***Review Article***

**Genetic profiling of quality** **traits 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: Quantitative Trait Loci, Genome-Wide Association Studies, Marker-Assisted Selection, Clustered Regularly Interspaced Short Palindromic Repeats, genomic selection.*

**1. INTRODUCTION**

Global cereal production has witnessed steady growth, reaching an estimated 9.9 billion tonnes in 2023—a 2% increase over the previous year. Dominating this output are three staple crops: wheat (*Triticum aestivum* L.), maize, and rice, which together account for nearly 91% of total cereal production. Among these, bread wheat holds a pivotal role in ensuring food security and meeting industrial demands worldwide (FAO, 2023). Bread wheat possesses distinctive physiochemical 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 growing global demand for wheat with specific quality attributes requires a deeper understanding 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. 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 genetics and environmental variables, necessitating a comprehensive strategy for their improvement.

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)**

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. Sharma *et al.,* (20) 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 (Fan *et al.,* 2024) 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.** *Overview of Wheat Breeding Toolkits and Associated QTL Markers*

This diagram provides an integrated view of the tools and genetic markers used in modern wheat breeding. The left section illustrates the Cluster Toolkit, symbolized by a blue square, which represents groups of related genetic markers identified through clustering methods. Adjacent to this, the Breeder’s Toolkit is depicted using three distinct shapes- a blue square, blue rectangle, and blue oval- each signifying different components critical for marker-assisted selection and genomic analysis.

At the center, the diagram maps the wheat genome landscape by displaying the three subgenomes (A, B, and D) as overlapping layers in varying shades of green and white, emphasizing the polyploid structure of bread wheat. To the right, a legend explains the symbols: the blue square, rectangle, and oval denote elements of the breeder’s toolkit; the red triangle represents quantitative trait loci (QTL) associated with milling quality; the green diamond is linked to starch quality QTLs; and the yellow star marks the ideal breeding outcomes or elite lines. Additional markers, such as those for gluten strength (green diamond), grain protein content (depicted as a green cloud), and pre-harvest sprouting resistance (represented by either a blue square or yellow star), further underline the connection between genetic determinants and industrially relevant traits.

Overall, the diagram encapsulates the multifaceted approach of combining genetic tools with detailed QTL mapping to enhance selection precision in wheat breeding programs.

**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 (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

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 *et al.,* 2002). 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). 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; Khurshid & Ahmad,2021;

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 make GWAS a powerful tool 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 (Hasan *et al.,* 2021; Toth *et al.,* 2018). MAS facilitates the identification of markers linked to starch synthesis enzymes, hence enhancing texture and processing characteristics (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 (Khurshid & Ahmad, 2021; Morris, 2002). These applications highlight the contribution of MAS 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 disulphide bonds in glutenin subunits. Deficiency compromises dough characteristics, rendering soil and tissue analysis essential for sulfur management (Zhao *et al.,* 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 during the blooming and grain-filling stages ensures 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 (Bana *et al.,* 2022).

**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 (Li *et al.,* 2022), while puroindolines modulate grain hardness, thereby affecting milling efficiency and flour texture (Wall *et al.,* 2011). In addition to macromolecules, non-starch polysaccharides (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 (Veloo *et al.,* 2023), while drought restricts starch deposition and shifts protein profiles, thereby affecting dough performance (Johansson *et al.,* 2020). 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 both genotypes and the environment, thereby 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.

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.,* 2003). 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. 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 1.** 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 compromise wheat quality by reducing protein content and starch accumulation through impaired enzyme activity and photosynthate distribution. Integrating genotype-by-environment models with molecular breeding enables the precise selection of stress-resilient alleles, fostering climate-adapted wheat cultivars. | Veloo *et al.,*  2023; Johansson *et al.,*  2020 |
| Multi-Omics Approaches for Quality Trait Dissection | Functional genomics, transcriptomics, and metabolomics reveal key regulatory genes influencing wheat’s industrial properties. | 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 dramatically reshaped by the integration of advanced genetic profiling, extensive quantitative trait loci mapping, marker-assisted selection, genomic selection, and a spectrum of cutting-edge 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 are 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. Ongoing innovation, multidisciplinary collaboration, and sustainable breeding methodologies are essential for achieving uniform industrial standards for food security.

Table 2: Significant advancements in generating high-yielding, superior-quality cultivars

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| --- | --- | --- | --- |
| **Category** | **Technology/Methodology** | **Achievements** | **References** |
| **Molecular Breeding** | Marker‐assisted selection, genomic selection, quantitative trait loci mapping, CRISPR, and other gene‐editing tools | Enables the precise introgression of desirable traits, leading to cultivars with enhanced yield, stress resilience, and superior grain quality | Rasheed *et al.,* 2019; Kaur *et al.,* 2023 |
| **Genetic Profiling** | High-throughput genotyping, whole-genome sequencing, association studies, principal component and path analysis | Facilitates the identification and characterization of key genetic loci and allelic variants linked to yield, quality, and adaptation traits, enabling targeted breeding | Prakash *et al.,* 2023; Kaur *et al.,* 2023 |
| **Agronomic Optimization** | Optimized nutrient management, tailored irrigation strategies, precise crop management, sustainable agronomy practices | Improves water use efficiency, grain yield, and quality under variable climatic conditions and ensures that agronomic inputs complement genetic gains from breeding programs | Mutanda *et al.,*2025; Farouk *et al.,* 2024 |

**COMPETING INTERESTS DISCLAIMER:**

The authors declare 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.

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