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GENETIC AND GENOMIC APPROACHES FOR IMPROVING NUTRIENT AND WATER USE EFFICIENCY IN CROP PLANTS: A REVIEW

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ABSTRACT

Climate change, resource depletion, and increasing global food demand necessitate the development of crop varieties with enhanced nutrient use efficiency (NUE) and water use efficiency (WUE). These traits are complex, polygenic, and strongly influenced by genotype $\times$ environment interactions. Conventional breeding has achieved limited gains due to low heritability and phenotyping challenges. Recent advances in genomic selection, genome-wide association studies, and CRISPR/Cas-mediated genome editing have significantly improved the precision of breeding for resource-use efficiency. Integration of physiological traits such as root system architecture, stomatal conductance, and biomass partitioning further enhances selection efficiency. Future breeding strategies must adopt systems-level integration of genomics, phenomics, and predictive analytics to develop climate-resilient and resource-efficient cultivars.

Key words: Nutrient use efficiency, Water use efficiency, Genomic selection, Root architecture, CRISPR/Cas9.

Introduction

Global agriculture faces mounting pressure to meet the food demands of a growing population under changing climatic conditions. Climate variability, including increased temperatures and erratic rainfall patterns, has already begun to reduce crop productivity and stability (Xiong *et al.*, 2022). Sustainable intensification is therefore essential to ensure food security while minimizing environmental degradation (Egli *et al.*, 2021).

Modern agriculture relies heavily on nitrogen fertilizers and irrigation, both of which have high environmental costs. Inefficient nitrogen use leads to leaching, eutrophication, and greenhouse gas emissions, while excessive irrigation contributes to groundwater depletion (Hatfield and Dold, 2019; Mallareddy *et al.*, 2023). Improving Nutrient Use Efficiency (NUE) and Water Use Efficiency (WUE) is therefore critical for sustainable crop production.

NUE refers to the efficiency with which plants acquire and utilize nutrients to produce yield, whereas WUE reflects the ratio of biomass production to water consumption (Farooq *et al.*, 2019). Complex genetic networks govern both traits and are strongly influenced by environmental conditions, necessitating integrated breeding strategies.

Although NUE and WUE are often treated as independent traits, increasing evidence indicates that they are physiologically and genetically interconnected. Water availability directly influences nutrient mobility in soil and uptake by roots, while nutrient status affects plant water relations through osmotic adjustment and stomatal behaviour. For example, nitrogen availability regulates leaf area development and photosynthetic capacity, which in turn influences transpiration rates and water demand. Conversely, water deficit conditions reduce nutrient

diffusion and mass flow toward roots, thereby limiting nutrient acquisition even in nutrient-rich soils. This bidirectional relationship suggests that improving NUE without considering WUE—or vice versa—may lead to suboptimal outcomes under field conditions (Farooq *et al.*, 2019; Hatfield and Dold, 2019). Therefore, breeding strategies must target combined resource-use efficiency rather than isolated trait improvement.

This review provides a comprehensive synthesis of current knowledge on breeding for improved nutrient and water use efficiency. It examines genetic and physiological determinants, evaluates recent methodological advancements, and discusses future prospects for integrating genomics, phenomics, and genome editing to develop climate-resilient, resource-efficient crop cultivars.

Conceptual Framework of Nutrient and Water Use Efficiency

Nutrient Use Efficiency (NUE) and Water Use Efficiency (WUE) are foundational indicators of sustainable crop production, reflecting the capacity of plants to convert limited resources into economic yield. Given their multidimensional nature, these efficiencies are interpreted at agronomic, physiological, and economic levels.

Nutrient Use Efficiency (NUE)

NUE broadly denotes the efficiency with which supplied nutrients are converted into harvestable yield (Moll *et al.*, 1982). At the agronomic level, NUE is commonly expressed as:

$$NUE = \frac{\text{Grain Yield}}{\text{Nutrient supplied}}$$

This formulation integrates nutrient uptake efficiency (ability of roots to acquire nutrients from soil) and nutrient utilization efficiency (Magray *et al.*, 2022). A conceptual representation of nutrient use efficiency across agronomic and physiological scales is presented in Fig. 1. Physiological NUE refers to internal processes governing nutrient assimilation, remobilization, and partitioning within

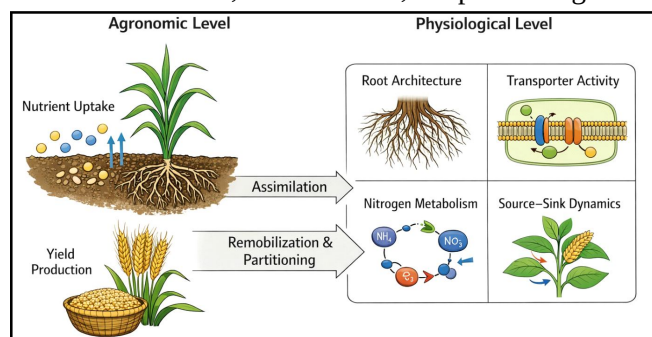


Fig. 1: Overview of nutrient use efficiency (NUE) from nutrient uptake to physiological regulation in plants.

plant tissues. Traits such as root architecture, transporter activity, nitrogen assimilation enzymes, and source–sink relationships play decisive roles in determining overall efficiency. Because NUE is strongly influenced by genotype × environment interactions and soil heterogeneity, its expression varies across agroecological contexts.

Water use Efficiency (WUE)

Water Use Efficiency (WUE) represents the relationship between biomass or grain yield and water consumed by the crop (Farooq *et al.*, 2019). Water use efficiency at agronomic and physiological scales is conceptually depicted in Fig. 2. At the whole-plant or agronomic scale, it is expressed as:

$$WUE = \frac{\text{Biomass or Yield}}{\text{Water used}}$$

At the physiological level, intrinsic WUE (*iWUE*) is defined as the ratio of net photosynthetic rate (*A*) to stomatal conductance (*g_s*) (Farquhar *et al.*, 1989):

$$IWUE = \frac{A}{g_s}$$

WUE can also be interpreted economically, where output value per unit of water applied is considered under irrigated systems. Physiological determinants of WUE include stomatal regulation, transpiration efficiency, photosynthetic capacity, and carbon allocation dynamics. Since water availability directly interacts with nutrient uptake and assimilation, NUE and WUE are biologically interconnected traits rather than independent parameters.

Physiological Basis of Resource Use Efficiency

Resource use efficiency in crops is governed by coordinated physiological processes regulating nutrient acquisition, water relations, carbon assimilation, and biomass partitioning. The key physiological processes governing nutrient and water use efficiency are illustrated

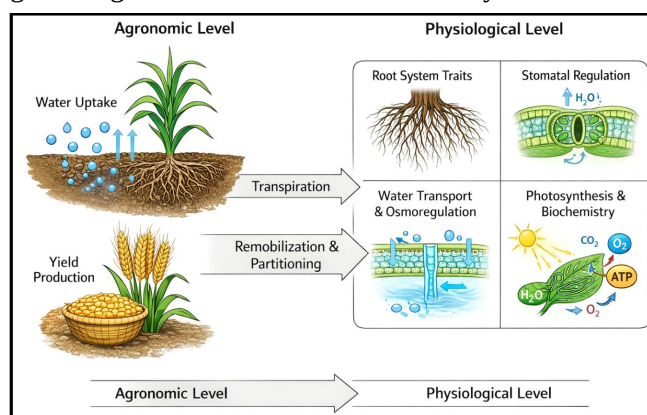


Fig. 2: Conceptual framework of water use efficiency (WUE) at agronomic and physiological levels.

in Fig. 3. Because NUE and WUE are mechanistically interconnected, understanding their physiological determinants is essential for targeted breeding.

Nutrient Uptake and Assimilation

Nutrient uptake is initiated at the root–soil interface through specialized membrane transport systems. Nitrate (NO_3^-) uptake is mediated primarily by high- and low-affinity nitrate transporters, whereas ammonium (NH_4^+) is absorbed via ammonium transport proteins. Root absorption efficiency depends on root surface area, membrane transport capacity, and soil nutrient availability (Islam *et al.*, 2022). Following uptake, nitrate is reduced and assimilated into amino acids through coordinated enzymatic pathways, ultimately contributing to protein synthesis and biomass accumulation. Nutrient transport from roots to shoots via the xylem and subsequent remobilization during reproductive stages are critical components of physiological NUE (Marschner, 2012; Muratore *et al.*, 2021). Variation in transporter activity, assimilation efficiency, and source–sink dynamics significantly influences nutrient productivity across genotypes.

Water Relations and Photosynthesis

Water acquisition occurs through roots and is driven upward via xylem transport, largely regulated by transpiration-induced tension. Under water deficit conditions, stomatal closure reduces CO_2 diffusion into leaves, limiting carboxylation efficiency and photosynthetic rate (Bauke *et al.*, 2022). Drought stress disrupts the photosynthetic apparatus and alters the activity of key Calvin cycle enzymes, including *Rubisco*, *PPDK*, *FBPase*, *NADP-ME*, and *PEPCase*. Reduced enzymatic efficiency impairs carbon fixation and biomass production (Taghvimi *et al.*, 2024). Simultaneously, stress-induced accumulation of reactive oxygen species (ROS) disturbs cellular redox balance, potentially damaging membranes and chloroplast structures (Hasanuzzaman

et al., 2020). Efficient antioxidant systems are therefore essential to maintain photosynthetic integrity under stress conditions. Intrinsic water use efficiency is tightly linked to stomatal conductance, transpiration regulation, and carbon assimilation capacity (Al-Salman *et al.*, 2024). Thus, WUE reflects the balance between water conservation and sustained photosynthetic performance.

Root System Architecture

Root system architecture (RSA) is a major determinant of both NUE and WUE, influencing soil exploration, nutrient interception, and water extraction. Traits such as root length density, root angle, lateral branching, and root depth distribution enhance resource capture under limiting conditions (Lynch, 2022). Several regulatory genes associated with root architecture have been identified across crops, including *EXO70A3* (root growth dynamics), *CKX2* (cytokinin metabolism influencing root development), *VRN1* (developmental regulation), and *egt2* (root growth angle modulation) (Alrajhi *et al.*, 2024). However, while gene-level discoveries provide mechanistic insights, breeding efforts increasingly focus on integrated RSA phenotypes rather than single-gene manipulation due to the polygenic control of root traits. Optimizing root architecture remains a promising avenue for improving combined nutrient and water acquisition efficiency under field conditions (Woods, 2023; Dudhe *et al.*, 2025).

Genetic Architecture of Resource Use Efficiency

Nutrient use efficiency (NUE) and water use efficiency (WUE) are complex quantitative traits governed by a highly polygenic genetic architecture. Unlike simple Mendelian traits, both NUE and WUE are controlled by numerous loci distributed across the genome, each contributing small additive effects along with significant non-additive interactions (Satya *et al.*, 2026). Genome-wide association studies and quantitative trait locus (QTL) mapping consistently suggest that these traits exhibit continuous phenotypic variation and relatively low heritability under field conditions, reflecting their sensitivity to environmental fluctuations (Borrill *et al.*, 2019; Sukumaran *et al.*, 2026).

A defining feature of resource-use efficiency traits is the substantial contribution of epistatic interactions, in which gene–gene interactions influence trait expression beyond individual-locus effects. In wheat, epistatic QTLs have been shown to play a major role in determining NUE, often contributing more to phenotypic variation than main-effect loci alone (Singh *et al.*, 2023). Such observations emphasize the limitation of selection strategies based solely on additive genetic effects and underscore the need

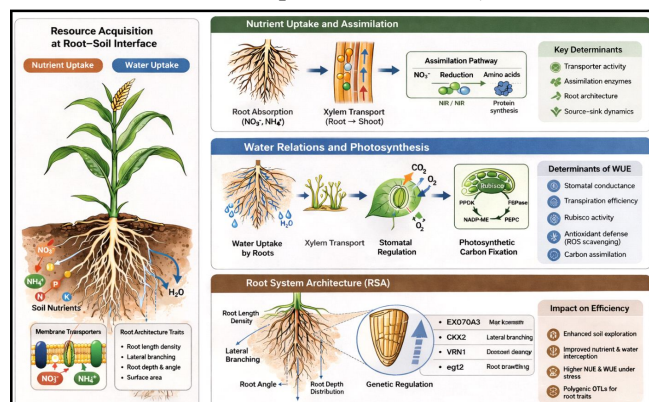


Fig. 3: Integrated physiological mechanisms governing nutrient and water use efficiency in crops.

for approaches that capture complex genetic interactions.

In addition to epistasis, pleiotropy further complicates the genetic architecture of NUE and WUE. Certain genomic regions simultaneously influence multiple physiological traits, such as biomass accumulation, transpiration efficiency, and yield components (Singh *et al.*, 2023). For example, pleiotropic QTLs associated with WUE in wheat have been mapped across multiple chromosomes, including QWue.acn-2B, which influences both water-use efficiency and productivity (Hui *et al.*, 2023). Such overlapping genetic control suggests coordinated regulation of carbon assimilation, water relations, and yield formation.

Another critical aspect shaping the genetic architecture of NUE and WUE is the strong influence of genotype $\times$ environment ($G \times E$) interactions. Environmental variables, including soil nutrient availability, moisture regimes, and temperature, modulate gene expression and physiological processes, leading to environment-specific trait manifestation (Jan *et al.*, 2025). As a result, QTLs identified under one set of conditions often show reduced or inconsistent effects in different environments. This conditional expression limits the stability and transferability of identified loci across agroecological zones.

Large-scale QTL analyses across major crops further reinforce the genome-wide and environment-dependent nature of these traits. In rice, meta-analyses integrating hundreds of QTLs have identified meta-QTL regions associated with nitrogen uptake and utilization, including candidate genes such as *OsNAR2.1* and *OsAMT1;1*, which are involved in nutrient transport mechanisms (Hongzhen *et al.*, 2023). The genetic architecture and distribution of QTLs associated with nutrient and water use efficiency across crop genomes are summarized in Fig. 4. Similarly, in wheat and maize, NUE-related loci are dispersed across multiple chromosomes, with each

locus explaining only a modest proportion of phenotypic variance (Shi *et al.*, 2022). A comparable pattern is observed for WUE, where QTLs related to transpiration efficiency, stomatal conductance, and biomass production are widely distributed and exhibit moderate, environment-dependent effects (Zhou *et al.*, 2025).

Collectively, these findings indicate that NUE and WUE are governed by complex, multilayered genetic networks involving additive effects, epistasis, pleiotropy, and strong environmental modulation. The dispersed genomic control, coupled with the limited stability of individual QTLs, poses significant challenges for conventional selection approaches. Representative QTLs associated with nutrient use efficiency and water use efficiency across major crops are summarized in Tables 1 and 2. Therefore, effective genetic improvement of resource-use efficiency requires integrative strategies that capture genome-wide variation and account for genotype $\times$ environment interactions, such as genomic selection and multi-environment evaluation frameworks.

Breeding Approaches for Improving Resource Use Efficiency

Conventional Breeding Approaches:

a. Phenotypic Selection: Phenotypic selection has historically been the primary method for improving resource-use efficiency, relying on observable traits such as grain yield under low-input conditions, biomass accumulation, chlorophyll content, and root architecture (Cudjoe, 2024). Indirect selection traits, including canopy temperature, stay-green phenotype, and carbon isotope discrimination ($\Delta^{13}C$), have been widely used as proxies for WUE and NUE in cereals (Singh *et al.*, 2023). However, phenotypic selection is constrained by strong genotype $\times$ environment interactions and environmental variability, which obscure genetic signals (Bataillon *et al.*, 2022). Moreover, these traits often represent cumulative physiological responses, limiting the ability to dissect component mechanisms (Dos Santos *et al.*, 2022). Although high-throughput phenotyping platforms and remote sensing technologies have improved precision, phenotypic selection alone remains insufficient for rapid improvement of highly polygenic traits (Nguyen *et al.*, 2025).

b. Hybridization and Backcross Breeding:

Hybridization and backcross breeding have facilitated the introgression of favorable alleles from landraces and wild relatives into elite cultivars, contributing to improved drought tolerance, root architecture, and nutrient responsiveness (Ahtisham *et al.*, 2025). Backcrossing is particularly effective for transferring major-effect loci

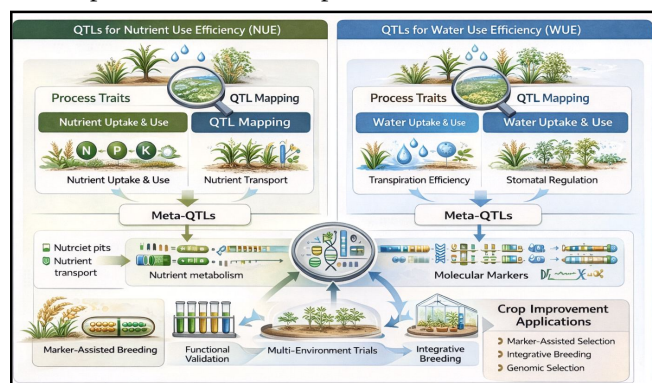


Fig. 4: Schematic representation of QTL mapping, molecular markers, and breeding strategies for NUE and WUE improvement.

Table 1: QTLs for nutrient use efficiency in various crops.

S. No.	Nutrient	Crop	Trait Category	Key Traits/Parameters	No. of QTLs	(PVE)	SAE	Reference
1	Nitrogen	Rice	NUE Components	N uptake, biomass, grain yield	13–43	6–18%	Partial	Zhou <i>et al.</i> , 2017; Senthilvel <i>et al.</i> , 2008
2	Nitrogen	Rice	Nitrogen Traits	Leaf/shoot N content, grain number	20–32	5–15%	No	Laza <i>et al.</i> , 2006; Cho <i>et al.</i> , 2007
3	Nitrogen	Rice	NUE & Stress	N-deficiency tolerance, total N, NUE	12–16	7–16%	Partial	Wei <i>et al.</i> , 2012; Senthilvel <i>et al.</i> , 2008
4	Nitrogen	Wheat	Uptake & Use Efficiency (Meta-QTL)	N uptake, root traits, biomass	Multiple MQTLs	8–22%	Yes	Saini <i>et al.</i> , 2021
5	Nitrogen	Rice	Dry Matter & Grain N	Grain N production, dry matter	28	6–14%	No	Piao <i>et al.</i> , 2009
6	Phosphorus	Rice	P Uptake (Pup1)	P uptake, tiller number	1 (Major QTL)	Up to 30%	Yes	Wissuwa <i>et al.</i> , 2002
7	Phosphorus	Rice	PUE Components	Biomass, yield, P translocation, HI	36	5–17%	Partial	Wang <i>et al.</i> , 2014
8	Phosphorus	Barley	PAE & PUE	Shoot/root dry weight, tillers	16	7–19%	Partial	Maharajan <i>et al.</i> , 2018
9	Phosphorus	Pearl millet	P Efficiency	Grain/stover P, flowering time	53	4–15%	No	Maharajan <i>et al.</i> , 2023
10	Phosphorus	Wheat	P Uptake & Biomass (Meta-QTL)	Shoot P uptake, biomass	~49	6–20%	Partial–Yes	Maharajan <i>et al.</i> , 2018
11	Nitrogen	Rice	Yield Components	Panicles, spikelets, grain filling	52	4–12%	No	Yue <i>et al.</i> , 2015

PVE: Phenotypic Variance Explained (PVE) (%) Range; **SAE:** Stability Across Environments

while preserving elite genetic backgrounds. However, its efficiency is limited for traits like NUE and WUE that are governed by numerous small-effect loci (Mallikarjuna *et al.*, 2022). While hybridization enhances genetic diversity, achieving stable gains in resource-use efficiency requires approaches capable of capturing genome-wide variation.

c. Recurrent Selection: Recurrent selection has been widely applied to accumulate favourable alleles for quantitative traits through repeated cycles of recombination and selection. This method is effective for exploiting additive genetic variance and improving traits such as biomass production, water-use traits, and nutrient uptake efficiency (Pathak *et al.*, 2025). However, long breeding cycles and environmental sensitivity limit the rate of genetic gain. Without integration of molecular tools, recurrent selection remains inefficient for complex traits characterized by epistasis and $G \times E$ interactions. Overall, conventional breeding approaches have contributed incremental improvements in NUE and WUE but are constrained by low heritability, polygenic control, and

environmental dependency. These limitations have driven the adoption of molecular and genomic strategies for more precise and efficient selection (Ali *et al.*, 2025). An overview of conventional and advanced breeding strategies for improving resource use efficiency is shown in Fig. 5.

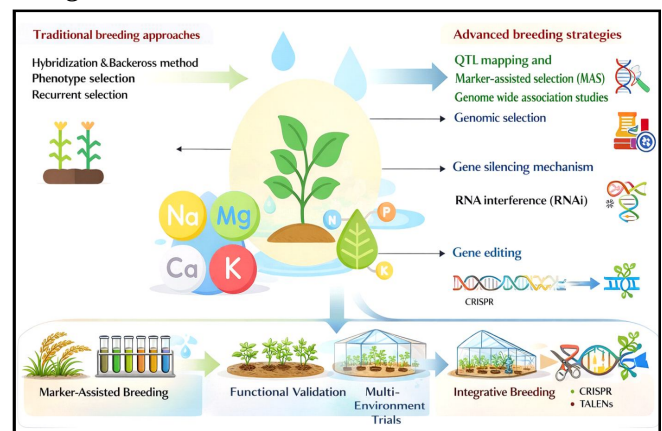


Fig. 5: Integrated breeding strategies combining conventional and molecular approaches for improving NUE and WUE.

Table 2: QTLs for water use efficiency in various crops.

S. No.	Crop	Trait Category	Traits / Parameters	Chromosome(s) / QTL Region	No. of QTLs	PVE	SAE	Reference
1	Maize	Stomatal & Yield Traits	Stomatal conductance (g_s), transpiration rate (TR), grain yield	Chr 6, Chr 7	~4	8–16%	Partial	Sarkar <i>et al.</i> , 2023
2	Barley	$\Delta^{13}C$ & Biomass under Drought	Carbon isotope discrimination ($\Delta^{13}C$), intrinsic WUE, biomass	Chr 2H, 3H, 4H, 5H, 7H	20+ clusters	5–18%	Partial	Raza <i>et al.</i> , 2019
3	Barley	Juvenile WUE Traits	Biomass WUE, water content under drought	Chr 3H, 5H, 6H, 7H	Multiple	6–15%	No	Wehner <i>et al.</i> , 2016
4	Rice	Intrinsic WUE	$\Delta^{13}C$ (proxy for WUE), transpiration efficiency	Chr 1–Chr 7	1–7 per population	Up to 19%	Partial	Fernando <i>et al.</i> , 2025
5	Wheat	WUE & Yield Components	$\Delta^{13}C$, chlorophyll content, grain weight	Chr 2B (QWue.acn-2B), Chr 1A, 7A	Multiple	7–22%	Partial –Y	Hui <i>et al.</i> , 2023
PVE: Phenotypic Variance Explained (PVE) (%) Range; SAE: Stability (Across Environments)								

Modern Breeding Approaches:

Modern breeding tools leverage advances in genomics and computational biology to improve selection accuracy for complex traits. These approaches enable the capture of genome-wide variation and facilitate the prediction of breeding values under diverse environmental conditions.

a. Marker-Assisted Selection (MAS):

MAS enables indirect selection of favourable alleles using molecular markers linked to QTLs controlling NUE and WUE-related traits (Syed *et al.*, 2020). It has been successfully applied to improve nitrogen uptake, root traits, and drought tolerance. However, MAS is most effective for traits governed by a few stable QTLs and is less suitable for highly polygenic traits with strong environmental interactions (Song *et al.*, 2023).

b. Genomic Selection (GS):

Genomic selection represents a major advancement for breeding complex traits by utilizing genome-wide markers to predict genomic estimated breeding values. GS captures both small-effect loci and epistatic interactions, making it highly suitable for NUE and WUE improvement (Ranjan *et al.*, 2021). GS enables early-generation selection and reduces reliance on extensive phenotyping, particularly when integrated with high-throughput phenomics. This approach significantly accelerates breeding cycles and enhances genetic gain under variable environments.

c. Genome-Wide Association Studies (GWAS):

GWAS provides high-resolution mapping of genetic loci associated with complex traits by leveraging natural

diversity. It has identified genomic regions controlling root architecture, stomatal conductance, nitrogen metabolism, and transpiration efficiency across crops. Although most GWAS-identified loci have small effects, they are valuable for refining candidate genes and supporting marker development. Multi-environment validation remains essential due to environmental sensitivity.

d. Genome Editing and Genetic Engineering:

Genome editing technologies, particularly CRISPR/Cas systems, have revolutionized crop improvement by enabling precise modification of genes associated with resource-use efficiency. Targeted editing of genes regulating nitrogen transport, assimilation, and stress responses has demonstrated significant improvements in NUE (Sathee *et al.*, 2022). Similarly, manipulation of stomatal traits and root architecture has improved WUE and drought tolerance (Chen *et al.*, 2022). DNA-free genome editing approaches further address regulatory and biosafety concerns, enhancing the applicability of genome editing in crop improvement.

Physiological Trait-Based Breeding for Enhanced Resource Use Efficiency

Improving nutrient use efficiency (NUE) and water use efficiency (WUE) requires a shift from yield-centric selection toward physiological trait-based breeding, where key processes governing resource acquisition, assimilation, and allocation are directly targeted (Singh *et al.*, 2022). Because NUE and WUE are emergent properties of multiple interacting physiological mechanisms, traits such as root system architecture, stomatal regulation, and biomass partitioning must be considered in an integrated framework rather than in isolation. This approach enables

the identification of ideotypes that maintain productivity under nutrient- and water-limited environments (Khadka *et al.*, 2020).

Root System Architecture and Resource Acquisition

Root system architecture (RSA) plays a central role in determining the efficiency of both water and nutrient acquisition by regulating soil exploration patterns. Traits such as root depth, root angle, root length density (RLD), and lateral branching influence the plant's ability to access deep soil moisture and intercept nutrients in spatially heterogeneous environments (Weemstra *et al.*, 2022). Increased root length density enhances the absorptive surface area, thereby improving nutrient uptake efficiency and water extraction, particularly under stress conditions. Deep and steep root systems are especially advantageous in drought-prone environments, where access to subsoil water reserves contributes to sustained transpiration and yield stability (Huang *et al.*, 2024). Despite significant advances in identifying RSA-associated QTLs and regulatory genes, including *EXO70A3*, *CKX2*, *VRN1*, and *EGT2*, their direct deployment in breeding programs remains limited due to phenotyping constraints and the polygenic nature of root traits (Abbas *et al.*, 2022). Consequently, breeding strategies are increasingly focused on selecting integrated root phenotypes that confer adaptive advantages under field conditions rather than targeting individual genes.

Stomatal Traits and Transpiration Efficiency

Stomatal traits are critical determinants of intrinsic water use efficiency (iWUE), as they regulate the balance between carbon assimilation and transpirational water loss. Stomatal density, size, and conductance collectively influence gas exchange dynamics and plant water status (Li *et al.*, 2025). Experimental evidence indicates that moderate reductions in stomatal density can enhance WUE without compromising photosynthetic capacity or yield, highlighting the potential of stomatal traits as effective breeding targets. The *ERECTA* gene, a receptor-like kinase, plays a significant role in regulating stomatal patterning and transpiration efficiency, with favorable alleles associated with improved biomass accumulation and yield (Li *et al.*, 2021; Li *et al.*, 2025). Carbon isotope discrimination ($\Delta^{13}\text{C}$) has emerged as a robust integrative proxy for WUE and has been successfully applied in wheat breeding programs to select for improved transpiration efficiency (Dong *et al.*, 2025). Cultivars such as *RAC875* demonstrate the effectiveness of combining optimized stomatal characteristics with drought adaptation traits to achieve yield stability under water-limited conditions (Aggarwal *et al.*, 2024).

Importantly, breeding for stomatal traits must balance water conservation with sufficient CO_2 uptake to avoid compromising photosynthesis. Therefore, the focus is on achieving optimal stomatal regulation rather than simply reducing stomatal conductance.

Biomass Partitioning and Harvest Index

Efficient biomass partitioning is essential to ensure that improvements in resource acquisition are effectively translated into economic yield. Harvest index (HI), defined as the ratio of grain yield to total above-ground biomass, reflects the efficiency of assimilate allocation from source tissues to reproductive sinks (Ren *et al.*, 2022). Under stress conditions, particularly drought and nutrient limitation, the remobilization of stored assimilates from vegetative tissues to developing grains becomes a critical determinant of yield stability. Enhanced partitioning efficiency improves nitrogen remobilization and grain filling, thereby contributing to higher NUE (Padhan *et al.*, 2023). Breeding strategies that optimize source–sink relationships, particularly during reproductive stages, have been shown to improve both yield and resource-use efficiency. However, excessive allocation to vegetative growth at the expense of reproductive development can reduce harvest index, highlighting the need for balanced trait selection.

The simultaneous improvement of NUE and WUE requires coordinated optimization of root architecture, stomatal regulation, and biomass allocation. These traits are functionally interconnected and collectively determine plant performance under resource-limited environments (Singh *et al.*, 2024). For instance, enhanced root systems improve resource acquisition, while efficient stomatal regulation minimizes water loss, and optimized biomass partitioning ensures effective utilization of acquired resources (Van Der Bom *et al.*, 2020).

Therefore, physiological trait-based breeding provides a holistic framework for developing crop ideotypes that maintain productivity under climate variability. Integrating these traits within genomics-assisted breeding programs offers a promising pathway for achieving sustainable improvements in resource-use efficiency.

Emerging Frontiers in Resource-Use Efficiency Breeding

The future improvement of nutrient use efficiency (NUE) and water use efficiency (WUE) relies on integrating advanced phenotyping, data-driven analysis, and precision genome engineering. High-throughput phenotyping platforms, including UAV-based imaging, thermal sensing, and multispectral analysis, enable rapid, non-destructive assessment of canopy temperature,

transpiration efficiency, biomass accumulation, and stress responses across breeding populations, thereby improving selection accuracy for complex physiological traits (Luna-Maldonado *et al.*, 2026). The integration of genomic, phenotypic, and environmental data enhances genomic prediction and strengthens selection for polygenic traits such as NUE and WUE (Amin *et al.*, 2025). Multi-omics approaches provide system-level insights into regulatory networks controlling nutrient uptake and drought adaptation (Fan *et al.*, 2025). In parallel, next-generation genome editing technologies, including multiplex CRISPR and base editing, allow precise modification of key regulatory genes associated with nutrient transport, root architecture, and stomatal regulation, supporting a shift toward predictive crop improvement (Khalid *et al.*, 2026).

Constraints and Bottlenecks

Despite technological advances, several barriers limit the effective deployment of resource-use-efficient cultivars. High-throughput phenotyping remains capital-intensive and technically demanding, particularly in low- and middle-income regions, where limited infrastructure and trained personnel constrain large-scale application (Eskandar *et al.*, 2026). Integration of multi-omics and large datasets is further challenged by platform incompatibility, lack of standardized analytical frameworks, and limited bioinformatics capacity, making accurate characterization of genotype–phenotype–environment interactions difficult (Jan *et al.*, 2025). In addition, regulatory uncertainty surrounding genome-edited crops delays commercialization in many regions, while public perception and heterogeneous policy frameworks hinder adoption (Molinari *et al.*, 2024). Socio-economic constraints, including weak extension systems, limited farmer participation, and misalignment between breeding targets and farmer needs, further reduce field-level impact. Addressing these limitations is essential to translate technological advances into sustainable improvements in nutrient and water use efficiency under changing climate conditions (Prasad *et al.*, 2024).

Conclusion

Enhancing nutrient use efficiency (NUE) and water use efficiency (WUE) is essential for developing climate-resilient cropping systems capable of sustaining productivity under increasing environmental and resource constraints. The quantitative and polygenic nature of these traits, strongly influenced by epistasis and genotype × environment interactions, requires breeding strategies beyond single-gene or single-trait improvement. Future gains will depend on trait pyramiding approaches that combine favorable alleles controlling root system

architecture, stomatal regulation, nitrogen assimilation, and biomass partitioning within elite genetic backgrounds. Integration of QTL mapping, genome-wide association studies, genomic selection, and precision genome editing enables coordinated improvement of multiple physiological components underlying resource efficiency. Equally important is integration across biological scales, linking gene networks and molecular pathways with whole-plant physiology, field performance, and farm-level adaptation. Adopting systems-based, multidisciplinary breeding strategies aligned with farmer needs will be critical to achieving sustainable improvements in NUE and WUE under climate change.

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