Molecular Plant Breeding 2025, Vol.16, No.1, 93-104
http://genbreedpublisher.com/index.php/mpb

Case Study Open Access

Case Study: Breeding Maize Varieties with High Protein Content

Qiaohong Ying, Qiong Chen, Kaozu Lei, Huazhou Liu
Zhejiang Kecheng Seed Industry Co., Ltd., Wenzhou, 325019, Zhejiang, China
Corresponding email: keseed@qq.com

Molecular Plant Breeding, 2025 Vol.16, No.1 doi: 10.5376/mpb.2025.16.0010
Received: 19 Jan., 2025
Accepted: 21 Feb., 2025
Published: 28 Feb., 2025

Preferred citation for this article:
Ying Q.B., Chen Q., Lei K.Z., and Liu H.Z., 2025, Case study: breeding maize varieties with high protein content, Molecular Plant Breeding, 16(1): 93-104 (doi: 10.5376/mpb.2025.16.0010)

Abstract This study gives an account of the breeding efforts of high-protein maize varieties, particularly Quality Protein Maize (QPM), and their potential to address malnutrition and improve the nutritional value of maize. Compared to conventional maize, QPM varieties contain higher levels of essential amino acids such as lysine and tryptophan, which are crucial for human and animal nutrition. Research has shown that the adoption of QPM significantly improves children's growth, indicating its potential to combat malnutrition in developing regions. However, QPM breeding still faces challenges, such as reduced yield and insufficient agronomic traits. Future research directions include integrating molecular breeding with conventional methods, exploring genetic loci associated with protein synthesis and stress tolerance, and developing QPM varieties that are both nutritionally superior and agronomically viable.

Keywords High-protein maize; Quality protein maize (QPM); Malnutrition; Molecular breeding; Essential amino acids

1 Introduction

As one of the three most widely grown cereal grains globally, maize plays a foundational role in the diets of millions. Accounting for approximately 15% of global protein intake and 20% of calories in many developing countries, maize has a unique position among staple crops for its calorie density and relative ease of production (Zarkadas et al., 1995). Its flexibility in various climates, from temperate to tropical zones, allows it to thrive where other crops may not, increasing its importance in food and feed systems globally (Denic et al., 2012). However, conventional maize varieties have limited amino acid profiles, which are deficient in lysine and tryptophan, reducing their overall biological value when consumed as a primary protein source.

Enhancing the protein content and quality of maize would address a significant nutritional gap. Conventional maize varieties are often low in essential amino acids such as lysine and tryptophan, leading to protein deficiency risks in populations heavily reliant on maize as a staple (Bhatnagar et al., 2004). Quality Protein Maize (QPM), developed to address these gaps, demonstrates superior nutritional value by offering a more complete amino acid profile, critical for both human health and animal feed efficiency. This biofortification effort not only raises the nutritional profile of the maize grain but also contributes to reducing health issues related to protein deficiency in vulnerable populations, particularly in developing countries (Tandzi et al., 2017).

Breeding high-protein maize varieties presents a range of challenges and opportunities. Key challenges include maintaining crop yield while improving protein content, ensuring genetic diversity, and achieving resilience to environmental stressors. Recent advances in molecular breeding techniques have allowed researchers to identify and target genes associated with enhanced protein levels and amino acid profiles. For example, genetic modification efforts have introduced markers like the *opaque-2* gene to help enhance lysine and tryptophan levels (Vasal, 2014). Traditional and molecular breeding methods alike continue to develop hybrids capable of maintaining nutritional value under variable conditions, such as low soil nitrogen or drought (Bello et al., 2014). These ongoing efforts to produce QPM varieties highlight the balancing act between enhancing protein quality and managing the practical limitations of crop performance.

This study aims to synthesize current research efforts in high-protein maize breeding, highlighting advancements in genetic selection, breeding methodologies, and the challenges faced in real-world application. It also seeks to examine the broader implications of QPM development for food security and public health, with a focus on sustainable adoption across different agronomic settings. In particular, the review will consider the effectiveness of different breeding strategies in maximizing nutritional yield without compromising the agronomic viability of the maize crop, thus supporting global efforts to meet rising nutritional demands.

2 Study Objectives and Relevance

2.1 Defining specific goals for protein enhancement in maize

The primary objective of breeding maize varieties with high protein content is to address the nutritional deficiencies prevalent in many developing regions. Quality Protein Maize (QPM) has been developed to contain higher levels of essential amino acids, particularly lysine and tryptophan, which are typically deficient in conventional maize varieties. For instance, QPM lines have been shown to possess nearly double the amount of lysine and tryptophan compared to non-QPM lines, significantly improving the protein quality of maize (Hossain et al., 2019; Amegbor et al., 2022). Additionally, the use of molecular marker-assisted selection (MAS) has accelerated the development of QPM cultivars, ensuring that these enhanced nutritional traits are effectively incorporated into new maize varieties (Vikal and Chawla, 2014).

Another specific goal is to ensure that the enhancement of protein content does not come at the expense of other agronomic traits such as yield. Studies have demonstrated that it is possible to select QPM lines with high protein and tryptophan levels without a yield penalty, making them viable for large-scale agricultural production (Amegbor et al., 2022). This balance is crucial for the adoption of QPM by farmers, as it ensures that the nutritional benefits do not compromise economic returns.

2.2 Addressing the role of protein-rich maize in combating malnutrition

Protein-energy malnutrition (PEM) is a significant health issue, particularly affecting pregnant women, the elderly, and children under the age of five. QPM has been identified as a sustainable solution to combat PEM due to its enhanced protein quality. The consumption of QPM has been linked to improved growth rates in children, with studies showing a 12% increase in weight and a 9% increase in height among infants and young children consuming QPM instead of conventional maize (Gunaratna et al., 2010). This demonstrates the potential of QPM to make a substantial impact on public health in regions where maize is a staple food.

Furthermore, the integration of QPM into the diets of populations in developing countries can lead to broader socio-economic benefits. By improving the nutritional status of these communities, QPM can contribute to better health outcomes, increased productivity, and reduced healthcare costs. The United Nations Sustainable Development Goals highlight the importance of nutrition in achieving progress in health, education, and poverty reduction, and QPM is a key component in these efforts (Hossain et al., 2019).

2.3 Examining global agricultural needs for nutrient-dense staple crops

The global agricultural landscape is increasingly focused on the need for nutrient-dense staple crops to address widespread malnutrition. Maize, being one of the top three cereal crops globally, plays a critical role in food security and nutrition. Enhancing the nutritional profile of maize through biofortification is a strategic approach to meet the dietary needs of populations with limited access to diverse foods (Figure 1) (Prasanna et al., 2020; Palacios-Rojas et al., 2020). Biofortified maize varieties, such as those enriched with quality protein, provitamin A, and zinc, are particularly impactful in rural areas where dietary supplements and fortified foods are less accessible (Prasanna et al., 2020).

Moreover, the development of nutrient-dense maize varieties aligns with the broader goals of sustainable agriculture. By improving the nutritional quality of staple crops, agricultural systems can contribute to better health outcomes without the need for significant changes in dietary habits or food systems. This approach is not only cost-effective but also sustainable, as it leverages existing agricultural practices and infrastructure (Welch, 2002). The success of QPM and other biofortified crops demonstrates the potential of plant breeding to address global nutritional challenges effectively.

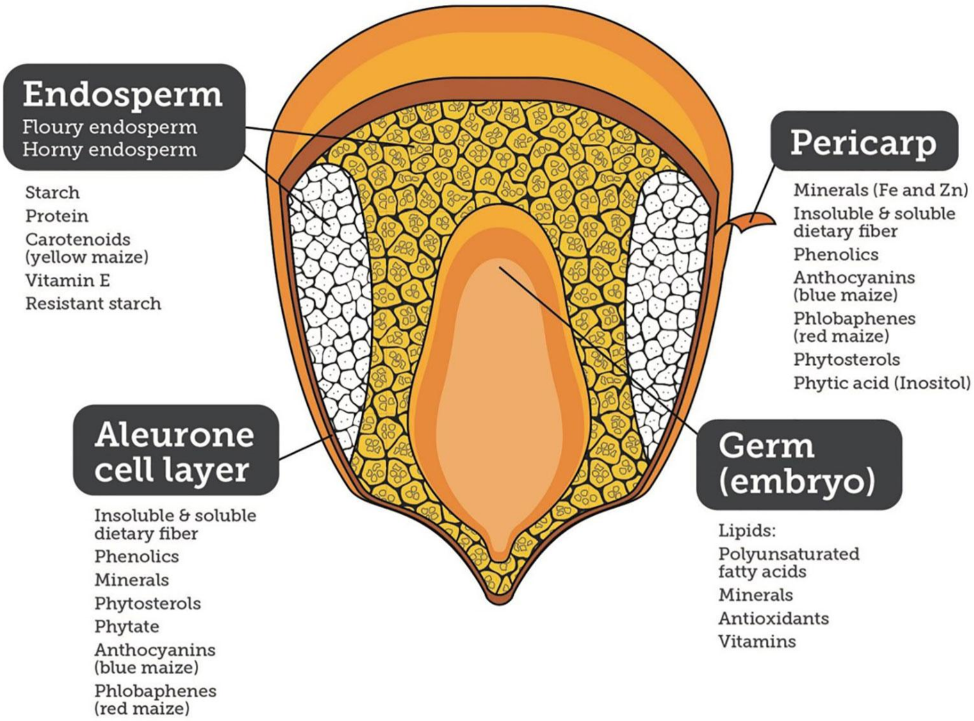

Figure 1 Nutritional quality of different components of a maize kernel (Adopted from Prasanna et al., 2020)

3 Comprehensive Methodological Framework

3.1 Strategic selection of diverse genetic maize varieties

The strategic selection of diverse genetic maize varieties is fundamental to breeding programs aimed at enhancing protein content. This process involves identifying and utilizing a wide range of genetic resources to ensure a broad genetic base. For instance, the study by Jaradat and Goldstein (2013) utilized multivariate statistical procedures to quantify total diversity and its components across 31 traits in 1348 maize accessions. This approach allowed for the identification of physical and color traits useful for selecting accessions with high protein and nutrient contents. Similarly, the research conducted by Okporie et al. (2013) sourced genetic materials from a gene bank and developed high-protein maize populations through three cycles of reciprocal recurrent selection.

Moreover, understanding the genetic diversity and population structure is crucial for predicting hybrid performance. Abu et al. (2021)'s study on tropical extra-early maturing quality protein maize (QPM) inbred lines under low soil nitrogen stress, assessed 110 inbred lines using SNP markers, revealing significant genetic distances and clustering based on endosperm color, pedigree, and selection history. This genetic variability is essential for breeding programs aiming to enhance protein content while maintaining other agronomic traits.

3.2 Detailed description of crossbreeding and selection methodologies

Crossbreeding and selection methodologies are pivotal in developing high-protein maize varieties. Mass selection, as described in the study by the Crop Science Society of America (Bletsos and Goulas, 1999), involves a two-step selection procedure. Plants with grain yield higher than 80% of the check-plant mean and protein concentration greater than the check-plant mean were selected. The four plants within each selection grid with the highest protein concentration were chosen, resulting in a final selection intensity of 5%. This method, although not particularly effective after three cycles, highlights the iterative nature of selection in breeding programs.

Reciprocal recurrent selection is another effective methodology. Okporie et al. (2013)'s study at Ebonyi State University demonstrated the development of high-protein maize populations through three cycles of this method. This approach involves selecting and intercrossing the best individuals from two populations to combine desirable traits. Additionally, the use of genomic selection (GS) can accelerate the breeding cycle by facilitating the rapid selection of superior genotypes. GS integrates genomic-enabled prediction models to enhance the efficiency of breeding programs, as discussed in a review on genomic selection in plant breeding (Crossa et al., 2017).

3.3 Design of experimental setups, including control groups and statistical analysis

Designing robust experimental setups is crucial for validating the effectiveness of breeding methodologies. Control groups and statistical analyses are integral components of these setups. For instance, Bletsos and Goulas, 1999’s study on mass selection for improving grain yield and protein in maize included check plants for environmental control, ensuring that the selection process accounted for environmental variability. The effectiveness of the selection was evaluated through direct field evaluations of different selection cycles, with statistical analyses confirming the trends observed during the selection process.

In another example, the study on the genetic diversity and inter-trait relationship of QPM inbred lines utilized genotype by trait biplot analysis to reveal associations between grain yield and other traits (Abu et al., 2021). This statistical approach helped identify inbred lines with high expressivity for desirable traits, facilitating indirect selection for high grain yield. Additionally, the participatory breeding program in Portugal employed multilocation field trials to compare initial populations with derived selection cycles (Alves et al., 2017; Zhou and Jiang, 2024), using microsatellites for molecular diversity analysis. This comprehensive experimental design ensured that the agronomic performance and genetic diversity were accurately assessed.

4 Genetic Approaches

4.1 Use of traditional breeding methods

Traditional breeding methods have been instrumental in developing maize varieties with enhanced protein content. These methods involve selecting and cross-breeding maize lines that exhibit desirable traits such as high protein levels, resistance to diseases, and adaptability to various environmental conditions. For instance, the development of Quality Protein Maize (QPM) has been a significant achievement in this regard.

QPM varieties have been bred to contain higher levels of essential amino acids like lysine and tryptophan, which are typically deficient in conventional maize varieties (Denic et al., 2008; Amegbor et al., 2022a). These breeding efforts have led to the creation of numerous QPM lines that not only improve nutritional value but also maintain competitive agronomic traits such as yield and disease resistance (Denic et al., 2008; Tandzi et al., 2017).

However, traditional breeding methods are not without challenges. The process is often time-consuming and labor-intensive, requiring multiple generations of selection to achieve the desired traits. Additionally, there is a need to balance between improving protein content and maintaining other important agronomic traits. For example, some QPM lines have been found to have lower protein content compared to non-QPM lines, although they exhibit higher levels of essential amino acids (Amegbor et al., 2022a). Despite these challenges, traditional breeding remains a cornerstone in the development of high-protein maize varieties, providing a foundation upon which modern techniques can build.

4.2 Application of molecular markers to identify high-protein traits

The application of molecular markers has revolutionized the breeding of high-protein maize varieties by enabling more precise and efficient selection of desirable traits. Molecular markers are DNA sequences that are associated with specific traits, such as high protein content, and can be used to track these traits in breeding populations. This approach, known as marker-assisted selection (MAS), allows breeders to identify and select plants that carry the desired traits at an early stage, thereby speeding up the breeding process (Tandzi et al., 2017; Sethi et al., 2023).

For example, studies have identified several quantitative trait loci (QTLs) associated with protein content and other nutritional traits in maize. These QTLs can be used as molecular markers to guide the selection of high-protein lines (Abu et al., 2021). Additionally, the use of single nucleotide polymorphism (SNP) markers has been shown to be effective in dissecting the genetic diversity and population structure of maize inbred lines, which is crucial for predicting hybrid performance and selecting parents for breeding programs (Abu et al., 2021). The integration of molecular markers into traditional breeding programs has the potential to significantly enhance the efficiency and accuracy of developing high-protein maize varieties.

4.3 Genetic modification and its role in enhancing protein content

Genetic modification (GM) offers a powerful tool for enhancing the protein content of maize by directly introducing or modifying genes associated with protein synthesis. Unlike traditional breeding, which relies on the natural variation and recombination of genes, genetic modification allows for the precise insertion of specific genes that can enhance protein content and quality. For instance, genetic engineering techniques have been used to increase the levels of essential amino acids such as lysine and tryptophan in maize kernels, thereby improving their nutritional value (Figure 2) (Amegbor et al., 2022; Sethi et al., 2023).

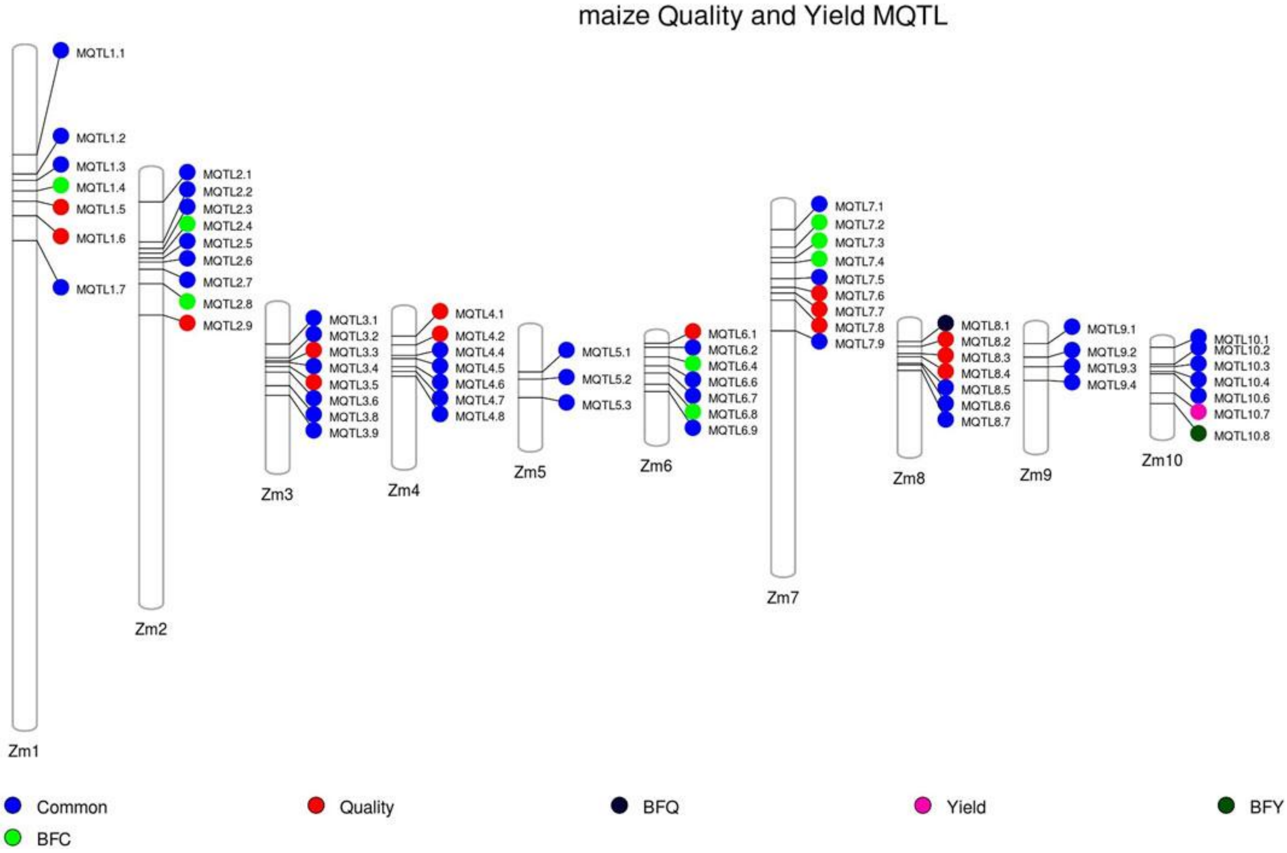

Figure 2 Distribution of MQTLs on different maize chromosomes (Adopted from Sethi et al., 2023)

Image caption: Common: MQTLs associated with both quality and yield-associated traits, BFQ: breeder-friendly quality trait MQTLs, BFY: breeder-friendly yield trait MQTLs, BFC: breeder-friendly common MQTLs (involving both quality and yield-related traits) (Adopted from Sethi et al., 2023)

One of the key advantages of genetic modification is its ability to overcome the limitations of traditional breeding. For example, while traditional breeding methods may struggle to simultaneously improve multiple traits due to genetic linkage and trade-offs, genetic modification can target specific genes without affecting other traits. This has been demonstrated in studies where genes associated with protein quality and yield-related traits were identified and manipulated to develop biofortified, high-yielding maize varieties (Sethi et al., 2023). However, the adoption of GM maize varieties is often hindered by regulatory, ethical, and public acceptance issues, which need to be addressed to fully realize the potential of this technology in enhancing maize protein content.

5 Environmental Considerations

5.1 Impact of climate on maize protein expression

Climate significantly influences the expression of protein in maize. Rising atmospheric CO2 levels have been shown to alter the protein composition of maize, with increases in certain protein fractions like glutelin and zein, while others like globulin and α-zein decrease. These changes can affect the nutritional value of maize, highlighting the need for breeding programs to consider future climate scenarios to maintain or improve protein quality (Wroblewitz et al., 2014). Additionally, climate-induced stresses such as drought and heat can impact maize yields and protein content. For instance, early quality protein maize (QPM) hybrids have been developed to tolerate combined drought and heat stress, which are anticipated to increase in frequency due to climate change (Bhadmus et al., 2021).

Moreover, the variability in gene expression under different environmental conditions can lead to heterogeneity in grain composition. Studies have shown that transcription factor gene expression in maize is highly variable across different genomic and environmental conditions, which can influence the levels of grain components like protein, oil, and amino acids (Harrigan et al., 2009). This variability underscores the importance of understanding and managing environmental impacts to stabilize protein expression in maize.

5.2 Adaptation of high-protein varieties to different regions

The adaptation of high-protein maize varieties to different regions is crucial for ensuring food security under changing climatic conditions. Breeding programs have successfully developed stress-tolerant maize cultivars for various regions, including sub-Saharan Africa, Asia, and Latin America, by integrating advanced breeding techniques and extensive on-farm testing (Prasanna et al., 2021). These efforts have led to the deployment of elite climate-resilient maize cultivars that can thrive in stress-prone environments.

Furthermore, the potential for crop production adaptation depends on the availability of future varieties that can cope with climate change. Studies suggest that a significant portion of global cropland may require new crop varieties to avoid yield loss due to climate change. Region-specific breeding efforts are essential to develop varieties that can adapt to local climatic conditions and maintain high protein content (Zabel et al., 2021). For example, modern maize hybrids in Northeast China have shown increased yield potential and resource use efficiency despite adverse climate changes, indicating successful adaptation to new conditions (Chen et al., 2013).

5.3 Soil and irrigation requirements

Soil and irrigation management play a vital role in the cultivation of high-protein maize varieties. Low soil nitrogen (N) stress can negatively impact grain yield and protein content. Breeding for nitrogen use efficiency (NUE) is essential to address food insecurity and improve grain quality. Studies have shown that low N conditions reduce grain yield, kernel weight, and protein content, while increasing starch content. Therefore, it is feasible to improve both grain yield and quality traits under low-N conditions through targeted breeding programs (Ertiro et al., 2022).

Irrigation practices also influence maize protein content. In regions with limited water availability, developing drought-tolerant maize varieties is critical. For instance, early QPM hybrids with tolerance to combined drought and heat stress have been identified as high-yielding and stable under such conditions (Bhadmus et al., 2021). Additionally, the integration of agronomic improvements, such as optimized irrigation schedules, can enhance maize yield and protein content. Research indicates that agronomic practices, along with climate and genetic factors, contribute significantly to yield gains in maize (Rizzo et al., 2022).

6 Challenges in Breeding

6.1 Balancing yield and protein enhancement

One of the primary challenges in breeding maize varieties with high protein content is achieving a balance between yield and protein enhancement. High-protein maize varieties often exhibit a trade-off with yield, as the genetic modifications that increase protein content can negatively impact other agronomic traits. For instance, studies have shown that while Quality Protein Maize (QPM) varieties have superior nutritional profiles, they often yield less compared to non-QPM varieties (Bhatnagar et al., 2004; Tandzi et al., 2017). This negative correlation between yield and protein content complicates breeding efforts, as breeders must carefully select for both traits without compromising one for the other.

Moreover, the relationship between grain yield and protein content is influenced by environmental factors such as soil nitrogen levels. Research indicates that low soil nitrogen stress can exacerbate the trade-off between yield and protein content, making it even more challenging to develop varieties that perform well under suboptimal conditions (Ertiro et al., 2022). Therefore, breeding programs must consider both genetic and environmental factors to achieve a balance between yield and protein enhancement.

6.2 Genetic diversity and maintaining resistance to diseases

Maintaining genetic diversity while enhancing protein content is another significant challenge in maize breeding. Genetic diversity is crucial for the resilience of maize varieties against diseases and environmental stresses. However, the focus on specific traits like high protein content can lead to a reduction in genetic diversity, making the crops more susceptible to diseases (Abu et al., 2021; Amegbor et al., 2022). For example, breeding programs that concentrate on high-lysine inbreds may inadvertently reduce the genetic pool, limiting the ability to introduce new traits such as disease resistance.

Additionally, the genetic loci associated with high protein content must be carefully managed to ensure that they do not compromise other important traits. Studies have identified multiple genetic loci that control protein synthesis factors, but these loci must be integrated into breeding programs without negatively affecting disease resistance or other agronomic traits (Tandzi et al., 2017; Sethi et al., 2023). Therefore, maintaining a broad genetic base while selecting for high protein content is essential for the long-term success of breeding programs.

6.3 Cost and scalability of breeding programs

The cost and scalability of breeding programs present another set of challenges. Advanced breeding techniques, such as molecular breeding and genome editing, offer the potential to accelerate the development of high-protein maize varieties. However, these technologies are often expensive and may not be accessible to breeding programs in developing countries (Cooper and Messina, 2022; Tandzi et al., 2017). The high cost of these technologies can limit their widespread adoption, making it difficult to scale up breeding efforts to meet global demand.

Furthermore, the scalability of breeding programs is also affected by the need for extensive field trials and evaluations. Breeding high-protein maize varieties requires rigorous testing across multiple environments to ensure that the new varieties perform well under different conditions. This process is time-consuming and resource-intensive, adding to the overall cost of breeding programs (Jaradat and Goldstein, 2013; Amegbor et al., 2022b). Therefore, finding cost-effective and scalable solutions is crucial for the successful development and dissemination of high-protein maize varieties.

7 Case Study Results

7.1 Summary of protein content improvements achieved

The breeding of maize varieties with high protein content has shown significant advancements. For instance, the introgression of the *opaque16 (o16)* gene into opaque2 (o2)-based parental inbreds resulted in hybrids with up to 91% more tryptophan and 76% more lysine compared to their recurrent parents (Sarika et al., 2018; Wang et al., 2024). This demonstrates a substantial improvement in the protein quality of maize, particularly in terms of essential amino acids. Additionally, Quality Protein Maize (QPM) lines have been developed to enhance the nutritional value of maize. These QPM lines, although having a slightly lower overall protein content (7% lower) than non-QPM lines, exhibit a higher quality index due to increased levels of tryptophan and lysine (Amegbor et al., 2022a). This indicates that the focus has been on improving the quality rather than the quantity of protein.

7.2 Yield outcomes compared to non-bred varieties

The yield outcomes of high-protein maize varieties have been mixed. Some studies have reported that QPM hybrids tend to yield less than commercial checks. For example, QPM hybrids evaluated in the southern U.S. environments yielded less than commercial checks, although they showed significant improvements in agronomic and kernel-quality traits (Bhatnagar et al., 2004). This suggests a trade-off between yield and protein quality in some cases. However, other studies have shown that it is possible to achieve high yields along with improved protein content. For instance, the reconstituted hybrids with the o16 gene showed similar grain yield and attributing traits to their original versions, indicating that high protein content can be achieved without compromising yield (Sarika et al., 2018). This highlights the potential for breeding strategies that do not sacrifice yield for nutritional quality.

7.3 Quality of protein achieved

The quality of protein in bred maize varieties has been significantly enhanced, particularly in terms of essential amino acids. The QPM lines, for example, have been shown to contain 1.9 times more tryptophan and double the quality index compared to non-QPM lines (Bhatnagar et al., 2004). This improvement is crucial as tryptophan and lysine are essential amino acids that are often deficient in regular maize.

Moreover, the introduction of the o16 gene alongside the o2 gene has led to hybrids with enhanced levels of lysine and tryptophan. These pyramided lines (o2o2/o16o16) exhibited up to 64% and 86% increases in lysine and tryptophan, respectively, over the original hybrids (Sarika et al., 2018). This dual-gene approach has proven effective in significantly boosting the amino acid profile of maize.

8 Nutritional Impact Assessment

8.1 Comparison of nutritional values with standard maize varieties

Quality Protein Maize (QPM) varieties have been developed to address the nutritional deficiencies found in standard maize varieties. Studies have shown that QPM varieties generally have a higher quality of protein due to increased levels of essential amino acids such as lysine and tryptophan. For instance, QPM lines were found to have 1.9 times more tryptophan and double the quality index compared to non-QPM lines, despite having a 7% lower overall protein content (Amegbor et al., 2022a). Additionally, QPM varieties have been shown to contain higher levels of other essential nutrients, such as carotenoids and tocopherols, which are crucial for human health (Chander et al., 2008).

In comparison to standard maize varieties, QPM has demonstrated superior nutritional profiles. For example, a study comparing northern adapted cultivars of common maize with QPM found that QPM had double the amount of lysine and arginine, and higher levels of tryptophan and cysteine, resulting in a better balance of essential amino acids (Zarkadas et al., 1995). This improved amino acid profile makes QPM a more nutritious option, particularly in regions where maize is a staple food and protein malnutrition is prevalent.

8.2 Protein bioavailability and digestibility

The bioavailability and digestibility of protein in QPM are critical factors that determine its nutritional efficacy. Research indicates that QPM varieties not only have higher levels of essential amino acids but also exhibit improved protein digestibility. For instance, the amino acid score of QPM, adjusted for digestibility, was found to be significantly higher than that of conventional maize varieties, indicating better protein quality (Zarkadas et al., 1995). This is particularly important for populations that rely heavily on maize as a primary protein source.

Moreover, transgenic QPM varieties have been developed to further enhance protein content and quality. A study on transgenic lysine-rich maize showed that the insertion of the lysine-rich *sb401* gene increased the total protein and lysine content, leading to an improved amino acid score and overall nutritive value (Tang et al., 2013). These advancements suggest that QPM can provide a more bioavailable and digestible protein source compared to standard maize varieties, thereby addressing protein malnutrition more effectively.

8.3 Implications for human health and diet quality

The enhanced nutritional profile of QPM has significant implications for human health and diet quality, particularly in developing countries where maize is a staple food. The increased levels of essential amino acids in QPM can help combat protein malnutrition, which is a major health issue in these regions. For example, a meta-analysis of community-based studies found that the consumption of QPM instead of conventional maize led to a 12% increase in the rate of growth in weight and a 9% increase in the rate of growth in height in infants and young children with mild to moderate undernutrition (Gunaratna et al., 2010).

Furthermore, the adoption of QPM varieties can improve overall diet quality by providing a more balanced intake of essential nutrients. The higher levels of carotenoids, tocopherols, and other micronutrients in QPM can contribute to better health outcomes, including improved immune function and reduced risk of chronic diseases (Chander et al., 2008; Prasanna et al., 2020). Therefore, the integration of QPM into the diets of populations that rely on maize as a staple food can have profound positive effects on public health and nutritional status.

9 Economic and Agricultural Implications

9.1 Potential for market adoption by farmers

The potential for market adoption of high-protein maize varieties by farmers is influenced by several factors, including the perceived benefits and the challenges associated with these varieties. Studies have shown that the adoption of quality protein maize (QPM) varieties can significantly improve nutritional outcomes for both human and livestock consumption, which can be a strong incentive for farmers to adopt these varieties (Tandzi et al., 2017). However, the adoption rate has been limited due to minimal collaboration between maize breeders, farmers, agricultural extension workers, and other stakeholders. This lack of collaboration can hinder the dissemination of information and the practical benefits of QPM varieties, making it essential to enhance participatory plant breeding and variety selection processes to improve adoption rates (Tandzi et al., 2017).

Moreover, the success of market adoption also depends on the agronomic performance of these high-protein maize varieties. Farmers are more likely to adopt new varieties if they are agronomically equal or superior to conventional varieties. For instance, in East Africa, the adoption of QPM was higher in areas where farmers participated in extension programs and were aware of the agronomic and nutritional benefits of QPM (Groote et al., 2016). Therefore, effective extension strategies that highlight both the agronomic and nutritional advantages of high-protein maize are crucial for increasing market adoption among farmers.

9.2 Cost-benefit analysis for high-protein maize cultivation

Conducting a cost-benefit analysis for high-protein maize cultivation involves evaluating the economic returns against the costs incurred in adopting these varieties. High-protein maize varieties, such as those developed through breeding programs, have shown potential for increased yields and improved nutritional content, which can translate into higher market prices and better economic returns for farmers (Jugenheimer, 1961). However, the initial costs of adopting these varieties, including the purchase of seeds and potential changes in farming practices, need to be considered. For example, the use of molecular breeding techniques to develop QPM varieties can be cost-prohibitive for farmers in developing regions, limiting their widespread adoption (Tandzi et al., 2017).

In addition to the direct economic benefits, high-protein maize cultivation can have significant welfare impacts. Studies in Zambia and South Africa have demonstrated that the adoption of improved maize varieties, including high-protein types, leads to increased crop incomes, improved food security, and reduced poverty levels among farming households (Khonje et al., 2015). These benefits highlight the importance of considering both the direct and indirect economic impacts when evaluating the cost-effectiveness of high-protein maize cultivation.

9.3 Government and policy support considerations

Government and policy support play a critical role in the successful adoption and cultivation of high-protein maize varieties. Policies that promote the dissemination of improved seed varieties and provide support for agricultural extension services can significantly enhance the adoption rates of high-protein maize. For instance, in South Africa, policies aimed at increasing the land under improved maize varieties, particularly among female farmers, have been shown to positively impact household food security and economic outcomes (Sinyolo, 2020). Such policies can help address the barriers to adoption and ensure that the benefits of high-protein maize are accessible to a broader range of farmers.

Furthermore, government support in the form of subsidies, training programs, and infrastructure development can facilitate the adoption of high-protein maize. In Ethiopia, gender-based decision-making and economic status were identified as key drivers of adoption, suggesting that targeted support for economically disadvantaged and gender-egalitarian households could enhance the adoption of improved maize varieties (Gebre et al., 2019). Additionally, policies that encourage participatory approaches in plant breeding and variety selection can help bridge the gap between research and practical application, ensuring that high-protein maize varieties meet the needs and preferences of local farmers (Tandzi et al., 2017).

10 Concluding Remarks

The breeding of maize varieties with high protein content, particularly Quality Protein Maize (QPM), has shown significant promise in addressing malnutrition and improving the nutritional value of maize. Studies have demonstrated that QPM varieties contain higher levels of essential amino acids such as lysine and tryptophan compared to conventional maize, which are crucial for human and animal nutrition. Additionally, the genetic variability and heritability of these traits suggest substantial opportunities for further improvement through selective breeding. The adoption of QPM has been shown to positively impact child growth rates, indicating its potential to combat undernutrition in developing regions. However, challenges such as lower overall protein content in some QPM lines and the need for better agronomic traits remain.

Future breeding research should focus on overcoming the agronomic limitations associated with QPM varieties, such as lower yields and poorer grain quality observed in some mutant lines. Integrating molecular breeding techniques with conventional methods could accelerate the development of QPM varieties that are both nutritionally superior and agronomically viable. Additionally, exploring the genetic loci associated with protein synthesis and stress tolerance can lead to the development of more resilient QPM varieties. Participatory plant breeding (PPB) and participatory variety selection (PVS) should be employed to enhance the adoption of QPM by involving farmers and other stakeholders in the breeding process. Furthermore, expanding the genetic base by incorporating diverse germplasm can help in developing hybrids with improved nutritional and agronomic traits.

The long-term impact of breeding high-protein maize varieties, particularly QPM, on global nutrition and agriculture could be profound. By improving the nutritional quality of maize, a staple food for a significant portion of the world's population, QPM can play a crucial role in reducing malnutrition and improving public health outcomes. Enhanced nutritional profiles of maize can also open new market opportunities for farmers, contributing to economic development in rural areas. Moreover, the success of QPM can serve as a model for biofortification efforts in other staple crops, further advancing global food security and nutrition. The integration of QPM into agro-food systems can thus lead to sustainable improvements in both human health and agricultural productivity.

Acknowledgments

We are grateful to Mrs. Jie Zhang for critically reading the manuscript and providing valuable feedback that improved the clarity of the text.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Abu P., Badu-Apraku B., Ifie B., Tongoona P., Melomey L., and Offei S., 2021, Genetic diversity and inter-trait relationship of tropical extra-early maturing quality protein maize inbred lines under low soil nitrogen stress, PLoS One, 16(6): e0252506.
https://doi.org/10.1371/journal.pone.0252506

Alves M., Belo M., Carbas B., Brites C., Paulo M., Mendes-Moreira P., Brites C., Bronze M., Šatović Z., and Patto M., 2017, Long‐term on‐farm participatory maize breeding by stratified mass selection retains molecular diversity while improving agronomic performance, Evolutionary Applications, 11: 254-270.
https://doi.org/10.1111/eva.12549

Amegbor I., Biljon A., Shargie N., Tarekegne A., and Labuschagne M., 2022a, Identifying quality protein maize inbred lines for improved nutritional value of maize in Southern Africa, Foods, 11(7): 898.
https://doi.org/10.3390/foods11070898

Amegbor I., Biljon A., Shargie N., Tarekegne A., and Labuschagne M., 2022b, Heritability and associations among grain yield and quality traits in quality protein maize (QPM) and non-QPM hybrids, Plants, 11(6): 713.
https://doi.org/10.3390/plants11060713

Bello B., Olawuyi J., Ige A., Mahamood J., Afolabi S., Azeez A., and Abdulmaliq Y., 2014, Agro-nutritional variations of quality protein maize (*Zea mays* L.) in Nigeria, Journal of Agricultural Sciences, Belgrade, 59: 101-116.
https://doi.org/10.2298/JAS1402101B

Bhadmus O., Badu-Apraku B., Adeyemo O., and Ogunkanmi A., 2021, Genetic analysis of early white quality protein maize inbreds and derived hybrids under low-nitrogen and combined drought and heat stress environments, Plants, 10(12): 2596.
https://doi.org/10.3390/plants10122596

Bhatnagar S., Betrán F., and Rooney L., 2004, Combining abilities of quality protein maize inbreds, Crop Science, 44: 1997-2005.
https://doi.org/10.2135/CROPSCI2004.1997

Bletsos E., and Goulas C., 1999, Mass selection for improvement of grain yield and protein in a maize population, Crop Science, 39: 1302-1305.
https://doi.org/10.2135/CROPSCI1999.3951302X

Chander S., Meng Y., Zhang Y., Yan J., and Li J., 2008, Comparison of nutritional traits variability in selected eighty-seven inbreds from Chinese maize (*Zea mays* L.) germplasm, Journal of Agricultural and Food Chemistry, 56(15): 6506-6511.
https://doi.org/10.1021/jf7037967

Chen X., Chen F., Chen Y., Gao Q., Yang X., Yuan L., Zhang F., and Mi G., 2013, Modern maize hybrids in Northeast China exhibit increased yield potential and resource use efficiency despite adverse climate change, Global Change Biology, 19(3): 923-936.
https://doi.org/10.1111/gcb.12093

Cooper M., and Messina C., 2022, Breeding crops for drought-affected environments and improved climate resilience, The Plant Cell, 35: 162-186.
https://doi.org/10.1093/plcell/koac321

Crossa J., Pérez-Rodríguez P., Cuevas J., Montesinos-López O., Jarquín D., Campos G., Burgueño J., González-Camacho J., Pérez-Elizalde S., Beyene Y., Dreisigacker S., Singh R., Zhang X., Gowda M., Roorkiwal M., Rutkoski J., and Varshney R., 2017, Genomic Selection in plant breeding: methods, models, and perspectives, Trends in Plant Science, 22(11): 961-975.
https://doi.org/10.1016/j.tplants.2017.08.011

Denic M., Chaque P., Fato P., Senete C., Mariote D., and Haag W., 2008, Approaches in breeding for high quality protein maize, Genetika, 40(3): 237-247.
https://doi.org/10.2298/GENSR0803237D

Denic M., Ignjatovic-Micic D., Stankovic G., Marković K., Zilic S., Lazić-Jančić V., Chaúque P., Fato P., Senete C., Mariote D., and Haag W., 2012, Role of genetic resources from different geographic and climatic regions in simultaneous breeding for high quality protein maize (HQPM) and stress tolerance, Genetika, 44: 13-23.
https://doi.org/10.2298/GENSR1201013D

Ertiro B., Das B., Kosgei T., Tesfaye A., Labuschagne M., Worku M., Olsen M., Chaikam V., and Gowda M., 2022, Relationship between grain yield and quality traits under optimum and low-nitrogen stress environments in tropical maize, Agronomy, 12(2): 438.
https://doi.org/10.3390/agronomy12020438

Gebre G., Isoda H., Rahut D., Amekawa Y., and Nomura H., 2019, Gender differences in the adoption of agricultural technology: The case of improved maize varieties in southern Ethiopia, Women's Studies International Forum, 76: 102264.
https://doi.org/10.1016/j.wsif.2019.102264

Groote H., Gunaratna N., Fisher M., Kebebe E., Mmbando F., and Friesen D., 2016, The effectiveness of extension strategies for increasing the adoption of biofortified crops: the case of quality protein maize in East Africa, Food Security, 8: 1101-1121.
https://doi.org/10.1007/s12571-016-0621-7

Gunaratna N., Groote H., Nestel P., Pixley K., and McCabe G., 2010, A meta-analysis of community-based studies on quality protein maize, Food Policy, 35: 202-210.
https://doi.org/10.1016/J.FOODPOL.2009.11.003

Harrigan G., Stork L., Riordan S., Reynolds T., Taylor J., Masucci J., Cao Y., LeDeaux J., Pandravada A., and Glenn K., 2009, Impact of environmental and genetic factors on expression of maize gene classes: relevance to grain composition, Journal of Food Composition and Analysis, 22: 158-164.
https://doi.org/10.1016/J.JFCA.2008.08.005

Hossain F., Sarika K., Muthusamy V., Zunjare R., and Gupta H., 2019, Quality protein maize for nutritional security, In: Qureshi A., Dar Z., and Wani S. (eds.), Quality breeding in field crops, Springer, Cham, Switzerland, pp.217-237.
https://doi.org/10.1007/978-3-030-04609-5_11

Jaradat A., and Goldstein W., 2013, Diversity of maize kernels from a breeding program for protein quality: I. physical, biochemical, nutrient, and color traits, Crop Science, 53: 956-976.
https://doi.org/10.2135/CROPSCI2012.07.0437

Jugenheimer R., 1961, Breeding for oil and protein content in maize, Euphytica, 10: 152-156.
https://doi.org/10.1007/BF00022206

Khonje M., Manda J., Alene A., and Kassie M., 2015, Analysis of adoption and impacts of improved maize varieties in Eastern Zambia, World Development, 66: 695-706.
https://doi.org/10.1016/J.WORLDDEV.2014.09.008

Okporie E., Chukwu S., and Onyishi G., 2013, Development of high protein populations of maize (*Zea mays* L.) from three cycles of reciprocal recurrent selection, IOSR Journal of Agriculture and Veterinary Science, 3: 22-26.
https://doi.org/10.9790/2380-0322226

Palacios-Rojas N., McCulley L., Kaeppler M., Titcomb T., Gunaratna N., Lopez-Ridaura S., and Tanumihardjo S., 2020, Mining maize diversity and improving its nutritional aspects within agro-food systems, Comprehensive Reviews in Food Science and Food Safety, 19(4): 1809-1834.
https://doi.org/10.1111/1541-4337.12552

Prasanna B., Cairns J., Zaidi P., Beyene Y., Makumbi D., Gowda M., Magorokosho C., Zaman-Allah M., Olsen M., Das A., Worku M., Gethi J., Vivek B., Nair S., Rashid Z., Vinayan M., Issa A., Vicente F., Dhliwayo T., and Zhang X., 2021, Beat the stress: breeding for climate resilience in maize for the tropical rainfed environments, Theoretical and Applied Genetics, 134: 1729-1752.
https://doi.org/10.1007/s00122-021-03773-7

Prasanna B., Palacios-Rojas N., Hossain F., Muthusamy V., Menkir A., Dhliwayo T., Ndhlela T., Vicente F., Nair S., Vivek B., Zhang X., Olsen M., and Fan X., 2020, Molecular breeding for nutritionally enriched maize: status and prospects, Frontiers in Genetics, 10: 1392.
https://doi.org/10.3389/fgene.2019.01392

Rizzo G., Monzon J., Tenorio F., Howard R., Cassman K., and Grassini P., 2022, Climate and agronomy, not genetics, underpin recent maize yield gains in favorable environments, Proceedings of the National Academy of Sciences of the United States of America, 119(4): e2113629119.
https://doi.org/10.1073/pnas.2113629119

Sarika K., Hossain F., Muthusamy V., Zunjare R., Baveja A., Goswami R., Bhat J., Saha S., and Gupta H., 2018, Marker-assisted pyramiding of opaque2 and novel opaque16 genes for further enrichment of lysine and tryptophan in sub-tropical maize, Plant Science, 272: 142-152.
https://doi.org/10.1016/j.plantsci.2018.04.014

Sethi M., Saini D., Devi V., Kaur C., Singh M., Singh J., Pruthi G., Kaur A., Singh A., and Chaudhary D., 2023, Unravelling the genetic framework associated with grain quality and yield-related traits in maize (*Zea mays* L.), Frontiers in Genetics, 14: 1248697.
https://doi.org/10.3389/fgene.2023.1248697

Sinyolo S., 2020, Technology adoption and household food security among rural households in South Africa: the role of improved maize varieties, Technology in Society, 60: 101214.
https://doi.org/10.1016/j.techsoc.2019.101214

Tandzi L., Mutengwa C., Ngonkeu E., Woin N., and Gracen V., 2017, Breeding for quality protein maize (QPM) varieties: a review, Agronomy, 7(4): 80.
https://doi.org/10.3390/agronomy7040080

Tang M., He X., Luo Y., Ma L., Tang X., and Huang K., 2013, Nutritional assessment of transgenic lysine-rich maize compared with conventional quality protein maize, Journal of the Science of Food and Agriculture, 93(5): 1049-1054.
https://doi.org/10.1002/jsfa.5845

Vasal S., 2002, Quality protein maize: overcoming the hurdles, Journal of Crop Production, 6: 193-227.
https://doi.org/10.1300/J144v06n01_11

Vikal Y., and Chawla J., 2014, Molecular interventions for enhancing the protein quality of maize, In: Chaudhary D., Kumar S., and Langyan S. (eds.), Maize: nutrition dynamics and novel uses, Springer, New Delhi, India, pp.49-61.
https://doi.org/10.1007/978-81-322-1623-0_4

Wang W., Zhu S.J., and Cheng J.H., 2024, The role of mineral fertilizers in enhancing maize nutritional value, Field Crop, 7(4): 222-231.

Welch R., 2002, Breeding strategies for biofortified staple plant foods to reduce micronutrient malnutrition globally, The Journal of Nutrition, 132(3): 495S-499S.
https://doi.org/10.1093/JN/132.3.495S

Wroblewitz S., Hüther L., Manderscheid R., Weigel H., Wätzig H., and Dänicke S., 2014, Effect of rising atmospheric carbon dioxide concentration on the protein composition of cereal grain, Journal of Agricultural and Food Chemistry, 62(28): 6616-6625.
https://doi.org/10.1021/jf501958a

Zabel F., Müller C., Elliott J., Minoli S., Jägermeyr J., Schneider J., Franke J., Moyer E., Dury M., François L., Folberth C., Liu W., Pugh T., Olin S., Rabin S., Mauser W., Hank T., Ruane A., and Asseng S., 2021, Large potential for crop production adaptation depends on available future varieties, Global Change Biology, 27(16): 3870-3882.
https://doi.org/10.1111/gcb.15649

Zarkadas C., Yu Z., Hamilton R., Pattison P., and Rose N., 1995, Comparison between the protein quality of northern adapted cultivars of common maize and quality protein maize, Journal of Agricultural and Food Chemistry, 43: 84-93.
https://doi.org/10.1021/JF00049A016

Zhou L., and Jiang L., 2024, Impact of integrated agronomic practices on maize yield and nutrient use efficiency, Field Crop, 7(2): 79-92.