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Improving Nutrient-Use Efficiency: Modern and Conventional Breeding Perspectives

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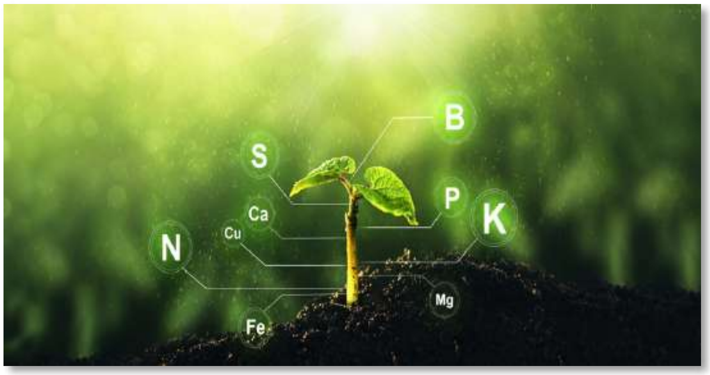
Since the beginning of crop domestication, humans have continuously improved crops to meet changing food and environmental demands. In the present era, agriculture faces increasing pressures from climate change, soil nutrient depletion, and rising global food needs. Enhancing nutrient-use efficiency (NuUE) has therefore become a critical target in crop improvement. Conventional breeding remains central to this goal through the selection of genotypes with superior nutrient uptake and the utilization of both cultivated and wild species to improve nutrient acquisition and assimilation. Mutation breeding has also contributed by generating novel traits and enabling the identification of nutrient-efficient lines.



The discovery of nutrient-related genes and QTLs through genetic mapping has further illuminated the molecular basis of nutrient absorption, transport, and utilization. However, the complex physiological and biochemical pathways underlying NuUE often limit the effectiveness of conventional breeding alone. Modern biotechnological tools—molecular markers, genomic selection, and genome editing techniques such as CRISPR–Cas—offer precise and accelerated avenues for improving NuUE. These methods facilitate targeted modification of key pathways and nutrient-responsive genes. Integrating traditional breeding with advanced biotechnologies provides a pathway to developing high-yielding varieties that require fewer fertilizers, ultimately contributing to a more sustainable and environmentally friendly agricultural system.

Agriculture in the 21st century faces three critical challenges. First, the global population is expected to reach 10 billion by 2050, placing immense pressure on global food production systems. Second, climate change—marked by rising temperatures, irregular rainfall, and frequent extreme weather events—threatens crop productivity and agroecosystem stability. Third, widespread micronutrient deficiencies or "hidden hunger" persist among populations dependent on staple crops lacking essential minerals.

Plants require mineral nutrients to support growth, metabolism, and stress tolerance. Macronutrients such as nitrogen, phosphorus, and potassium are particularly vital for yield, quality, and vigour. However, nutrient acquisition and utilization efficiency are often limited by environmental and physiological constraints. A large proportion of applied fertilizers is lost through leaching, volatilization, and runoff, contributing to soil degradation, water pollution, and higher production costs.

Improving nutrient-use efficiency (NuUE) is therefore a priority for modern agriculture. As nutrient uptake and utilization are under strong genetic control, plant breeding presents a powerful strategy for enhancing NuUE. Nutrient-efficient varieties can reduce fertilizer requirements, minimize nutrient losses, lower input costs, and enhance performance under nutrient-deficient conditions. Thus, breeding for improved NuUE is essential for meeting future food demands while ensuring environmental sustainability.

Conventional Approaches to Improve Nutrient-Use Efficiency

Conventional strategies for enhancing NuUE rely primarily on traditional breeding and agronomic practices. Classical plant breeding focuses on selecting and crossing genotypes with superior nutrient uptake, efficient root systems, and improved nutrient assimilation. As the root system is the primary organ responsible for acquiring water and nutrients from the soil (Ramakrishna et al., 2019), improving root architecture has become central to NuUE enhancement.

Several studies report strong associations between nitrogen uptake and root traits such as rooting depth, root hair length, root diameter, and cellular structure (Wang et al., 2023). For example, increased root length density significantly improved nitrogen and phosphorus assimilation in maize, contributing to a 22% increase in grain yield (Chen et al., 2022). In Brassica napus, Wang et al. (2014) developed an N-efficient line (D4-15) through hybridization, which showed improved yield performance compared to N-inefficient genotypes.

Mutation breeding is another conventional method for creating novel genetic variability. A notable example is the dominant male-sterile mutant Ms44 in maize (Fox et al., 2017), where a single amino acid substitution caused male sterility and reduced nitrogen allocation to tassels. This allowed greater nitrogen partitioning to ears, enhancing kernel number and increasing yield by 4–8.5% under low-nitrogen conditions.

Challenges of Conventional Breeding and Modern Solutions for Improving NuUE

Although conventional breeding has contributed significantly to NuUE improvement, it faces several limitations:

1. Slow and Labour-Intensive Processes

Repeated cycles of crossing and field evaluations delay the development of improved lines.

Modern Solution: Molecular markers, marker-assisted selection (MAS), and genomic selection (GS) accelerate breeding by enabling early and precise identification of NuUE-related genotypes.

2. Complex, polygenic nature of NuUE traits

NuUE traits are quantitative and environmentally influenced, making phenotypic selection difficult. **Modern Solution:** QTL mapping and marker-assisted backcrossing allow precise introgression of nutrient-efficiency QTLs.

3. Limited Genetic Variation Within Crop Gene Pools

Conventional breeding relies heavily on existing germplasm.

Modern solution: Genetic engineering and transgenic approaches enable the introduction of beneficial genes from diverse species, expanding the genetic base.

4. Difficulty Improving Complex Physiological Traits

Processes such as biological nitrogen fixation or modification of metabolic pathways are hard to manipulate using traditional methods.

Modern solution: Genome-editing tools (CRISPR/Cas, TALENs, ZFNs) enable precise gene modification without altering overall genomic integrity.

Genome-Based Strategies for Improving NuUE

Advances in molecular genetics have enabled the identification of genes and QTLs underlying key physiological traits. Linkage mapping and association mapping are the two primary methods used for dissecting quantitative traits.

- Genome-wide association studies (GWAS) scan the entire genome to identify marker–trait associations (Risch & Merikangas, 1996).
- Candidate-gene association mapping focuses on genes with known or suspected functions (Bangarwa et al., 2020).

These tools, along with genome sequencing and high-throughput genotyping, have greatly accelerated the identification of QTLs governing nutrient uptake and utilization.

Key QTL Discoveries in Rice

- **Nitrogen Use Efficiency:** 13 QTLs identified for NUE-related traits (Zhou et al., 2017; Obara et al., 2001).
- **Potassium-Use Efficiency:** Four QTLs discovered in IR64/Azucena cross affecting height, tillering, and biomass (Wu et al., 1998).
- **Phosphorus Uptake:** The major QTL Pup1 was fine-mapped (Wissuwa et al., 2002) and successfully introgressed into *Improved Samba Mahsuri* using MAS (Swamy et al., 2020), enhancing P-deficiency tolerance without compromising yield or quality.

Integrating these QTLs into breeding pipelines will accelerate the development of nutrient-efficient cultivars, especially for low-input farming systems.

Modern Biotechnological Approaches for Improving NuUE

Modern biotechnologies offer unmatched precision and speed in improving NuUE.

1. Genome Editing

CRISPR/Cas and related technologies enable targeted modification of genes involved in:

- nitrogen uptake and assimilation (e.g., NPF6.1, NPF4.5, AAP1, AAP5),
- regulation of nitrogen metabolism (GRF4, NLP1, MYB61),
- phosphorus uptake and signalling (PHT1–PHT5, PHR1, PHR2).

For example, modifying GS1.1 in wheat improved nitrogen-use efficiency (Wang et al., 2020).

2. Transgenic Approaches

Transgenic interventions introduce beneficial genes from unrelated species. Key examples include:

Table 1. Genetically modified crops with improved nutrient-use efficiency

Crop	Gene Overexpressed	Major Features	Reference
Arabidopsis, Rice, Tomato	AVP1/AVP1D	Enhanced root branching; increased P acquisition	Yang et al., 2014
Rice	OsNRT1.1B + OsNR2	Increased nitrate uptake and assimilation; improved tillering and yield	Gao et al., 2019
Maize	Raf2	Increased Rubisco content; improved carbon assimilation and stress resilience	Eshenour et al., 2024

These advancements expand the breeding landscape beyond the limitations of traditional gene pools.

Conclusion and Future Prospects

Improving nutrient-use efficiency is vital for increasing crop productivity while reducing environmental impacts. Advances in high-throughput phenotyping, genome mapping, and biotechnology have greatly enhanced the ability to identify and manipulate genes associated with NuUE. Root architecture traits, molecular markers, favourable QTLs, and genome-edited alleles offer promising avenues for developing climate-resilient, nutrient-efficient cultivars.

Future efforts should focus on multidisciplinary integration—combining phenomics, genomics, genome editing, and field-level validation—to develop varieties that perform consistently across diverse agroecosystems. Utilizing contrasting genotypes such as the N-efficient *B. napus* line D4-15 will aid in QTL discovery and the development of superior cultivars. Overall, a combination of conventional breeding, molecular tools, and biotechnology will be crucial for building a sustainable agricultural future.

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