



International Journal of Agriculture and Nutrition

ISSN Print: 2664-6064
ISSN Online: 2664-6072
NAAS Rating (2025): 4.69
IJAN 2025; 7(12): 11-19
www.agriculturejournal.net
Received: 16-09-2025
Accepted: 19-10-2025

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Use of genomic prediction and GWAS to breed for drought tolerance in common beans: Nurturing resilient crops in a thirsty world - A review

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DOI: <https://www.doi.org/10.33545/26646064.2025.v7.i12a.321>

Abstract

Common beans (*Phaseolus vulgaris* L.), play a crucial role in enhancing food security and promoting sustainable agriculture in developing countries. Its production has however been significantly impacted by drought in the Sub-Saharan Africa, exacerbating the problems of food security and economic stability across various regions. This has necessitated tailored adaptation strategies to mitigate the adverse effects of drought on its production and food security in the region that include breeding for drought tolerance. Drought tolerance in agriculture holds significant potential for enhancing crop resilience and ensuring food security, particularly in the face of climate change and increasing water scarcity. Integrating drought tolerance into breeding programs should involve several advanced strategies that include Genomic prediction and Genome-Wide Association Studies (GWAS) as exceptionally powerful and sophisticated instruments for dissecting and elucidating the complex genetic underpinnings associated with drought tolerance. In the realm of agricultural research, it is imperative that future investigations meticulously integrate multi-environment phenotyping techniques alongside comprehensive genomic data in order to more effectively elucidate the intricate interactions between genotype and environment, with a particular emphasis on the vast and diverse gene pools of bean varieties.

Keywords: Drought tolerance, genomic prediction, genome-wide association studies, common beans

Introduction

Legumes, particularly common beans (*Phaseolus vulgaris* L.), play a crucial role in enhancing food security and promoting sustainable agriculture in developing countries. They are nutrient-dense, providing high levels of protein, dietary fiber, and essential minerals, which are vital for combating malnutrition in low-income populations (Uebersax *et al.*, 2022, Lisciani *et al.*, 2024) [81, 46]. Legumes also contribute to sustainable agricultural practices through symbiotic nitrogen fixation, reducing the need for chemical fertilizers and improving soil health (Islam *et al.*, 2022, Uebersax *et al.*, 2022) [77, 81]. Their short growth cycle allows for crop diversification, which is essential in adapting to climate variability and ensuring stable food production (Uebersax *et al.*, 2022, Wondaferew *et al.*, 2024) [81, 91]. Additionally, underutilized legumes like marama beans and Bambara groundnuts exhibit high drought tolerance and nutritional value, presenting opportunities for sustainable food sources in regions facing climate challenges (Aderinola & Duodu, 2024) [1]. Overall, the integration of legumes into agricultural systems supports both nutritional needs and environmental sustainability, making them a key component in addressing food security issues in developing nations.

Drought significantly impacts bean production in Sub-Saharan Africa, exacerbating the problems of food security and economic stability across various regions. The frequency and intensity of drought events have escalated, particularly post-1990, leading to increased crop failures and water scarcity, with the Sahara region experiencing the most severe trends (Ogunrinde *et al.*, 2025, Lombe *et al.*, 2024) [57, 47]. Vulnerable populations, especially those in lower income brackets, face income reductions of up to 40%, as they lack the resources to adapt or recover from drought impacts (Pignède, 2025). The effects vary regionally; for instance, Central Africa experiences heightened nutritional risks linked to socio-economic instability, while Northern Africa faces severe agricultural and water insecurity due to extreme drought conditions (Sharma *et al.*, 2024) [73]. Overall, the complex interplay of

climatic, economic, and social factors necessitates tailored adaptation strategies to mitigate the adverse effects of drought on bean production and food security in the region (Lombe *et al.*, 2024, Sharma *et al.*, 2024) [47, 73].

Drought tolerance in common beans

Drought tolerance in common beans (*Phaseolus vulgaris* L.) is a multifaceted trait influenced by genetic, physiological, and agronomic factors. Research has identified specific genotypes, such as CAL96 and DAB541, that exhibit enhanced drought resilience through mechanisms like the overexpression of drought-responsive genes (PvDREB1F and PvDREB5A) and improved antioxidative stress responses, which correlate with biomass production under drought conditions (Pholo-Tait *et al.*, 2024) [59]. Additionally, studies on landrace accessions from Italy revealed significant variability in drought tolerance, with certain genotypes maintaining higher yields under water scarcity, emphasizing the importance of morpho-physiological traits in predicting drought resilience (Alicandri *et al.*, 2024) [3]. Furthermore, the application of foliar treatments, such as iron nanoparticles and ascorbic acid, has been shown to enhance growth and antioxidant defenses, thereby mitigating drought stress effects (Yilmaz, 2024) [95]. Agronomic evaluations of Andean genotypes highlighted the role of water use efficiency and assimilate partitioning in achieving drought tolerance, with specific genotypes identified as promising candidates for breeding programs (Hamabwe *et al.*, 2024) [28]. Lastly, the diversity in stomatal and hydraulic responses among common bean genotypes suggests that both isohydric and anisohydric strategies contribute to drought resilience, indicating a complex interplay of physiological adaptations (Buckley *et al.*, 2024) [9].

In Uganda, the cultivation of drought-tolerant bean varieties is crucial due to the frequent occurrence of drought conditions that significantly impact agricultural productivity. Recent studies have identified several bean genotypes with enhanced drought resistance, which are being integrated into breeding programs to improve yields under water-scarce conditions. The Lechinta genotype, known for its high drought stress resistance, has shown superior adaptability compared to other genotypes like M-2087 and A-1988, which originate from the Mesoamerican and Andean gene pools, respectively (Galan *et al.*, 2024) [20]. Additionally, improved varieties such as Flor de Mayo Eugenia and Negro 8025 have demonstrated significant drought tolerance, with yields of 1,905 and 1,843 kg ha⁻¹ under drought conditions, respectively, compared to higher yields under irrigated conditions (Rivera, 2024) [19]. These varieties have been developed through breeding programs that focus on traits such as water use efficiency, relative water content, and root/shoot ratio, which are crucial for drought resistance (Verheyen *et al.*, 2024) [82]. The integration of genetic and molecular insights, such as the expression of genes related to stress response and signaling, further enhances the development of drought-tolerant varieties (Ponce *et al.*, 2024) [61]. The use of the Target Population of Environments (TPE) approach has also been instrumental in identifying and targeting genotypes that perform well under specific drought conditions in East Africa, including Uganda (Jha *et al.*, 2024) [35]. These efforts

collectively aim to ensure sustainable bean production and food security in the face of climate change.

Physiology & phenotyping of drought tolerance

Drought tolerance in agriculture holds significant potential for enhancing crop resilience and ensuring food security, particularly in the face of climate change and increasing water scarcity. Integrating drought tolerance into breeding programs involves several advanced strategies. Molecular breeding tools, such as Quantitative Trait Loci (QTL) mapping and Genome-Wide Association Studies (GWAS), have been instrumental in identifying genes linked to drought tolerance in crops like maize, which can be exploited for breeding applications (Rasheed *et al.*, 2023) [63]. Marker-Assisted Selection (MAS) and Genomic Selection (GS) are pivotal in reducing environmental impacts and enhancing the efficiency of breeding programs by facilitating the introgression of valuable traits from diverse germplasm collections (Rauf *et al.*, 2016) [64]. Additionally, the use of High-Throughput Phenotyping Platforms (HTPPs) allows for the evaluation of physiological responses to drought at early growth stages, improving the efficiency of breeding drought-tolerant wheat varieties (Khadka *et al.*, 2020) [41]. The integration of conventional and molecular breeding methods, alongside the introduction of drought-tolerant, underutilized crops, can enhance agricultural resilience to water deficiency (Rosero *et al.*, 2020) [67]. At institutions like ICRISAT, efforts are focused on identifying and mapping QTL for specific drought-tolerance traits, such as stay-green in sorghum and root traits in chickpea, to improve crop performance under water-limited conditions (Serraj *et al.*, 2005) [72]. These comprehensive approaches, combining advanced genetic tools and phenotyping techniques, are crucial for developing drought-tolerant cultivars that can sustain productivity in challenging environments.

Drought tolerance in plants involves a complex interplay of physiological, biochemical, and molecular mechanisms that enable them to survive water scarcity. Key strategies include osmotic adjustment, which helps maintain cellular turgor, and the synthesis of protective proteins such as dehydrins that mitigate dehydration stress (Haghpahanah *et al.*, 2024) [26]. Additionally, plants enhance their root systems for improved water uptake and exhibit morphological adaptations like leaf rolling and increased cuticle thickness to reduce transpiration (Shil, 2023) [74]. Hormonal signaling, particularly involving abscisic acid, plays a crucial role in regulating stomatal closure and water conservation (Ilyas *et al.*, 2021) [32]. Antioxidant systems are activated to counteract oxidative stress caused by reactive oxygen species, with enzymes like superoxide dismutase and catalase being pivotal in this defense (Hashmi *et al.*, 2023) [29]. Furthermore, the integration of genetic approaches, including transgenic methods, is being explored to enhance drought resilience in crops, ensuring food security in the face of climate change (Batool *et al.*, 2024, Shil, 2023) [5, 74]. Phenotyping techniques play a crucial role in identifying and characterizing drought-tolerant traits in crops by enabling the assessment of various physiological and morphological traits that contribute to drought resilience. Root phenotyping, for instance, allows researchers to evaluate Root System Architecture (RSA), which is vital for water uptake and recovery from drought stress, highlighting traits such as root length and surface area that are linked to

genetic loci associated with drought tolerance (Dutta & Sarma, 2022) ^[17]. High-Throughput Phenotyping (HTP) methods facilitate the non-destructive analysis of large-scale phenotypic data, thus enhancing the understanding of plant responses to drought and enabling the identification of key traits like limited transpiration, which conserves water during stress (Kim *et al.*, 2021, Sarkar *et al.*, 2022) ^[43, 70]. Furthermore, comprehensive phenotyping approaches have led to the identification of consistent markers, such as stomatal density and canopy temperature depression, which can be utilized for early selection in breeding programs aimed at developing drought-tolerant cultivars (Tuberosa, 2012, Toum *et al.*, 2022) ^[80, 79]. Collectively, these techniques provide a robust framework for dissecting the genetic basis of drought tolerance, ultimately guiding the development of resilient crop varieties.

GWAS results in common bean (Plus comparative legume examples)

Genome-Wide Association Studies (GWAS) in common bean (*Phaseolus vulgaris*) significantly enhance the understanding of genetic variation in legume crops by identifying key genetic loci associated with important agronomic traits. For instance, GWAS has revealed SNPs linked to traits such as cooking time, water uptake, and micronutrient concentrations (Fe and Zn), which are crucial for addressing nutritional deficiencies in human diets (Binagwa *et al.*, 2020) ^[6]. Additionally, studies have identified major QTLs for disease resistance, such as rust and scab, highlighting the genetic basis for resilience against pathogens, which is vital for crop yield stability (Wu *et al.*, 2022, Oriama *et al.*, 2024) ^[92, 58]. Furthermore, GWAS has facilitated the discovery of Quantitative Trait Nucleotides (QTNs) associated with seed mineral content, thereby providing genetic resources for breeding programs aimed at improving nutritional quality (Gunjača *et al.*, 2021) ^[23]. Collectively, these findings underscore the utility of GWAS in dissecting the complex genetic architecture of common bean, paving the way for enhanced breeding strategies in legume crops (Jurado *et al.*, 2024) ^[40].

Genome-Wide Association Studies (GWAS) in common bean (*Phaseolus vulgaris*) reveal both similarities and differences when compared to other legume species. A notable similarity is the identification of significant SNPs associated with various traits, such as root traits under aluminum toxicity, micronutrient content, and disease resistance, which is also observed in legumes like soybean and pea (Ambachew & Blair, 2021, Binagwa *et al.*, 2020, Izquierdo *et al.*, 2023) ^[4, 6, 33]. However, differences arise in the specific genetic loci and candidate genes identified; for instance, common bean studies have highlighted unique QTLs for rust resistance and aluminum tolerance that differ from those found in other legumes (Wu *et al.*, 2022, Izquierdo *et al.*, 2023) ^[92, 33]. Additionally, the heritability of traits in common bean, ranging from 0.67 to 0.92, suggests a polygenic inheritance pattern that may vary in other legumes (Ambachew & Blair, 2021) ^[4]. Overall, while GWAS findings in common bean align with broader legume research, they also underscore the distinct genetic architecture and adaptive strategies of this species.

Comparative analysis of GWAS results across legume species, including the common bean, can indeed accelerate the discovery of novel genes by leveraging the genetic diversity and shared evolutionary history among these crops.

The integration of GWAS with interspecific lines, as demonstrated in the study of common bean and tepary bean, has already identified novel loci associated with drought tolerance, highlighting the potential of cross-species analysis to uncover adaptive genetic variations (López-Hernández *et al.*, 2022) ^[48]. Furthermore, the use of meta-analysis and comparative genomics, as seen in the identification of orthologous MQTL-YC shared across common bean, soybean, and pea, underscores the value of cross-species approaches in refining genomic regions related to seed yield components (Izquierdo *et al.*, 2023) ^[33]. The development of methods to identify conserved genes underlying GWAS loci across multiple species, as applied to ionomic traits in various crops, further supports the notion that comparative genomics can reveal previously unknown genes by focusing on evolutionarily conserved regions (Whitt *et al.*, 2023) ^[87]. Additionally, the challenges and advancements in GWAS, such as the integration of multi-omics data and machine learning, are crucial for enhancing the resolution of genetic mapping and facilitating the discovery of novel genes across leguminous crops (Ding, n.d.). These approaches collectively suggest that comparative GWAS can significantly contribute to molecular breeding by identifying candidate genes that are conserved across species, thereby accelerating the development of improved legume varieties with enhanced traits such as yield, nutrient content, and stress resistance.

Genomic prediction: Theory and applied studies in beans and other legumes

Key factors influencing genomic prediction accuracy in beans and other legumes include training population size, genetic diversity, and the choice of genomic prediction models. Research indicates that optimal training population size is crucial, as larger populations can enhance prediction accuracy, but diminishing returns may occur beyond a certain threshold (Alemu *et al.*, 2024) ^[2]. Additionally, the inclusion of Genotype × Environment Interactions (GEI) in models has been shown to significantly improve accuracy, particularly for traits with low heritability (Haile *et al.*, 2020) ^[27]. The effectiveness of different statistical models, such as Bayesian methods and GBLUP, also plays a vital role, with some models outperforming others depending on the presence of large effect Quantitative Trait Loci (QTL), (Silva *et al.*, 2021) ^[75]. Furthermore, environmental covariates may not always enhance prediction accuracy, especially in extreme conditions (Widener *et al.*, 2021) ^[88]. Overall, a combination of these factors is essential for optimizing genomic prediction in breeding programs.

Applied studies in genomic prediction significantly enhance crop yield and disease resistance in legume species by leveraging advanced genomic tools and methodologies. Genome-Wide Association Studies (GWAS) have identified key genetic markers associated with disease resistance, such as those linked to *Phakopsora pachyrhizi* resistance in soybeans, which can improve selection accuracy in breeding programs (Xiong *et al.*, 2023) ^[93]. Additionally, genomic selection models, including Bayesian LASSO, have demonstrated high predictive accuracy for complex traits, facilitating the rapid development of disease-resistant cultivars (Xiong *et al.*, 2023) ^[93]. The integration of genomic resources and high-throughput phenotyping technologies allows for the identification of genetic determinants of resistance to diseases like *Ascochyta* blight

and Fusarium wilt in various legumes (Jha *et al.*, 2022, Jha *et al.*, 2023) [36, 37]. Furthermore, the application of these genomic approaches not only accelerates breeding cycles but also contributes to sustainable agricultural practices by reducing reliance on chemical inputs (Ding, n.d.). Overall, these advancements are crucial for improving food security and agricultural resilience in the face of climate change and increasing disease pressures (James & Bala, 2024, Jha *et al.*, 2022) [34, 37].

Genomic prediction in legumes is underpinned by various theoretical frameworks that leverage advanced genomic technologies and statistical models. Key approaches include Genomic Selection (GS), which utilizes marker profiles to predict the performance of untested genotypes, thereby facilitating the selection process in breeding programs (Howard *et al.*, 2022) [31]. The integration of Machine Learning (ML) methods, such as Random Forest and Extreme Gradient Boosting, has shown promise in enhancing predictive performance, particularly for nonlinear phenotypes, compared to traditional parametric methods (Farooq *et al.*, 2023) [18]. Additionally, robust statistical models, like the minimum density power divergence estimator, have been developed to address complexities in genomic data, improving heritability estimation and prediction accuracy (Chowdhury *et al.*, 2024) [10]. Compared to other plant species, legumes benefit from a rich genomic resource base, including reference genomes and high-density molecular markers, which are crucial for optimizing breeding strategies and improving crop yields in challenging environments (Bohra *et al.*, 2020, Dai *et al.*, 2021) [8, 14].

The widespread adoption of Genomic Selection (GS) in legume breeding programs faces several significant challenges. High genotyping costs and the necessity for large training populations hinder effective implementation, as many breeding programs, particularly in the public sector, struggle with limited resources and funding (M *et al.*, 2024, Wartha & Lorenz, 2022) [85]. Additionally, the complexity of genetic architectures in legumes, characterized by multiple minor effect alleles, complicates the accurate prediction of traits, making it difficult to achieve reliable results across diverse environments and populations (Haile *et al.*, 2020, Merrick *et al.*, 2022) [27, 51]. Furthermore, the integration of GS into traditional breeding practices requires optimization of existing methodologies, including field designs and data management, which can be resource-intensive (Sdasd, 2022). Lastly, ethical concerns regarding genetic diversity and data access further complicate the landscape for adopting GS in legume breeding (M *et al.*, 2024).

Models used in genomic selection

In Genomic Selection (GS), several statistical models are commonly employed to predict Genomic Estimated Breeding Values (GEBVs). The Genomic Best Linear Unbiased Prediction (GBLUP) model is widely used due to its effectiveness in estimating marker effects across various traits (Mrode and Pocrnic, 2023, Terakado *et al.*, 2021) [21, 78]. Bayesian methods, including BayesA, BayesB, BayesC, and improved Bayesian least absolute shrinkage and selection operator (IBLASSO), have also gained popularity, often providing superior prediction accuracy, particularly in the presence of large effect quantitative trait loci (QTL) (Mrode and Pocrnic, 2023, Terakado *et al.*, 2021, Khan *et al.*, 2023) [21, 78, 42]. Additionally, machine learning approaches, such as Support Vector Machines (SVM) and

ensemble methods like Multiple Kernel Ensemble (MKE), have shown promising results, enhancing prediction performance through optimized hyperparameters (Wang *et al.*, 2023) [84]. Overall, the choice of model can significantly influence prediction accuracy, with Bayesian methods and GBLUP being among the most prevalent in current genomic selection practices (Mrode and Pocrnic, 2023, Khan *et al.*, 2023) [21, 42].

Machine Learning (ML) models and traditional linear models exhibit distinct differences in accuracy and computational efficiency within Genomic Selection (GS). While traditional methods, such as linear mixed models and regularized regression, have demonstrated strong predictive performance and computational efficiency, particularly in handling high-dimensional data, ML models often provide enhanced accuracy by accommodating complex, non-linear relationships (Sinha & Desai, 2023, Hay, 2024, Lourenço *et al.*, 2024) [76, 30, 49]. However, the computational demands of ML can be significant, with increased complexity leading to higher costs without guaranteed improvements in predictive accuracy (John *et al.*, 2022, Lourenço *et al.*, 2024) [38, 49]. For instance, while the GBLUP model outperformed ML models in certain scenarios, ML techniques like Random Forest showed superior performance in specific traits (Hay, 2024) [30]. Overall, the choice between ML and traditional models in GS should consider the specific dataset and trait characteristics, as both approaches have their merits and limitations (Jones *et al.*, 2023, Lourenço *et al.*, 2024) [39, 49].

Combining GWAS and genomic prediction: Strategies and case studies

Current strategies for integrating Genome-Wide Association Studies (GWAS) with genomic prediction to enhance accuracy in complex trait prediction focus on leveraging functional genomic annotations and advanced statistical models. One prominent method, SBayesRC, combines GWAS summary statistics with functional annotations, significantly improving prediction accuracy by 14% in European ancestry and up to 34% in cross-ancestry contexts, outperforming traditional methods like SBayesR and LDpred (Zheng *et al.*, 2024, Zeng *et al.*, 2023) [99, 97]. Additionally, the GWABLUP approach enhances genomic predictions by weighting SNPs based on GWAS findings, yielding up to 10% more reliable predictions compared to standard GBLUP models (Meuwissen *et al.*, 2024) [52]. Furthermore, integrating biological prior knowledge from GWAS into Bayesian models has shown to optimize genomic selection accuracy for traits in livestock, achieving improvements of up to 14.60% (Zhao *et al.*, 2024) [98]. These strategies highlight the importance of combining genomic data with functional insights to refine predictions for complex traits across diverse populations.

Combining Genome-Wide Association Studies (GWAS) with genomic prediction techniques enhances the identification of causal variants and genes associated with complex diseases by integrating diverse data sources and methodologies. Recent advancements propose frameworks that leverage GWAS summary statistics alongside gene expression and biological pathway data, significantly improving gene prioritization accuracy. For instance, methods like FLAMES integrate SNP-to-gene linking and network-based approaches, allowing for more precise predictions of causal genes in complex loci, particularly where traditional methods struggle (Weeks *et al.*, 2020,

Schipper & Posthuma, 2023) [86, 71]. Additionally, unified statistical frameworks have been developed to compute the probability of each gene being affected by causal variants, facilitating the rediscovery of known disease genes and uncovering novel ones with biological relevance (McManus *et al.*, 2022, Gonin, 2022) [50, 22]. This multifaceted approach not only enhances the understanding of genetic architecture but also addresses the limitations of association signals in revealing underlying causal mechanisms (Simone, 2022). Successful case studies demonstrating the effectiveness of combining GWAS and Genomic Prediction (GP) in breeding programs are evident across various crops and livestock. For instance, a study on wheat breeding for Septoria tritici blotch resistance identified 24 marker-trait associations through GWAS, which, when integrated with GP, improved prediction accuracy from 0.49 to 0.58, showcasing the potential for selecting superior lines based on Genomic-Estimated Breeding Values (GEBVs, Zakieh *et al.*, 2023) [96]. Similarly, research on pre-harvest sprouting tolerance in wheat revealed 171 Main-Effect Quantitative Trait Nucleotides (M-QTNs) and achieved genomic prediction accuracies ranging from 0.41 to 0.55, highlighting the utility of GWAS in enhancing GP models (Kumar *et al.*, 2022). Furthermore, a comprehensive analysis across 14 datasets indicated an average increase of 26.31% in prediction accuracy when genomic information was utilized, underscoring the critical role of genomic data in improving breeding outcomes (Montesinos-López *et al.*, 2023) [54]. These examples illustrate the synergistic benefits of integrating GWAS and GP in both plant and animal breeding programs (Ren *et al.*, 2024) [65].

Breeding pipelines: MAS, MABC, GS, genomic mating

The integration of Marker-Assisted Selection (MAS) and Marker-Assisted Backcrossing (MABC) with Genomic Selection (GS) significantly enhances the efficiency of breeding pipelines by leveraging the strengths of each method. MAS utilizes molecular markers to identify and select for specific traits, while GS employs genome-wide data to predict genetic merit, thus improving accuracy in selecting complex traits (Verma *et al.*, 2024, M *et al.*, 2024) [83]. This combined approach allows breeders to exploit both simple and polygenic traits, leading to faster development of superior cultivars and improved crop yields (Kumar *et al.*, 2024, Sandhu *et al.*, 2022) [44, 69]. Moreover, the integration facilitates the use of advanced genomic tools, such as high-throughput phenotyping and machine learning, which further accelerates breeding cycles and enhances genetic diversity management (Degen & Müller, 2023, Sandhu *et al.*, 2022) [15, 69]. Overall, this synergy not only streamlines the breeding process but also addresses challenges related to genetic architecture and resource allocation, ultimately promoting sustainable agricultural practices (M *et al.*, 2024, Degen & Müller, 2023) [15].

Genomic mating strategies offer several advantages over traditional Marker-Assisted Selection (MAS) and Marker-Assisted Backcrossing (MABC) approaches in crop and animal breeding. These strategies leverage genome-wide marker data to predict genetic potential with high accuracy, enhancing breeding efficiency and enabling the selection of complex traits such as yield and disease resistance more effectively than MAS, which relies on specific markers for simpler traits (Verma *et al.*, 2024, M *et al.*, 2024) [83]. Additionally, Genomic Selection (GS) can accelerate

breeding cycles and improve genetic diversity, addressing long-term sustainability concerns (Moeinizada *et al.*, 2020) [53]. However, limitations include high genotyping costs, the necessity for large training populations, and potential ethical issues regarding genetic diversity and data access (M *et al.*, 2024). Furthermore, while genomic mating can optimize short-term gains, it may inadvertently compromise long-term genetic potential if not managed carefully (Moeinizada *et al.*, 2020, Wolfe *et al.*, 2021) [90, 53]. Thus, while genomic strategies present transformative opportunities, they also require careful implementation to balance immediate and future breeding goals.

The integration of Marker-Assisted Selection (MAS), Marker-Assisted Backcrossing (MABC), Genomic Selection (GS), and genomic mating in breeding pipelines can significantly accelerate genetic gain and improve breeding outcomes. Genomic selection, which utilizes genome-wide information to predict genetic merit, has been shown to enhance genetic gain by reducing breeding cycle times and increasing selection accuracy, as demonstrated in rice and macadamia breeding programs (Biswas *et al.*, 2023, O'Connor *et al.*, 2021) [7, 56]. The combination of GS with MAS allows for a more comprehensive selection process by exploiting genetic markers for both simple and polygenic traits, thereby improving functional trait development and breeding efficiency (Verma *et al.*, 2024) [83]. In sugarcane, an integrated approach that combines GS with high-throughput phenotyping and genotyping, machine learning, and speed breeding has been proposed to overcome challenges related to its complex genome, thus accelerating genetic gain (Sandhu *et al.*, 2022) [69]. Furthermore, the application of GS in plant breeding, inspired by its success in livestock, highlights its potential to enhance genetic improvement of complex traits, especially when integrated with other breeding tools and platforms (Xu *et al.*, 2020) [94]. The synergy between these methods not only expedites the development of superior cultivars but also supports sustainable agriculture and global food security by promoting the rapid recycling of parents and increasing the rate of genetic improvement (Biswas *et al.*, 2023, Verma *et al.*, 2024) [7, 83].

Future perspectives: Enviromics, climate adaptation, wild introgressions

Future perspectives for genomic prediction in the context of enviromics, climate adaptation, and wild introgressions highlight the integration of environmental data with genomic information to enhance breeding strategies. Enviromics, which utilizes environmental attributes to predict genotype performance, can significantly improve selection accuracy across diverse environments, particularly under climate change scenarios (Resende *et al.*, 2021, Cooper & Messina, 2021) [66, 11]. The application of landscape genomics further aids in understanding adaptive potential and genomic vulnerabilities, allowing for tailored conservation strategies that enhance resilience in species facing climate stressors (Li *et al.*, 2025, Ruegg *et al.*, 2018) [45, 68]. Additionally, incorporating genotype by-environment interactions into genomic prediction models is crucial for optimizing breeding outcomes, as these interactions can influence trait expression across varying conditions (Crossa *et al.*, 2022) [13]. Collectively, these advancements suggest a promising future for genomic prediction, emphasizing the need for interdisciplinary approaches that combine

genomics, ecology, and agronomy to address the challenges posed by climate change and biodiversity loss.

The integration of enviromics into genomic prediction significantly enhances the accuracy of climate-resilient crop and animal breeding programs by addressing genotype-by-environment interactions (G×E) and improving selection efficiency. Enviromics, which encompasses high throughput environmental data, allows for a more nuanced understanding of how environmental factors influence phenotypic expression and performance across diverse conditions. For instance, studies have shown that incorporating environmental information alongside genomic and phenomic data can lead to substantial improvements in prediction accuracy, with gains averaging 49.19% in wheat breeding programs (Montesinos-López *et al.*, 2024) [55]. Additionally, the development of Environment-Phenotype Associations (EPA) facilitates the recycling of historical G×E data, enhancing the predictive power of models by reducing dimensionality and connecting phenotypic responses to environmental variations (Costa-Neto *et al.*, 2022) [12-13]. This approach not only aids in identifying candidate genes for stress resilience but also optimizes resource allocation in breeding programs, ultimately contributing to the development of crops and animals better suited to withstand climate change challenges (Winans *et al.*, 2024).

Conclusions & recommendations

Drought serves as a significant and formidable constraint on the production of common beans, particularly in regions where water resources are severely limited and scarcity is a prevalent concern. The methodologies of Genomic Prediction (GP) and Genome-Wide Association Studies (GWAS) function as exceptionally powerful and sophisticated instruments for dissecting and elucidating the complex genetic underpinnings associated with drought tolerance, thereby hastening the breeding process aimed at producing resilient and robust varieties of beans. By enhancing the precision of selection processes and effectively shortening the duration of breeding cycles, these advanced genomic approaches pave the way for the development of bean cultivars that are capable of maintaining yield and productivity even under conditions of constrained water availability.

In the realm of agricultural research, it is imperative that future investigations meticulously integrate multi-environment phenotyping techniques alongside comprehensive genomic data in order to more effectively elucidate the intricate interactions between genotype and environment, with a particular emphasis on the vast and diverse gene pools of bean varieties. The confluence of Genomic Prediction (GP) methodologies and Genome-Wide Association Studies (GWAS) with additional genomics approaches holds the potential to substantially enhance our understanding of the underlying mechanisms that confer drought tolerance in these vital crops. Furthermore, it is crucial for policymakers and relevant stakeholders to allocate appropriate resources and investments towards the education and training of breeders, the development of easily accessible genomic resources, and the fortification of seed systems, so as to guarantee that the enhanced varieties of drought-tolerant crops are successfully disseminated to farmers who are situated in regions that are particularly

vulnerable to climate variability. Ultimately, such comprehensive efforts are essential to ensure that advancements in agricultural science translate into practical benefits for those who rely on these crops for their livelihoods, particularly in the face of escalating environmental challenges.

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