Physical Education, Health and Social Sciences

https://journal-of-social-education.org **E-ISSN: 2958-5996**

P-ISSN: 2958-5988

Enhancing Wheat Quality and Nutritional Value: Insights into Genetic Basis, Biotechnological Tools, and Environmental Influences

Saima Majeed*[1], Sana Afzal[2], Azka Muneer[3], Faiqa Abid[4], Mohammad Ilyas[5], Abdul Latif Khan Tipu[6], Khatir Ali [7]

[1] Government College University Faisalabad.
***Corresponding Author**: saimamajeed653@gmail.com
[2] Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. sanafzal437@gmail.com
[3] Department of Plant Breeding and Genetics, Faculty of Agriculture, University of Agriculture, Faisalabad. azkamuneer96@gmail.com
[4] Department of Agronomy, Islamia University Bahawalpur. faiqaabid761@gmail.com
[5] Department of Botany, Abdul Wali Khan University Mardan. ilyas.uop014@gmail.com
[6] Economic Botany Section, Regional Agricultural Research Institute Bahawalpur. gtipu117@gmail.com
[7] Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. khatirali34521@gmail.com

DOI: https://doi.org/10.63163/jpehss.v4i1.1068

Abstract

Wheat (Triticum aestivum L.) is a critical global staple, providing ~19% of caloric intake and ~21% of protein needs, yet modern cultivars often suffer from reduced micronutrient density due to yield-focused breeding. This review synthesizes the genetic architecture of wheat quality traits, including seed storage proteins (glutenins and gliadins), key loci such as Gpc-B1 (NAM-B1) for enhanced grain protein content (GPC), iron, and zinc remobilization, and genes governing grain hardness and starch quality. Biotechnological advances, particularly CRISPR/Cas9 multiplexing for reducing gluten allergenicity, increasing resistant starch, and knocking out negative regulators like TaGW2 for improved yield-quality synergy, are highlighted alongside RNA interference and marker-assisted/genomic selection strategies. Multi-omics integration reveals spatiotemporal dynamics during grain development, while environmental factors nitrogen-sulfur balance, foliar biofortification, and climate stressors like elevated CO_2, heat, and drought significantly influence nutritional and processing quality. Genotype-by-environment interactions are addressed through stability models (AMMI and GGE biplots). Regulatory landscapes vary globally, with emerging flexibility for gene-edited products. Integrated approaches combining genetics, biotechnology, agronomy, and supportive policies hold promise for developing nutritionally superior, resilient wheat cultivars to combat hidden hunger and ensure food security.

Keywords: Wheat Quality, Grain Protein Content, Seed Storage Proteins, Crispr/Cas9, Biofortification, Gpc-B1/NAM-B1, Genotype-By-Environment Interaction, Climate Change, Multi-Omics, Genomic Selection

1. Introduction

The global agricultural landscape is currently undergoing a paradigm shift, transitioning from a historical focus on absolute yield metrics to a more integrated approach that prioritizes nutritional density, end-use functionality, and environmental resilience (Arslan et al., 2023). Common wheat (Triticum aestivum L.) occupies a central position in this evolution, serving as a foundational staple that provides approximately 19.0% of the world's caloric intake and 20.8% of daily protein requirements (Khalid et al., 2023). As the global population approaches an estimated 9.7 billion by 2050, the demand for wheat is projected to increase significantly, necessitating a 70.0% rise in total food production (Haque et al., 2021). However, this quantitative requirement is complicated by the qualitative deficiencies prevalent in modern cultivars, where decades of selection for high-yielding varieties have frequently led to the erosion of micronutrient density and a narrowing of the genetic diversity essential for adapting to a volatile climate (Gudi et al., 2022). The emergence of hidden hunger a state of micronutrient deficiency occurring despite adequate caloric intake now affects billions, particularly in regions where wheat remains the primary dietary source (Sparling et al., 2024). Consequently, enhancing wheat's nutritional profile and processing quality has become a critical objective for ensuring global food security and public health (Beshah et al., 2025).

2. The Genetic Architecture of Wheat Quality and End-Use

Wheat's unique status among cereals is primarily derived from its complex polyploid genome and the unique viscoelastic properties of its storage proteins, which enable the production of a diverse array of food products, from leavened breads and pasta to biscuits and noodles (Kou et al., 2023). Hexaploid bread wheat contains three distinct but related subgenomes (A, B, and D), a result of two separate interspecific hybridization events (Li et al., 2025). This complexity provides a vast reservoir of genetic variation but also presents significant challenges for trait improvement and functional genomics research (Norman et al., 2023).

2.1. Classification and Functional Role of Seed Storage Proteins Functionality

The technological quality of wheat is largely determined by the composition and concentration of seed storage proteins (SSPs), which are traditionally classified based on their solubility into four fractions: albumins, globulins, gliadins, and glutenins (Zheng et al., 2018). While albumins and globulins primarily perform metabolic functions and are rich in essential amino acids, the gliadin and glutenin fractions collectively termed gluten constitute up to 85.0% of the total grain protein content (GPC) and are the primary drivers of dough rheology (Lubieniechi et al., 2025).

Glutenins are further subdivided into high-molecular-weight glutenin subunits (HMW-GS) and low-molecular-weight glutenin subunits (LMW-GS). These subunits form large, polydisperse aggregates known as glutenin macropolymers (GMP), stabilized by intermolecular disulfide bonds (Wieser & Kieffer, 2001). HMW-GS are the most critical components for dough elasticity and strength, whereas LMW-GS contribute to both resistance to extension and dough extensibility. The Glu-1 loci, located on the long arms of chromosomes 1A, 1B, and 1D, encode the HMW-GS (Ma et al., 2003). Although the wheat genome theoretically contains six HMW-GS genes, silencing of specific alleles particularly the Ay subunit results in most cultivars expressing only three to five subunits (Wang et al., 2021). Recent research highlights that re-expressing these silenced genes, such as the 1Ay allele, can simultaneously improve GPC and grain yield, effectively breaking the traditional negative correlation between these two traits (Che et al., 2025).

Gliadins, on the other hand, are monomeric proteins that provide dough with its characteristic viscosity and extensibility. However, specific alpha-gliadin epitopes are the primary triggers for celiac disease, an autoimmune disorder affecting approximately 1.0% of the global population (Huang et al., 2025). Balancing the functional requirements of the milling and baking industries with the health needs of consumers is a primary challenge for contemporary breeding programs (Sanchez-Leon et al., 2018).

Table 1: Classification and Functional Properties of Seed Storage Protein Fractions

Protein Fraction	Sub-components	Primary Function	Genetic Loci
Glutenins	HMW-GS, LMW-GS	Elasticity, dough strength, GMP formation	Glu-1 (A1, B1, D1), Glu-3 (Kou et al., 2023; Wieser & Kieffer, 2001)
Gliadins	alpha, beta, gamma, omega-gliadins	Viscosity, extensibility, allergenicity	Gli-1, Gli-2 (Arslan et al., 2023; Zheng et al., 2018)
Albumins	Metabolic proteins	Enzyme activity, nutritional value	Various
Globulins	7S globulin	Energy storage, falling number regulation	Various (Kumar et al., 2018)

2.2. Genetic Mapping of Quality Traits: From QTLs to GWAS

The polygenic nature of wheat quality traits necessitates the use of advanced mapping techniques to identify the underlying quantitative trait loci (QTLs). Over 367 QTLs have been identified for GPC alone, distributed across all 21 chromosomes, explaining phenotypic variance ranging from 0.6% to 66.0%. Major GPC QTLs are frequently mapped to chromosomes 2A, 2B, 3A, 4A, 6B, 7A, and 7B (Kumar et al., 2018).

A cornerstone of wheat nutritional improvement is the Gpc-B1 locus (also known as NAM-B1) on chromosome 6BS. This locus encodes an NAC-family transcription factor that regulates the remobilization of nutrients (nitrogen, zinc, and iron) from senescing leaves to the developing grain (LiuZhang al., 2024). The introgression of Gpc-B1 from wild emmer wheat (Triticum turgidum ssp. dicoccoides) into modern cultivars has been shown to increase GPC by up to 10.0%, alongside significant increases in zinc and iron concentrations, without necessarily compromising grain weight if managed appropriately (Saini et al., 2022).

The development of high-density genetic maps and the utilization of Genome-Wide Association Studies (GWAS) have further refined our understanding of the genetic basis of quality traits (Subedi et al., 2023). GWAS provides greater resolution than traditional linkage mapping by leveraging historical recombination events in diverse populations (Gudi et al., 2022). For instance, a GWAS on 327 wheat accessions over multiple years identified stable QTLs for grain protein concentration on chromosomes 1B, 1D, 2A, and 7D (Shewry, 2009). Similarly, grain hardness a critical trait for milling is primarily controlled by the Pina-D1 and Pinb-D1 genes on chromosome 5DS, which encode friabilin proteins. Mutations in these genes differentiate hard wheat from soft wheat, impacting starch damage during milling and subsequent water absorption in dough (Marcotuli et al., 2022).

Table 2: Key Genetic Loci and Candidate Genes Influencing Wheat Quality and Grain Development

Trait	Key Gene/Locus	Chromosome	Biological Impact
Protein Content	Gpc-B1 (NAM-B1)	6BS	Enhances nitrogen, Fe, and Zn remobilization (Kou et al., 2023; Kumar et al., 2018)
Grain Hardness	Pina-D1, Pinb-D1	5DS	Controls endosperm texture and milling quality (Kumar et al., 2018)

Grain Weight	TaGW2	6A	Negative regulator; knockout increases grain size (Arslan et al., 2023; Haque et al., 2021)
Falling Number	QFN.sau-1B.2	1BL	Regulates alpha-amylase activity and sprout resistance (Gudi et al., 2022)
Starch Quality	TaSBEIIa	2A, 2B, 2D	Controls amylose/amylopectin ratio and resistant starch (Arslan et al., 2023)

3. Biotechnological Tools for Precision Breeding

The complexity of the wheat genome has historically limited the efficacy of traditional breeding methods, which are often time-consuming and labor-intensive (Salem et al., 2025). The advent of targeted genome editing technologies, most notably the CRISPR/Cas9 system, has provided researchers with a powerful toolkit to bypass these limitations and introduce specific modifications into elite cultivars (Haque et al., 2021).

3.1. CRISPR/Cas9: Revolutionizing Polyploid Wheat Improvement

The CRISPR/Cas9 system operates by using a single-guide RNA (sgRNA) to direct the Cas9 endonuclease to a specific genomic locus, where it generates a double-strand break (DSB) (Karmacharya, 2021). In polyploid wheat, the ability of CRISPR/Cas9 to achieve "multiplexing" simultaneously targeting the A, B, and D homoeologs is its most transformative feature. This allows for the complete knockout of redundant genes that govern undesirable traits (Lubieniechi et al., 2025).

3.1.1. Nutritional and Health Enhancement

One of the most promising applications of CRISPR/Cas9 in wheat is the reduction of gluten allergenicity (Tariq et al., 2023). By designing sgRNAs that target conserved regions of the alpha-gliadin gene family, researchers have successfully generated wheat lines with an 85.0% reduction in immunoreactive epitopes, offering a potential dietary solution for celiac patients without eliminating the technological properties of the grain (Sanchez-Leon et al., 2018). Additionally, targeting the starch branching enzyme IIa (TaSBEIIa) has resulted in high-amylose wheat with significantly increased resistant starch content, which provides substantial health benefits for colon health and blood glucose management (Basu et al., 2023).

3.1.2. Yield and Quality Synergy

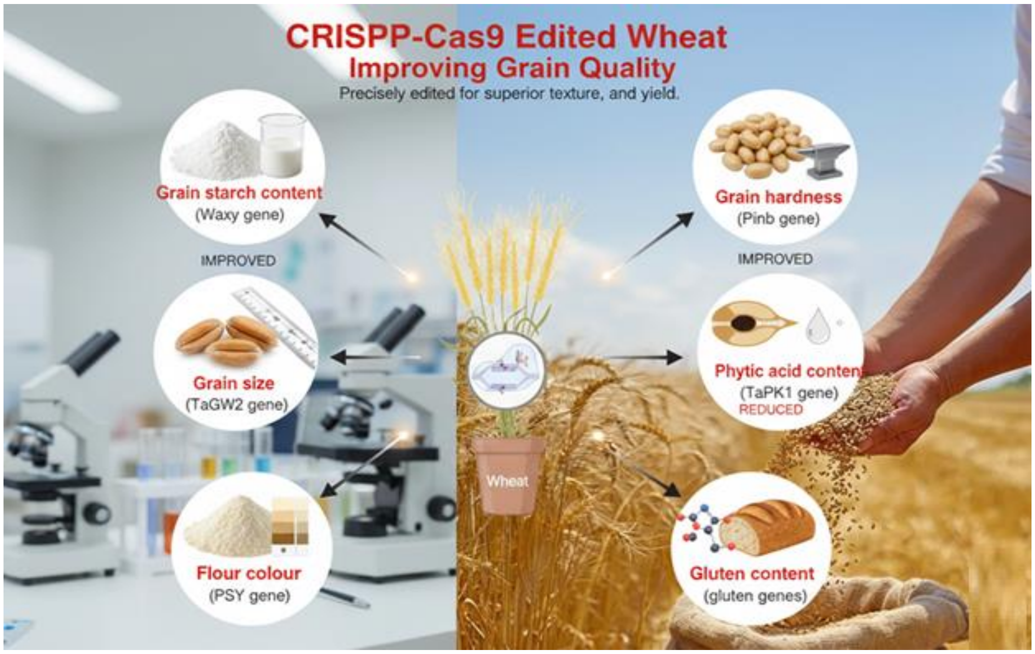
CRISPR/Cas9 has also been utilized to target negative regulators of yield and quality. Knocking out the TaGW2 gene, an E3 ubiquitin ligase, results in increased grain width and length, thereby boosting thousand-kernel weight (TKW) and overall yield potential (LI et al., 2024). Similarly, targeting TaGASR7, a gibberellin-regulated gene, has been shown to elevate grain length across diverse varietal backgrounds (Chachar et al., 2024). These applications demonstrate that biotechnology can be used to improve multiple complex traits simultaneously, a task that would take decades through conventional crossing (Jamil et al., 2025).

3.2. RNA Interference (RNAi) and Non-Transgenic Approaches

While CRISPR/Cas9 focuses on DNA modification, RNA interference (RNAi) targets the transcriptome, utilizing double-stranded RNA (dsRNA) to silence specific genes through the degradation of their mRNA (Liang et al., 2023). This technology has been particularly effective in developing resistance to biotic stresses through host-induced gene silencing (HIGS), where the plant is engineered to produce dsRNA that targets essential genes in invading pathogens or pests (Zand Karimi et al., 2022).

For nutritional improvement, RNAi has been used for the biofortification of wheat, altering metabolic pathways to enhance the accumulation of micronutrients or bioactive compounds. However, the transgenic nature of most RNAi applications has faced significant regulatory hurdles and public skepticism (Saakre et al., 2024). Emerging alternatives, such as spray-induced gene silencing (SIGS), offer a non-transgenic path forward by applying dsRNA directly to the plant's surface, providing a faster and potentially more acceptable means of trait modification (Baysal et al., 2022).

Figure 1. Precision Genome Editing Applications for Enhancing Wheat End-Use Quality and Yield.



3.3. Modern Molecular Breeding Strategies: MAS and Genomic Selection

Beyond direct genome modification, molecular marker technologies have drastically improved the efficiency of selection within breeding programs. Marker-assisted selection (MAS) integrates molecular markers such as Simple Sequence Repeats (SSR), Single Nucleotide Polymorphisms (SNP), and Kompetitive Allele Specific PCR (KASP) to track specific genes or QTLs through generations (Poland & Rutkoski, 2016). MAS is highly effective for traits controlled by a few major genes, such as disease resistance (Lr, Sr, Yr genes) or HMW-GS composition (Collard & Mackill, 2008). For instance, MAS facilitated the development of a commercial cultivar with improved dough quality in just five years, compared to twelve years via traditional methods (Wang et al., 2018).

For complex, polygenic traits like grain yield and GPC, genomic selection (GS) has emerged as the preferred strategy. GS utilizes high-throughput genotyping to capture the effects of thousands of markers across the entire genome, allowing for the prediction of breeding values (GEBVs) for individuals in a population (Gudi et al., 2022). By training models on a reference population with both genotypic and phenotypic data, breeders can select superior genotypes in progeny generations without the need for extensive field trials, significantly accelerating the rate of genetic gain (Kumar et al., 2018).

Table 3: Comparison of Modern Biotechnological and Marker-Based Breeding Tools

Technology	Mechanism	Primary Advantage	Typical Applications
CRISPR/Cas9	DNA cleavage (DSB)	High precision, multiplexing, transgene-free potential	Knocking out TaGW2, alpha-gliadins, TaSBEIIa (Haque et al., 2021; Arslan et al., 2023)
RNAi	mRNA degradation	Specific gene silencing without DNA change	Disease resistance, metabolic engineering (Haque et al., 2021)
MAS	Marker-trait linkage	Rapid selection of major alleles	Disease resistance pyramiding (Fhb1, Yr), dough quality (Collard & Mackill, 2008; Wang et al., 2018)
Genomic Selection	Whole-genome prediction	Captures minor QTL effects	Improving GPC, yield stability, complex environmental traits (Gudi et al., 2022; Poland & Rutkoski, 2016)

4. Multi-Omics Integration and Grain Development Dynamics

A comprehensive understanding of wheat quality requires an integrated analysis of the molecular processes occurring during grain development (Fan et al., 2025). The transition from flowering (anthesis) to physiological maturity is a highly coordinated sequence of biological events governed by the interplay of the genome, transcriptome, proteome, and metabolome (Li et al., 2025).

4.1. The Spatiotemporal Transcriptomic Atlas

Recent research has focused on delineating the spatiotemporal transitions that occur within the grain's tissues the embryo, endosperm, and seed coat. High-resolution temporal atlases have identified a critical developmental window at approximately 7 days post-anthesis (DPA) (Zhi et al., 2023). During this phase, metabolic programming is established, with genes involved in cell division and carbohydrate biosynthesis reaching peak expression to determine the final potential for grain weight and size (Peirats-Llobet et al., 2023).

As development progresses, the focus shifts from primary metabolism to the biosynthesis and accumulation of storage components. Genes and proteins involved in starch synthesis (e.g., ADP-glucose pyrophosphorylase) and SSP assembly become dominant (Yao et al., 2024). Joint analysis of the transcriptome and metabolome has revealed that pathways such as the citrate cycle (TCA), carbon fixation, and amino acid metabolism (alanine, aspartate, and glutamate) are significantly enriched during this transition, highlighting the energetic cost of protein accumulation (Sheng et al., 2025).

4.2. Insights from Proteomics and Metabolomics

Proteomic profiling has been instrumental in characterizing the response of wheat to environmental stressors and nutrient availability (Satrio et al., 2024). Techniques such as liquid chromatography-tandem mass spectrometry (LC-MS/MS) have allowed for the identification of stress-responsive proteins, including heat shock proteins (HSPs) and antioxidant enzymes like superoxide dismutase (SOD) and catalase (CAT), which help maintain cellular integrity during terminal heat or drought stress (Sparling et al., 2024).

Metabolomics provides a snapshot of the chemical end-products of gene expression. In colored wheat varieties, metabolomic analysis has identified over 500 essential nutrients, including high concentrations of anthocyanins and flavonoids in the seed coat (Saini et al., 2020). These compounds not only contribute to the aesthetic appeal of the grain but also serve as potent antioxidants with significant health benefits (Halder et al., 2022). Interestingly, studies have shown that immature green kernels often possess higher levels of certain beneficial compounds, such as polyphenols and vitamins, than mature grains, suggesting potential for developing functional foods from less mature harvests (Sramkova et al., 2009).

Table 4: Integration of Different Multi-Omics Levels for Understanding Wheat Quality

Omics Level	Focus	Key Findings in Wheat Quality
Transcriptomics	Gene expression patterns	Identification of 7 DPA as critical for grain weight; discovery of TaABI3-B1 (Li et al., 2025)
Proteomics	Protein composition and activity	Characterization of HMW-GS/LMW-GS accumulation; stress protein identification (Wang et al., 2021)
Metabolomics	Chemical end-products	Flavonoid pathways in colored wheat; lipid and organic acid dynamics (Saini et al., 2020; Zheng et al., 2018)
Ionomics	Mineral composition	Micronutrient accumulation (Fe, Zn, Se) during grain filling (Sramkova et al., 2009)

5. Environmental Influences and Agronomic Management

While genetic potential sets the upper limit for wheat quality, environmental conditions and management practices dictate the extent to which this potential is realized. The interaction between nutrient management and climate change is a critical determinant of grain composition (Collier et al., 2024).

5.1. Nitrogen and Sulfur Synergy

The accumulation of protein in wheat grains is heavily dependent on nitrogen (N) availability. However, nitrogen fertilization alone is often insufficient to ensure optimal dough quality. Sulfur (S) is a vital co-factor, as it is a constituent of the amino acids cysteine and methionine, which are essential for the formation of the disulfide bonds that stabilize the glutenin macropolymer (Wieser & Kieffer, 2001).

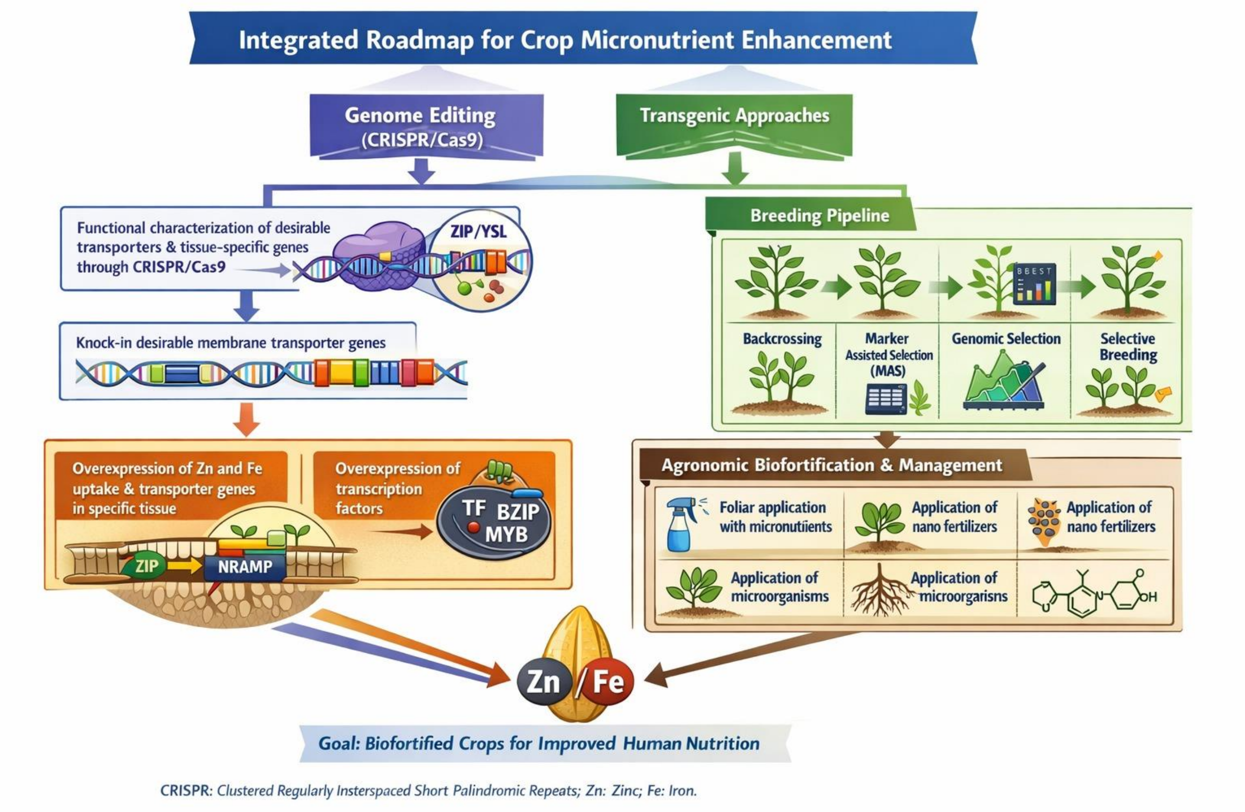
A critical parameter in agronomic management is the nitrogen-to-sulfur (N:S) ratio. For wheat, an N:S ratio between 15:1 and 18:1 is generally recommended to optimize protein quality and N-use efficiency (Preston, 2024). Adequate sulfur fertilization (30-60 kg S/ha under normal N levels) has been shown to increase the content of HMW-GS and promote the formation of large GMP particles (greater than 60 micrometers), which are positively correlated with dough elasticity (Abdalla et al., 2025). Conversely, excessive sulfur application (90 kg S/ha) or nitrogen application in the absence of sulfur can lead to the accumulation of low-molecular-weight sulfur-poor proteins and free asparagine, the latter of which is a precursor to acrylamide formation during high-temperature processing (Beshah et al., 2025; Timms et al., 1981).

5.2. Biofortification and Nutrient Density

Biofortification strategies both genetic and agronomic are being deployed to combat micronutrient deficiencies. Agronomic biofortification involves the foliar application of mineral fertilizers, such as zinc sulfate (ZnSO4), ferrous sulfate (FeSO4), and sodium selenate (Cakmak, 2008). Foliar application of selenium (Se) during the heading and grain-filling stages has been found to significantly increase grain Se content without impacting yield, while simultaneously reducing the concentration of anti-nutrients like phytic acid (Dhaliwal et al., 2022).

Innovative agronomic tools, such as the organo-mineral fertilizer complex "Complexon," have demonstrated remarkable results in increasing yield (up to 64.5%) while enhancing flour output and reducing cellulose content. These complexes often contain amino acids and micronutrients that activate bioactive components and improve plant nutrition under stressful conditions (Yeritsyan et al., 2024).

Figure 2. Integrated Breeding and Biotechnological Strategies for Wheat Biofortification.



CRISPR: Clustered Regularly Insterspaced Short Palindromic Repeats; Zn: Zinc; Fe: Iron.

5.3. The Challenge of Climate Change: Elevated CO2, Heat, and Drought

The ongoing rise in atmospheric CO2 (eCO2) presents a profound challenge to wheat quality. While eCO2 stimulates photosynthesis in C3 plants like wheat, leading to potential yield increases of 21.0% to 35.0%, it simultaneously causes a significant reduction in grain protein and mineral density a phenomenon known as the "dilution effect" (Sparling et al., 2024).

Under eCO2 conditions (projected to reach 550 ppm by 2050), protein content in wheat can decrease by 7.0% to 15.0%, and in some cases, reductions of up to 65.0% have been reported in specific experimental setups (Myers et al., 2014). This decrease is often accompanied by significant declines (up to 50.0%) in essential micronutrients like zinc and iron (Sparling et al., 2024). Furthermore, the increase in carbohydrate production under eCO2 may contribute to higher levels of dietary starch, potentially exacerbating issues like diabetes and obesity while failing to address protein-energy malnutrition (Zampieri et al., 2017).

Concurrent stressors like terminal heat and drought further complicate the quality outlook. Heat stress during the grain-filling period reduces the duration of starch accumulation and impairs the activity of enzymes like starch synthase, leading to shriveled grains and reduced flour extraction (Ashraf, 2014). Interestingly, heat and drought stress often increase the percentage of protein by reducing carbohydrate accumulation, but this protein is frequently of lower quality, characterized by an increased gliadin-to-glutenin ratio and higher concentrations of phytic acid (Lama et al., 2023).

Table 5: Differential Impacts of Climate Change and Nutrient Interactions on Wheat Functionality

Environmental Stress	**Effect on Yield**	**Effect on GPC**	**Effect on Minerals (Fe, Zn)**	**Functional Impact**
Elevated CO2	Increase (+16-35%)	Decrease (-7-15%)	Significant decrease	Reduced dough strength, dilution of minerals (Kimball, 2016; Myers et al., 2014; Sparling et al., 2024)
Heat Stress	Decrease	Increase (percentage)	Decrease (bioavailability)	Increased gliadin, reduced grain size (Ashraf, 2014; Zampieri et al., 2017)
Drought Stress	Decrease	Increase (percentage)	Variable	Improved water-use efficiency at cost of yield (Ashraf, 2014; Sparling et al., 2024)
N-S Interaction	Increase	Significant increase	Synergistic increase	Optimized GMP size and dough elasticity (Litke et al., 2017; Wieser & Kieffer, 2001; Zhang et al., 2007)

6. Quantitative Modeling of Genotype-by-Environment (GxE) Interactions

A fundamental challenge in breeding is the inconsistent performance of genotypes across different environments, a phenomenon known as the Genotype-by-Environment (GxE) interaction. To ensure the release of stable, high-quality cultivars, breeders utilize sophisticated statistical models to analyze Multi-Environment Trials (MET) (Ahmed et al., 2011).

6.1. AMMI and GGE Biplot Models

Two primary multivariate approaches are utilized for stability analysis: the Additive Main Effects and Multiplicative Interaction (AMMI) model and the Genotype main effect plus Genotype-by-Environment interaction (GGE) biplot analysis (Al-Ghumaiz et al., 2025).

The AMMI model uses ANOVA to partition the main effects (Genotype and Environment) and Principal Component Analysis (PCA) to explain the residual interaction (Mehareb et al., 2022). This model is particularly effective at identifying genotypes with broad or specific adaptation. For instance, in a study across four locations in Punjab, India, the AMMI model revealed that while yield was heavily influenced by GxE, the genotype had a more significant impact on GPC, suggesting that quality may be a more stable target for selection than yield (Mullualem et al., 2024).

The GGE biplot focuses on the G and GE components, offering visual tools to identify the "ideal genotype" one that combines high mean performance with the shortest stability vector (indicating high stability). GGE biplots are also used to define "mega-environments," regions where the ranking of genotypes remains consistent, allowing for more targeted breeding efforts (Wodebo et al., 2023).

6.2. Stability Indices and Selection

To complement visual models, several stability indices are calculated, including the AMMI Stability Value (ASV) and the Yield Stability Index (YSI). A lower ASV indicates a more stable genotype across environments (Purchase et al., 2000). For example, the genotype IC8 was identified in long-term trials as highly stable under both organic and conventional fertilization regimes, making it an ideal candidate for sustainable production systems (Hossain et al., 2023). In Zimbabwe, the selection of genotypes G5 and G8 was based on their combination of high grain yield and stability, which outperformed existing check varieties (Greveniotis et al., 2023).

Table 6: Comparative Results of Multi-Environment Trials (MET) Using Stability Models

Location	Key Findings	Best Genotypes	Model Used
Punjab, India	Genotype impact on GPC greater than Environment impact	BWL7508, BWL7511	AMMI/GGE (Gudi et al., 2022)
Ethiopia (Highlands)	Significant GxE for yield components	BWRVT/76, BWRVT/40	GGE Biplot (BWRVT, 2024)
South Ethiopia	Significant location variance (82%)	G8 (stable), G11 (yielder)	AMMI/GGE (Al-Ghumaiz et al., 2025)
Zimbabwe	Crossover effects in different years	G5, G8	GGE Biplot (CBI of Zimbabwe, 2024)
Saudi Arabia	Organic vs. Conventional stability	IC8	AMMI (Al-Ghumaiz et al., 2025)

7. The Global Regulatory and Policy Landscape

The adoption of modern biotechnological tools in wheat improvement is inextricably linked to the diverse and shifting regulatory frameworks established by different nations. The distinction between "Genetically Modified Organisms" (GMOs) and "Gene-Edited" products remains a central point of global divergence (Lubieniechi et al., 2025).

7.1. Regulatory Divergence and Trade Challenges

In the European Union, the regulatory environment has historically been highly restrictive. A 2018 ruling by the European Court of Justice initially classified all gene-edited organisms as GMOs, subjecting them to a rigorous and costly approval process that has essentially halted commercial development in the region for decades (Lubieniechi et al., 2025). However, as of 2024-2025, there is a significant legislative movement toward a more science-based framework. The European Commission has proposed a separate category (Category 1 NGT) for plants that could have occurred naturally or through conventional breeding, exempting them from many GMO-style restrictions to support the "Farm to Fork" sustainability strategy (Caradus, 2023).

In contrast, countries like the United States, China, Japan, and several Latin American nations have adopted more flexible, product-focused regulations. China, in particular, has accelerated its approval timelines for gene-edited products to just 1-2 years, granting the first commercial approval for a gene-edited wheat variety in May 2024 (Rudenko et al., 2023). India has also exempted SDN1 and SDN2 categories of gene-edited crops (those without foreign DNA) from the stringent biosafety assessments required for transgenic crops (Clark et al., 2024).

Africa is emerging as a critical region for adaptive regulation. Nigeria, Kenya, Malawi, and Ethiopia have published guidelines that distinguish between conventional, intermediate, and transgenic products, applying a case-by-case review process that aims to foster local innovation while ensuring food safety (Spök et al., 2022).

7.2. Economic Implications for Small-Scale Breeders

One of the primary consequences of strict GMO regulation is the high cost of entry, which often limits the use of advanced biotechnology to large multinational corporations (Ramsay et al., 2022). By adopting more flexible regulations for gene editing, countries can lower the regulatory costs, enabling small and medium-sized enterprises (SMEs) and public research institutions to develop niche varieties adapted to local markets and environmental conditions (Fu et al., 2024).

8. Future Perspectives and Strategic Integration

The challenge of enhancing wheat quality in a changing world requires a holistic strategy that transcends the traditional boundaries of genetics, agronomy, and food science. The future of wheat improvement lies in the "synergistic amalgamation" of diverse methodologies (Gudi et al., 2022). The integration of high-resolution spatiotemporal multi-omics data with machine learning-based genomic selection models (Beyer et al., 2024). will allow for "breeding by design," where genotypes can be mathematically optimized for specific end-use environments. The utilization of crop wild relatives through advanced introgression techniques will remain essential for restoring the genetic diversity lost during the Green Revolution (Norman et al., 2023).

Furthermore, as climate change alters the primary metabolic processes of the wheat plant, agronomic practices must evolve in tandem. Precision agriculture tools, including remote sensing (NDVI and LAI) to monitor nitrogen and sulfur needs in real-time, will be critical for maintaining grain quality under eCO2 and heat stress (Litke et al., 2017). The development of wheat varieties with reduced allergenicity and enhanced resistant starch content through CRISPR/Cas9 (Sanchez-Leon et al., 2018) will continue to expand the market for wheat-based products, ensuring that this ancient crop remains a cornerstone of human health and global food security in the 21st century. Additionally, implementing site-specific herbicide and nutrient management strategies, as explored by, will further stabilize yields and quality across variable terrains (Dhaliwal et al., 2022). Through the convergence of precise genetic tools, nuanced agronomic management, and supportive global policies, it is possible to develop wheat cultivars that are not only highly productive but also nutritionally superior and resilient to the existential threats of the coming decades (Khalid et al., 2023).

Finally, novel metabolic interventions such as the application of gamma-aminobutyric acid (GABA) are showing promise in protecting grains under stress. Studies have shown that GABA application can mitigate the effects of salt and endoplasmic reticulum (ER) stress by activating antioxidant pathways and promoting the accumulation of mineral nutrients and phenolics in wheat seedlings (Kumari et al., 2024). These types of interventions, which transform precursors like AB-ald into gamma-aminobutyric acid, could provide additional tools for enhancing the nutritional value and stress resilience of wheat crops in challenging environments (Abdalla et al., 2025).

Conclusion

Enhancing wheat quality and nutritional value demands a multifaceted strategy that synergizes genetic insights, precision biotechnological tools, and adaptive agronomic practices amid accelerating climate change. The genetic complexity of polyploid wheat, exemplified by storage protein loci and major QTLs like Gpc-B1, provides a foundation for targeted improvements in GPC, micronutrient density, and end-use functionality. CRISPR/Cas9 and related technologies enable precise modifications to reduce allergenicity, boost resistant starch, and optimize yield-quality trade-offs, while multi-omics approaches illuminate grain development dynamics and stress responses. Environmental influences, including nutrient synergies and climate stressors, underscore the need for integrated management to realize genetic potential. Stability analyses and flexible regulations will facilitate the deployment of resilient cultivars. Ultimately, converging these elements will produce wheat varieties that are high-yielding, nutritionally enhanced, and sustainable, safeguarding global food security and public health in the face of future challenges.

References

Abdalla, M. A., Sumon, M. M., & Mühling, K. H. (2025). Improvement of cereal-and legume-derived protein quality with selenium and sulfur for plant food production. Journal of the Science of Food and Agriculture, 105(11), 5611-5623.

Abdullah, M. A., Khan, J., Awais, M., & Shoukat, A. (2023). Enhancing the Productivity of Wheat (Triticum spp.) Via Genetic and Environmental Variability: A Review. Asian Journal of Biochemistry, Genetics and Molecular Biology, 15(4), 8-14.

Abdullah, M. A., Khan, J., Awais, M., & Shoukat, A. (2023). Enhancing the Productivity of Wheat (Triticum spp.) Via Genetic and Environmental Variability: A Review. Asian Journal of Biochemistry, Genetics and Molecular Biology, 15(4), 8-14.

Al-Ghumaiz, N. S., Al-Otayk, S. M., & Alzamil, A. A. (2025). Phenotypic stability and adaptability of wheat genotypes under different fertilization systems: Long-term insights from AMMI and GGE biplot models. *Frontiers in Plant Science*, 16, 1693316. https://doi.org/10.3389/fpls.2025.1693316

Arslan, M., Kim, S., Kou, X., Awan, F. S., & Ozturk, M. (2023). Advances in bread wheat production through CRISPR/Cas9 technology: A comprehensive review of quality and other aspects. *Planta*, 258(1), 55. https://doi.org/10.1007/s00425-023-04183-5

Awais, M., Rasheed, S., Asad, R. A. A., Annum, N., Abid, F., Zaman, M., & ur Rehman, Z. (2024). CRISPR/Cas9 and Modern Breeding Tools for Genetic Improvement of Maize Seeds. Global Research Journal of Natural Science and Technology, 2(3).

Awais, M., Rasheed, S., Asad, R. A. A., Annum, N., Abid, F., Zaman, M., & ur Rehman, Z. (2024). CRISPR/Cas9 and Modern Breeding Tools for Genetic Improvement of Maize Seeds. Global Research Journal of Natural Science and Technology, 2(3).

Basu, U., Riaz Ahmed, S., Bhat, B. A., Anwar, Z., Ali, A., Ijaz, A., ... & Mushtaq, M. (2023). A CRISPR way for accelerating cereal crop improvement: Progress and challenges. Frontiers in Genetics, 13, 866976.

Baysal, Ö., & Bastas, K. K. (2022). Host-Induced Gene Silencing: Approaches in Plant Disease Management. In Microbial Biocontrol: Sustainable Agriculture and Phytopathogen Management: Volume 1 (pp. 33-50). Cham: Springer International Publishing.

Beshah, A., Muhie, S. H., Alomari, D., & Napoli, M. (2025). Enhancing nutritional value of common wheat: Impacts of foliar selenium application on grain quality and safety. *Field Crops Research*, 330, 109969. https://doi.org/10.1016/j.fcr.2025.109969

Caradus, J. R. (2023). Processes for regulating genetically modified and gene edited plants. GM Crops & Food, 14(1), 1-41.

Chachar, Z., Fan, L., Chachar, S., Ahmed, N., Narejo, M. U. N., Ahmed, N., ... & Qi, Y. (2024). Genetic and genomic pathways to improved wheat (Triticum aestivum L.) yields: A review. Agronomy, 14(6), 1201.

Che, R., Liu, B., Chao, Y., Bian, Y., Xie, L., Li, L., ... & Cao, S. (2025). Deciphering the genetic architecture and regulatory mechanism underlying the accumulation of seed storage proteins in wheat. Journal of Experimental Botany, eraf351.

Chirag, S., Sarfraz, H., Akram, J., Salman, M., Awais, M., Mehmood, S., Ali, K., Khurshid, C. M. R., Rahman, S., Ahmad, J., Akhtar, N., & Ali, Q. (2025). Cotton genetic improvement for insect resistance: Integrating plant breeding and entomological approaches for sustainable pest management. Physical Education, Health and Social Sciences, 3(4), 379–397.

Chirag, S., Sarfraz, H., Akram, J., Salman, M., Awais, M., Mehmood, S., Ali, K., Khurshid, C. M. R., Rahman, S., Ahmad, J., Akhtar, N., & Ali, Q. (2025). Cotton genetic improvement for insect resistance: Integrating plant breeding and entomological approaches for sustainable pest management. Physical Education, Health and Social Sciences, 3(4), 379–397.

Clark, L. F., & Hobbs, J. E. (2024). International Regulation of Gene Editing Technologies in Crops: Current Status and Future Trends (p. 118). Springer Nature.

Collier, G. R., Spaner, D. M., & Beres, B. L. (2024). Learning to balance wheat G× E× M interactions in response to a changing climate—The case for ultra-early planting systems. Agronomy Journal, 116(2), 395-414.

Dhaliwal, S. S., Sharma, V., Shukla, A. K., Verma, V., Kaur, M., Shivay, Y. S., ... & Hossain, A. (2022). Biofortification—A frontier novel approach to enrich micronutrients in field crops to encounter the nutritional security. Molecules, 27(4), 1340.

Fan, B. L., Chen, L. H., Chen, L. L., & Guo, H. (2025). Integrative multi-omics approaches for identifying and characterizing biological elements in crop traits: current progress and future prospects. International Journal of Molecular Sciences, 26(4), 1466.

Flores-García, B. D., Fatunla, O., Adeleye, A. O., Babagana, M., Nkereuwem, M. E., Awais, M., & Manbe, M. Y. (2023). Making Sustainable Agriculture Possible Through the Utilization of Plant-Microbe Interactions. SciWaveBulletin, 1(1), 34-40.

Flores-García, B. D., Fatunla, O., Adeleye, A. O., Babagana, M., Nkereuwem, M. E., Awais, M., & Manbe, M. Y. (2023). Making Sustainable Agriculture Possible Through the Utilization of Plant-Microbe Interactions. SciWaveBulletin, 1(1), 34-40.

Fu, J. (2024). The Long-term Impact of GMO Plants on Agricultural Economy: Opportunities and Challenges. GMO Biosafety Research, 15.

Greveniotis, V., Bouloumpasi, E., Zotis, S., Korkovelos, A., Kantas, D., & Ipsilandis, C. G. (2023). Genotype-by-environment interaction analysis for quantity and quality traits in faba beans using AMMI, GGE models, and stability indices. Plants, 12(21), 3769.

Gudi, S., Saini, D. K., Gill, R., Kumar, A., & Sandhu, S. S. (2022). Application of AMMI and GGE biplot models for wheat quality traits stability analysis. *Frontiers in Genetics*, 13, 1001904. https://doi.org/10.3389/fgene.2022.1001904

Halder, T., Choudhary, M., Liu, H., Chen, Y., Yan, G., & Siddique, K. H. (2022). Wheat proteomics for abiotic stress tolerance and root system architecture: current status and future prospects. Proteomes, 10(2), 17.

Haque, S., Nazir, S., Ahmad, S., Liu, J., & Haque, E. (2021). Application of CRISPR/Cas9 in wheat genetic improvement: A comprehensive overview. *Biotechnology and Molecular Biology*, 2021(3978). https://bioscipublisher.com/index.php/bm/article/html/3978/

Haroon, M., Shehu, U. A., Ali, S., Haq, A., Essa, Y., Junaid, M., & Jan, A. (2025). Red Rot Disease of Sugarcane: Current Status, Pathogen Biology, and Integrated Management Strategies. Global Research Journal of Natural Science and Technology.

Hossain, M. A., Sarker, U., Azam, M. G., Kobir, M. S., Roychowdhury, R., Ercisli, S., ... & Golokhvast, K. S. (2023). Integrating BLUP, AMMI, and GGE models to explore GE interactions for adaptability and stability of winter lentils (Lens culinaris Medik.). Plants, 12(11), 2079.

Huang, C., Pang, J., Li, Z., Qu, M., Feng, Z., Ren, W., ... & Ji, W. (2025). Seed Storage Protein Identification and Transcriptome Analysis Reveal the Molecular Mechanisms of Wheat Quality Formation. Journal of Agricultural and Food Chemistry.

Jamil, M., Ahmad, W., Sanwal, M., & Maqsood, M. F. (2025). Gene editing and GWAS for digital imaging analysis of wheat grain weight, size and shape are inevitable to enhance the yield. Cereal Research Communications, 1-20.

Jan, A., Adil, S., Ali, T., Ahmed, B., Ahmed, Z., & Hussain, Z. (2025). Desert and medicinal plants as novel sources of antimicrobial agents for crop protection. Planta Animalia, 4(3), 197-218.

Jan, A., Adil, S., Ali, T., Ahmed, B., Ahmed, Z., & Hussain, Z. (2025). Desert and medicinal plants as novel sources of antimicrobial agents for crop protection. Planta Animalia, 4(3), 197-218.

Jan, A., Ali, T., Chirag, S., Ahmed, S., Ali, M., Wali, S., ... & Ullah, K. (2025). Eco-Friendly Management of Insect Pests and Plant Diseases Using Botanical Extracts. Global Research Journal of Natural Science and Technology.

Jan, A., Ali, T., Chirag, S., Ahmed, S., Ali, M., Wali, S., ... & Ullah, K. (2025). Eco-Friendly Management of Insect Pests and Plant Diseases Using Botanical Extracts. Global Research Journal of Natural Science and Technology.

Jan, A., Hussain, Z., Ullah, A., Ahmed, Z., Bakhsh, B. P., Latif, A., ... & Ahmed, M. (2025). Sugarcane Whip Smut: A Comprehensive Review of Pathogen Biology, Epidemiology, and Control Measures. Annual Methodological Archive Research Review, 3(5), 211-232.

Jan, A., Hussain, Z., Ullah, A., Ahmed, Z., Bakhsh, B. P., Latif, A., ... & Ahmed, M. (2025). Sugarcane Whip Smut: A Comprehensive Review of Pathogen Biology, Epidemiology, and Control Measures. Annual Methodological Archive Research Review, 3(5), 211-232.

Jan, A., Razzaq, F., Umair, M., Ullah, I., Shamsullah, S., Uzair, M., Ikram, M., Ayyaz, M., & Ali, T. (2025). Cotton Leaf Curl Disease: Pathogen Diversity, Whitefly Ecology, and Integrated Management Approaches. Planta Animalia, 4(4), 363-371.

Jan, A., Razzaq, F., Umair, M., Ullah, I., Shamsullah, S., Uzair, M., Ikram, M., Ayyaz, M., & Ali, T. (2025). Cotton Leaf Curl Disease: Pathogen Diversity, Whitefly Ecology, and Integrated Management Approaches. Planta Animalia, 4(4), 363-371.

Jan, A., Shaikh, G. Y., Ullah, S., Saddam, S., Ali, T., u Rehman, A., ... & Ahmed, M. (2025). In-vitro antifungal activity of medicinal plant extracts against Fusarium oxysporum causing wilt in okra. Indus Journal of Bioscience Research, 3(8), 406-414.

Jan, A., Shaikh, G. Y., Ullah, S., Saddam, S., Ali, T., u Rehman, A., ... & Ahmed, M. (2025). In-vitro antifungal activity of medicinal plant extracts against Fusarium oxysporum causing wilt in okra. Indus Journal of Bioscience Research, 3(8), 406-414.

Karmacharya, A. (2022). Molecular mapping of QTL for genetic transformation-related trait and CRISPR/Cas9-mediated gene editing in wheat (Doctoral dissertation, North Dakota State University).

Kimball, B. A. (2016). Grain production in a changing climate: Elevated CO2, heat and moisture stress. *GRDC Update Papers*, 2016(3). https://grdc.com.au/resources-and-publications/grdc-update-papers/tab-content/grdc-update-papers/2020/03/grain-production-in-a-changing-climate-elevated-co2,-heat-and-moisture-stress

Kou, X., Fang, Z., Fang, Y., Yu, H., & Zhao, Y. (2023). Fine mapping of quantitative trait loci for grain protein content in a recombinant inbred line population of wheat. *Frontiers in Plant Science*, 14, 12702865. https://doi.org/10.3389/fpls.2023.12702865

Kumar, A., Verma, P., Singh, R., & Gupta, P. K. (2018). Quantitative trait locus (QTL) mapping for quality traits of wheat based on high density genetic map combined with bulked segregant analysis RNA-seq (BSR-Seq). *Frontiers in Plant Science*, 9, 600788. https://doi.org/10.3389/fpls.2020.600788

Lama, S., Leiva, F., Vallenback, P., Chawade, A., & Kuktaite, R. (2023). Impacts of heat, drought, and combined heat–drought stress on yield, phenotypic traits, and gluten protein traits: capturing stability of spring wheat in excessive environments. Frontiers in Plant Science, 14, 1179701.

Li, L., Zhi, Y., Li, S., Guo, Y., & Zhang, L. (2025). Integrated multi-omics reveals the molecular basis underlying wheat grain development and identifies TaYAK1-2D as a positive grain weight regulator. *Plants*, 14(24), 3868. https://doi.org/10.3390/plants14243868

Li, S., Zhang, Y., Liu, Y., Zhang, P., Wang, X., Chen, B., ... & Mao, H. (2024). The E3 ligase TaGW2 mediates transcription factor TaARR12 degradation to promote drought resistance in wheat. The Plant Cell, 36(3), 605-625.

Liang, Y., Li, C., Mangauthia, S. K., & Biswal, A. K. (2023). Precision genetic technologies for cereal functional genomics. Journal of Plant Biochemistry and Biotechnology, 32(4), 673-687.

LiuZhang, X., & Liu, X. (2024). High-Density Genetic Mapping in Wheat: Methodologies and Achievements. Triticeae Genomics and Genetics, 15.

Lubieniechi, J. P., Rosado, A., Tachikawa, M., Sprink, T., & Akinbo, O. (2025). Genome editing in agriculture: Regulatory challenges and trade implications. *Frontiers in Bioengineering and Biotechnology*, 13, 1609110. https://doi.org/10.3389/fbioe.2025.1609110

Marcotuli, I., Soriano, J. M., & Gadaleta, A. (2022). A consensus map for quality traits in durum wheat based on genome-wide association studies and detection of ortho-meta QTL across cereal species. Frontiers in Genetics, 13, 982418.

Mehareb, E. M., Osman, M. A. M., Attia, A. E., Bekheet, M. A., & Abo Elenen, F. F. (2022). Stability assessment for selection of elite sugarcane clones across multi-environment based on AMMI and GGE-biplot models. Euphytica, 218(7), 95.

Mullualem, D., Tsega, A., Mengie, T., Fentie, D., Kassa, Z., Fassil, A., ... & Astatkie, T. (2024). Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (Triticum aestivum L.) genotypes using AMMI and GGE biplot analyses. Heliyon, 10(12).

Noor, R. N., Atiq, M., Usman, M., Jan, A., Nawaz, A., Iqbal, S., ... & Rajput, N. A. (2025). Physiology, Epidemiology and Fungicidal Subdual Strategies for whip smut of sugarcane Caused by Sporisoriums Scitamineum.

Noor, R. N., Atiq, M., Usman, M., Jan, A., Nawaz, A., Iqbal, S., ... & Rajput, N. A. (2025). Physiology, Epidemiology and Fungicidal Subdual Strategies for whip smut of sugarcane Caused by Sporisoriums Scitamineum.

Noor, S., Nawaz, A., Ahmed, M., Akhtar, H., Ahmed, K., Irshad, M. S., ... & Jan, A. (2025). Beneficial Fungi and Bacteria as Biocontrol Agents against Fungal and Bacterial Plant Pathogens. Global Research Journal of Natural Science and Technology, 3(1).

Noor, S., Nawaz, A., Ahmed, M., Akhtar, H., Ahmed, K., Irshad, M. S., ... & Jan, A. (2025). Beneficial Fungi and Bacteria as Biocontrol Agents against Fungal and Bacterial Plant Pathogens. Global Research Journal of Natural Science and Technology, 3(1).

Norman, A., Luo, G., Jones, K., Garcia-Ruiz, H., & Eckardt, N. (2023). Improving disease resistance in wheat: Application of CRISPR-mediated genome editing to manipulate susceptibility and resistance genes. *Frontiers in Genome Editing*, 7, 1542487. https://doi.org/10.3389/fgeed.2025.1542487

Peirats-Llobet, M., Yi, C., Liew, L. C., Berkowitz, O., Narsai, R., Lewsey, M. G., & Whelan, J. (2023). Spatially resolved transcriptomic analysis of the germinating barley grain. Nucleic Acids Research, 51(15), 7798-7819.

Preston, C. (2024). Watch nitrogen to sulfur ratios to optimize crop growth. *Smart Nutrition MST*. https://smartnutritionmst.com/news-research/watch-nitrogen-to-sulfur-ratios-to-optimize-crop-growth/

Ramsay, T., Robinson, B., Coche, I., Hackett, K., & Emerson, C. (2022). Ethical aspects of GMO regulation in the EU: regulating new plant breeding techniques as GM has negative effects on sustainability, diversity and inclusion. The EMBO Reports, 23(9), EMBR202255583.

Roonjha, M. A., Roonjho, R., Ali, M., Anas, M., Khalid, H., & Jan, A. (2025). Aphid-Transmitted Plant Viruses: Epidemiology and Integrated Vector Management. International Journal of Agriculture Innovations and Cutting-Edge Research (HEC Recognised), 3(3), 109-126.

Roonjha, M. A., Roonjho, R., Ali, M., Anas, M., Khalid, H., & Jan, A. (2025). Aphid-Transmitted Plant Viruses: Epidemiology and Integrated Vector Management. International Journal of Agriculture Innovations and Cutting-Edge Research (HEC Recognised), 3(3), 109-126.

Rudenko, L., Plunkett, L. M., Kornum, A., Röcklinsberg, H., Sørensen, D. B., & Gjerris, M. (2023). An overview of the regulation of genetically altered animals in research. Biotech Animals in Research, 23-72.

Saakre, M., Jaiswal, S., Rathinam, M., Raman, K. V., Tilgam, J., Paul, K., ... & Pattanayak, D. (2024). Host-delivered RNA interference for durable pest resistance in plants: advanced methods, challenges, and applications. Molecular Biotechnology, 66(8), 1786-1805.

Saini, D. K., Chopra, Y., Singh, J., Sandhu, K. S., Kumar, A., Bazzer, S., & Srivastava, P. (2022). Comprehensive evaluation of mapping complex traits in wheat using genome-wide association studies. Molecular Breeding, 42(1), 1.

Salem, K. F., & Eid, N. A. (2025). Modern Breeding Strategies and Tools in Bread Wheat (Triticum aestivum L.). In Breeding and Biotechnology of Grass and Bast Fiber Crops (pp. 343-393). Cham: Springer Nature Switzerland.

Satrio, R. D., Fendiyanto, M. H., & Miftahudin, M. (2024). Tools and techniques used at global scale through genomics, transcriptomics, proteomics, and metabolomics to investigate plant stress responses at the molecular level. In Molecular dynamics of plant stress and its management (pp. 555-607). Singapore: Springer Nature Singapore.

Sheng, Y., Wang, X., Lin, G., & Chen, M. (2025). Single-nucleus multi-omics reveals the impact of drought stress on the development of soybean endosperm. Plant Communications, 6(10).

Sparling, J., Myers, S. S., Loladze, I., Chang, T., & Ekele, J. U. (2024). Impact of elevated atmospheric carbon dioxide (eCO2) concentrations on crop productivity and nutritional quality: A review. *Environmental and Experimental Botany*, 218, 12061828. https://doi.org/10.1016/j.envexpbot.2025.12061828

Spök, A., Sprink, T., Allan, A. C., Yamaguchi, T., & Dayé, C. (2022). Towards social acceptability of genome-edited plants in industrialised countries? Emerging evidence from Europe, United States, Canada, Australia, New Zealand, and Japan. Frontiers in genome editing, 4, 899331.

Subedi, M., Ghimire, B., Bagwell, J. W., Buck, J. W., & Mergoum, M. (2023). Wheat end-use quality: State of art, genetics, genomics-assisted improvement, future challenges, and opportunities. Frontiers in Genetics, 13, 1032601.

Tariq, A., Mushtaq, M., Yaqoob, H., Bhat, B. A., Zargar, S. M., Raza, A., ... & Mir, R. A. (2023). Putting CRISPR-Cas system in action: a golden window for efficient and precise genome editing for crop improvement. GM Crops & Food, 14(1), 1-27.

Ullah, S., Riaz, M., Awais, M., Kashani, S. A., Mohammad, S., & Jan, A. (2026). Molecular breeding innovations for high-quality Basmati rice: Strengthening aroma, yield, and resistance to key diseases. Physical Education, Health and Social Sciences, 4(1), 114–124.

Ullah, S., Riaz, M., Awais, M., Kashani, S. A., Mohammad, S., & Jan, A. (2026). Molecular breeding innovations for high-quality Basmati rice: Strengthening aroma, yield, and resistance to key diseases. Physical Education, Health and Social Sciences, 4(1), 114–124.

Wodebo, K. Y., Tolemariam, T., Demeke, S., Garedew, W., Tesfaye, T., Zeleke, M., ... & Sharma, M. (2023). AMMI and GGE biplot analyses for mega-environment identification and selection of some high-yielding oat (Avena sativa L.) genotypes for multiple environments. Plants, 12(17), 3064.

Yao, J., Chu, Q., Guo, X., Shao, W., Shang, N., Luo, K., ... & Fan, L. (2024). Spatiotemporal transcriptomic landscape of rice embryonic cells during seed germination. Developmental cell, 59(17), 2320-2332.

Yeritsyan, S., Yeritsyan, L., Jhangiryan, T., Barseghyan, M., & Grigoryan, K. (2024). Enhancing wheat yield and nutritional quality through organo-mineral fertilizer application. *Functional Food Science*, 4(1), 1604. https://doi.org/10.31665/ffsh.2024.1604

Zand Karimi, H., & Innes, R. W. (2022). Molecular mechanisms underlying host-induced gene silencing. The Plant Cell, 34(9), 3183-3199.

Zhang, X., Li, Y., Khan, A., Ali, M., Chen, J., Shen, L., Zhu, A., Chang, G., Yin, C., Wang, Z., & Sun, Z. (2025). Multi-omics identifies key genetic and metabolic networks regulating spike organ development in wheat. *The Plant Cell*, 37(11), koaf250. https://doi.org/10.1093/plcell/koaf250