TaNRT1.1B and TaARE1 gene editing is used to enhance nitrogen use efficiency (NUE), which consequently enables wheat to be grown in low nutrient soils without reducing or lowering full yield.

Enhancing the Grain Quality Traits

The concept of grain quality in wheat is broadly defined in terms of physical, nutritional, and processing qualities that define its appropriateness to diverse final applications like bread, pasta, and the production of biscuits (Yu et al., 2024). Besides the increase in yield, precision gene editing will be an effective means of enhancing these quality characteristics as it will be possible to target the genes that determine the composition of grains, their nutritional value, and end-use functionality, as well as food safety. The key areas of concern are to enhance the quality of proteins and gluten, starch structure, enriching the micronutrients and decreasing the anti-nutritional constituents.

- **Protein and Gluten Quality**

The strength of the dough and the quality of baking is determined by wheat glutenins and gliadins (Tiwari et al., 2024). The modification of TaGluD-1 and alteration of 2 clusters of 2(gliadin) genes have yielded low-gluten or gluten-free lines of wheat, which are suitable in celiac-patients and niche markets (Peng et al., 2017).

- **Micronutrient Content**

CRISPR-based biofortification has been done on genes such as TaVIT2 (iron transporter) and NAS (nicotianamine synthase) to enhance the level of iron and zinc in grains without affecting yield (Harrington, et al., 2024).

- **Smaller Anti-Nutritional Factors.**

Anti-nutritional elements such as phytic acid inhibit uptake of minerals. Manipulation of TaIPK1 has also been effective in lowering phytic acid levels and increasing the bioavailability of micronutrients.

Table 1: Some of the critical Target Genes to enhance the quality traits of the grains in wheat using Precision Gene Editing (Sánchez-Leon et al., 2018, Wang et al., 2014, Zeng et al., 2020, Ahmad et al., 2024, Kumar et al., 2019, Gupta et al., 2024).

Trait Category	Target Gene(s)	Function/Role	Editing Strategy	Expected/Observed Outcome
Protein and Gluten Quality	<i>Glu-1Ax, Glu-1By, Glu-1Dy</i>	Encode high-molecular-weight glutenin subunits determining dough strength and elasticity	Gene activation or promoter editing	Enhanced gluten polymerization, improved dough strength
	α -Gliadin, γ -Gliadin	Encode prolamins storage proteins, major gluten allergens	Gene knockout via CRISPR/Cas9	Reduced gluten content, low-allergen or gluten-free wheat lines
	<i>TaGluD1, TaSPA</i>	Regulate seed storage protein synthesis	Gene modulation for balanced expression	Optimized protein composition and bread-making quality
Starch Composition and Functionality	<i>TaWaxy</i> (GBSSI)	Catalyzes amylose synthesis	Gene knockout	Low-amylose, soft-texture wheat suitable for noodles and pastries
	<i>TaSBEIIa, TaISA1, TaSSIV</i>	Control starch branching and granule structure	Gene editing to alter enzyme activity	Modified starch structure; high-amylose (resistant starch) or improved processing quality
Micronutrient Biofortification	<i>TaVIT2, TaNAS2</i>	Regulate iron and zinc sequestration and transport	Gene knockout or upregulation	Increased Fe and Zn accumulation in endosperm (biofortified wheat)
	<i>TaZIP4, TaSAMS</i>	Involved in Zn/Fe uptake and assimilation	Gene activation	Enhanced micronutrient uptake and nutritional value
Reduction of Anti-Nutritional Factors	<i>TaIPK1, TaMIPS</i>	Control phytic acid biosynthesis	Gene knockout	Lower phytic acid content; improved mineral bioavailability
	α -Amylase/Trypsin inhibitor genes	Encode allergenic proteins	Gene deletion	Reduced allergenicity and improved digestibility
Grain Texture, Color, and Storage Stability	<i>Pina-D1, Pinb-D1</i>	Encode puroindoline proteins determining grain hardness	Gene editing (gain or loss of function)	Tailored grain hardness; improved milling quality
	<i>TaLOX1, TaLTP1</i>	Control lipid oxidation and flavor stability	Gene knockout	Improved storage quality and extended shelf life

Case Studies and Recent Advances

A number of successful cases of precision gene editing have shown that it is capable of enhancing yield and quality character in wheat. TaGW7 knock-out has been demonstrated to cause a substantial increase in grain width and weight, with no impact on plant height or flowering, and thus yield potential increases without any unwanted pleiotropic effects (Wang et al., 2018). In a similar manner, TaDEP1 triple editing of all the three homoeologs led to a smaller plant structure and higher grain yield, which shows the strength of multiplex editing in enhancing structure and productivity (Zhang et al., 2021). CRISPR/Cas9-mediated editing of various alpha-gliadin genes in high-quality bread wheat varieties have effectively led to low immunoreactive gluten content, which generate low-gluten wheat lines that can be consumed by celiac disease or gluten intolerant individuals (Sánchez-Leon et al., 2018). All these studies indicate that the use of gene editing technology can be diversified to fine-tune the effects of complex polygenic traits to maximize yield and architecture and nutritional traits at the same time.

Challenges and consideration

Although it can transform the world, the use of the precision gene editing in the wheat improvement is fraught with several concerns and issues. The off-target effects are still an issue and unwanted edits at non-target genomic regions may take place, which can alter gene activity or stability. Nevertheless, with the development of whole-genome sequencing technology and the optimization of guide RNA design algorithms, such risks have significantly decreased, due to the increased precision in target site selection and validation. The other significant issue is the regulatory uncertainty as some nations like the United States and Japan do not apply genetically modified crop laws to genes-edited crops that do not include foreign DNA, other countries such as the European Union enforce a strict regulatory framework. Such absence of international agreement is a hindrance to international business and commercialization. Moreover, the technical complexity of wheat polyploid genome; it is complex to modulate and to edit all the copies of a gene that are homoeologous in hexaploid wheat, but this is

required to provide full and stable expression of the trait. Finally, there are ethical and social acceptance problems, as gene editing is often confused with transgenic modification in the opinion of the population. Hence, science communication and population education is essential to raise awareness, emphasize the accuracy and safety of gene editing, and make people more accepting and trusting of these technologies in agriculture.

Future Perspectives:

It can be assumed that the future of gene editing in wheat will be even more complex and will incorporate the use of modern molecular and breeding technologies to make it more efficient and precise. Among the avenues is multiplex editing, which is capable of targeting several genes related to yield, quality and stress tolerance simultaneously, and, therefore, enhances the generation of multi-trait elite cultivars. Moreover, new tools have emerged, including base editing and prime editing, which enable extremely specific single-nucleotide editing without generating double-strand break, which reduces the problem of genomic instability and off-target effects. These methods give exquisite control of gene activity, allowing small and yet advantageous modifications in complicated properties. Genetic improvements in breeding through the combination of speed breeding and genomic selection and gene editing further improve breeding performance through decreased generation time, and allowing rapid trait stacking and the issue of improved cultivars faster. In addition, the productivity and quality improvement are only anticipated to be the limit of gene editing, which is also offered to climate resilience, where genes like DREB, HSP70 and SnRK2 associated with enhanced heat and drought stress tolerance can be targeted. All these innovations will lead to the establishment of new generation wheat species that are high yielding, nutritious, and capable of withstanding the environmental changes.

Conclusion

Wheat (*Triticum aestivum* L.) is one of the staples of the world food security as it forms a significant source of caloric and nutritional value to the world population of billions. Though use of conventional breeding methods has helped in improvement of yield and quality, in many cases there is a constraint of such breeding methods due to long breeding cycles, genetic linkage drag, and complicated environmental interactions. The invention of modern biotechnological tools, specifically, CRISPR/Cas-based gene editing, has transformed the process of wheat improvement by allowing specific, efficient, and heritable alterations in the target genes. With this technology, they can now offer new prospects to improve the complex qualities like yield of grain, nutritional content and resistance to stresses without the use of foreign DNA, hence, increasing its acceptability by the people and regulatory capability in most places. Precision gene editing is an innovative and revolutionary technology that supplements and improves traditional and genomic-assisted breeding schemes. The ability to perform specific gene manipulation that relates to yield potential, grain quality and resilience, including CRISPR/Cas9, Cas12a, base editing, and prime editing especially when used in multiplex mode, provides the opportunities to reprogram the polyploid genome of wheat to a level that has never been achieved before. These technologies together with the use of speed breeding, marker-assisted selection, and genomic prediction can hasten the creation of the next generation of wheat cultivars with better productivity, nutritional value and adaptability. After all, the intersection of the sophisticated gene editing with the current breeding approaches is the answer to sustainable wheat improvement. This will be critical towards addressing the increasing food and nutrition security needs in the 21 st century so that wheat will continue to be productive and resilient to global climate and resource pressures.

Acknowledgement

I am highly grateful towards Department of Botany, PMCOE Shri Neelkantheswar Government Post Graduate College, Khandwa, Madhya Pradesh, India for the encouragement provided to carry on research works.

Financial support and sponsorship

Nil.

Conflicts of interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

References

1. Ahmar, S., Usman, B., Hensel, G., Jung, K. H., & Gruszka, D. (2024). CRISPR enables sustainable cereal production for a greener future. *Trends in Plant Science*, 29(2), 179-195.
2. Gupta, O. P., Singh, A., Pandey, V., Sendhil, R., Khan, M. K., Pandey, A., ... & Singh, G. (2024). Critical assessment of wheat biofortification for iron and zinc: a comprehensive review of conceptualization, trends, approaches, bioavailability, health impact, and policy framework. *Frontiers in Nutrition*, 10, 1310020.
3. Harrington, S. A., Connorton, J. M., Nyangoma, N. I., McNelly, R., Morgan, Y. M., Aslam, M. F., ... & Balk, J. (2023). A two-gene strategy increases iron and zinc concentrations in wheat flour, improving mineral bioaccessibility. *Plant physiology*, 191(1), 528-541.
4. Hillary, V. E., & Caesar, S. A. (2019). Application of CRISPR/Cas9 genome editing system in cereal crops. *The Open Biotechnology Journal*, 13(1).
5. Kumar, R., Kaur, A., Pandey, A., Mamrutha, H. M., & Singh, G. P. (2019). CRISPR-based genome editing in wheat: a comprehensive review and future prospects. *Molecular biology reports*, 46(3), 3557-3569.
6. Lawrenson, T., Clarke, M., Kirby, R., Forner, M., Steuernagel, B., Brown, J. K., & Harwood, W. (2024). An optimised CRISPR Cas9 and Cas12a mutagenesis toolkit for Barley and Wheat. *Plant Methods*, 20(1), 123.

7. Lawrenson, T., Clarke, M., Kirby, R., Forner, M., Steuernagel, B., Brown, J. K., & Harwood, W. (2024). An optimised CRISPR Cas9 and Cas12a mutagenesis toolkit for Barley and Wheat. *Plant Methods*, 20(1), 123.
8. Li, A., Hao, C., Wang, Z., Geng, S., Jia, M., Wang, F., ... & Mao, L. (2022). Wheat breeding history reveals synergistic selection of pleiotropic genomic sites for plant architecture and grain yield. *Molecular Plant*, 15(3), 504-519.
9. Li, J., Jiao, G., Sun, Y., Chen, J., Zhong, Y., Yan, L., ... & Xia, L. (2021). Modification of starch composition, structure and properties through editing of TaSBEIIa in both winter and spring wheat varieties by CRISPR/Cas9. *Plant biotechnology journal*, 19(5), 937-951.
10. Liang, Z., Chen, K., Li, T., Zhang, Y., Wang, Y., Zhao, Q., ... & Gao, C. (2017). Efficient DNA-free genome editing of bread wheat using CRISPR/Cas9 ribonucleoprotein complexes. *Nature communications*, 8(1), 14261.
11. Ma, Y.-X., Yang, S., & Lang, S.-P. (2024). *Application of CRISPR/Cas9 in wheat genetic improvement*. *Bioscience Methods*, 15(6), 315-326.
12. Ni, P., Zhao, Y., Zhou, X., Liu, Z., Huang, Z., Ni, Z., Sun, Q., & Zong, Y. (2023). Efficient and versatile multiplex prime editing in hexaploid wheat. *Genome Biology*, 24, 156.
13. Ni, P., Zhao, Y., Zhou, X., Liu, Z., Huang, Z., Ni, Z., Sun, Q., & Zong, Y. (2023). Efficient and versatile multiplex prime editing in hexaploid wheat. *Genome Biology*, 24, 156.
14. Peng, A., Chen, S., Lei, T., Xu, L., He, Y., Wu, L., ... & Zou, X. (2017). Engineering canker-resistant plants through CRISPR/Cas9-targeted editing of the susceptibility gene Cs LOB 1 promoter in citrus. *Plant biotechnology journal*, 15(12), 1509-1519.
15. Qian, Q., Hu, W., Yu, Y., Liu, Y., Tian, Y., Zhang, X., & Min, D. (2025). Overexpression of TaCR4-A positively regulates grain size in *Triticum aestivum*. *BMC Plant Biology*, 25(1), 1273.
16. Sánchez-León, S., Gil-Humanes, J., Ozuna, C. V., Giménez, M. J., Sousa, C., Voytas, D. F., & Barro, F. (2018). Low-gluten, nontransgenic wheat engineered with CRISPR/Cas9. *Plant biotechnology journal*, 16(4), 902-910.
17. Singh, T., HM, M., Singh, R., Jaiswal, J. P., Wadhwa, Z., Kumar, R., ... & Tiwari, R. (2025). Comprehensive approaches to design efficient gRNA for SDN1-CRISPR/Cas9 genome editing in wheat. *Frontiers in Genome Editing*, 7, 1579165.
18. Tiwari, V. K., Saripalli, G., Sharma, P. K., & Poland, J. (2024). Wheat genomics: genomes, pangenomes, and beyond. *Trends in Genetics*.
19. Wang, W., Pan, Q., Tian, B., Yu, Z., Davidson, D., Bai, G., ... & Akhunov, E. (2025). Non-additive dosage-dependent effects of TaGS3 gene editing on grain size and weight in wheat. *Theoretical and Applied Genetics*, 138(2), 38.
20. Wang, W., Simmonds, J., Pan, Q., Davidson, D., He, F., Battal, A., ... & Akhunov, E. (2018). Gene editing and mutagenesis reveal inter-cultivar differences and additivity in the contribution of TaGW2 homoeologues to grain size and weight in wheat. *Theoretical and Applied Genetics*, 131(11), 2463-2475.
21. Wang, W., Tian, B., Pan, Q., Chen, Y., He, F., Bai, G., ... & Akhunov, E. (2021). Expanding the range of editable targets in the wheat genome using the variants of the Cas12a and Cas9 nucleases. *Plant biotechnology journal*, 19(12), 2428-2441.
22. Wang, Y., Cheng, X., Shan, Q., Zhang, Y., Liu, J., Gao, C., & Qiu, J. L. (2014). Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. *Nature biotechnology*, 32(9), 947-951.
23. Yigider, E., Taşpınar, M. S., & Agar, G. (2023). Advances in bread wheat production through CRISPR/Cas9 technology: A comprehensive review of quality and other aspects. *Planta*, 258, 55.
24. Yu, Z., Yunusbaev, U., Fritz, A., Tilley, M., Akhunova, A., Trick, H., & Akhunov, E. (2024). CRISPR-based editing of the ω - and γ -gliadin gene clusters reduces wheat immunoreactivity without affecting grain protein quality. *Plant Biotechnology Journal*, 22(4), 892-903.
25. Zeng, D., Liu, T., Ma, X., Wang, B., Zheng, Z., Zhang, Y., ... & Liu, Y. G. (2020). Quantitative regulation of Waxy expression by CRISPR/Cas9-based promoter and 5'UTR-intron editing improves grain quality in rice. *Plant Biotechnology Journal*, 18(12), 2385.
26. Zhang, J., Zhang, H., Li, S., Li, J., Yan, L., & Xia, L. (2021). Increasing yield potential through manipulating of an ARE1 ortholog related to nitrogen use efficiency in wheat by CRISPR/Cas9. *Journal of integrative plant biology*, 63(9), 1649-1663.