***Review Article***

**Genetic profiling of quality ch****aracteristics for industrial applications and agronomic practices in bread wheat (*Triticum aestivum* L.).**

**ABSTRACT**

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| Bread wheat (*Triticum aestivum* L.) is a globally important crop due to its extensive use in food and industrial applications. This review aims to consolidate recent advancements in genetic profiling and agronomic practices that influence key quality parameters such as protein content, gluten strength, and starch composition—traits critical for baking, brewing, and bioethanol production. The review synthesizes research employing molecular tools such as quantitative trait loci (QTL) mapping, genome-wide association studies (GWAS), and marker-assisted selection (MAS). It also incorporates findings from agronomic practices including nutrient management, water optimization, and genotype-environment interactions that affect trait expression. Progress in molecular breeding has identified key genomic regions linked to industrially relevant quality traits. The integration of high-throughput genotyping with phenotypic evaluation has accelerated the identification of superior alleles. Agronomic strategies complement genetic approaches by enhancing trait expression under field conditions. However, practical application of these findings in breeding and agronomy remains limited. Emerging technologies such as genomic selection and CRISPR-based gene editing show strong potential but require further validation and infrastructure for widespread adoption. A synergistic approach combining molecular tools with precision agronomy is essential for advancing wheat quality to meet industrial standards. Continued investment in interdisciplinary research and technology transfer is critical to translate genetic gains into sustainable, high-quality wheat production systems. |

*Keywords: QTL, GWAS, MAS, CRISPR, genomic selection.*

**1. INTRODUCTION**

*Triticum aestivum* L., often known as bread wheat, is the most extensively farmed cereal crop globally and plays a crucial role in industry and food security. It constitutes over 30% of global grain output and is a vital crop for human nutrition and caloric intake (Shiferaw *et al*., 2013). Bread wheat possess distinctive physicochemical properties that render it essential for several industrial applications, such as baking, pasta making, bioethanol generation, and animal feed, in addition to its role as a staple crop. The increasing global demand for wheat with particular quality attributes necessitates a deeper comprehension of the genetic regulation of these traits and the agronomic practices to enhance them (Ray *et al*., 2013).The quality attributes of bread wheat may be broadly categorized as grain quality, milling quality, and end-use quality (Cappelli *et al*., 2021). Grain quality encompasses attributes such as test weight, kernel hardness (Lillemo *et al*., 2006), and protein content, whereas milling quality pertains to flour production and extraction rates (Gupta *et al*., 1993). End-use quality encompasses attributes such as dough rheology, gluten strength, and baking performance, which are of paramount importance for industrial processing (Güçbilmez *et al*., 2019). These characteristics are governed by complex interactions between hereditary and environmental variables, necessitating a comprehensive strategy for their improvement.

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| Quality Parameter | Genetic Determinants | Agronomic Influences | Industrial Impact |
| Grain Protein Content (GPC) | Gpc-B1, Glu-1, Glu-3 loci | Nitrogen fertilization, water stress | Baking quality, dough strength |
| Gluten Strength & Dough Rheology | HMW-GS & LMW-GS subunits | Sulfur availability, late-season nitrogen application | Elasticity, gas retention in bread |
| Starch Composition (Amylose/Amylopectin Ratio) | GBSS, SSII, SBE genes | Irrigation timing, temperature stress | Texture, viscosity for pasta/baking |
| Milling Efficiency & Flour Yield | Puroindoline genes (Pin-a, Pin-b) | Grain hardness, crop rotation | Flour extraction rate, energy use |
| Water Absorption & Baking Performance | Glutenin to Gliadin Ratio | Drought stress, soil nutrient balance | Moisture retention, crumb texture |

Table 1. Key Genetic and Agronomic Determinants of Industrial Quality in Bread Wheat

Genetic profiling provides a robust method to elucidate the genetic processes governing quality attributes in bread wheat. Progress in genomics, transcriptomics, and proteomics has enabled the identification of quantitative trait loci (QTLs), candidate genes, and molecular markers linked to essential qualitative traits. High-molecular-weight glutenin subunits (HMW-GS) and low-molecular-weight glutenin subunits (LMW-GS) have been thoroughly

investigated for their contributions to dough elasticity and extensibility (Shewry *et al*., 2003). Likewise, genes involved in starch synthesis, including those that code for granule-bound starch synthase (GBSS) and starch-branching enzymes, substantially affect the amylose-to-amylopectin ratio, which is a crucial factor in baking quality. Apart from genetic breakthroughs, agronomic practices are essential for enhancing wheat quality. Nutrient management, irrigation practices, and crop rotation substantially influence grain composition and processing characteristics. Nitrogen administration increases protein content, hence directly influencing gluten strength and dough performance (Ghimire *et al*., 2021). Likewise, exact water management techniques have demonstrated an impact on kernel growth and milling quality, underscoring the necessity for a comprehensive approach to crop management. The amalgamation of genetic and agronomic solutions presents significant promise to improve wheat quality for industrial applications. Recent improvements in genomic selection, gene editing technologies like a CRISPR-Cas9, and high-throughput phenotyping systems have significantly expedited wheat improvement. These developments provide the exact alteration of quality characteristics, hence allowing for the creation of wheat types customized to certain industrial specifications.

This paper seeks to deliver a thorough analysis of the genetic profiling of quality indicators in bread wheat, highlighting their significance for industrial applications. It also emphasizes the agronomic strategies that enhance genetic methods to attain the required quality results. This study aims to provide significant insights into the diverse efforts necessary to improve the commercial usability of bread wheat by integrating recent breakthroughs and research findings.

**2. Genetic Characterization of Industrial Quality Attributes**

**2.1 Mapping of Quantitative Trait Loci (QTL)**

Quantitative trait locus (QTL) mapping utilizes linkage analysis and genome-wide association studies (GWAS) to pinpoint chromosomal areas harboring genes that contribute to phenotypic variance in quality characteristics. QTL mapping has significantly enhanced the comprehension of the genetic regulation of wheat quality parameters. Numerous QTLs have been found for protein content, a critical quality parameter of bread. McCartney *et al*. (2006) identified 99 QTLs across 18 chromosomes that regulated 41 quality characteristics in bread wheat. A very stable gene area was identified on chromosome 4D, encompassing 20 of these QTLs. Additionally, ten additional QTLs, primarily associated with bread mixing characteristics (mixograph and farinograph performance), baking quality, and starch functionality, were identified in proximity to a QTL for time to maturity on chromosome 7D.

Mann *et al*. (2009) identified two high-frequency QTLs for grain protein content on chromosomes 3A and 7A across three of five locations, whereas two QTLs for dough rheology exhibited remarkable consistency across all five locations, with significant Glu-B1 and Glu-D1 loci seen. Carter *et al*. (2012) identified two QTL clusters on chromosomes 3B and 4D linked to milling quality and starch functionality characteristics. Boehm Jr. *et al*. (2018) identified four stable genomic areas on chromosomes 1BL, 2DS, 7AS, and 7BS, with several colocalizing QTLs regulating various end-use quality characteristics, such as grain protein content, water absorption, and flour production.

Grain hardness, a quality attribute of industrial significance, is another critical industrial characteristic (Jolly *et al*., 1996). Igrejas *et al*. (2002) found Quantitative Trait Loci (QTLs) that govern grain hardness (Hard), as well as the concentration of puroindoline-a (Pin-a) and puroindoline-b (Pin-b) in wheat. The most substantial QTL for the three phenotypes was identified on the short arm of chromosome 5D, closely associated with the mta9 allele, which governs the levels of puroindoline-a. A significant QTL associated with grain hardness was identified on the long arm of chromosome 5D, highlighting the genetic intricacy of this key trait.



**Fig.1.** The Landscape of the Wheat Genome

**2.1.1 Integration of QTL Mapping with Agronomic Metrics**

Comprehending the genetic foundation of agronomic and qualitative characteristics in wheat is crucial for improving its market value and industrial uses. These characteristics, influenced by genetic interactions and environmental variables, substantially affect end-use quality. Elangovan *et al*. (2011) discovered quantitative trait loci (QTLs) associated with sedimentation volume (Sv), grain protein content (Gpc), thousand grain weight (Tgw), and test weight (Tw)—crucial determinants of wheat marketability.

Through Composite Interval Mapping (CIM), 68 quantitative trait loci (QTLs) were found across seven chromosomes, with nine exhibiting clustering. The Additive Main Effects and Multiplicative Interaction (AMMI) model validated the genotype-by-environment (G × E) interactions, emphasizing their significance in trait expression. Several QTLs were co-localized, indicating a common genetic regulation of numerous agronomic variables, hence emphasizing the necessity for combined genetic and agronomic approaches in wheat enhancement.

**2.1.2 Genome-Wide Association Studies (GWAS)**

Genome-Wide Association Studies (GWAS) have revolutionized genetic research by facilitating the discovery of genomic areas associated with complex features essential for industrial applications in bread wheat (*Triticum aestivum* L.) (Rahimi *et al*., 2019). Utilizing natural genetic diversity, GWAS identifies associations between phenotypic variables and genotypic data, offering significant insights for wheat breeding initiatives.

The hexaploid genome of bread wheat, including six sets of chromosomes, poses both obstacles and possibilities for genetic study. The considerable genetic variety renders GWAS an essential instrument for identifying marker-trait associations (MTAs) associated with quality parameters such as grain hardness, protein content, and gluten strength—vital elements for commercial wheat products (Bhatta *et al*., 2018; Vishwakarma *et al*., 2024). In addition to quality indicators, GWAS facilitates the identification of genetic areas linked to agronomic qualities like as yield potential, disease resistance, and drought tolerance, which are crucial for enhancing productivity and sustainability (Alvarado *et al*., 2020).

***2.1.2.1 GWAS Methodology and Its Significance***

 Genome-wide association studies (GWAS) employ a systematic methodology to find genetic variations that affect wheat characteristics.

**(i). Genotyping:** Advanced methodologies such as single nucleotide polymorphism (SNP) arrays and next-generation sequencing (NGS) are employed to identify genetic variants (Yang *et al*., 2020; Collard *et al*., 2005).

**(ii). Phenotyping:** Phenotyping involves the collection of data on variables such as grain protein content (GPC), gluten strength, and milling quality across several contexts to evaluate genotype-by-environment (G×E) interactions (Campbell *et al*., 2001; Said *et al*., 2022).

**(iii). Statistical Analysis:** Techniques such as mixed linear models (MLMs) and Bayesian methods discern significant marker-trait associations (MTAs) and assess their influence (Malik *et al*., 2021).

**(iv). Validation:** Identified MTAs are evaluated across various contexts and genetic backgrounds to confirm their reliability and robustness (Tsai *et al*., 2020).

Genome-wide association studies (GWAS) continue to be an effective instrument in wheat breeding, enabling the creation of high-yield, stress-resistant, and commercially viable wheat varieties using precise genetic methodologies.

**Fig.2.** Genome-Wide Association Study Methodology for Wheat Trait Identification

Genome-wide association studies (GWAS) have transformed the identification of genetic loci that regulate complex quantitative features in bread wheat (*Triticum aestivum* L.). In contrast to conventional linkage mapping, it identifies numerous loci with minor effects that cumulatively impact essential industrial quality attributes (Tadesse *et al*., 2020). Genome-wide association studies (GWAS) have substantially aided in the identification of genetic loci linked to grain protein content (GPC) and kernel hardness, both critical for wheat quality. GPC influences baking efficacy, dough elasticity, and nutritional profile (Shewry, 2009). Significant loci associated with GPC have been discovered on chromosomes 2A, 6B, and 7D, influencing protein accumulation and gluten strength (Groos *et al*., 2003; Gupta *et al*., 2010; Saieed *et al*., 2010). Kernel hardness, which affects milling efficiency and flour characteristics, has been thoroughly investigated by GWAS. The Puroindoline A (Pina-D1) and Puroindoline B (Pinb-D1) genes located on chromosome 5D distinguish between soft and hard wheat types, influencing their appropriateness for cakes, pastries, bread, and pasta (Morris, 2002; Giroux & Morris, 1997; Morris & Rose, 1996). By combining marker-assisted selection (MAS) with genome-wide association studies (GWAS), breeders can integrate advantageous genetic variants to improve wheat quality and yield. Ongoing developments in genotyping and

statistical techniques provide GWAS a potent instrument for genomics-assisted enhancement of wheat (Breseghello & Sorrells, 2006).

**2.2 Marker-Assisted Selection (MAS) in the Enhancement of Bread Wheat**

Marker-Assisted Selection (MAS) combines molecular genetics with conventional breeding, improving efficiency and accuracy in wheat enhancement initiatives. This facilitates the prompt recognition of advantageous characteristics, hence decreasing both duration and expense in cultivar development (Collard & Mackill, 2008). Molecular markers associated with essential agronomic and industrial features enhance the precision and efficacy of breeding through marker-assisted selection (Gupta *et al*., 2005).

**2.2.1 Utilization of MAS in Industrial Quality Attributes**

MAS has significantly enhanced grain protein content (GPC), gluten strength, starch composition, and milling efficiency, all vital for commercial applications such as bread-making, pasta manufacture, and biscuit manufacturing. The Gpc-B1 gene has been selected to improve GPC, a crucial factor in bread-making quality (Uauy *et al*., 2006). Moreover, MAS enhances gluten strength by choosing high- and low-molecular-weight glutenin subunits at the Glu-1 and Glu-3 loci, hence improving dough elasticity and gas retention (Payne *et al*., 1987; Branlard *et al*., 2001). MAS facilitates the identification of markers linked to starch synthesis enzymes, hence enhancing texture and processing characteristics (Zeng *et al*., 1997; Christopher *et al*., 2007). It also improves milling efficiency and flour yield by focusing on indicators associated with grain hardness, regulated by the Puroindoline a and Puroindoline b genes (Giroux & Morris, 1997; Morris, 2002). These applications highlight MAS's contribution to the development of wheat cultivars suited for industrial requirements.

**3. Agronomic Strategies for Quality Improvement in Bread Wheat**

Genetic variables influence the quality potential of bread wheat (*Triticum aestivum* L.), whereas agronomic methods are essential for enhancing grain quality for industrial use. Effective fertilizer management, irrigation, crop rotation, insect control, and planting techniques are crucial to comply with the stringent requirements of the milling and baking sectors.

**Management of Nutrients:** A crucial factor in grain protein content (GPC), affecting gluten strength. Dividing treatments throughout planting and subsequent growth phases elevates protein concentrations, whereas late-season foliar spray further augments GPC (DuPont *et al*., 2003).Crucial for gluten flexibility, since it establishes disulfide bonds in glutenins. Deficiency compromises dough characteristics, rendering soil and tissue analysis essential for sulfur management (Zhao *et al*., 1997, 1999).Phosphorus (P), potassium (K), zinc, and iron indirectly affect grain growth and quality, highlighting the necessity for balanced fertilization.

**Water Resource Management:** Water availability influences starch accumulation, grain mass, and protein content. Moderate water stress can enhance protein concentration, hence boosting grain protein content (GPC), but severe stress diminishes both yield and quality. Irrigation throughout the blooming and grain-filling stages guarantees maximum yield (Goodling *et al*., 2003).

**Crop Rotation and Soil Stewardship:** Legume rotations enhance soil nitrogen content, hence decreasing need on fertilizers. Soils rich in organic matter improve nutrient absorption and grain quality (Kirkegaard *et al*., 2008).

**Management of Diseases and Pests:** Pathologies such as rusts and Fusarium head blight (FHB) diminish starch accumulation and contaminate grains with mycotoxins. Integrated pest management (IPM), encompassing resistant cultivars, crop rotation, and fungicides, reduces quality losses (McMullen *et al*., 2012).

**Planting Schedule and Density:** The ideal planting period synchronizes growth with advantageous climatic circumstances, facilitating enough grain development. Elevated plant density may diminish grain size and test weight, whereas insufficient density leads to resource underutilization. Appropriate harvest time, drying, and storage inhibit grain degradation (Frederick *et al*., 1995; Hylnka, 1964).

**4. Mechanisms Driving Quality Enhancements in Bread Wheat**

The quality enhancement in bread wheat (Triticum aestivum L.) is intricately governed by the interplay of genetic, agronomic, and environmental factors. A refined understanding of protein architecture, starch composition, and bioactive constituents has substantially contributed to precision breeding and cultural methodologies. Protein content and quality are fundamentally regulated by nitrogen metabolism, with enzymes like nitrate reductase, nitrite reductase, and glutamine synthetase playing pivotal roles in amino acid biosynthesis, while the Gpc-B1 gene facilitates nitrogen remobilization into the grain (Howarth et al., 2008; Quraishi et al., 2011; Uauy et al., 2006). The synthesis of gluten, governed by the Glu-1 and Glu-3 loci encoding gliadins and glutenins, significantly determines dough strength and elasticity, and sulfur fertilization has been shown to augment gluten quality (Shewry et al., 2002; Altenbach et al., 2003; Hurkman et al., 2013). Concurrently, starch quality traits are shaped by biosynthetic enzymes such as AGPase, starch synthases (SS), and branching enzymes (SBE), which influence gelatinization behavior and end-use texture (Tetlow et al., 2004). In waxy wheat lines, reduced GBSSI activity alters amylose content (Nakamura et al., 1995), while puroindolines modulate grain hardness, thereby affecting milling efficiency and flour texture (Wall et al., 2011). In addition to macromolecules, non-starch polysaccharides like arabinoxylans and β-glucans enhance dough hydration and rheological performance (Courtin & Delcour, 2002), and lipids such as glycolipids and phospholipids aid in gas retention during baking (Shevkani et al., 2017). Polyphenolic compounds, predominantly found in the aleurone layer, exhibit potent antioxidant properties (Yazar et al., 2023). The expression of these traits is further modulated by genotype-environment (G×E) interactions, which dictate variability in grain quality across different environments. These interactions may manifest as crossover, wherein genotype rankings shift across conditions, or as non-crossover, involving changes in performance magnitude without altering rank stability. Environmental stressors such as high temperatures during grain filling can influence starch and protein deposition, altering amylose/amylopectin ratios and glutenin cross-linking (Stone et al., 1994), while drought restricts starch deposition and shifts protein profiles, thereby affecting dough performance (Flagella et al., 2002). Nutrient factors like nitrogen and sulfur availability affect protein synthesis and gluten strength, with genotypic variation in uptake efficiency contributing further to G×E variability (Guttieri et al., 2004). Excess or inadequate light also alters quality metrics, either by limiting photosynthesis or inducing heat stress (Yang et al., 2006). Biotic pressures such as Fusarium head blight (FHB) not only affect yield and toxin levels but also interact with genotypic resistance traits, influencing quality outcomes (McMullen et al., 2012). These complexities necessitate targeted breeding strategies, utilizing multi-environment trials (METs) and analytical models such as AMMI and GGE biplots for adaptation assessment (Crossa et al., 2006). Genomic selection models that incorporate G×E effects further optimize predictive power. Agronomic practices tailored to genotype-specific responses, such as variable nitrogen regimes, strategic irrigation, and stress-responsive sowing schedules, can mitigate the adverse effects of abiotic stress. Underpinning these interactions are molecular mechanisms involving differential gene expression in response to environmental stimuli, regulating stress responses, nutrient metabolism, and developmental timing, while epigenetic modifications modulate these expression patterns. Hence, a comprehensive strategy integrating molecular biology, agronomy, and statistical modeling is critical for the development of resilient wheat varieties with consistent, high-quality end-use properties.

**5. The Influence of Agronomic Practices on Bread Wheat Quality**

Genetics establish the qualitative potential of wheat, whereas agronomic methods dictate its actualization. These behaviors influence genotypes and surroundings, hence affecting milling and baking characteristics.

**5.1 Enhancing Nutrient Accessibility**

Nitrogen Management: Divided nitrogen treatments enhance grain protein content (GPC) and gluten strength. Late-season foliar nitrogen enhances protein accumulation, whereas precision agriculture optimizes application rates (Bly *et al*., 1997).

Sulfur (S) is crucial for gluten elasticity, since it facilitates the formation of disulfide bonds in glutenins. Nutrient deficiencies diminish quality, requiring soil analysis and specific fertilizer (Salvagiotti *et al*., 2009). Phosphorus (P), potassium (K), zinc, and iron facilitate grain formation and metabolic functions, hence improving overall quality.

This comprehensive strategy guarantees uniform wheat quality by addressing genetic, environmental, and agronomic aspects to effectively fulfill industry requirements.

**6. Genetic Profiling of Quality Attributes in *Triticum aestivum***

Genetic profiling, employing molecular and genomic methodologies, has revolutionized bread wheat (*Triticum aestivum* L.) breeding by facilitating accurate selection for quality attributes. In contrast to conventional phenotypic assessment, genetic profiling immediately detects genomic areas, allelic variants, and molecular markers associated with advantageous features, hence expediting breeding initiatives.

Genetic profiling delineates key quantitative trait loci (QTLs) that influence grain quality traits in bread wheat, achieved through both QTL mapping in bi-parental populations and association studies using diverse germplasm panels. Modern approaches such as genome-wide association studies (GWAS), leveraging SNP arrays and genotyping-by-sequencing (GBS), have emerged as powerful tools for dissecting complex phenotypes associated with quality parameters (Gupta et al., 2008; Yu et al., 2006). The candidate gene strategy, informed by established biochemical pathways, guides gene-focused investigations targeting specific traits like starch biosynthesis and gluten protein quality. Once QTLs or candidate genes are identified, characterization of genetic variation—particularly SNPs and insertions/deletions—provides insights into allelic forms that confer superior trait expression, thereby facilitating marker-assisted selection (MAS) for desirable phenotypes (Collard et al., 2005). Functional analyses of these alleles deepen the understanding of how they regulate gene expression, protein activity, and associated enzymatic pathways. MAS expedites breeding efforts by enabling early selection based on genotypic data, circumventing the limitations of phenotypic evaluation, which is often laborious and environmentally sensitive (Xu et al., 2008). Complementing this, genomic selection (GS) employs genome-wide markers to predict breeding values, enhancing efficiency particularly for polygenic traits governed by numerous loci (Meuwissen et al., 2001). The advent of next-generation sequencing has significantly broadened the capacity to uncover novel genes and regulatory elements at a genome-wide scale (Kumar et al., 2015). Furthermore, integrative 'omics' approaches—encompassing transcriptomics, proteomics, and metabolomics—have enriched the molecular understanding of wheat quality traits (Shewry et al., 2009). In parallel, CRISPR-mediated gene editing now offers precise genome modifications aimed at improving key quality attributes (Zhang et al., 2019). These genomic advances translate effectively into wheat breeding through strategies like trait stacking and gene pyramiding, which allow the accumulation of multiple favorable alleles to enhance complex quality characteristics. Genetic profiling also enables introgression of beneficial alleles from diverse germplasm, including landraces and wild relatives, while minimizing linkage drag (Tanksley et al., 1996). Altogether, the convergence of genetic profiling, MAS, GS, and advanced genomic tools establishes a robust framework for breeding wheat varieties tailored to industrial demands. Not merely a supplementary technique, genetic profiling has become indispensable in enhancing wheat quality traits by accelerating selection cycles, improving precision, facilitating trait dissection, and harnessing novel alleles. When aligned with agronomic optimization, this integrative approach holds the key to ensuring a sustainable supply of premium-quality wheat to meet evolving global market and food industry requirements.

**Future Prospects**

The future of wheat breeding is set for significant breakthroughs propelled by advanced genomic and computational technology. CRISPR-based gene editing provides unparalleled accuracy in altering genes that determine wheat quality, enabling the swift improvement of characteristics such as protein composition, gluten flexibility, and starch structure. Simultaneously, multi-omics methodologies that incorporate genomes, transcriptomics, proteomics, and metabolomics will yield enhanced understanding of the molecular pathways governing quality attributes, allowing more precise breeding techniques.

The deployment of genomic prediction models and AI-based breeding techniques will expedite genetic advancements. Machine learning methods for genomic selection (GS) are anticipated to enhance predictive breeding, enabling breeders to identify high-performing genotypes without the need for extensive field experiments. Furthermore, precision agricultural methodologies, such as remote sensing, phenomics, and high-throughput screening, will improve field-based selection, guaranteeing optimal agronomic management aligned with genetic potential.

Notwithstanding these gains, obstacles persist, especially in tackling climatic unpredictability, resource constraints, and the intricate genetic framework of quality attributes. Future research should prioritize the development of climate-resilient wheat cultivars that combine stress tolerance with enhanced processing attributes. Furthermore, the synchronization of international breeding initiatives, accessible genetic databases, and advancements in bioinformatics will be essential for expediting data-driven breeding.

The integration of genetic engineering, artificial intelligence, and sustainable agronomy will shape the future of wheat enhancement. Collaborations among molecular biologists, agronomists, data scientists, and industry stakeholders will be crucial for developing future wheat varieties that satisfy industrial requirements and environmental sustainability objectives. Ongoing research, innovation, and technology integration will transform the wheat breeding sector to enhance global food security and industrial efficiency, rendering high-quality wheat more accessible and adaptable to future problems.

**Table 2.** Emerging Trends and Challenges in Genetic Profiling of Wheat Quality

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| Emerging Trend | Significance | Key References |
| Integration of MAS and GS for Industrial Traits | MAS and GS are increasingly combined to improve selection accuracy for wheat quality traits like dough strength, flour yield, and starch composition. | Meuwissen et al., 2001; Breseghello & Sorrells, 2006 |
| AI-Driven Genomic Selection and Machine Learning | AI models improve breeding efficiency by predicting genotypic responses to environmental variations. Machine learning refines GS models for quality trait prediction. | Crossa et al., 2017; Malik et al., 2021 |
| Climate-Resilient Breeding for Wheat Quality | Heat stress and drought affect protein content and starch accumulation. Developing climate-resilient wheat requires integration of G×E models with molecular breeding. | Stone et al., 1994; Flagella et al., 2002 |
| Multi-Omics Approaches for Quality Trait Dissection | Functional genomics, transcriptomics, and metabolomics reveal key regulatory genes influencing wheat’s industrial properties. | Shewry et al., 2009; Kumar et al., 2015 |
| CRISPR-Based Precision Breeding for Quality Traits | Enables direct editing of genes affecting gluten quality, starch biosynthesis, and milling properties. | Zhang et al., 2019; Yigider et al., 2023 |
| Sustainable Breeding and Resource Efficiency | Precision agriculture and AI-driven decision-making optimize fertilizer use, irrigation, and planting strategies to enhance wheat quality while reducing environmental impact. | Lal, 2010; Gooding et al., 2003 |

**Conclusion**

The evolution of wheat (*Triticum aestivum* L.) breeding has been transformed by the incorporation of genetic profiling, quantitative trait loci (QTL) mapping, marker-assisted

selection (MAS), genomic selection (GS), and sophisticated genomic technologies. These methodologies have markedly improved the accuracy and efficacy of breeding programs focused on enhancing industrial quality attributes, including grain protein content, gluten strength, starch composition, and milling efficiency. The capacity to discern and delineate significant alleles using molecular markers and genome-wide association studies (GWAS) has empowered breeders to make more educated choices, hence expediting genetic advancement. Apart from genetic improvements, agronomic methods and genotype-by-environment (G×E) interactions are crucial for achieving the qualitative potential of wheat. The strategic use of fertilizer management, irrigation, crop rotation, and planting techniques is essential for maximizing grain output and processing characteristics. Comprehending the interaction between environmental variables and genetic potential has facilitated the development of more adaptable and robust breeding practices, assuring consistent performance throughout varied growth circumstances.

Wheat research has achieved significant advancements in generating high-yielding, superior-quality cultivars by integrating molecular breeding, genetic profiling, and agronomic optimization. Achieving uniform industrial standards necessitates ongoing innovation, multidisciplinary collaboration, and sustainable breeding methodologies.

**COMPETING INTERESTS DISCLAIMER:**

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

**References**

1. Alemu, A., El Baouchi, A., El Hanafi, S., Kehel, Z., Eddakhir, K., & Tadesse, W. 2021. Genetic examination of grain protein content and dough quality characteristics in superior spring bread wheat (*Triticum aestivum*) lines by association research. Journal of Cereal Science, Volume 100, Article 103214.
2. Altenbach, S. B., DuPont, F. M., Kothari, K. M., Chan, R., Johnson, E. L., and Lieu, D. 2003. Temperature, water, and fertilizer affect the timing of critical stages in grain formation of US spring wheat.Journal of Cereal Science, 37(1), 9-20.
3. Alvarado, G., Rodríguez, F. M., Pacheco, A., Burgueño, J., Crossa, J., Vargas, M., ... Lopez-Cruz, M. A. 2020. META-R: A software application for the analysis of data derived from multi-environment plant breeding studies.The Crop Journal, 8(5), 745-756.
4. Bhatta, M., Morgounov, A., Belamkar, V., and Baenziger, P. S. 2018. A genome-wide association research identifies new genomic areas associated with grain yield and yield-related characteristics in drought-stressed synthetic hexaploid wheat. International Journal of Molecular Sciences, 19(10), 3011.
5. Bhave, M., & Morris, C. F. 2008. Molecular genetics of puroindolines and associated genes: allelic variation in wheat and other grasses. Plant Molecular Biology, 66, 205-219.
6. Bly, A. G., and Woodard, H. J. 2003. The timing of foliar nitrogen spray affects the grain production and protein content of hard red winter and spring wheat. Agronomy Journal, 95(2), 335-338.
7. Boehm Jr, J. D., Ibba, M. I., Kiszonas, A. M., See, D. R., Skinner, D. Z., and Morris, C. F. 2018. Genetic examination of kernel texture (grain hardness) in a bi-parental population of hard red spring wheat (*Triticum aestivum* L.).Journal of Cereal Science, volume 79, pages 57-65.
8. Branlard, G., Dardevet, M., Saccomano, R., Lagoutte, F., and Gourdon, J. 2001. Genetic variability of wheat storage proteins and the quality of bread wheat.Euphytica, Volume 119, Issue 1, Pages 59-67.
9. Breseghello, F., & Sorrells, M. E. 2006. Association mapping of kernel size and milling quality in wheat (*Triticum aestivum* L.) cultivars. Genetics, 172(2), 1165-1177.
10. Cappelli, A., and Cini, E. 2021. Challenges and possibilities in the production chains of wheat flour, pasta, bread, and bakery products: A thorough evaluation of innovations and enhancement tactics to augment sustainability, productivity, and product quality.Sustainability, Volume 13, Issue 5, Page 2608.
11. Carter, A. H., Garland-Campbell, K., Morris, C. F., and Kidwell, K. K. 2012. Chromosomes 3B and 4D are linked to several milling and baking quality features in a soft white spring wheat (*Triticum aestivum* L.) population.Theoretical and Applied Genetics, volume 124, pages 1079-1096.
12. Christopher, M. J., Williamson, P. M., Michalowitz, M., Jennings, R., Lehmensiek, A., Sheppard, J., & Banks, P. (2007). Simple sequence repeat markers linked to three quantitative trait loci for black point resistance can enhance selection populations in bread wheat.Australian Journal of Agricultural Research, 58(9), 867-873.
13. Collard, B. C., and Mackill, D. J. 2008. Marker-assisted selection: a method for precise plant breeding in the twenty-first century.Philosophical Transactions of the Royal Society B: Biological Sciences, 363(1491), 557-572.
14. Collard, B. C., Jahufer, M. Z. Z., Brouwer, J. B., and Pang, E. C. K. 2005. An overview of markers, quantitative trait loci (QTL) mapping, and marker-assisted selection for the enhancement of crops: fundamental principles.Euphytica, 142, 169-196.
15. Collard, B. C., Jahufer, M. Z. Z., Brouwer, J. B., and Pang, E. C. K. 2005. An overview of markers, quantitative trait loci (QTL) mapping, and marker-assisted selection for the enhancement of crops: fundamental principles.Euphytica, volume 142, pages 169-196.
16. Courtin, C. M., and Delcour, J. A. 2002. Arabinoxylans and endoxylanases in the production of bread from wheat flour.Journal of Cereal Science, 35(3), 225-243.
17. Crossa, J., Burgueño, J., Cornelius, P. L., McLaren, G., Trethowan, R., and Krishnamachari, A. 2006. Modeling genotype-environment interaction using additive genetic covariances across relatives to forecast breeding values of wheat genotypes. Crop Science, 46(4), 1722-1733.
18. Crossa, J., Pérez-Rodríguez, P., Cuevas, J., Montesinos-López, O., Jarquín, D., de los Campos, G., ... & Pérez-Elizalde, S. 2017. Genomic selection in plant breeding: methodologies, models, and viewpoints. Trends in Plant Science, Volume 22, Issue 11, Pages 961-975.
19. DuPont, F. M., and Altenbach, S. B. 2003. The molecular and biochemical effects of environmental variables on the growth of wheat grain and protein production.Journal of Cereal Science, 38(2), 133-146.
20. Elangovan, M., Dholakia, B. B., Rai, R., Lagu, M. D., Tiwari, R., Gupta, R. K., & Gupta, V. S. 2011. Identification of quantitative trait loci linked to agronomic characteristics in bread wheat (*Triticum aestivum* L.).J. Wheat Res., 3(1), 14-23.
21. Flagella, Z., Rotunno, T., Tarantino, E., Di Caterina, R., and De Caro, A. 2002. Alterations in wheat storage proteins resulting from induced experimental water shortage stress. Journal of Cereal Science, Volume 35, Issue 1, Pages 13-22.
22. Frederick, J. R., and Camberato, J. J. 1995. Effects of water and nitrogen on winter wheat in the southern Coastal Plain: II. Physiological responses.Agronomy Journal, 87(3), 527-533.
23. Garcia, M., Eckermann, P., Haefele, S., Satija, S., Sznajder, B., Timmins, A., ... & Fleury, D. 2019. Genome-wide association analysis of grain production in a varied array of spring wheat (*Triticum aestivum* L.) assessed in southern Australia.PLoS One, 14(2), e0211730.
24. Ghimire D., Das S., Mueller N. D., Creech C. F., Santra D., Baenziger P. S., Easterly A. C., Maust B., Maharjan B. Investigated the impact of cultivars and nitrogen management on wheat grain yield and protein content. Agronomy Journal. 2021;113:4348−4368. https://doi.org/10.1002/agj2.20836
25. Giroux, M. J., and Morris, C. F. 1997. A glycine to serine substitution in puroindoline b correlates with wheat grain hardness and reduced levels of starch-surface friabilin.Theoretical and Applied Genetics, volume 95, pages 857-864.
26. Gooding, M. J., Ellis, R. H., Shewry, P. R., and Schofield, J. D. 2003. Impact of limited water supply and elevated temperatures on the grain filling, desiccation, and quality of winter wheat.Journal of Cereal Science, 37(3), 295-309.
27. Groos, C., Robert, N., Bervas, E., and Charmet, G. 2003. Genetic examination of grain protein content, grain production, and thousand-kernel weight in *Triticum aestivum*.Theoretical and Applied Genetics, volume 106, pages 1032-1040.
28. Güçbilmez, Ç. M., Şahin, M., Akçacık, A. G., Aydoğan, S., Demir, B., Hamzaoğlu, S., ... & Yakışır, E. 2019. Assessment of the GlutoPeak test for forecasting the quality of bread wheat flour, its rheological characteristics, and baking efficacy.Journal of Cereal Science, 90, 102827.
29. Gupta, P. K., Kumar, J., Mir, R. R., and Kumar, A. 2010. Marker-assisted selection as an element of traditional plant breeding.Plant Breeding Reviews, 33(4), 145-217.
30. Gupta, P. K., Rustgi, S., and Kulwal, P. L. 2005. Linkage disequilibrium and association research in higher plants: current state and future potential.Plant Molecular Biology, 57, 461-485.
31. Gupta, P. K., Rustgi, S., and Mir, R. R. 2008. High-throughput DNA markers based on arrays for the enhancement of crops.Heredity, 101(1), 5-18.
32. Gupta, R. B., Khan, K., and Macritchie, F. 1993. Biochemical foundation of flour characteristics in bread wheat. I. Impact of fluctuations in the amount and size distribution of polymeric proteins.Journal of Cereal Science, 18(1), 23-41.
33. Guttieri, M., Bowen, D., Dorsch, J. A., Raboy, V., and Souza, E. 2004. Identification and characterisation of a wheat variety with reduced phytic acid content.Crop Science, 44(2), 418-424.
34. Howarth, J. R., Parmar, S., Jones, J., Shepherd, C. E., Corol, D. I., Galster, A. M., ... Hawkesford, M. J. 2008. Coordinated expression of amino acid metabolism in response to nitrogen and sulfur deprivation during wheat grain filling.Journal of Experimental Botany, 59(13), 3675-3689.
35. Hurkman, W. J., Vensel, W. H., Tanaka, C. K., Whitehand, L., and Altenbach, S. B. 2009. Impact of elevated temperature on albumin and globulin accumulation in the endosperm proteome of growing wheat grains.Journal of Cereal Science, 49(1), 12-23.
36. Hylnka, I. 1964. Chemistry and Technology of Wheat.
37. Igrejas, G., Leroy, P., Charmet, G., Gaborit, T., Marion, D., & Branlard, G. 2002. Mapping quantitative trait loci for grain hardness and puroindoline content in wheat (*Triticum aestivum* L.).Theoretical and Applied Genetics, volume 106, pages 19-27.
38. Jolly, C. J., Glenn, G. M., and Rahman, S. 1996. The GSP-1 genes are associated with the grain hardness locus (Ha) located on wheat chromosome 5D.Proceedings of the National Academy of Sciences, 93(6), 2408-2413.
39. Kierkegaard, J., Christen, O., Krupinsky, J., & Layzell, D. 2008. Advantages of break crops in temperate wheat cultivation.Field Crops Research, 107(3), 185-195.
40. Kumar, V., Singh, A., Mithra, S. A., Krishnamurthy, S. L., Parida, S. K., Jain, S., ... & Mohapatra, T. 2015. Genome-wide association analysis of salt tolerance in rice (Oryza sativa).DNA Research, 22(2), 133-145.
41. Lal, R. 2010. Administering soils and ecosystems to reduce anthropogenic carbon emissions and enhance global food security.Bioscience, 60(9), 708-721.
42. Landjeva, S., Korzun, V., and Börner, A. 2007. Molecular markers: current and prospective contributions to the characterisation and breeding of the wheat genome.Euphytica, volume 156, pages 271-296.
43. Lillemo, M., Chen, F., Xia, X., William, M., Peña, R. J., Trethowan, R., & He, Z. 2006. Puroindoline alleles associated with grain hardness in CIMMYT bread wheat germplasm.Journal of Cereal Science, 44(1), 86-92.
44. Malik, P., Kumar, J., Singh, S., Sharma, S., Meher, P. K., Sharma, M. K., ... & Sharma, S. 2021. Single-trait, multi-locus, and multi-trait genome-wide association studies employing four distinct models for yield characteristics in bread wheat.Molecular Breeding, volume 41, pages 1-21.
45. Mann, G., Diffey, S., Cullis, B., Azanza, F., Martin, D., Kelly, A., ... Morell, M. K. 2009. Genetic regulation of wheat quality: interactions across chromosomal areas influencing protein quantity and composition, dough rheology, and baking qualities of sponge and dough.Theoretical and Applied Genetics, volume 118, pages 1519-1537.
46. McCartney, C. A., Somers, D. J., Lukow, O., Ames, N., Noll, J., Cloutier, S., ... & McCallum, B. D. 2006. Quantitative Trait Locus study of quality characteristics in the spring wheat cross RL4452×‘AC Domain’.Plant Breeding, Volume 125, Issue 6, Pages 565-575.
47. McMullen, M., Bergstrom, G., De Wolf, E., Dill-Macky, R., Hershman, D., Shaner, G., and Van Sanford, D. 2012. A coordinated initiative to combat an adversary of wheat and barley: Fusarium head blight.Plant Disease, 96(12), 1712-1728.
48. Meuwissen, T. H., Hayes, B. J., and Goddard, M. 2001. Forecasting total genetic value with genome-wide dense marker maps.Genetics, 157(4), 1819-1829.
49. Morris, C. F. 2002. Puroindolines: the molecular genetic foundation of wheat grain toughness.Plant Molecular Biology, 48, 633-647.
50. Morris, C. F. 2002. Puroindolines: the molecular genetic foundation of wheat grain toughness.Plant Molecular Biology, 48, 633-647.
51. Nakamura, T., Yamamori, M., Hirano, H., Hidaka, S., and Nagamine, T. 1995. Cultivation of waxy (amylose-deficient) wheat varieties.Molecular and General Genetics, MGG, 248, 253-259.
52. Neumann, K., Kobiljski, B., Denčić, S., Varshney, R. K., and Börner, A. 2011. Genome-wide association mapping: a case study in *Triticum aestivum* L. (bread wheat).Molecular breeding, 27, 37-58.
53. Payne, P. I., Nightingale, M. A., Krattiger, A. F., and Holt, L. M. 1987. The correlation between HMW glutenin subunit composition and the bread-making qualities of British wheat cultivars.Journal of the Science of Food and Agriculture, 40(1), 51-65.
54. Quraishi, U. M., Abrouk, M., Murat, F., Pont, C., Foucrier, S., Desmaizieres, G., ... & Salse, J. 2011. The dissection of a nitrogen usage efficiency ortho-metaQTL in bread wheat by a cross-genome map reveals coordinated cereal genome evolution.The Plant Journal, 65(5), 745-756.
55. Rahimi, Y., Bihamta, M. R., Taleei, A., Alipour, H., and Ingvarsson, P. K. 2019. A genome-wide association analysis of agronomic variables in bread wheat identifies novel potential alleles for prospective breeding initiatives.BMC Plant Biology, 19, 1-19.
56. Ray, D. K., Mueller, N. D., West, P. C., and Foley, J. A. 2013. Yield trends are inadequate to achieve a twofold increase in world agricultural output by 2050.PloS One, 8(6), e66428.
57. Said, A. A., MacQueen, A. H., Shawky, H., Reynolds, M., Juenger, T. E., and El-Soda, M. 2022. Genome-wide association mapping of genotype-environment interactions influencing yield-related parameters of spring wheat cultivated under three irrigation regimes.Environmental and Experimental Botany, Volume 194, Article 104740.
58. Saieed, M. A. U. 2022.Identification and characterisation of new genes that enhance wheat grain yield (Doctoral dissertation, Murdoch University).
59. Salvagiotti, F., Castellarín, J. M., Miralles, D. J., and Pedrol, H. M. 2009. Sulfur fertilizer enhances nitrogen utilization efficiency in wheat by augmenting nitrogen absorption.Field Crops Research, 113(2), 170-177.
60. Shevkani, K., Singh, N., Bajaj, R., and Kaur, A. 2017. A review of wheat starch manufacturing, structure, functioning, and uses.International Journal of Food Science and Technology, 52(1), 38-58.
61. Shewry, P. R. 2009. Wheat.Journal of Experimental Botany, 60(6), 1537-1553.
62. Shewry, P. R., Halford, N. G., Belton, P. S., and Tatham, A. S. 2002. The composition and characteristics of gluten: a resilient protein derived from wheat grain.Philosophical Transactions of the Royal Society of London. Series B: Biological Sciences, 357(1418), 133-142.
63. Shewry, P. R., Halford, N. G., Tatham, A. S., Popineau, Y., Lafiandra, D., and Belton, P. S. 2003. The high molecular weight components of wheat glutenin and their influence on wheat processing characteristics.Advances in Food and Nutrition Research, 45, 219–302. https://doi.org/10.1016/s1043-4526(03)45006-7
64. Shiferaw, B., Smale, M., Braun, H. J., Duveiller, E., Reynolds, M., and Muricho, G. 2013. Crops that sustain the global population 10. Historical achievements and forthcoming obstacles regarding the significance of wheat in global food security.Food Security, 5, 291-317.
65. Stone, P. J., and Nicolas, M. E. 1994. Wheat cultivars exhibit significant variability in their grain production and quality responses to brief episodes of post-anthesis heat stress.Functional Plant Biology, Volume 21, Issue 6, Pages 887-900.
66. Tadesse, W., Ogbonnaya, F. C., Jighly, A., Sanchez-Garcia, M., Sohail, Q., Rajaram, S., and Baum, M. 2015. Genome-wide association analysis of yield and grain quality characteristics in winter wheat genotypes.PloS One, 10(10), e0141339.
67. Tetlow, I. J., Morell, M. K., and Emes, M. J. 2004. Recent advancements in the comprehension of starch metabolism control in higher plants.Journal of Experimental Botany, 55(406), 2131-2145.
68. Tsai, H. Y., Janss, L. L., Andersen, J. R., Orabi, J., Jensen, J. D., Jahoor, A., & Jensen, J. 2020. Genomic prediction and genome-wide association studies of yield, quality, and disease-related characteristics in spring barley and winter wheat.Scientific Reports, 10(1), 3347.
69. Uauy, C., Distelfeld, A., Fahima, T., Blechl, A., and Dubcovsky, J. 2006. A NAC gene that regulates senescence enhances the protein, zinc, and iron content in wheat grains.Science, 314(5803), 1298-1301.
70. Vishwakarma, M. K., Bhati, P. K., Kumar, U., Singh, R. P., Kumar, S., Govindan, V., ... Joshi, A. K. 2024. Genetic analysis of enhanced quality attributes and agronomic characteristics using genome-wide association mapping in bread wheat (T. aestivum L.).Frontiers in Plant Science, 15, Article 1419227.
71. Wall, M. L. 2011.The surface of starch granules: Technological and biological ramifications of puroindoline and host-pathogen interactions. University of Ottawa, Canada.
72. Wrigley, C. W., and Morris, C. F. 1996. Enhancing the quality of grains through breeding. In Cereal Grain Quality (pp. 321-369). Dordrecht: Springer Netherlands.
73. Xu, Y., and Crouch, J. H. 2008. Marker-assisted selection in plant breeding: Transitioning from research to application.Crop Science, 48(2), 391-407.
74. Yang, J., and Zhang, J. 2006. Grain development of cereals during soil desiccation.New Phytologist, 169(2), 223-236.
75. Yang, Y., Chai, Y., Zhang, X., Lu, S., Zhao, Z., Wei, D., ... & Hu, Y. G. 2020. Multi-locus GWAS of quality attributes in bread wheat: identifying additional candidate genes and potential regulatory networks.Frontiers in Plant Science, 11, 1091.
76. Yazar, G., & Rosell, C. M. 2023. Fat substitutes in baked goods: Their influence on rheological characteristics and overall product quality.Critical Reviews in Food Science and Nutrition, 63(25), 7653-7676.
77. Yigider, E., Taspinar, M. S., and Agar, G. 2023. Enhancements in bread wheat production by CRISPR/Cas9 technology: A thorough examination of quality and other factors.Planta, 258(3), 55.
78. Yu, J., and Buckler, E. S. 2006. Genetic association mapping and genomic structure of maize.Current Opinion in Biotechnology, 17(2), 155-160.
79. Zeng, M., Morris, C. F., Batey, I. L., and Wrigley, C. W. 1997. Factors contributing to the variability in starch gelatinization, pasting, and gelation characteristics in wheat.Cereal Chemistry, 74(1), 63-71.
80. Zhang, X., Qin, W., Chen, S., Shao, L., and Sun, H. 2017. Yield and water use efficiency responses of winter wheat to water stress during the past three decades: A case study on the North China Plain.Agricultural Water Management, 179, pages 47-54.
81. Zhao, F. J., Hawkesford, M. J., & McGrath, S. P. (1999). Assimilation of sulfur and its impact on the productivity and quality of wheat.Journal of Cereal Science, 30(1), 1-17.
82. Zhao, F. J., McGrath, S. P., Salmon, S. E., Shewry, P. R., Quayle, R., Withers, P. J. A., ... Monaghan, J. 1997. Optimizing sulfur inputs for the breadmaking quality of wheat.Aspects of Applied Biology, volume 50, pages 199-205.