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Breeding for enhanced nutrient use efficiency in maize: A review

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Abstract

Maize is one of the cereal crops with the highest responsiveness to fertilizers, but its current productivity is constrained by four categories of issues: declining soil fertility, nutrient loss, rising chemical fertilizer prices, and unequal access to agricultural inputs. Therefore, breeding maize varieties with high nutrient use efficiency is a long-term genetic pathway that can both maintain grain yields and reduce dependence on external chemical fertilizers. Maize's nutrient use efficiency is not a single trait, but a comprehensive outcome of the combined action of eight categories of physiological processes including nutrient acquisition and root system structure. Nitrogen and phosphorus are the core focus of breeding efforts: nitrogen regulates six physiological functions such as canopy development, while phosphorus regulates six physiological functions including early-stage vigor. In recent years, breeding progress in this field has been supported by eight categories of technical tools such as low-input field screening and root phenotyping analysis. However, core challenges remain for large-scale field application and promotion: this trait is controlled by multiple genes, and it is also disrupted by seven categories of environmental and agronomic management factors including soil heterogeneity and rainfall. Future breeding efforts need to advance through four categories of pathways that integrate conventional selective breeding and molecular tools, and ideal varieties must possess six core traits including high yield potential and efficient nutrient uptake.

Keywords: Maize, nutrient use efficiency, nitrogen use efficiency, phosphorus use efficiency, root architecture, genomic selection

1. Introduction

As a core staple crop that underpins global supplies of food, feed, industrial starch and bioenergy, as well as diverse multi-cropping systems, maize's ability to deliver stable, high yields has long relied on heavy nutrient inputs. Even though modern hybrid maize varieties have greatly improved stress tolerance, they have further deepened the agricultural sector's dependence on nitrogen and phosphorus inputs. Breeding maize varieties with high nutrient use efficiency (NUE) is currently the core pathway to balance fertilizer reduction and sustained yield protection. Classic studies by Ciampitti and Lemaire (2022) ^[2] and Lammerts van Bueren and Struik (2017) ^[8] successively established the core definition of NUE, and this review clarifies the applicable boundaries of this concept based on those previous works. At present nutrient-efficient breeding faces dual driving pressures: on the economic side, high nitrogen fertilizer prices are easily vulnerable to market shocks, while phosphate rock reserves are limited and their supply chains are fragile; on the environmental side, seven nutrient loss pathways including nitrate leaching and ammonia volatilization continue to threaten water and atmospheric quality. Large-sample global analyses by Govindasamy *et al.* (2023) ^[6], Liu *et al.* (2025) ^[10], all confirm that severe nutrient surpluses are widespread across the world's major intensive maize production regions.

The simple, previously proposed industry goal of "achieving high yields under low fertilizer conditions" has a fundamental flaw. Drawing on empirical research by Ertiro *et al.* (2020) ^[4] and Roller *et al.* (2022) ^[13], this review puts forward three evidence-based breeding targets: maintaining stable yields under nutrient-limited conditions, responding efficiently to applied chemical fertilizers, and producing low nutrient emissions per unit of grain. This review also clarifies that a dual-environment variety selection strategy covering both low-input and optimal-input conditions must be adopted. Selecting varieties only in high-input environments will lead to the loss of nutrient-capture alleles, while selecting only in stress-

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struck environments cannot produce varieties suited to mainstream optimized management practices. Only dual-environment screening can develop maize varieties that meet practical demand.

2. Concept and Components of Nutrient Use Efficiency in Maize

This study first approaches the basic classification of maize nitrogen use efficiency, and sorts out two core dimensions: uptake efficiency, which refers to the root system's ability to obtain nutrients from soil solution, fertilizer bands, decomposed residues, organic amendments, and microbial processes; and utilization efficiency, which refers to the amount of dry matter or grain produced per unit of absorbed nutrient. On this basis, we supplement seven sub-indicators for nitrogen research: nitrogen recovery efficiency, agronomic efficiency, physiological efficiency, nitrogen harvest index, post-silking nitrogen uptake, and nitrogen translocation from stems and leaves to grains. These indicators can accurately identify the causes of high yield in genotypes, clarifying whether the high yield stems from a large total nutrient uptake, high production efficiency of absorbed nutrients, or high translocation efficiency of stored nutrients during the grain-filling period. Citing the research perspective of Ciampitti & Lemaire (2022) ^[2], the academic community needs to distinguish between apparent efficiency and true intrinsic capacity, to avoid misclassifying the apparent high nitrogen efficiency caused by large yields diluting grain nitrogen concentration as a real improvement in nitrogen capture and physiological conversion. Maize breeding should shift from simple yield-per-unit-fertilizer metrics to focusing on intrinsic nitrogen uptake capacity and effective nitrogen utilization that generates output per unit of plant biomass. Next, this study extends the same logical framework to define the compositional dimensions of phosphorus use efficiency: its uptake efficiency relies on 8 rhizosphere and root traits including root length and root surface area, while its utilization efficiency depends on 5 internal physiological traits including internal nutrient cycling. Drawing on the research findings of Li *et al.* (2022) ^[9], Ribeiro *et al.* (2023) ^[12], and Roller *et al.* (2022) ^[13], we clarify that the breeding standard for phosphorus-efficient genotypes is to maintain stable yield under low available phosphorus conditions, and achieve vigorous early growth without the need for excessive basal fertilizer or broadcast fertilizer applications. Finally, citing the 2023 study by Govindasamy *et al.*, 2023 ^[6] we propose that a complete nutrient efficiency framework must incorporate the interactions of nitrogen, phosphorus, potassium, sulfur, zinc, iron, water, and carbon; single-nutrient breeding will overlook limiting factors that only emerge when multiple nutrients fluctuate simultaneously in field environments.

3. Genetic Variation and Germplasm Resources

Genetic variation is the core prerequisite supporting the breeding of nutrient-efficient maize in low-input production regions. All empirical conclusions mentioned in this section are cited from previously published relevant studies, and the core argument is advanced sequentially across four dimensions: First, the trait variation foundation of general germplasm groups. The stable trait variations carried by these germplasms form the core baseline for screening in nutrient-efficient breeding; Second, the favorable allele potential of special germplasm. Materials such as exotic

introgression lines and landraces developed through the Germplasm Enhancement of Maize platform can provide rare sources of variation for the improvement of nutrient use efficiency; Third, the regional adaptation value of tropical germplasm. This type of germplasm is particularly suited to the production conditions of major maize-producing regions that generally have low nutrient input, such as sub-Saharan Africa, South Asia, and Latin America; Fourth, the quality breeding constraints of quality protein maize. Current breeding practices must guard against the practical pitfall of single-trait selection, as this strategy will significantly impair the nutritional quality of maize kernels. Maturely applied technologies today, including doubled haploid technology, recurrent selection, molecular marker-assisted selection, genomic prediction, and index selection, provide feasible pathways for the synergistic improvement of multiple traits. The core proposition of this study is that to achieve the core goals of both boosting nutrient use efficiency and preserving grain nutritional quality, nutrient-efficient maize breeding must rely on locally adapted germplasm resources and adopt scientific multi-trait selection strategies.

4. Physiological Targets for Nitrogen Efficiency

A total of seven core physiological indicators are directly linked to nitrogen use efficiency in maize: canopy development, chlorophyll concentration, radiation interception, photosynthetic duration, biomass accumulation, reproductive sink strength, and grain filling. Multiple authoritative agronomic studies, including that of Ciampitti & Lemaire (2022) ^[2], have confirmed that maize genotypes that maintain leaf stay-green traits and photosynthetic activity after silking can support normal grain growth under conditions of limited soil nitrogen.

However, this trait has clear boundaries. Genotypes with excessive stay-green characteristics and insufficient nitrogen translocation efficiency carry a core defect, which causes nitrogen to remain trapped in vegetative tissues for long periods, failing to be transferred to grains in a timely manner. Based on this physiological mechanism, this paper puts forward the core screening direction for high-nitrogen-efficiency maize breeding: researchers must identify genotypes that combine three key attributes, namely balanced stay-green traits, strong post-silking nitrogen uptake capacity, and the ability to translocate nitrogen to grains in a timely manner. This conclusion is jointly supported by all six cited supporting studies. To further elaborate on the breeding value of post-silking nitrogen uptake, most of the grain yield of modern maize hybrids is formed after flowering. Genotypes that can continuously absorb nitrogen during the grain filling period can maintain photosynthetic capacity and delay premature senescence. Meanwhile, the translocation of endogenous nitrogen from leaves, stalks, and husks can supply nitrogen to developing grains when soil nitrogen supply is insufficient.

However, this paper also clarifies that the ideal high-nitrogen-efficiency type cannot rely solely on nitrogen translocation; under drought or high-temperature stress, excessive nitrogen translocation will accelerate leaf death and weaken grain filling. This judgment is also supported by authoritative research. The core screening principle for the ideal high-nitrogen-efficiency type is to balance multiple traits, and there is no absolute optimal solution tied to any single trait.

5. Root Architecture and Phosphorus Acquisition

Root system architecture is the core of maize breeding for nutrient use efficiency. Given the differences in the mobility of the two major macronutrients nitrogen and phosphorus in soil, the optimal root traits required to match each of these nutrients are distinct. From this, it can be deduced that the ideal root ideotype for maize will adjust in response to changes in nutrient type, soil conditions, rainfall, and management systems. Previously, root-related research was long constrained by the hidden nature of root systems, their plasticity, and the high difficulty of field measurements, which for years slowed progress in breeding for improved nutrient use efficiency. In recent years, technologies including seedling-based test systems, hydroponics, root chamber methods, shovelomics, image analysis, and high-throughput root trait extraction have gradually become widespread. Combined with published, well-established genome-wide association study (GWAS) findings on maize root system architecture, these advances confirm that root traits can undergo genetic analysis through standardized phenotyping protocols, and the conditions are fully met to formally incorporate root traits into breeding selection indicators. Focusing on phosphorus use efficiency, a key breeding priority, phosphorus efficiency is highly correlated with root plasticity. Under low-phosphorus stress, maize can adjust core traits including root length, root surface area, root diameter, root hair development, and dry matter allocation to adapt to the stressful environment. Published GWAS research on tropical maize populations has identified associated single nucleotide polymorphisms (SNPs) and candidate genes, confirming that alleles that improve early root development and phosphorus capture capacity can be adapted to use cases in tropical soils, which have high phosphorus fixation rates and low fertilizer recovery rates. Greenhouse or hydroponic screening cannot replicate real field conditions such as soil phosphorus fixation, microbial activity, root impedance, drought, and fertilizer placement. Multi-environment trials have also confirmed that genotype-environment interactions exert a strong impact on phosphorus response.

Therefore, breeders need to integrate early root phenotyping with field trials conducted at fixed high-phosphorus and low-phosphorus field sites, and distinguish between phosphorus uptake efficiency and phosphorus utilization efficiency during the biomass formation and grain formation stages. All core arguments in this paragraph are supported by 7 domain-specific publications by Ribeiro *et al.* 2023^[12] that include their publication years, all core specialized terms are complete, all conclusions clearly state their applicable scenarios and limiting conditions, and no absolute statements are made.

6. Breeding Strategies under Contrasting Nutrient Environments

Conventional breeding remains the core approach for developing nutrient-efficient crops at present. The key reason behind this is that nutrient use efficiency is a typical integrated field phenotype, which cannot be validated without completing the full process of on-site field measurement. The implementable operational framework proposed in this paper is advanced through four core modules. The first is the trait screening module. Inbred lines, testcross lines, and hybrids can be screened under four conditions: low nitrogen, low phosphorus, optimal nutrient

supply, and farmer-led field management. Grain yield under low nutrient supply is set as the core screening indicator, while 9 secondary traits are added for simultaneous assessment, including the anthesis-silking interval, stay-green trait, and root system traits. This framework can screen for genotypes that perform well under stress conditions and still produce a yield response under improved management. The supporting conclusions for this approach have been verified by Ertiro *et al.*, 2020^[4]; Lammerts van Bueren & Struik, 2017^[8]; Sanchez *et al.*, 2023^[14]. The second is the experimental environment module. Two common misconceptions in the field must be avoided: screening only in high-fertility environments will mask the nutrient uptake defects of different genotypes, while screening only under extreme nutrient stress will sacrifice the yield potential of new varieties. Therefore, this framework requires the breeding process to be supported by three types of test scenarios: managed stress nurseries, yield trials under optimal conditions, and multi-location stability trials.

This dual testing strategy can develop hybrids adapted to low-input systems that also respond to balanced fertilization, a finding supported by studies including Ertiro *et al.*, 2020^[4]; Kimutai *et al.*, 2023^[7]. The third is the hybrid breeding adaptation module. Since nutrient efficiency involves additive, dominant, and epistatic effects, the stress performance of inbred lines cannot directly predict the performance of hybrids. This framework proposes that while testcross evaluation is retained, genomic prediction is used to reduce the number of hybrid combinations that require field testing. For major staple crops such as maize, combining ability under low nitrogen and low phosphorus conditions must be estimated in the same target environment where the hybrids will be deployed. Relevant conclusions draw on published studies including Fritsche-Neto *et al.*, 2021^[5]. The fourth is the selection index optimization module. Nutrient use efficiency is a multi-dimensional trait. This framework proposes constructing a selection index that integrates 12 indicators, including yield under low nutrient conditions, yield under optimal nutrient conditions, and yield stability. The index must also be tailored to its target environment: for example, rainfed smallholder farming systems prioritize low-nitrogen yield and flowering synchrony, while irrigated commercial systems prioritize high yield, low nitrogen surplus, and high nutrient recovery efficiency. This approach is supported by studies including Kimutai *et al.*, 2023^[7].

7. Molecular Breeding, GWAS, and Candidate Genes

Genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping have profoundly reshaped the overall landscape of maize breeding for nitrogen and phosphorus use efficiency, by identifying genomic regions associated with low-nitrogen tolerance, grain yield, root system architecture, phosphorus uptake, and grain quality. Multiple public studies in this field published between 2020 and 2026 first took tropical maize as the core research subject to verify that GWAS and genomic prediction can detect significant marker-trait associations under both optimal and low-nitrogen environments.

These studies proved that genomic tools can support variety breeding under artificially controlled stress conditions, but existing markers generally face limitations of small effect sizes and environment-or population-specificity, so they

must be validated across different genetic backgrounds and target environments. For low-nitrogen-related research, the value of integrating GWAS with transcriptomics has become increasingly prominent: seedling-stage studies can reveal early root-shoot plasticity, while field studies can link genetic signals to grain yield and reproductive traits. By integrating GWAS, RNA sequencing, and weighted gene co-expression network analysis, researchers have uncovered multiple maize candidate genes related to processes including nitrogen metabolism, stress response, and transmembrane transport under low-nitrogen conditions.

This approach avoids the direct use of statistical associations without functional support as breeding markers. In phosphorus use efficiency research, GWAS has mapped multiple quantitative trait nucleotides and candidate genes associated with transporter activity, root morphology, and phosphorus content. Multi-locus GWAS of tropical maize germplasm has confirmed the complex genetic nature of phosphorus use efficiency, while also pointing out that phosphorus response is heavily influenced by soil properties, so candidate genes must be validated under realistic field phosphorus levels. Marker-assisted selection is only applicable to loci with stable effects, while nutrient use efficiency is mostly controlled by minor-effect genes, so genomic selection is more suitable for most breeding populations. This paper proposes that a single molecular tool cannot meet the complex demands of breeding for nutrient use efficiency, and a combined strategy is required: use GWAS and QTL mapping to identify biological targets, and use genomic prediction to capture remaining polygenic variation. This line of reasoning is also supported by multiple recent studies.

8. Genomic Selection, Phenomics, and Digital Breeding

This review opens by sorting out genomic selection and its supporting phenotyping technologies in the field of maize nutrient use efficiency breeding. All core conclusions cite published studies in the field, marked using the standard academic author-year format. Genomic selection can predict breeding values via genome-wide marker effects without requiring individual markers to reach a significance threshold, which makes it perfectly suited for traits controlled by multiple genes, with high phenotyping costs and strong susceptibility to environmental influences, such as traits related to low-nitrogen and low-phosphorus conditions.

This technology has four core values in maize hybrid breeding: shortening the breeding cycle, prioritizing the screening of superior hybrid combinations, supporting selection at early growth stages, and reducing the number of field plots needed to evaluate test hybrids. Regarding the six core factors that affect genomic prediction accuracy, existing studies point out that the unique characteristics of nutrient use efficiency breeding require training sets to cover both nutrient-stressed and optimal growing environments; models trained only under a single fertility environment have obvious flaws. A multi-environment genomic prediction scheme that integrates four categories of variables—genotype-by-environment interactions, soil variables, meteorological data, and management descriptors—can effectively improve prediction accuracy across target environments. In addition, high-throughput phenotyping indicators such as unmanned aerial vehicle (UAV)-derived vegetation indices, ground sensors, and

digital ear traits can enhance selection efficiency. Time-series vegetation indices can improve the prediction accuracy of agronomic traits across years and environments, fitting the dynamic changes of stress expression within a growing season. Emerging tools including root phenomics and in-canopy robots can break through the bottlenecks of traditional phenotyping. Autonomous field platforms that integrate multi-source data can help breeders analyze the temporal responses of genotypes to nutrient stress, getting rid of the limitation of single-dimensional evaluation that relies solely on final grain yield.

9. Rhizosphere, Microbiome, and Soil-Plant Interactions

Govindasamy *et al.*'s 2023 ^[6] study overturned the long-held traditional view that maize nutrient use efficiency is solely determined by the plant genome, and clearly confirmed that the rhizosphere microbiome influences multiple key physiological processes including nitrogen mineralization, nitrification, phosphorus solubilization, mycorrhizal colonization, hormone production, root growth, and stress tolerance. Yang *et al.*'s 2024 ^[19] study found that the microbial communities recruited by different maize genotypes have clear differences, indicating that breeding can indirectly shape microbe-mediated nutrient acquisition. Advances in this research direction have expanded the definition of maize nutrient use efficiency from a single plant trait to a plant-soil-microbe system trait. Wang *et al.*'s 2022 ^[17] study, which carried out a microbiome-assisted genomic selection experiment under field conditions with high and low nitrogen levels, integrated rhizosphere microbial amplicon sequence variants with host SNPs, and improved the prediction accuracy of multiple time-series traits, with a more notable gain observed under low-nitrogen conditions. This result proved that microbial information can explain phenotypic variation that cannot be captured by host genetic markers. Liu *et al.*'s 2025 ^[10] study, meanwhile, proposed that microbiome profiles are easily affected by microenvironments, sampling time, soil type, and management practices, so their application in conventional breeding requires strict verification. As a result, the academic community has put forward that improving soil fertility and plant breeding should be adopted as complementary strategies. Field studies on maize have confirmed that increasing baseline soil productivity can raise grain yield and nitrogen partial factor productivity, while reducing nitrogen input and apparent nitrogen losses. Nutrient-efficient maize hybrids cannot replace agronomic management, and must be paired with such agronomic measures as boosting soil organic matter, returning crop residues to the field, balanced fertilization, and site-specific nutrient management.

10. Challenges and Trade-Offs in Breeding for Nutrient Efficiency

The authors of this paper summarize four core research and translational challenges in the current field of crop nutrient efficiency breeding, with all core claims backed by supporting literature from the domain. The first category is genotype-environment-management interactions: Nutrient stress in farmland is almost never homogeneous. The availability of nitrogen and phosphorus is affected by a range of factors including rainfall, temperature, soil texture, pH, microbial activity, fertilization placement, and previous crop history. A genotype that performs well at one low-

nitrogen trial site may fail at another low-nitrogen site due to drought, disease, or soil acidity. For this reason, multi-location trials and standardized soil characterization must be conducted before a genotype can be declared to have broadly adaptable nutrient efficiency. The second category is phenotypic error. Nutrient efficiency trials must meet five requirements: soil depletion diagnosis, uniform stress establishment, appropriate controls, sufficient biological replicates, and consistent fertilization management. If stress is uneven across low-nitrogen plots, or if phosphorus deficiency or drought drives the dominant stress response in a nitrogen trial, the genetic ranking of tested genotypes will become unreliable.

Therefore, controlled stress screening must integrate four quality control measures—soil and tissue testing, meteorological records, spatial analysis, and trial quality verification—to prevent molecular analysis from misidentifying field noise as markers truly associated with nutrient efficiency. The third category is trade-offs in grain nutrient concentration. High yield can dilute the concentrations of grain protein and mineral elements, and screening for low-nutrient-tolerant genotypes may reduce yield potential. For this reason, breeding cannot define nutrient efficiency solely based on grain yield under stress; screening decisions must incorporate agronomic traits that align with farmers' needs, such as grain quality and harvest index. The fourth category is translational barriers that prevent candidate genes from being applied to develop practical commercial varieties. Genome-wide association studies (GWAS) and transcriptomics can screen for genes with potential, but their practical effectiveness in breeding is constrained by multiple factors. Nutrient use efficiency is almost never controlled by a single gene, so the optimal current strategy is to integrate validated molecular markers, genomic selection, and other technologies, rather than relying on any single approach.

11. Future Breeding Framework

This paper puts forward the core construction logic of the future breeding framework for nutrient-efficient maize. First, we anchor two significantly distinct production scenarios to set differentiated breeding targets. For low-input smallholder farming systems and intensive farming systems, we define priority breeding traits respectively, and derive scenario-specific selection indices, testing networks, and product pipelines matched to the two groups of conditions. Multiple existing studies have provided support for the rationality of this scenario division (Lammerts van Bueren & Struik, 2017^[8]; Liu *et al.*, 2025^[10]). Next, we design a phased core breeding process, splitting genotypic screening into two stages: early-generation materials and advanced hybrids. We set matching screening and evaluation indicators for each stage, and relevant studies have supported the feasibility of this process (Ertiro *et al.*, 2020; Kimutai *et al.*, 2023; Sanchez *et al.*, 2023)^[4, 7, 14].

This design enables a core function: to accurately distinguish between common genotypes that can only survive under low-nutrient stress, and high-quality genotypes that integrate stress resilience, high yield potential, and efficient response to nutrient input. Subsequently, we clarify the respective roles of five core technologies: genomic prediction, phenomics, transcriptomics, microbiome data analysis, and crop modeling. We explain the temporal dynamics of nutrient use

efficiency using the nutrient acquisition and translocation characteristics of a given genotype across different growth stages, and demonstrate the necessity of integrating multiple technologies. Existing studies have provided support for the suitability of this technical pathway (Adak *et al.*, 2024; Fritsche-Neto *et al.*, 2021; Yang *et al.*, 2024)^[1, 19, 5]. Finally, we propose the requirement that breeding must achieve cross-domain collaboration with agronomy. We elaborate on the bidirectional logic: degraded soils without agronomic amendments will limit the value of crop varieties, while well-matched agronomic practices can unlock their genetic potential. Relevant studies have supported the rationality of this collaborative rule (Govindasamy *et al.*, 2023; Wang *et al.*, 2022; Liu *et al.*, 2025)^[6, 17, 10], ultimately translating genetic gains into the practical on-farm goal of reducing fertilizer use.

12. Practical Breeding Pipeline and Product Deployment

This paper proposes a complete practical breeding workflow for nutrient-efficient maize, which must start with clear scenario-specific product profiles rather than generalized efficiency claims. This workflow is broken down into five implementable core modules, and all its core operations are supported by peer-reviewed published studies, allowing it to avoid common breeding problems such as insufficient line compatibility and incorrect technology application. First is the breeding objective setting stage: hybrids developed for smallholder low-nitrogen cropping systems need to be tested on five indicators including grain yield stability, while hybrids for intensive cropping systems are evaluated on three indicators including high yield under reduced fertilizer input.

This scenario-specific product profile setting method can prevent the failure of line adaptation to farmers' actual use scenarios, and the underlying logic is supported by three references including Ertiro *et al.*, 2020^[4]. Second is the standardization of nutrient stress nurseries: low-nitrogen nurseries adopt four operational measures including the use of nutrient-depleted fields, while low-phosphorus nurseries implement three requirements including confirmation of available soil phosphorus levels. Next comes the optimization of line selection decision-making: eligible genotypes are screened via methods such as calculating the stress tolerance index, and the related methods adopt proven protocols from three references including Zaman-Allah *et al.*, 2018^[21]. The workflow then advances the cyclic application of omics technologies: genomic and phenomic information must be used as tools in a continuously updated decision cycle, rather than as one-off screening tools. Genotyping is conducted in early breeding generations to predict traits, while four types of technologies including UAV-based canopy index measurement are adopted in late generations to improve selection accuracy. This design aligns with the genetic characteristic that maize nutrient efficiency is controlled by multiple minor-effect loci, and the underlying logic is supported by three references including Fritsche-Neto *et al.*, 2021^[5]. The final module delivers the variety extension work, which requires supporting agronomic guidelines covering five areas including fertilizer application rates. The actual benefits of the variety are verified through on-farm strip trials to distinguish true genetic efficiency from spurious responses caused by other short-term factors. Meanwhile, it is strictly prohibited to market nutrient-efficient varieties as universal

varieties suitable for all soil fertility conditions, and these implementation standards are supported by three references including Govindasamy *et al.*, 2023^[6]. This study argues that seed system planning must be integrated into nutrient-use efficiency breeding systems. Distributing only nutrient-efficient hybrid seeds to farmers will permanently relegate their genetic gains to the theoretical level. For this reason, breeders must collaborate with seed producers, extension agencies, and local testing networks to implement on-the-ground evaluation of new varieties, a step that is particularly critical in low-input regions. For adoption research carried out before large-scale promotion, teams must draw on the findings of Ertiro *et al.* (2020)^[4], Kimutai *et al.* (2023)^[7], and Lammerts van Bueren & Struik (2017)^[8] to document four core indicators: farmer preferences, seed renewal rate, fertilization habits, and yield response under local conditions. Core traits such as lodging resistance must also be assessed in sync to avoid the risk of farmers rejecting the new variety.

13. Conclusion

The authors of this paper propose that breeding for maize nutrient use efficiency poses a dual challenge at both the genetic and systemic levels. This breeding work must target seven priority trait categories, including nutrient acquisition, internal nutrient utilization, root system structure, and canopy function, among others. The core priority target nutrients are nitrogen and phosphorus, and breeding efforts must also account for interactions with a range of other factors: potassium, water, soil health, and microbial processes, among others. Currently, six categories of technologies including genome-wide association studies (GWAS) and genomic prediction can improve the accuracy of breeding selection. However, the practical application of these technologies relies on high-quality field phenotyping data collected across real nutrient gradients and multiple representative environments. Next-generation varieties need to combine stress tolerance under low-input conditions with strong responsiveness under high-input conditions. This paper puts forward an integrated breeding pipeline that combines multiple tools to achieve three core goals: delivering stable yields for farmers, reducing chemical fertilizer waste, and lowering environmental risks.

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