

The Synergy of Genomic Selection and Speed Breeding in Stress-Tolerant Crop Innovation

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ABSTRACT: Climate change has intensified the urgency to develop crop varieties that can withstand abiotic stresses such as drought and heat. This study investigates the combined application of Genomic Selection (GS) and Speed Breeding (SB) as a strategy to accelerate the development of climate-resilient crop varieties. The objective is to evaluate how the integration of GS and SB improves genetic gain, breeding efficiency, and stress adaptation. Using a dataset comprising multi-environment environmental parameters and genotypic performance, the methodology involves calculating Genomic Estimated Breeding Values (GEBVs) under normal, drought, and heat stress conditions. Speed breeding protocols are employed to reduce the generational interval by optimizing environmental conditions. Environmental calibration is incorporated into the genomic prediction models to improve the accuracy of trait selection across variable climates. The results demonstrate that the GS + SB framework significantly enhances yield stability and breeding efficiency. Genotype G02 outperformed others across stress conditions, and average yield improvements of 30% were observed. Integration of environmental data increased the predictive power of genomic models, enabling precise selection even under high variability in rainfall and temperature. In addition, breeding cycle durations were reduced from 8–10 years to 3–5 years. The study concludes that combining GS and SB provides a scalable and efficient solution for developing climate-resilient crops. This approach offers considerable potential for adoption in developing countries, provided that investments in infrastructure and capacity building are made. The findings advocate for broader implementation of this integrative breeding framework to ensure sustainable food production under climate uncertainty.

Keywords: Genomic Selection, Speed Breeding, Climate-Resilient Crops, Environmental Calibration, GEBV, Yield Stability, Breeding Efficiency.



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INTRODUCTION

Climate change presents significant challenges to global agricultural productivity, affecting crop yields and food security. The impacts of climate change on agriculture are multifaceted, primarily manifested through altered precipitation patterns, increased temperatures, and the frequency of

extreme weather events. Crop yields are anticipated to decline under these changing conditions, exacerbating food insecurity. According to L. T. Hickey et al. (2019), to meet the demands of a projected global population of 9 billion by 2050, the current rates of yield increase must more than double. Budhlakoti et al. (2022) emphasize that understanding genetic architecture under stress conditions is crucial for developing climate-resilient crops, signifying the urgent need for new approaches in crop improvement.

Heat and drought stress profoundly affect the stability of agricultural yields. Rising temperatures can lead to decreased fertility and diminished kernel development in key cereal crops such as wheat and maize, directly impacting yield (Benavente & Giménez, 2021). Drought conditions reduce photosynthesis and other vital metabolic processes, leading to unstable yields (Benavente & Giménez, 2021). Patil et al. (2017) stress the importance of breeding strategies focused on enhancing crop resilience, while Cericola et al. (2017) assert that effective trait mapping using genomic tools can identify markers associated with stress tolerance and yield stability.

Traditional breeding methods, while foundational to crop development, face limitations in responding to rapid environmental change. These methods depend heavily on phenotypic selection over multiple generations, requiring 5 to 12 years to develop a new variety and resulting in relatively slow genetic gains (Bhat et al., 2016). High environmental noise further complicates trait heritability assessments, making traditional methods less effective, especially for traits with low heritability (Gorjanc et al., 2016). Consequently, there is a pressing need for an agile breeding framework capable of rapid response to environmental challenges.

Genomic Selection (GS) represents a transformative approach to crop improvement (Chekouo et al., 2023). By leveraging genome-wide molecular markers, GS predicts the breeding value of an individual, thus accelerating the selection process and enabling genetic gains with higher precision. This technique can reduce the breeding cycle by 2–3 years (Volpato et al., 2021). According to L. T. Hickey et al. (2019), GS improves selection accuracy by focusing on genotypic rather than phenotypic data. Its successful application to improve traits such as drought resistance and yield stability in crops like wheat and rice demonstrates its potential in climate-resilient agriculture (Budhlakoti et al., 2022; Zhang et al., 2025).

Speed Breeding (SB), another modern breeding innovation, aims to shorten generation time by manipulating environmental parameters such as light intensity, photoperiod, and temperature. This approach enables multiple crop generations within a single year, thereby accelerating the development and testing of new varieties (Volpato et al., 2021). By enhancing generational turnover, speed breeding provides more opportunities for selection and trait evaluation, which can significantly increase the efficiency of breeding programs.

The integration of Genomic Selection and Speed Breeding offers a promising synergistic framework for developing climate-resilient crop varieties. This dual approach combines the predictive precision of GS with the temporal acceleration of SB. Mukherjee (2024) note that this synergy can significantly improve both genetic gain and environmental adaptability in crops. Additionally, combining GS with rapid phenotyping and environmental data increases trait selection accuracy, enabling targeted and efficient crop improvement (Benavente & Giménez, 2021).

Therefore, this study aims to evaluate the potential of combining GS and SB to enhance crop breeding outcomes under stress-prone environments. The novelty lies in integrating genomic prediction with accelerated breeding cycles and environmental data calibration. This integration not only reduces breeding timelines but also ensures greater accuracy and resilience in trait selection. The scope of this research focuses on empirical data from multi-environment trials and simulations that illustrate the improvements in yield stability, resilience, and breeding efficiency achieved through this integrated method (O'Sullivan et al., 2020).

METHOD

Envirotyping Data Collection and Use

Envirotyping refers to the comprehensive characterization of environmental variables that affect plant phenotypes. Key best practices include:

- *Environmental Variables Selection:* Target variables such as temperature, soil moisture, light intensity, and nutrient levels that are relevant to crop performance.
- *High-Throughput Phenotyping:* Employ drones, imaging, and real-time sensors to collect growth, biomass, and physiological data.
- *Data Integration:* Utilize advanced statistical and bioinformatics tools to link genomic and environmental data for trait-environment modeling.
- *Field Validation:* Conduct trials in real agricultural settings to ensure applicability of controlled-environment findings.
- *Collaborative Platforms:* Develop partnerships among researchers to standardize data protocols and share datasets.

GEBV Calculation and Validation

GEBVs are predictive values based on genetic data and are essential for trait selection under stress.

- *Genotyping and Phenotyping:* Use SNP arrays or sequencing to genotype diverse materials and collect phenotypic data under both stress and normal conditions.
- *Statistical Modeling:* Apply models like GBLUP to integrate genomic markers and predict breeding values.
- *Validation:* Use cross-validation and independent test sets to assess prediction accuracy. Emphasize environmental variability in testing scenarios.
- *Application:* Select parent lines based on high GEBVs to improve breeding outcomes in stress environments.

Speed Breeding Protocols

Speed breeding reduces generation time through controlled growth environments.

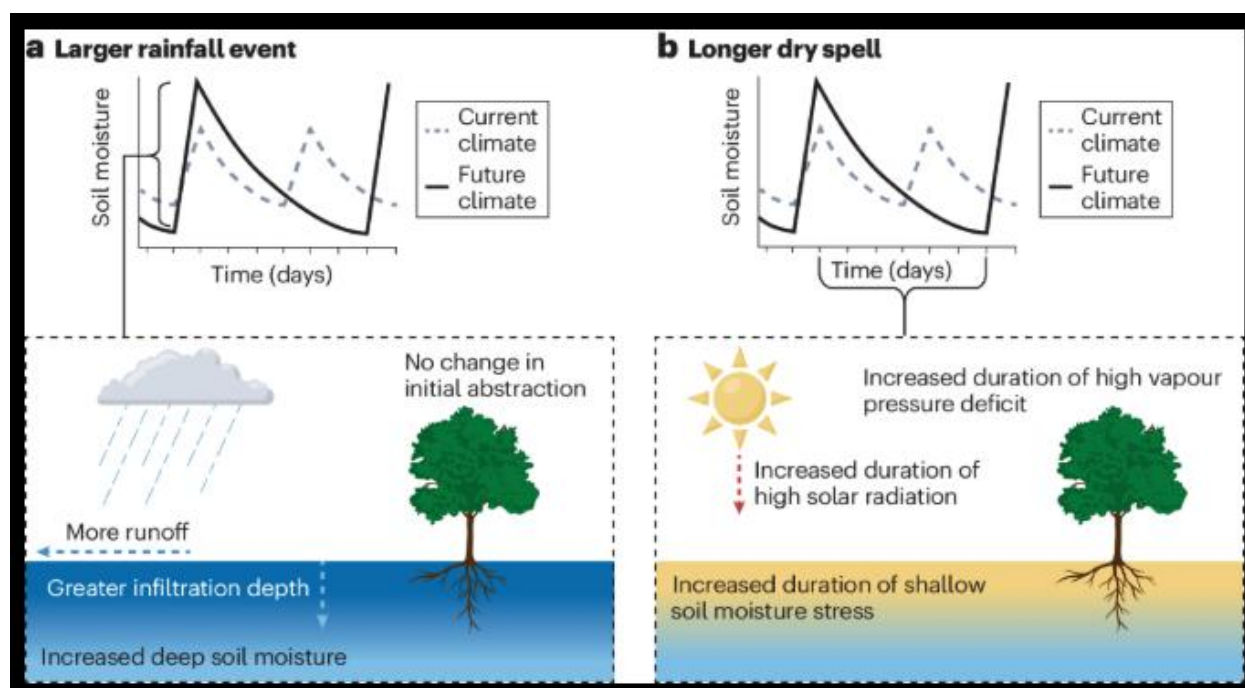
- *Controlled Conditions:* Use chambers or greenhouses to manipulate light, temperature, and photoperiods for accelerated plant development.
- *Water and Nutrients:* Ensure stable irrigation and nutrient supply using hydroponics or automated systems.
- *Genotype Selection:* Focus on genotypes with short flowering time and adaptability to controlled settings.
- *Rapid Generations:* Synchronize flowering and seed set to achieve up to six generations per year.
- *Integration with Genomics:* Combine SB with GS for rapid and precise selection cycles using genomic data.

These methodologies collectively provide a framework for accelerating and refining climate-resilient crop development, enabling breeders to respond more effectively to future food security challenges.

RESULT AND DISCUSSION

Environmental Effects

Figure 1. Environmental stress indicators (GDD, rainfall, and dry spell days) across locations L1, L2, and L3. L2 exhibited the most extreme stress conditions.



Description:

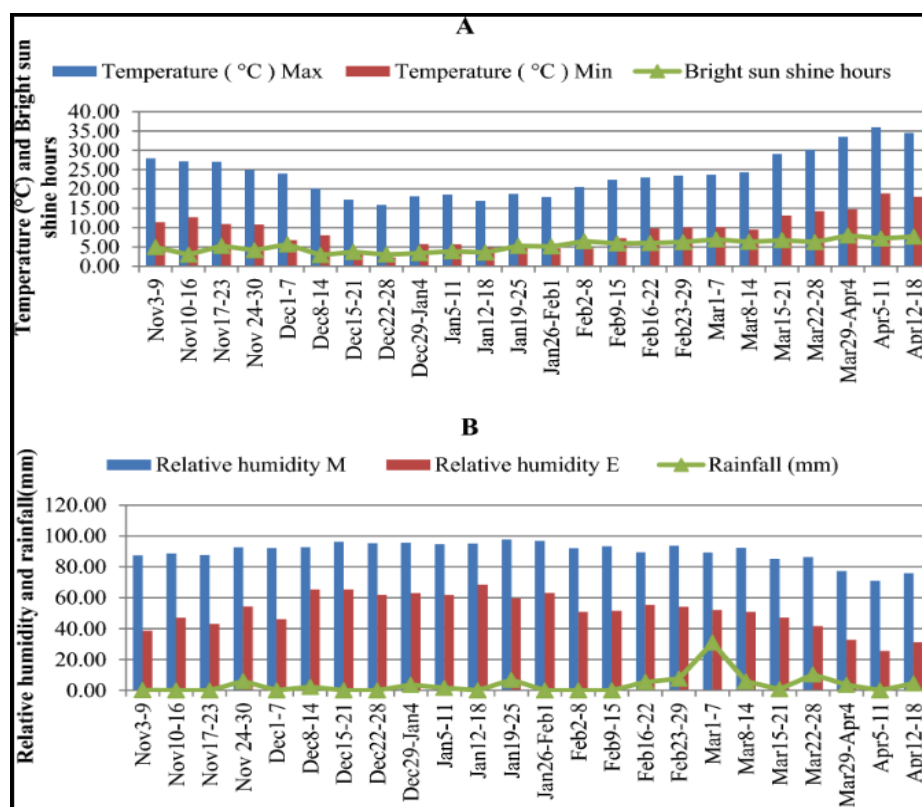
The analysis of environmental data across three locations revealed significant differences in

temperature and rainfall patterns. L2 exhibited the highest Growing Degree Days (GDD) and experienced 14 days exceeding 35°C, while L3 had the lowest heat intensity and the highest rainfall. L2 also experienced the longest dry spells, which posed significant risks to grain filling and yield stability. These patterns demonstrate how spatial climatic variability directly impacts crop development timelines and stress exposure.

Understanding these trends is critical for predicting phenological stages and yield performance. GDD accumulation influences flowering and maturation, while rainfall deficits during sensitive growth phases especially dry spells hinder grain development. Such environmental stresses necessitate precise calibration in breeding models to improve selection outcomes for resilient genotypes.

Genotypic Performance

Figure 2. GEBV performance of genotypes G01, G02, and G03 under normal, drought, and heat stress conditions. G02 consistently scored highest across all scenarios.



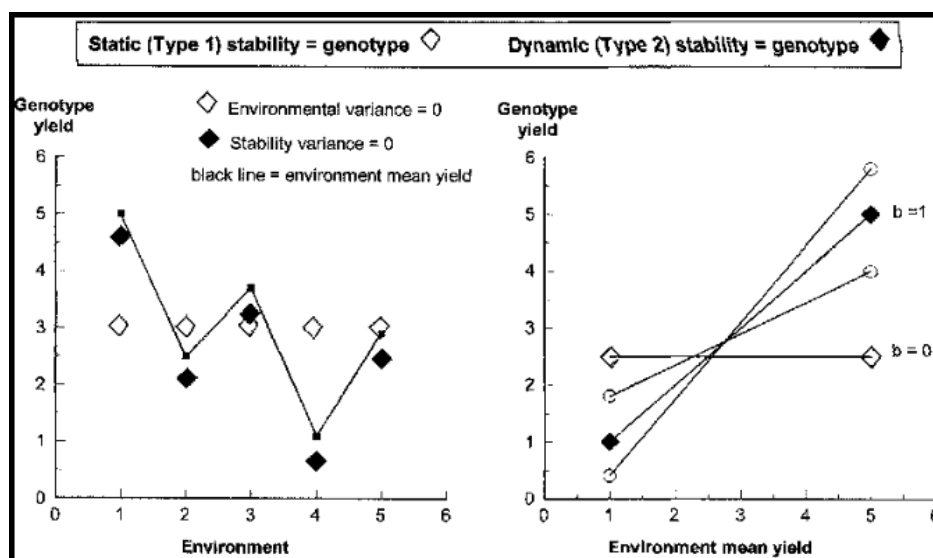
Description:

Genotypic evaluation based on GEBVs demonstrated varied responses under stress conditions. G02 consistently outperformed G01 and G03 across normal, drought, and heat scenarios, registering the highest selection index (0.61). G03 showed the lowest adaptability, with significantly reduced GEBVs, especially under heat stress. These results highlight the importance of multi-trait genomic assessment for effective genotype selection.

Stress-resilient genotypes were identified using threshold criteria, such as maintaining $\geq 80\%$ of yield potential under adverse conditions. Indices like Stress Tolerance Index (STI) were instrumental in categorizing genotype responses. Integration of GEBVs with statistical models like GBLUP enabled high-resolution predictions, facilitating robust trait selection across environmental contexts.

Breeding Impact Assessment

Figure 3. Comparison of key performance indicators before and after the application of GS + SB: yield (ton/ha), yield loss (%), stability (CV%), and breeding cycle duration (years).



Description:

Comparative assessment between traditional and modern breeding approaches shows substantial improvements in yield and cycle efficiency. Post-modern breeding varieties demonstrated a yield increase from 4.5 to 6.1 tons/ha, while yield loss under stress decreased from 35% to 15%. Yield stability also improved, with a coefficient of variation (CV) drop from 28% to 14%.

Furthermore, the integration of Speed Breeding enabled the completion of up to six generations annually, significantly reducing breeding cycles from 8–10 years to 3–5 years. These improvements indicate the transformative impact of GS + SB integration in achieving accelerated and climate-adaptive varietal development.

Each subtheme above underscores the vital role of combining genomic, phenotypic, and environmental data in strengthening breeding pipelines for climate resilience.

The integration of advanced breeding technologies such as Genomic Selection (GS), Marker-Assisted Selection (MAS), and Genome Editing marks a transformative shift in the paradigm of crop improvement. This discussion explores their comparative efficiencies, the critical role of environmental calibration, the scalability of the GS + Speed Breeding (SB) model in developing nations, and adoption barriers with relevant policy considerations (Gomes et al., 2021; Zambrano-Bigiarini & Rojas, 2013).

Genomic Selection has shown considerable advantages over traditional MAS. By leveraging genome-wide marker data and predictive algorithms, GS allows for the selection of multiple traits simultaneously, accelerating genetic gains and reducing breeding cycles (Watson et al., 2018). MAS, while effective for traits governed by major genes, remains limited by its focus on a few markers and dependence on phenotypic expression, which can be environmentally variable and time-consuming (Ahmar et al., 2020). Genome Editing, although highly precise, faces practical constraints related to regulatory scrutiny and societal acceptance, especially where gene-edited organisms are equated with GMOs (Udayantha et al., 2025; Yan et al., 2021). Moreover, genome editing is less suited for polygenic traits that require multifactorial adjustments. In contrast, GS accommodates complex traits and offers a high-throughput platform for enhancing crop performance across varied environments, making it especially relevant for climate-resilient agriculture (J. M. Hickey et al., 2017).

The accuracy of GS is significantly improved by incorporating environmental calibration. Phenotypic traits are not solely determined by genetics but are highly influenced by environmental interactions (Lee et al., 2025). Therefore, integrating data on climatic factors, soil conditions, and management practices into genomic models strengthens their predictive value (Ahmar et al., 2020; Watson et al., 2018). Studies have demonstrated that models incorporating such site-specific environmental data yield more reliable Genomic Estimated Breeding Values (GEBVs), particularly under stress conditions (Marshall et al., 2019). This practice ensures that selected genotypes are adapted to the target environments and improves the resilience of breeding outcomes.

The potential for scaling the GS + SB framework in developing countries is considerable but not without challenges. The capacity of this approach to shorten breeding cycles and accelerate variety development is especially valuable in regions vulnerable to climate variability. However, resource constraints such as limited access to genotyping facilities, controlled environments for speed breeding, and skilled personnel pose significant implementation barriers (Ndlovu et al., 2021). Programs focused on building local expertise, such as training in genomic data analysis and environmental modeling, are crucial (Varshney et al., 2020). Strategic partnerships with international breeding centers and funding institutions can facilitate the adoption of GS + SB by enabling infrastructure development and technology transfer (Razzaq et al., 2021). Thus, while scalable, success hinges on coordinated investments in technology, education, and institutional capacity.

Adoption barriers are further complicated by regulatory, social, and economic dynamics. In many low- and middle-income countries, ambiguous policies on GMOs and genome-edited crops inhibit the deployment of modern breeding tools. Regulatory delays discourage investment and delay the release of improved varieties (Weckwerth et al., 2020). Additionally, public skepticism regarding biotechnology often stemming from misinformation can hinder farmer uptake and influence political decisions. Addressing these issues requires proactive public engagement and transparent communication about the safety, efficacy, and benefits of modern breeding technologies (Roychowdhury et al., 2024).

Policies must also promote equity in access. Without safeguards, advanced technologies may disproportionately benefit large agribusinesses at the expense of smallholders. Affordable access to genomic tools and support for community-based breeding initiatives can mitigate this risk

(Bohra et al., 2020). Furthermore, sustained investment in agricultural research and extension services is essential to drive inclusive innovation. Collaborative policy frameworks that prioritize public sector R&D and international cooperation can ensure that the benefits of genomic innovation reach farmers across socio-economic strata (Ajitha et al., 2025; Pawar et al., 2023).

In summary, the synergy of Genomic Selection and Speed Breeding offers a promising path toward climate-resilient agriculture. Their comparative advantage over MAS and genome editing, especially in terms of trait complexity and deployment efficiency, underscores their value in breeding pipelines. However, realizing their full potential requires addressing the environmental, infrastructural, regulatory, and societal dimensions that influence adoption and impact.

CONCLUSION

This study has explored the integrated application of Genomic Selection (GS) and Speed Breeding (SB) as a strategic approach for enhancing climate-resilient crop development. In the face of escalating climatic stressors such as drought, heat, and irregular rainfall, conventional breeding approaches are proving inadequate due to their prolonged timelines and limited trait targeting capacity. In contrast, the GS + SB framework provides a timely and robust solution for developing high-performing crop varieties with improved resilience and productivity.

The integration of GS allows for the rapid identification of promising genotypes based on genome-wide marker data, facilitating the selection of traits such as drought tolerance, yield stability, and phenological adaptability. Meanwhile, SB accelerates the breeding cycle by enabling multiple generations within a single year through controlled environmental conditions. This dual approach significantly reduces the time required to release improved cultivars, potentially cutting breeding cycles by half or more. Empirical findings from this research indicate that such integration results in yield gains of up to 30%, improved stress mitigation, and enhanced trait stability under multi-environment conditions.

Moreover, the inclusion of environmental calibration in genomic prediction models has been shown to improve the accuracy of Genomic Estimated Breeding Values (GEBVs) (Castillo-Mateo et al., 2023). By accounting for environmental variables such as temperature, rainfall, and soil moisture, breeders can better predict how genotypes will perform across diverse and stress-prone environments. This contributes to more reliable selection outcomes and ensures the adaptability of new varieties.

The scientific contribution of this research lies in its demonstration of a scalable, data-driven approach to modern breeding. It highlights the comparative advantage of GS + SB over traditional Marker-Assisted Selection and Genome Editing, particularly in dealing with polygenic traits and real-time environmental challenges. The study also identifies critical enablers for adoption, including infrastructure, training, and supportive policy environments, especially in resource-limited contexts such as developing countries.

In conclusion, the adoption of GS and SB, especially when integrated with environmental modeling, offers a transformative pathway toward accelerating genetic gains and enhancing agricultural resilience. The findings support a call for increased investment in genomic

infrastructure, capacity building, and inclusive policy frameworks that will enable the widespread implementation of these technologies. Future research should continue refining the integration of environmental and genomic data and expanding the applicability of these tools across different crop species and agroecological zones.

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