

Accelerating Genetic Gains in Cowpea through Rapid-Cycle Genomic Selection for Nutrient-Use Efficiency

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ABSTRACT: Cowpea (*Vigna unguiculata* L. Walp.) serves as a critical protein source and soil fertility enhancer in sub-Saharan African smallholder systems, yet poor nutrient-use efficiency (NUE) under low-input conditions constrains productivity. Genetic improvement of NUE offers a pathway to sustainable yield gains while reducing fertilizer dependency. This review synthesizes advances in genomic selection (GS) and rapid-cycle genomic selection (RGS) for accelerating genetic improvement of NUE-related traits in cowpea. We examine the physiological and genetic underpinnings of NUE encompassing nutrient uptake, utilization, and agronomic efficiency and review progress in phenotyping, genotyping, and prediction modeling for these traits. Evidence from cereals and legumes demonstrates that integrating GS with speed-breeding or off-season nurseries can double annual genetic gain (ΔG per year) by reducing breeding cycle duration. Simulation studies indicate that optimal training population design, high-throughput phenotyping, and multi-environment genomic models are essential for maintaining prediction accuracy and managing inbreeding in RGS pipelines. Implementation opportunities include expanding cowpea genomic resources, adopting cost-effective genotyping platforms, and strengthening institutional capacity through CGIAR–NARS partnerships. Persistent

challenges include balancing short-term gains with long-term genetic diversity, integrating socioeconomic preferences into selection indices, and reducing phenotyping costs for resource-constrained programs. We conclude with a roadmap emphasizing pilot RGS deployment in African cowpea breeding networks to validate empirical performance for NUE improvement. These strategies can substantially accelerate genetic gain and advance climate-resilient, nutrient-efficient cowpea production systems.

KEYWORDS: Nutrient-use efficiency; Genomic selection; Rapid-cycle genomic selection; Genetic gain; High-throughput phenotyping; Genotyping-by-sequencing

1. INTRODUCTION

1.1 Importance of Cowpea in Food Security and Smallholder Systems

Cowpea (*Vigna unguiculata*) represents a strategic crop for food and nutritional security in sub-Saharan Africa, where it significantly supports smallholder farmer livelihoods. Its importance stems from exceptional adaptability to marginal environments, high nutritional value, and critical roles in sustainable farming systems (Masemola et al., 2023). As a protein-rich source containing essential amino acids, including lysine and tryptophan, cowpea addresses widespread nutritional deficiencies in low-income communities (Bengoechea, 2023; Masemola et al., 2023). Beyond nutrition, cowpea exhibits nutraceutical properties including anti-inflammatory and anti-diabetic activities that enhance its value as a health-promoting food (Bengoechea, 2023).

Economically, cowpea cultivation and marketing generate income for rural households, contributing to poverty alleviation and resilience in fragile farming systems (Ayalew & Yoseph, 2022). Emerging cowpea-based food products, such as *Akara* and *Moin-moin*, have created additional market opportunities, increasing income generation and dietary diversity (Asiwe, 2023). Agronomically, cowpea enhances soil fertility through biological nitrogen fixation, reducing synthetic fertilizer dependence and promoting ecological intensification (Ayalew & Yoseph, 2022). Its drought tolerance and capacity to thrive in arid and semi-arid regions make it a dependable crop under climate change scenarios.

However, productivity constraints persist, including insect pest infestations, limited seed access, and excessive reliance on synthetic pesticides that pose environmental and health risks (Agyekum et al., 2016; Rabe et al., 2023). Integrated pest management and strengthening informal seed systems represent promising interventions (Agyekum et al., 2016; Rabe et al., 2023). Furthermore, cowpea's deep cultural and dietary significance underscores its importance for food sovereignty and agro-biodiversity preservation. Despite these benefits, climate variability, pest pressures, and limited genetic improvement efforts highlight the need for innovative breeding strategies to realize cowpea's full potential in smallholder systems.

1.2 Nutrient-Use Efficiency (NUE)

Nutrient-use efficiency (NUE) constitutes a central concept in sustainable agriculture, reflecting plant capacity to utilize applied or available nutrients effectively for biomass and yield production. Broadly, NUE is defined as crop yield per unit of nutrient input, though specific indices including partial factor productivity, nutrient recovery efficiency, and leaf-level NUE provide nuanced perspectives on nutrient utilization (Andualem et al., 2024; Jayara et al., 2023; Sarkar & Baishya, 2017). Cowpea, in particular, plays a crucial role in food safety and NUE context, contributing to income for smallholders, climate resilience, soil fertility, and nutrition (Figure 1).

The importance of NUE lies in its capacity to enhance agricultural sustainability. Improved NUE reduces fertilizer waste, lowers production costs, and minimizes nutrient losses to the environment, thereby curtailing soil degradation, eutrophication, and greenhouse gas emissions (Rawal et al., 2022; Singh et al., 2019). For smallholder farmers, optimizing NUE translates into reduced input costs and higher profitability (Sarkar & Baishya, 2017). Strategies for improving NUE encompass integrated nutrient management, precision agriculture, and development of crop varieties with enhanced nutrient uptake and utilization efficiencies (Andualem et al., 2024).

Nevertheless, NUE improvement faces challenges. High efficiency does not always coincide with maximum yield, as efficiency often peaks under low-input conditions (Singh et al., 2019). Furthermore, soil heterogeneity, climatic variability, and nutrient cycling dynamics complicate efforts to achieve consistent improvements across diverse environments (Congreves et al., 2021). These challenges emphasize the importance of genetic improvement strategies that complement agronomic interventions to sustainably enhance NUE in crops such as cowpea.

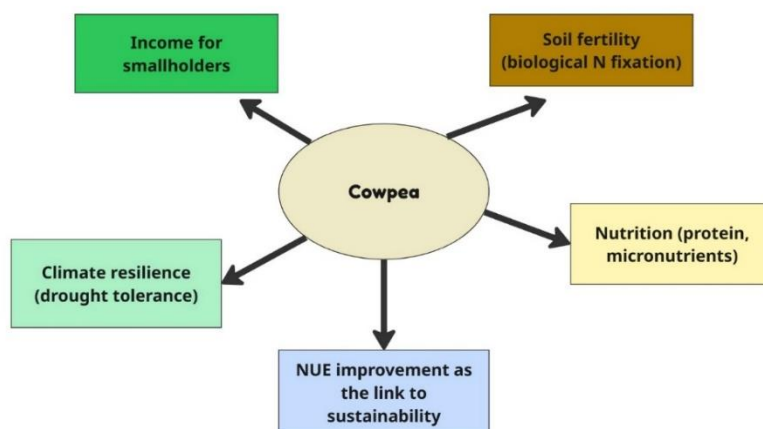


Figure 1. Role of cowpea in food security and NUE context

1.3 Rationale for Genomic Selection and Rapid-Cycle Approaches

Conventional cowpea breeding has been constrained by long generation times, limited genetic diversity exploitation, and environmental variability, all of which slow improved variety delivery. Genomic selection (GS) and rapid-cycle genomic selection (RCGS) have emerged as transformative breeding approaches addressing these limitations by accelerating genetic gains. GS leverages genome-wide marker information to predict breeding values, enabling earlier and more accurate selection compared to traditional phenotypic or marker-assisted selection (Crain et al., 2021). When combined with rapid cycling, GS reduces breeding cycle length, thereby multiplying the rate of genetic gain per unit time.

Evidence from diverse crops highlights the effectiveness of these approaches. In tropical maize, RCGS increased grain yield by 0.225 t ha⁻¹ per cycle while enabling two breeding cycles annually. Similar results have been reported in wheat and ryegrass, where recurrent genomic selection delivered genetic gains up to 12.3% for grain yield within three cycles (Byrne et al., 2024; Dreisigacker et al., 2023). These advances demonstrate GS potential to accelerate genetic improvement for complex traits including drought tolerance, nutrient efficiency, and resilience to biotic and abiotic stresses (Das et al., 2020).

Challenges remain, particularly in maintaining prediction accuracy across breeding populations and ensuring genetic diversity preservation under rapid cycles (Dunkel et al., 2017). Furthermore, the polygenic nature of traits like NUE requires sophisticated models capable of capturing gene-by-environment interactions (Das et al., 2020). Despite these limitations, integrating GS and RCGS in cowpea breeding provides a compelling rationale for re-engineering breeding pipelines to address food security and sustainability challenges.

1.4 Scope and Objectives of the Review

This review synthesizes current knowledge on accelerating genetic gains in cowpea through rapid-cycle genomic selection, with particular emphasis on enhancing nutrient-use efficiency. It examines the agronomic and nutritional importance of cowpea in smallholder systems, explores definitions, significance, and challenges associated with NUE, and evaluates the potential of genomic selection and rapid-cycle approaches in overcoming breeding bottlenecks. The review draws on lessons from other crops to inform cowpea improvement, highlights research gaps, and outlines future directions for integrating NUE-focused breeding into cowpea programs. By doing so, it aims to provide a framework for harnessing advanced genomic tools to accelerate development of cowpea cultivars that are nutritionally efficient, climate-resilient, and suitable for resource-limited farming systems.

2. NUTRIENT-USE EFFICIENCY IN COWPEA

2.1 Components of NUE: Uptake, Utilization, Agronomic Efficiency

Nutrient-use efficiency (NUE) in cowpea is determined by physiological and agronomic components: nutrient uptake efficiency, utilization efficiency, and agronomic efficiency (Table 1). Uptake efficiency reflects plant capacity to acquire nutrients from soil, shaped by root architecture, rhizosphere interactions, and soil fertility management. Utilization efficiency refers to the capacity of absorbed nutrients to be assimilated and converted into biomass and yield, while agronomic efficiency quantifies yield increase per unit of applied nutrient (Jayara et al., 2023; Sarkar & Baishya, 2017).

As illustrated in Figure 2, these components are interconnected, with uptake efficiency influenced by root traits and biological nitrogen fixation, utilization efficiency driven by biomass partitioning and nitrogen remobilization, and agronomic efficiency reflecting overall NUE performance. Cowpea demonstrates considerable variability in nutrient uptake efficiency due to genetic differences in root traits such as length and density, which influence phosphorus (P) acquisition (Krasilnikoff et al., 2003) (Table 1). Micronutrient management, including combined application of molybdenum (Mo), iron (Fe), and zinc (Zn), enhances nodulation, nitrogen fixation, and nutrient accumulation (Dhaliwal et al., 2022). Similarly, organic amendments including farmyard manure and bio-fertilizers improve soil health and nutrient uptake efficiency while reducing dependence on synthetic fertilizers (Sharma et al., 2023). Phosphorus management remains particularly critical, with varieties such as Pusa Dharni demonstrating enhanced efficiency under optimized P application (Singh et al., 2022). These findings highlight the importance of integrating genetic, agronomic, and ecological approaches to strengthen NUE in cowpea.

Table 1. Components of nutrient-use efficiency (NUE) in cowpea

Component	Definition	Key Traits / Measurement Methods	References
Uptake Efficiency	Ability to acquire nutrients from soil	Root length, density, nodulation; nutrient content in tissues	Dhaliwal et al., 2022; Krasilnikoff et al., 2003
Utilization Efficiency	Conversion of absorbed nutrients into yield	Nitrogen remobilization, biomass partitioning, harvest index	Sharma et al., 2023; Singh et al., 2022
Agronomic Efficiency	Yield gain per unit of applied nutrient	Grain yield vs. fertilizer input, nutrient recovery efficiency	Jayara et al., 2023; Sarkar & Baishya, 2017

Conceptual Venn diagram showing the three major components of NUE (uptake efficiency, utilization efficiency, and agronomic efficiency). Uptake efficiency reflects root and rhizosphere traits determining nutrient acquisition; utilization efficiency relates to internal remobilization and partitioning processes; agronomic efficiency represents yield per unit of applied nutrient (Figure 2).

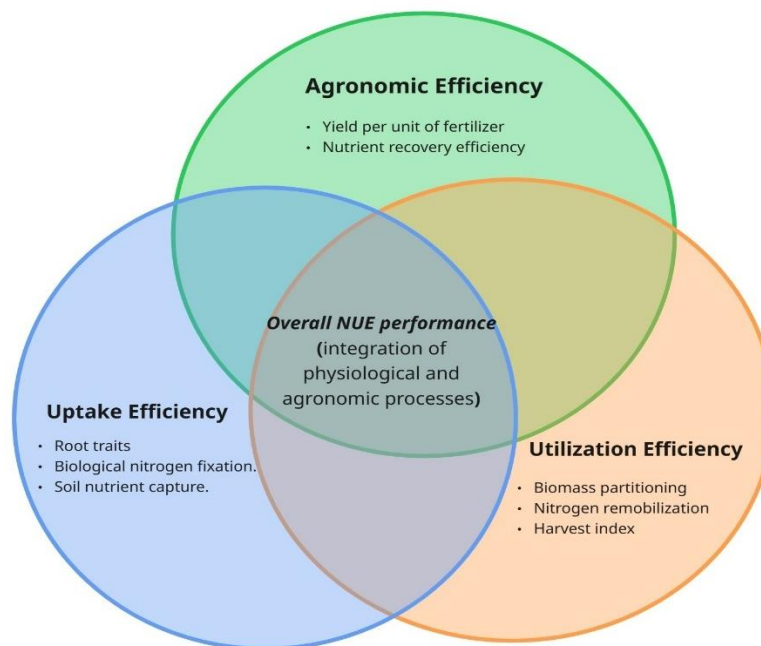


Figure 2. Components of nutrient-use efficiency (NUE)

2.2 Methods for Measuring NUE Traits

Assessing NUE in cowpea requires diverse methodological approaches that capture both physiological and agronomic dimensions. Nitrogen-use efficiency can be partitioned into supply, uptake, and utilization components by measuring crop yield, nitrogen concentration in grain, and post-harvest soil nitrogen. Physiological methods extend this analysis across the crop life cycle, assessing grain-specific nitrogen efficiency and uptake dynamics (Weih et al., 2014).

Recent advances include near-infrared spectroscopy (NIRS) for non-destructive prediction of cowpea nutritional quality, offering a cost-effective alternative to wet chemistry methods (Ndiaye et al., 2023). Molecular genetics also provide powerful tools, enabling identification of genes and markers linked to nutrient uptake and assimilation. However, divergent results across methods highlight the importance of long-term, multi-environment evaluations to achieve robust NUE estimates (Quan et al., 2021). This integrative approach ensures that both physiological processes and ecological contexts are adequately represented in NUE assessments.

2.3 Genetic Architecture and Heritability of NUE

The heritability of NUE traits in cowpea is central to their potential for genetic improvement. Significant genetic variability has been documented for traits linked to nitrogen fixation, phosphorus use, and yield components, providing a foundation for selection (Singh, 2018). Broad-sense heritability estimates for traits such as plant height, seed weight, and pod number per plant are consistently high, indicating strong genetic control and responsiveness to selection (Sheidu et al., 2023).

Marker-assisted selection further enhances breeding efficiency by targeting single nucleotide polymorphisms (SNPs) associated with phosphorus stress tolerance and other nutrient-related traits (Ravelombola et al., 2017). This integration of conventional heritability estimates with molecular tools offers opportunities to accelerate genetic gains. Nevertheless, genotype $\times$ environment (G $\times$ E) interactions complicate trait stability, requiring breeding strategies that combine high heritability with adaptability across heterogeneous environments (Laidig et al., 2024; Nguyen & Kant, 2018).

2.4 Environmental Influences and G $\times$ E Interactions

Environmental variation plays a pivotal role in shaping NUE expression in cowpea, with G $\times$ E interactions strongly influencing yield stability and nutrient content. Multi-environment studies in Nigeria, Ethiopia, and Brazil have demonstrated that some genotypes such as G21, G25, and MNC02-675F-4-9 exhibit stable performance across environments, while others display specificity to particular agro-ecologies (Kindie et al., 2021; Popoola et al., 2024; Sousa et al., 2018). Nutrient content, particularly micronutrients like Fe, Mn, and Zn, also varies with environmental conditions, as shown by differential performance of TVU-14196 and Meterlong Bean in South African trials (Gerrano et al., 2022).

Analytical approaches such as GGE biplot analysis and REML/BLUP mixed models have proven effective in quantifying G $\times$ E effects, identifying broadly adapted genotypes, and delineating mega-environments (Carvalho et al., 2017; Filho et al., 2017) (Figure 3). However, environmental conditions such as soil fertility and moisture often exert stronger influences than genetic potential, underscoring the importance of breeding for resilience alongside efficiency (Agele et al., 2018). Ultimately, integrating G $\times$ E insights into breeding programs is essential for developing cowpea cultivars with consistent NUE across diverse production systems. Systems diagram depicting environmental drivers and their interactions influencing NUE in cowpea. Arrows link soil fertility, climate, management practices, and genetic background to overall NUE performance (Figure 3). Feedback interactions represent G $\times$ E effects that determine stability across contrasting environments.

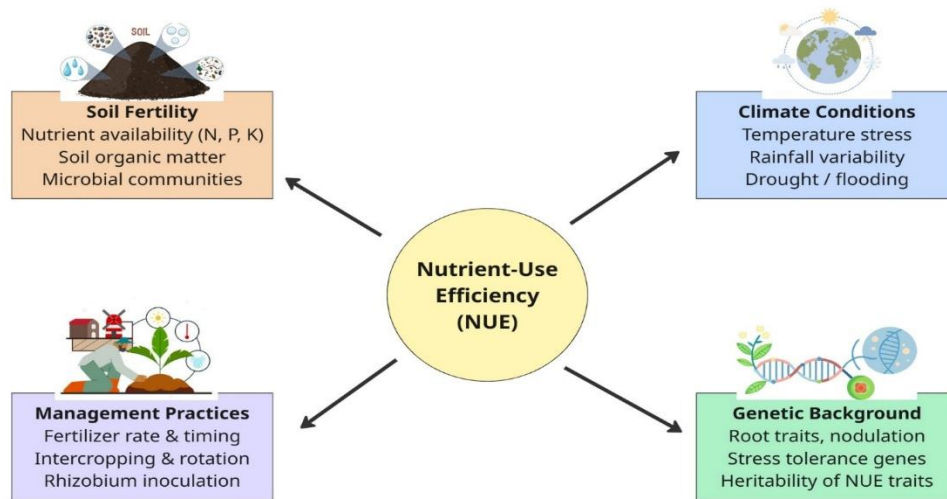


Figure 3. Environmental influences and G×E on NUE

3. GENOMIC SELECTION AND RAPID-CYCLE GENOMIC SELECTION (RGS)

3.1 Principles of Genomic Selection (GS)

Genomic selection (GS) represents a paradigm shift in breeding by using genome-wide molecular markers to predict the genomic estimated breeding value (GEBV) of individuals, bypassing the need for prior QTL identification (Newell & Jannink, 2014). The process begins with training a prediction model using phenotypic and genotypic data from a reference population, which is then applied to predict untested individuals (Howard et al., 2022). Advances in next-generation sequencing and high-density SNP genotyping platforms have improved marker coverage, enhancing predictive accuracy (Gidamo, 2022). This makes GS particularly effective for complex, polygenic traits such as NUE, where traditional marker-assisted selection has limited power.

3.2 What Makes RGS Different: Shortening the Breeding Cycle

Rapid-cycle genomic selection (RGS) builds on GS by dramatically reducing breeding cycle time, thereby increasing genetic gain per unit time. By leveraging genomic predictions for early selection and combining them with accelerated generation turnover, RGS achieves multiple cycles per year (Crain et al., 2021). Integration with speed breeding techniques that controlled photoperiod and temperature regimes further shortens cycle length, allowing rapid recombination and fixation of desirable alleles (Watson et al., 2019) (Figure 4).

Applications in maize and wheat demonstrate that RGS can deliver annual genetic gains of 6–14% for yield and stress tolerance traits (Das et al., 2020; Dreisigacker et al., 2023). These advances highlight RGS as a powerful strategy to accelerate improvement of nutrient efficiency and stress resilience in cowpea, traits that are otherwise slow to develop through conventional breeding. Schematic overview illustrating the integration of genomic selection (GS) and rapid-cycle genomic selection (RGS) within cowpea breeding pipelines. The diagram highlights the iterative process of genotyping, phenotyping, genomic prediction, and accelerated recombination to shorten breeding cycles and enhance nutrient-use efficiency (NUE) (Figure 4).

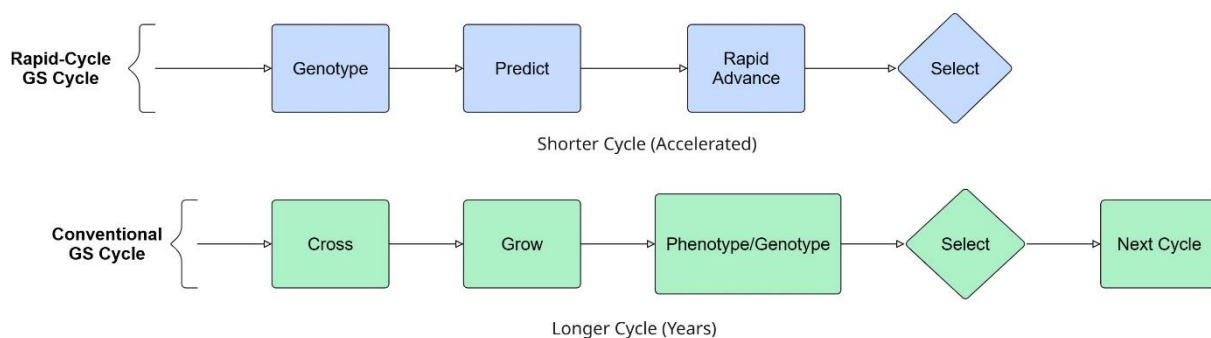


Figure 4. Principles of Genomic Selection vs. Rapid-Cycle GS

3.3 Simulation Tools (e.g., AlphaSimR) for Predicting Genetic Gain

Simulation platforms such as AlphaSimR provide breeders with powerful means to model complex breeding strategies, predict genetic gain, and optimize GS pipelines before field implementation. AlphaSimR enables simulation of entire breeding populations, including haplotype sequences, pedigree structures, and QTN effects (Faux et al., 2016). Such tools allow breeders to test scenarios involving training set size, marker density, and trait heritability, all of which affect GS accuracy.

Incorporating speed breeding and doubled-haploid methods into simulations further enhances capacity to evaluate rapid-cycle strategies (Rocha et al., 2023). Importantly, simulations have shown that GS accuracy is highly sensitive to training population composition and marker-trait linkage

disequilibrium, underscoring the need for continuous model updating during breeding cycles. This modeling capacity is particularly valuable for NUE-related traits, which are often difficult to phenotype directly.

3.4 Lessons Learned from Cereals and Other Legumes

The application of GS and RGS in cereals has provided critical lessons for legume improvement. In maize and wheat, GS has demonstrated superior efficiency for polygenic traits, while RGS has delivered rapid genetic gains without compromising diversity (Dreisigacker et al., 2023). These experiences emphasize the importance of multi-trait prediction models to balance NUE improvement with other key traits (Das et al., 2020). Legumes, once considered genomic orphans, now benefit from expanded resources such as genetic linkage maps, HapMaps, and transcriptome assemblies (Bohra et al., 2019; Salgotra & Stewart, 2022). Genomic-assisted breeding has been successfully applied in chickpea, pigeonpea, and groundnut to enhance resilience and nutritional quality (Jha et al., 2022). In lentil, GS has achieved higher prediction accuracy and genetic gains compared with conventional methods (Gebremedhin et al., 2024). These findings confirm the potential of GS and RGS to accelerate cowpea improvement, provided that investments in phenotyping infrastructure and population improvement are sustained (Varshney et al., 2019).

4. PHENOTYPING FOR NUE IN COWPEA

4.1 Traditional Phenotyping Methods: Strengths and Limitations

Traditional phenotyping approaches, including manual measurements of morphological and physiological traits, have long been foundational for NUE research in cowpea. These methods provide detailed insights into root and shoot traits, nodulation, and biomass partitioning, which are crucial for understanding nitrogen dynamics (Sinha et al., 2020). They are effective for capturing phenotypic diversity across germplasm collections and validating results from advanced tools (Amusa & Igbari, 2023; Souza et al., 2024).

However, their limitations include labor intensiveness, time consumption, and susceptibility to environmental variability, which complicate genetic interpretation of NUE-related traits (Nguyen & Kant, 2018). Low throughput further restricts their application in large-scale breeding programs. These constraints underscore the need for complementary high-throughput methods.

4.2 High-Throughput Phenotyping Tools and Proxies

Advances in high-throughput phenotyping technologies have transformed NUE research by enabling large-scale, precise, and rapid trait assessment. Techniques such as near-infrared spectroscopy (NIRS) facilitate evaluation of protein and starch content in cowpea seed, supporting non-destructive screening across diverse germplasm (Padhi et al., 2022). Imaging tools including hyperspectral, multispectral, and RGB-based systems offer detailed measurements of canopy development and nutrient status (Madurapperumage et al., 2024).

Digital biomarkers derived from image-based platforms further improve assessment of growth and nutrient response, enhancing selection efficiency for NUE (Banerjee et al., 2020). Integration of these technologies accelerates breeding pipelines while reducing reliance on nitrogen fertilizers, thereby supporting sustainability (Nguyen & Kant, 2018; Reddy et al., 2025). A comparison of traditional and high-throughput phenotyping methods highlights the benefits and limitations of each approach (Table 2). While traditional methods are detailed and accessible, they are labor-intensive and low-throughput, making them suitable for small trials and validation studies. In contrast, high-throughput methods are rapid, scalable, and precise, but require significant infrastructure and expertise, making them ideal for large populations and NUE-related traits.

Table 2. Comparison of traditional vs high-throughput phenotyping methods

Phenotyping Approach	Strengths	Limitations	Suitability for Cowpea
Traditional (manual, destructive)	Detailed, low-cost, accessible	Labor-intensive, low throughput, environment-sensitive	Useful for small trials; validation studies
High-throughput (imaging, NIRS, UAVs)	Rapid, scalable, precise; non-destructive	Costly, requires infrastructure and expertise	Suitable for large populations, NUE-related traits

Side-by-side comparison of conventional manual phenotyping versus modern high-throughput platforms (HTP). Traditional methods rely on destructive sampling and are cost-effective but labor-intensive and low in throughput, whereas HTP integrates imaging, UAVs, and spectral tools to deliver rapid, non-destructive trait measurement (Figure 5). Adapted from Crain et al. (2018), this figure underscores the role of HTP in enhancing prediction accuracy for NUE-related traits.

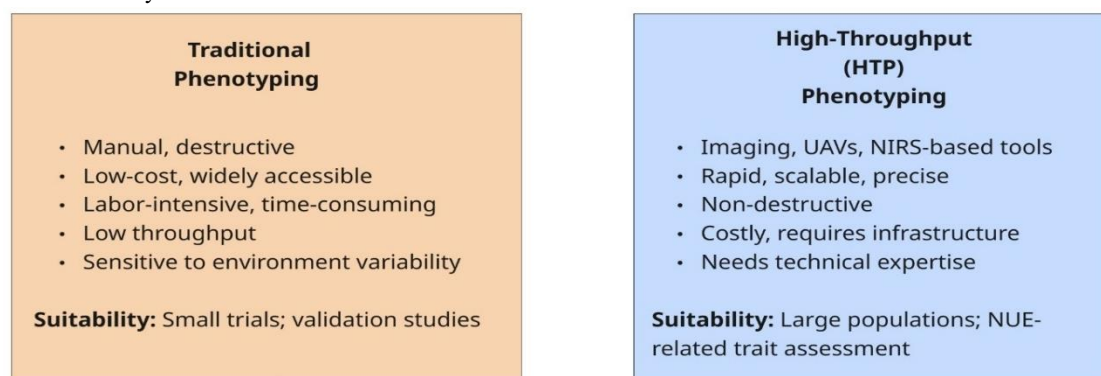


Figure 5. Phenotyping methods for NUE

4.3 Root Traits and Nutrient Acquisition Efficiency

Root morphology and architecture are central to nitrogen uptake efficiency in cowpea. Traits such as root length, branching density, and biomass allocation enhance soil exploration and nitrogen capture (Lynch et al., 2023). High root-to-shoot ratios further improve NUE by prioritizing nutrient acquisition structures (Schneider & Lynch, 2021).

Breeding for optimized root traits has been facilitated by high-throughput imaging, genome-wide association studies (GWAS), and computational modeling, which allow precise identification of genotypes with superior root systems (Paez-Garcia et al., 2015; Zaffar et al., 2024). Nevertheless, field validation remains essential to confirm trait expression under variable soil and climatic conditions (McGrail et al., 2020).

4.4 Multi-Environment Trial Designs for Capturing NUE Variability

Multi-environment trials (METs) are critical for understanding NUE trait performance across diverse production systems. Statistical approaches such as REML/BLUP and GGE biplot analyses provide robust insights into genotype stability and adaptability (Sousa et al., 2018, 2019). For example, cowpea varieties BRS Tumucumaque and MNC00-595F-27 were identified as stable and high-yielding across Brazilian environments, confirming MET utility for trait evaluation.

Integration of METs with high-throughput phenotyping enhances the ability to capture G×E interactions, ensuring that NUE traits selected under controlled conditions are transferable to field realities (Nguyen & Kant, 2018). This holistic framework acknowledges the role of genotype × environment × management (G×E×M) interactions, which are essential for translating NUE improvements from individual genotypes to whole cropping systems.

5. GENOTYPING AND TRAINING POPULATION DESIGN

5.1 Genotyping Platforms (GBS, SNP Chips, DArTseq)

Advances in genotyping platforms have transformed genomic selection by enabling high-throughput, cost-effective, and precise detection of genetic variation. Genotyping-by-sequencing (GBS) has gained traction in plant breeding owing to its flexibility and scalability. By reducing genome complexity through restriction enzyme digestion, GBS allows consistent sequencing across populations, offering broad genome coverage while minimizing ascertainment bias (Bajgain et al., 2016; Heffelfinger et al., 2014). Its adaptability to diverse genomes and amenability to multiplexing make it well-suited for genome-wide association studies (GWAS) and genomic selection.

SNP chips, such as Illumina Infinium arrays, remain widely used because of their high genotyping accuracy, ease of analysis, and reproducibility (Hyten, 2022). Despite higher costs per data point compared to GBS, their robustness makes them appropriate for breeding programs requiring precise and uniform marker datasets. DArTseq represents a mid-density alternative that combines the breadth of GBS with the consistency of SNP chips (Table 3). This platform has demonstrated success in tracking complex traits such as disease resistance in potato breeding (Endelman et al., 2024). The choice among platforms depends on trade-offs between cost, coverage, and analytical simplicity, with GBS increasingly favored in legumes like cowpea where flexibility and affordability are priorities. A comparison of genotyping platforms highlights their respective advantages and limitations (Table 3), informing the selection of the most suitable platform for genomic selection in cowpea breeding programs.

Table 3. Genotyping Platforms for Genomic Selection

Platform	Cost & Coverage	Advantages	Limitations
GBS	Low cost, genome-wide coverage	Flexible, scalable, detects novel variants	Missing data, requires imputation
SNP Chips	High cost, fixed coverage	High accuracy, reproducible, easy analysis	Limited to predefined SNPs, less flexible
DArTseq	Moderate cost, mid-density coverage	Combines benefits of GBS and SNP chips	Lower resolution than high-density arrays

5.2 Marker Density and Imputation Considerations

Marker density and genotype imputation are pivotal for optimizing prediction accuracy in genomic selection. Medium-density panels ($\approx 1,500$ SNPs) have been shown to capture up to 97% of the prediction accuracy of high-density platforms, suggesting that extremely dense marker sets may not be necessary in all cases (Sleper et al., 2025). Imputation allows breeders to cost-effectively infer missing genotypes, thereby expanding effective marker density and training set size (Jacobson et al., 2015).

Imputation accuracy depends on reference population size, genetic relatedness, and algorithm choice. Tools such as Beagle and FImpute leverage linkage disequilibrium and pedigree information to enhance accuracy (Barjasteh et al., 2019; He et al., 2015). However, imputation benefits plateau beyond certain density thresholds, requiring careful cost-benefit analysis in cowpea breeding. Thus, medium-density genotyping combined with strategic imputation offers an efficient compromise between cost and prediction performance.

5.3 Training Population Size, Diversity, and Relatedness

Training population (TP) design strongly influences genomic prediction accuracy, as it determines the relationship between training and validation populations. Larger TPs generally enhance accuracy, as shown in strawberry where prediction accuracy continued to increase with $>3,000$ individuals (Sleper et al., 2025). However, genetic diversity and relatedness play a critical balancing role. While broad diversity can improve robustness across environments, low relatedness between training and validation populations decreases prediction accuracy, as reported in salmon and cassava (Fraslin et al., 2021).

For cowpea, breeding programs must optimize TP design by ensuring sufficient size while maintaining adequate relatedness to target populations. Selective genotyping of individuals from diverse genetic backgrounds, combined with periodic TP updates, can sustain prediction accuracy across

breeding cycles (Cossa et al., 2021). This balance is particularly important for NUE traits, where environmental sensitivity and polygenic architecture demand robust training datasets.

5.4 Multi-Trait and Multi-Environment Prediction Models

Multi-trait and multi-environment genomic prediction models represent advanced approaches for improving selection efficiency. Multi-trait models exploit genetic correlations between traits, enhancing prediction accuracy for traits with low heritability or limited phenotypic data. In cowpea, integrating NUE with yield, drought tolerance, and disease resistance can improve overall selection response.

Multi-environment models account for G×E interactions, enabling breeders to identify genotypes with stable performance across environments or specific adaptation to target agro-ecologies. Bayesian and machine learning approaches have shown promise in capturing complex trait architectures and non-additive effects (Montesinos-López et al., 2021). For cowpea breeding, these models offer pathways to simultaneously improve NUE and other priority traits while managing environmental variability.

6. EVIDENCE FOR GS IN COWPEA AND RELATED LEGUMES

6.1 Cowpea Genomic Resources and Diversity Studies

Cowpea genomic resources have expanded substantially in recent years, providing a foundation for genomic selection. The release of the cowpea reference genome and development of high-density SNP panels have enabled genome-wide association studies (GWAS) and identification of quantitative trait loci (QTLs) associated with complex traits, including drought tolerance, disease resistance, and nutritional quality (Boukar et al., 2019; Salgotra & Stewart, 2022). GS models integrating these genome-wide markers are increasingly employed to predict breeding values and accelerate genetic gain (Jain et al., 2017; Wang et al., 2018).

Complementary approaches such as marker-assisted backcrossing (MABC) and marker-assisted recurrent selection (MARS) continue to play roles in improving simpler traits, but GS provides greater power for polygenic traits like NUE (Jain et al., 2017). Notable progress includes development of climate-resilient varieties combining tolerance to abiotic stress with resistance to pests and diseases (Sindhu et al., 2019). However, challenges remain in scaling GS adoption due to limitations in regeneration systems, efficiency of gene transfer, and the need for optimized training populations that account for genotype × environment interactions.

6.2 Genomic Selection Applications in Cowpea (Current State)

Current applications of genomic selection in cowpea remain limited compared to major cereals, but pilot studies demonstrate its feasibility. Marker-assisted selection has been successfully applied for traits such as aphid resistance, Striga resistance, and pod borer tolerance (Boukar et al., 2019). However, full implementation of GS for complex traits like NUE requires expanded phenotyping capacity, larger training populations, and validation across multiple environments.

Recent initiatives by CGIAR centers and national programs have begun to establish the infrastructure necessary for GS deployment, including genotyping facilities, data management systems, and capacity building for bioinformatics (Varshney et al., 2019). These efforts position cowpea breeding programs to transition from marker-assisted selection to full genomic selection, particularly for traits that are difficult or expensive to phenotype.

6.3 Evidence from Related Legumes (Soybean, Common Bean, Groundnut)

Insights from other legumes reinforce the potential of GS for enhancing NUE. Soybean demonstrates high nitrogen fixation efficiency, deriving 61% of nitrogen from the atmosphere in North America and up to 78% in Brazil (Peoples et al., 2021). Groundnut also contributes substantially, fixing 150–200 kg N ha⁻¹ through symbiotic associations, with %Ndfa ranging from 72% to 77%. By contrast, common bean shows lower nitrogen fixation efficiency, with an average %Ndfa of 38% (Peoples et al., 2021).

Genomic-assisted breeding has been applied to these legumes with promising outcomes. In soybean, molecular tools have been used to enhance nodulation and NUE under water- and phosphorus-limited conditions (Jin et al., 2022). In chickpea and lentils, GS has improved yield-related traits and stress adaptation, with accuracies ranging from moderate to high (Roorkiwal et al., 2016). These advances illustrate the feasibility of transferring similar GS frameworks to cowpea, provided that adequate phenotyping and training populations are available.

6.4 Reported Heritability and Prediction Accuracies for NUE-Related Traits

Heritability and genomic prediction accuracies for NUE traits vary widely across crops, reflecting differences in genetic architecture, environments, and modeling approaches. In tropical maize, nitrogen utilization efficiency showed moderate heritability (0.49 under high-N conditions) but dropped under low-N inputs (0.22), underscoring the sensitivity of estimates to nutrient availability (Torres et al., 2018). In lentils, heritability estimates for NUE-related traits ranged from 0.24 to 0.66, with genomic prediction accuracies between 0.34 and 0.83 depending on the model used (Gebremedhin et al., 2024).

Comparable findings are reported in chickpea, where yield-related traits linked to NUE exhibited prediction accuracies ranging from 0.14 to 0.91, with the highest values for seed weight (Roorkiwal et al., 2016). Maize studies further confirm that prediction accuracy improves when training populations include both parents of hybrids, with accuracies up to 0.78 (Mastrodomenico et al., 2019). A summary of reported heritability and prediction accuracies for NUE-related traits in legumes is presented in Table 4, highlighting the range of estimates and the potential for genomic improvement of NUE in these crops.

Table 4. Reported heritability and prediction accuracies for NUE-related traits in legumes

Species	Trait	Heritability (h ²)	Prediction Accuracy	Reference
Maize	Nitrogen utilization efficiency	0.22–0.49	Up to 0.78	Mastrodomenico et al., 2019; Torres et al., 2018
Lentil	NUE-related traits	0.24–0.66	0.34–0.83	Gebremedhin et al., 2024; Haile et al., 2019
Chickpea	Yield, seed weight	Moderate	0.14–0.91	Roorkiwal et al., 2016

7. SIMULATION STUDIES AND EXPECTED GAINS

7.1 Predicted ΔG per Cycle vs. ΔG per Year under RGS

Simulation studies provide critical insights into the potential of rapid-cycle genomic selection (RGS) to accelerate genetic gain. Genetic gain per cycle (ΔG per cycle) represents improvement achieved within a single breeding cycle, while genetic gain per year (ΔG per year) accounts for cycle frequency. RGS fundamentally alters this relationship by reducing cycle length, thereby multiplying annual genetic gain even when per-cycle gains remain modest (Gaynor et al., 2020).

In maize, RGS achieved ΔG per year values 1.5 to 2 times higher than conventional breeding by enabling two cycles annually. Similarly, wheat breeding simulations demonstrated that reducing cycle length from 5 years to 2 years through speed breeding and genomic selection could double annual genetic gain (Dreisigacker et al., 2023). In ryegrass, RGS delivered genetic gains of 12.3% for grain yield within three cycles, demonstrating the power of accelerated recombination combined with genomic prediction (Byrne et al., 2024).

For cowpea, simulation studies suggest that implementing RGS could achieve similar gains, particularly for traits like NUE that are difficult to phenotype and have moderate heritability. However, realizing these gains requires careful optimization of training population size, prediction accuracy, and selection intensity (Crain et al., 2021).

7.2 Risks of Accelerated Cycles: Inbreeding and Variance Loss

While RGS offers substantial benefits, accelerated breeding cycles pose risks related to inbreeding and loss of genetic variance. Rapid selection can quickly fix favorable alleles but simultaneously reduce effective population size, leading to inbreeding depression and loss of long-term selection response. Simulations in dairy cattle and crops have shown that without proper management, RGS can deplete genetic variance within 5–10 cycles, compromising future breeding progress (Gorjanc et al., 2015).

In cowpea, where genetic diversity is already limited in some breeding populations, these risks are particularly concerning. Loss of rare alleles that may be valuable for future trait improvement such as novel pest resistance or climate adaptation represents a significant long-term cost (Dunckel et al., 2017). Furthermore, inbreeding can reduce fitness traits such as vigor and fertility, offsetting gains in target traits like NUE.

7.3 Strategies to Mitigate Risks (Optimal Contribution, Diversity Management)

Several strategies can mitigate the risks of inbreeding and variance loss in RGS programs. Optimal contribution selection (OCS) balances genetic gain with maintenance of genetic diversity by constraining the contribution of superior individuals to the next generation (Gorjanc et al., 2015). This approach has been successfully applied in animal breeding and is increasingly adopted in plant breeding programs.

Genomic diversity indices, such as expected heterozygosity and genomic relationship matrices, provide tools for monitoring and managing diversity in real-time (Cossa et al., 2021). Periodic introduction of new germplasm into training populations can replenish genetic variance, though this must be balanced against potential reductions in prediction accuracy due to increased genetic distance (Fraslin et al., 2021). For cowpea, integrating landraces and wild relatives into breeding populations offers a pathway to maintain diversity while pursuing rapid genetic gain.

7.4 Optimization of Selection Intensity and Cycle Length

Optimizing selection intensity and cycle length is critical for maximizing long-term genetic gain under RGS. High selection intensity accelerates short-term gains but increases inbreeding and variance loss, while moderate intensity preserves diversity at the cost of slower progress (Gaynor et al., 2020). Simulation studies suggest that an optimal balance exists, typically involving selection of 10–20% of candidates per cycle (Gorjanc et al., 2015).

Cycle length optimization depends on crop biology, phenotyping capacity, and infrastructure. For cowpea, speed breeding protocols enabling 4–8 generations per year have been demonstrated (Edet & Ishii, 2022), though practical implementation in resource-limited settings may support 2–3 cycles annually. Economic modeling indicates that even modest reductions in cycle length can substantially improve cost-effectiveness of breeding programs by accelerating variety release and adoption (Crain et al., 2021).

8. INTEGRATING RGS INTO COWPEA BREEDING PIPELINES

8.1 Role of Speed Breeding and Off-Season Nurseries

Speed breeding and off-season nurseries are key enablers of RGS in cowpea. Speed breeding employs controlled environment facilities with extended photoperiods and optimal temperature regimes to accelerate plant development, enabling multiple generations per year (Watson et al., 2019). In cowpea, protocols have been developed that achieve up to 8 generations annually using growth chambers and immature seed harvest (Edet & Ishii, 2022).

Off-season nurseries complement speed breeding by utilizing geographic locations with favorable climates during the off-season of primary breeding sites. For African cowpea programs, nurseries in contrasting agro-ecologies enable year-round field evaluations of homozygous lines, reducing cultivar development timelines (Walia, 2024). However, challenges such as infrastructure costs, genotype-specific responses, and stress effects of accelerated growth must be carefully managed. Addressing these limitations through optimized protocols and investment in controlled-environment facilities is essential for mainstreaming RGS in cowpea pipelines.

Flowchart summarizing the sequential steps in implementing GS and RGS for NUE improvement. The process begins with germplasm characterization and training-population development, followed by genotyping, phenotyping, genomic prediction, and selection of superior genotypes based on genomic estimated breeding values (GEBVs). Rapid-cycle advancement through off-season nurseries accelerates recombination and reduces cycle time (Figure 7).



Figure 6. GS/RGS Pipeline in Cowpea Breeding

8.2 Cost–Benefit Considerations in Low-Resource Programs

Successful integration of RGS in cowpea requires balancing efficiency gains with affordability, particularly in low-resource settings. Speed breeding can be implemented with minimal infrastructure beyond standard growth chambers, making it accessible to national breeding programs with constrained budgets (Edet & Ishii, 2022). Furthermore, cost-effective genotyping methods such as targeted resequencing can reduce per-sample costs by up to 35%, as demonstrated in peanut breeding (Sung et al., 2024).

Genomic resources, including SNP panels and the UCR Minicore collection, provide cost-efficient platforms for trait dissection and genomic prediction in cowpea (Muñoz-Amatriain et al., 2021). Nevertheless, challenges such as limited phenotyping capacity and initial investment in infrastructure remain significant barriers. Cost–benefit analyses suggest that incremental integration of RGS, supported by capacity building and donor partnerships, can mitigate these constraints while maximizing long-term returns in breeding efficiency.

8.3 Institutional Capacity, Partnerships, and Infrastructure Needs

Integrating RGS into cowpea pipelines requires robust institutional capacity and infrastructure for data management, genotyping, and phenotyping. Centralized data management systems such as Breedbase facilitate handling of large genotypic and phenotypic datasets, improving decision-making in breeding (Morales et al., 2022). High-throughput genotyping platforms, coupled with marker-assisted selection, accelerate trait introgression for pest and disease resistance.

On the phenotyping side, advanced field and controlled-environment platforms are necessary to capture NUE and stress-related traits at scale. Despite these opportunities, public-sector breeding programs often lack resources to sustain high-tech infrastructure. Investment in collaborative frameworks linking CGIAR centers, national agricultural research systems (NARS), and private sector actors can help bridge resource gaps while enhancing knowledge exchange (Parmar et al., 2021). Building human capacity in data analytics and bioinformatics is equally critical to support adoption of genomics-assisted breeding.

8.4 Participatory Approaches to Ensure Adoption of NUE Varieties

For RGS-enabled cowpea varieties to achieve widespread impact, participatory approaches must be embedded in breeding pipelines. Farmer participation ensures that breeding objectives align with local agronomic needs, culinary preferences, and market traits (Egbadzor et al., 2015). Participatory varietal selection (PVS) in Mozambique and Ghana has demonstrated that farmer-led evaluations enhance adoption by ensuring varieties meet socio-cultural and economic expectations.

Gender-responsive breeding is equally important, as women often play central roles in cowpea production, processing, and marketing (Friedmann et al., 2024). Integrating gender analysis into breeding programs ensures that varietal traits address the specific needs and preferences of women farmers, thereby improving adoption rates and impact (Bacud et al., 2024). For NUE varieties, participatory approaches can help identify traits that reduce labor requirements, improve food quality, and enhance profitability under diverse farming systems.

9. DEBATES AND OPEN QUESTIONS

9.1 Trade-off Between Genomic Prediction Accuracy and Breeding Cycle Speed

A central debate in RGS concerns the trade-off between genomic prediction accuracy and breeding cycle speed. Rapid cycling reduces time for phenotyping, potentially compromising training population quality and prediction accuracy (Crain et al., 2021). Some argue that maintaining longer cycles with more extensive phenotyping preserves accuracy and reduces risk of selecting inferior genotypes.

However, empirical evidence suggests that moderate reductions in prediction accuracy can be offset by increased cycle frequency, resulting in net gains in annual genetic improvement (Gaynor et al., 2020). For cowpea NUE, where phenotyping is expensive and time-consuming, accepting slightly lower per-cycle accuracy in exchange for more frequent selection may be optimal. Ongoing research is needed to define accuracy thresholds below which RGS becomes counterproductive.

9.2 Managing Genetic Diversity and Inbreeding in Rapid-Cycle Breeding Programs

Managing genetic diversity under RGS remains a contentious issue. Critics argue that rapid selection inevitably depletes diversity, limiting future breeding options and increasing vulnerability to emerging pests and diseases (Dunckel et al., 2017). Proponents counter that with appropriate diversity management strategies such as optimal contribution selection and periodic germplasm introgression-RGS can maintain adequate diversity while achieving rapid gains (Gorjanc et al., 2015).

For cowpea, where genetic bottlenecks have occurred historically, this debate is particularly relevant. Balancing short-term productivity gains with long-term genetic resource conservation requires explicit breeding objectives that incorporate diversity metrics alongside trait improvement targets. Transparent reporting of diversity trends in breeding populations is essential for informed decision-making.

9.3 Resource Allocation in Breeding: High-Throughput Phenotyping versus Genotyping

Resource allocation between phenotyping and genotyping represents another key debate. High-throughput phenotyping (HTP) can improve training population quality and prediction accuracy but requires substantial investment in equipment and expertise (Crain et al., 2018). Conversely, investing in genotyping capacity enables larger populations to be screened but may not improve accuracy if phenotypic data is limiting.

Simulation studies suggest that optimal allocation depends on trait heritability, phenotyping cost, and population structure (Crain et al., 2021). For low-heritability traits like NUE, investment in HTP may yield greater returns by improving phenotype quality. For high-heritability traits, expanding genotyping capacity may be more cost-effective. Cowpea programs must tailor resource allocation to their specific trait priorities and budget constraints.

9.4 Genotype-by-Environment Interaction (G×E) and Stability of Genomic Selection Models

The stability of genomic selection models across environments is a critical concern for cowpea breeding in Africa, where production systems are highly heterogeneous. G×E interactions can reduce prediction accuracy when models trained in one environment are applied in another (Jarquin et al., 2017). Multi-environment genomic prediction models that explicitly account for G×E have shown promise in wheat and maize but require extensive phenotyping across environments (Bancic et al., 2023).

For cowpea NUE, where environmental factors strongly influence trait expression, developing robust multi-environment models is essential. This may require regional breeding networks that share phenotypic and genotypic data, enabling models to capture G×E patterns across African agro-ecologies. Alternatively, breeding for broad adaptation rather than specific adaptation may simplify selection while maintaining acceptable performance across environments.

9.5 Socioeconomic Trade-offs and Farmer Adoption: Aligning Breeding Objectives with Local Preferences

Aligning breeding objectives with farmer preferences remains a persistent challenge. While breeders prioritize traits like NUE and yield, farmers often value characteristics such as grain color, cooking time, and market demand (Marennya et al., 2022). Misalignment between breeding objectives and farmer preferences is a major cause of low adoption rates for improved varieties.

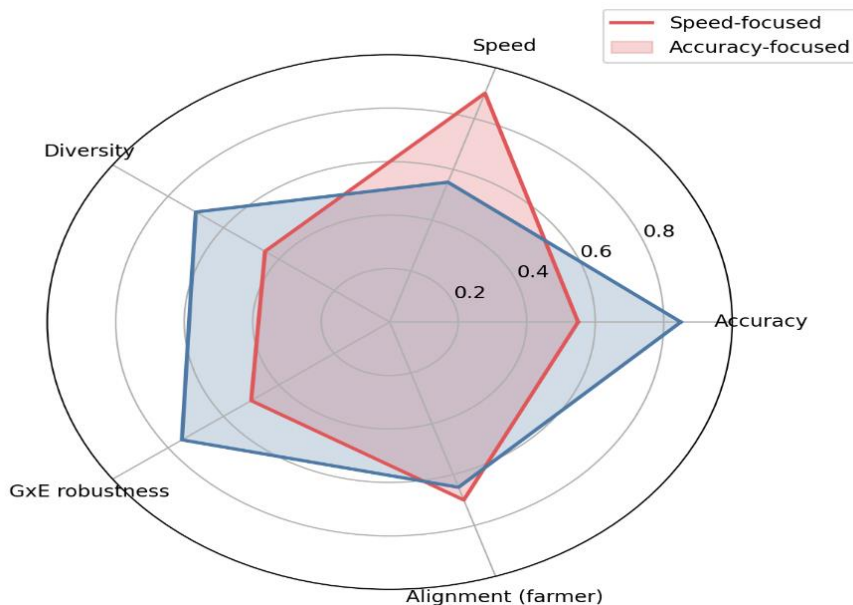
Gender and social marginalization further complicate this issue, as different farmer groups may have divergent preferences (Bacud et al., 2024). For example, women may prioritize processing qualities and nutritional content, while men focus on yield and market value. Participatory breeding approaches that engage diverse stakeholder groups in variety evaluation and selection can help bridge these gaps (Gesesse et al., 2023). For NUE varieties, demonstrating tangible benefits such as reduced fertilizer costs and improved profitability will be critical for farmer adoption.

Table 5 outlines key trade-offs and considerations for implementing rapid-cycle genomic selection (RGS) in cowpea, emphasizing the importance of balancing accuracy, genetic diversity, phenotyping, genotyping, and socioeconomic factors. Qualitative depiction of the principal trade-offs influencing implementation of rapid-cycle genomic selection (RGS) for nutrient-use efficiency (NUE) in cowpea.

Table 5. Summary of major trade-offs and implementation considerations in rapid-cycle genomic selection (RGS) for cowpea

Trade-off Theme	Description / Mechanism	Evidence & Implications	Key References
Accuracy vs Cycle Speed	Shorter cycles reduce phenotypic information per round, potentially lowering model accuracy.	Moderate cycle reduction (< 50 %) maintains > 90 % accuracy if training data large & connected.	Norman et al., 2017
Genetic Diversity vs Gain	Re-selecting high GEBVs each cycle can shrink allelic variance.	Inbreeding rate ≈ 0.02 – 0.04 per cycle under unconstrained RGS; use optimal-contribution selection to control it.	Festa & Whetten, 2021
Phenotyping Genotyping Investment	High-throughput phenotyping (HTP) costly but enhances prediction of NUE traits.	Combining cheap genotyping (GBS) + targeted HTP (leaf spectra, UAV indices) maximizes cost efficiency.	Crain et al., 2018 Bacud et al., 2024
G×E Complexity & Model Stability	GS models trained in few environments often fail in new ones.	Multi-environment and enviromic models raise accuracy by 15–30 % across locations.	Jarquín et al., 2020; Crossa et al., 2021
Socioeconomic Alignment	Breeding targets must fit local market & farmer preferences for uptake.	Participatory selection and seed-system linkages essential for adoption of NUE-efficient varieties.	Adebisi & Lucero-Prisno, 2022

The radar diagram contrasts five interacting dimensions selection speed, prediction accuracy, genetic-diversity maintenance, phenotyping/genotyping investment, and socio-economic alignment based on evidence from recent genomic-selection simulations and breeding-program analyses (Figure 8). Higher speed improves annual gain but can reduce prediction reliability and genetic variance; balanced investment in data collection and participatory breeding is required to sustain long-term progress.

**Figure 7. Conceptual visualization of key trade-offs in rapid-cycle genomic selection for cowpea**

10. FUTURE DIRECTIONS AND RESEARCH PRIORITIES

10.1 Need for Empirical GS Studies Targeting NUE in Cowpea

Despite theoretical promise, empirical studies demonstrating GS effectiveness for NUE in cowpea remain scarce. Most evidence comes from simulation or extrapolation from other crops. Field-based validation studies are urgently needed to confirm prediction accuracies, quantify genetic gains, and identify optimal breeding strategies under African conditions.

These studies should evaluate multiple prediction models, training population designs, and phenotyping approaches to establish best practices. Collaboration between CGIAR centers and national programs can facilitate multi-location trials that capture G×E interactions and validate model transferability across environments.

10.2 Optimizing Training Population Design under African Conditions

Training population design requires optimization for African cowpea production systems, which differ substantially from conditions in developed countries where most GS research has been conducted. Factors such as soil fertility gradients, water availability, and pest pressure create unique selection environments that may not be captured in standard training populations.

Research priorities include determining optimal training population size for cowpea NUE, evaluating the value of including landraces and wild relatives, and assessing the frequency of training population updates needed to maintain prediction accuracy. Cost-effective strategies for training population development in resource-limited settings are particularly important.

10.3 Developing Cost-Effective Phenotyping Pipelines

High-throughput phenotyping remains a bottleneck for GS implementation in cowpea. Developing cost-effective phenotyping pipelines that balance accuracy, throughput, and affordability is a critical research priority. Near-infrared spectroscopy (NIRS) for seed nutrient content and UAV-based imaging for canopy traits offer promising starting points.

Integration of phenotyping proxies such as leaf chlorophyll content as an indicator of nitrogen status can further reduce costs while maintaining adequate prediction accuracy. Validation of these proxies under diverse field conditions is needed to ensure reliability. Collaborative phenotyping platforms that serve multiple breeding programs can improve cost-effectiveness through economies of scale.

10.4 Multi-Environment GS Models for NUE and Yield Stability

Developing robust multi-environment GS models for NUE and yield stability is essential for cowpea improvement in Africa. These models must account for complex G×E interactions while remaining computationally tractable for resource-limited programs. Bayesian and machine learning approaches show promise but require extensive validation.

Research should focus on identifying environmental covariates that explain G×E patterns, enabling more accurate predictions in untested environments. Integration of crop growth models with genomic prediction may offer additional predictive power by mechanistically linking genotype, environment, and phenotype.

10.5 Pilot Implementation of Rapid-Cycle GS in Cowpea Programs

Pilot implementation of RGS in selected African cowpea breeding programs is needed to demonstrate feasibility and quantify benefits under operational conditions. These pilots should evaluate different RGS strategies including speed breeding, off-season nurseries, and combinations thereof to identify optimal approaches for different program contexts.

Comprehensive economic analysis of pilot programs will inform scaling decisions and investment priorities. Lessons learned regarding infrastructure requirements, capacity building needs, and operational challenges will be invaluable for broader RGS adoption across cowpea breeding networks.

11. CONCLUSIONS

Synthesis of Opportunities and Challenges

Rapid-cycle genomic selection offers transformative potential for accelerating genetic improvement of nutrient-use efficiency in cowpea. Opportunities include leveraging expanded genomic resources, cost-effective genotyping platforms, and high-throughput phenotyping technologies to achieve annual genetic gains 1.5 to 2 times higher than conventional breeding. Evidence from cereals and other legumes demonstrates the feasibility of this approach for complex, polygenic traits like NUE.

However, significant challenges remain. Phenotyping NUE traits at scale requires substantial investment in infrastructure and expertise. Managing genetic diversity under rapid selection cycles demands explicit strategies to prevent inbreeding and variance loss. Ensuring that improved varieties meet farmer preferences and achieve high adoption rates requires participatory approaches and gender-responsive breeding. For resource-limited African breeding programs, balancing these opportunities and challenges while maintaining cost-effectiveness is a central concern.

Roadmap for Breeders and Researchers

A practical roadmap for implementing RGS in cowpea breeding includes several key steps. First, establish or expand genomic resources, including reference populations, SNP panels, and genotyping capacity. Second, develop cost-effective phenotyping pipelines that balance accuracy and throughput, prioritizing traits most relevant to farmer needs. Third, pilot RGS strategies in selected breeding programs to validate effectiveness and refine protocols.

Fourth, invest in institutional capacity, including data management systems, bioinformatics expertise, and collaborative networks linking CGIAR centers, NARS, and farmers. Fifth, implement diversity management strategies to ensure long-term breeding progress and genetic resource conservation. Finally, engage farmers and other stakeholders throughout the breeding process to ensure that improved varieties address real-world needs and achieve high adoption rates.

Final Thoughts on Accelerating Genetic Gain for NUE in Cowpea

Accelerating genetic gain for nutrient-use efficiency in cowpea is essential for achieving sustainable intensification of African agriculture. Rapid-cycle genomic selection provides a powerful tool for this purpose, but its successful implementation requires careful attention to technical, economic, and social dimensions. By integrating advanced genomic tools with participatory breeding approaches and strategic partnerships, cowpea breeding programs can deliver varieties that are more productive, resource-efficient, and responsive to farmer needs.

The path forward demands sustained investment in research, infrastructure, and capacity building. It also requires adaptive management, as breeding strategies must evolve in response to emerging challenges such as climate change, evolving pest pressures, and shifting market demands. With appropriate support and strategic implementation, RGS can substantially accelerate genetic gain for NUE and contribute to food security, poverty alleviation, and environmental sustainability in smallholder farming systems across sub-Saharan Africa.

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