THE SCIENCE WORLD
A Monthly e Magazine
ISSN:2583-2212
October, 2025 Vol.5(10), 9449-9453

Popular Article

Genomic Selection for Climate-Resilient Crops: Accelerating Breeding for Climate Change

Ravleen Kaur Badwal[1*], Pavan Chouksey[2], Rohit[3]
[1]Ph.D. Scholar, Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, M.P.- 482004
[2]PhD Scholar, Department of Plant Biotechnology, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur
[3]M.Sc., Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana -125004
*Corresponding author email: ravleenkaur01@jnkvv.org
DOI:10.5281/ScienceWorld.17496152

Abstract

Climate change threatens global agriculture through rising temperatures, unpredictable rainfall, and extreme weather, reducing crop yields. Genomic selection (GS), using high-throughput genotyping and predictive modelling, enables breeders to efficiently select traits like drought tolerance, heat resilience, and stable yield. This article reviews GS fundamentals, models, and the integration of machine learning and multi-omics data, with case studies in rice, while discussing challenges and opportunities for implementing GS in diverse and resource-limited environments.

Keywords: climate change; genomic selection (GS); climate resilient.

Introduction

Climate change is impacting agriculture, with crop yields projected to drop 10–25% by 2050 due to drought and heat stress (IPCC, 2022). Conventional breeding is often too slow to keep up. Genomic selection (GS), introduced by Meuwissen et al. (2001), uses genome-wide markers to predict breeding values for complex traits, reducing the need for extensive field phenotyping. GS accelerates selection cycles and improves traits critical for climate resilience, such as drought and heat tolerance. Advances in high-throughput genotyping, phenotyping, and machine learning have further enhanced GS. This article reviews GS applications in developing climate-resilient rice, highlighting methods, achievements, challenges, and prospects for food security.

Genomic Selection: Definition

Genomic selection is a breeding approach that uses genome-wide molecular markers to predict the genetic merit of individuals, allowing early and accurate selection for complex traits (Meuwissen et al., 2001).

Genomic Selection Framework

GS involves training a statistical model to predict genomic estimated breeding values (GEBVs) using a training population with both genotypic (e.g., SNP markers) and phenotypic data. The model is then applied to a breeding population to select individuals with desirable traits. Key steps include:

- Genotyping: High-density SNP arrays or genotyping-by-sequencing (GBS) to capture genome-wide variation.
- Phenotyping: Precise measurement of climate-relevant traits (e.g., yield under drought, heat stress response) in controlled or field conditions.
- Model Training: Statistical models (e.g., GBLUP, Bayesian methods) or machine learning algorithms (e.g., random forests, neural networks) to correlate genotypes with phenotypes.
- Validation and Selection: Cross-validation to assess prediction accuracy, followed by selection of high-GEBV individuals for breeding.

Statistical Tools and Packages for Implementing Genomic Selection

Several tools and packages have been developed for the evaluation of genomic prediction and implementation of GS, some of which are discussed in table 1.

Table 1. Overview of Statistical Tools and Packages for Implementing Genomic Selection in Crop Breeding.

Model / Tool (Full Form)	**Type**	**Key Features**
RR-BLUP (Ridge Regression Best Linear Unbiased Prediction)	Linear / Mixed	Estimates marker effects assuming equal variance; additive effects
GBLUP (Genomic Best Linear Unbiased Prediction)	Linear / Mixed	Uses genomic relationship matrix; like RR-BLUP
BRR (Bayesian Ridge Regression)	Linear / Mixed	Linear model with shrinkage of marker effects

BayesA (Bayesian Model A)	Bayesian	Marker-specific variances; normally distributed effects
BayesB (Bayesian Model B)	Bayesian	Some markers zero effect; others variable
BayesC / BayesCπ (Bayesian Model C / Cπ)	Bayesian	Mixture of BayesA and BayesB
Bayes LASSO (Bayesian Least Absolute Shrinkage and Selection Operator)	Bayesian	Bayesian shrinkage using LASSO
RF (Random Forest)	Machine Learning	Tree-based ensemble; captures non-linear effects
SVM (Support Vector Machine)	Machine Learning	Kernel-based regression/classification
MT-BLUP (Multi-Trait Best Linear Unbiased Prediction)	Multi-Trait	Uses correlations between traits for prediction
MT-Bayes (Multi-Trait Bayesian Model)	Multi-Trait / Bayesian	Multi-trait Bayesian model
STGS (Single-Trait Genomic Selection)	Hybrid / Tool	Single-trait GS; supports RR-BLUP, LASSO, SVM, RF, ANN
MTGS (Multi-Trait Genomic Selection)	Hybrid / Tool	Multi-trait GS; supports MRCE, KMLASSO, MLASSO
rrBLUP package (R package rrBLUP)	Tool	R package; linear models and cross-validation

Case Study: Genomic Selection for Grain-Filling Characteristics in Rice

Grain filling strongly influences rice yield but is hard to improve through conventional breeding due to its quantitative nature and environmental sensitivity. Yabe et al. (2018) evaluated ~400 rice accessions using ~700K SNPs and applied GS models (GBLUP, BayesA, BayesB), achieving prediction accuracies of 0.45–0.70. GS outperformed traditional selection, offering higher accuracy and greater expected genetic gain, showing its potential to enhance grain-filling efficiency and yield stability under climate stress.

Advantages of Genomic Selection (GS)

Faster Breeding Cycles: Early-generation selection reduces breeding duration by 30–50%.

- Improved Prediction Accuracy: Captures additive and non-additive effects for complex traits.
- Multi-Trait Selection: Simultaneously predicts correlated traits for balanced improvement.
- Integration of Multi-Omics Data: Enhances accuracy by capturing G × E interactions.
- Efficient Resource Use: Reduces large-scale field trials, saving time and costs.
- Climate Resilience: Targets drought, heat, and salinity tolerance for stable yields.

Challenges

- Training Population Diversity: Narrow genetic bases reduce model applicability; include landraces/wild relatives.
- Environmental Variability: G × E interactions require multi-environment trials.
- Cost & Accessibility: High-throughput genotyping is expensive; low-cost GBS and shared resources help.

Factors Affecting Prediction Accuracy

- Marker Density: Higher density improves accuracy; moderate density (~2000 SNPs) often sufficient.
- Bayesian Model Convergence: High-density markers may slow MCMC in Bayes models.
- SNP Quality: Intergenic SNPs and $MAF > 0.1$ improve prediction.
- Population Size & Relatedness: Larger, related populations yield higher accuracy.
- Trait Heritability: High-heritability traits predict better; low-heritability traits need more data.
- Model Choice: BLUP, GBLUP, RR-BLUP, Bayesian, RKHS handle complex traits well.
- Missing Data: Multi-trait models (MTGS) can compensate using correlated traits.

Future Directions and Conclusion:

Genomic selection (GS) is a powerful tool for developing climate-resilient crops, offering high prediction accuracy and shorter breeding cycles. Integrating GS with speed breeding, gene editing (e.g., CRISPR), and portable sequencing technologies can accelerate crop improvement, even in resource-limited regions. While successful in maize and rice, wider adoption requires addressing costs, germplasm diversity, and environmental variability.

Collaborative frameworks and public-private partnerships are essential to make GS accessible and secure global food systems against climate change.

References

Crossa, J., et al. (2023). Genomic selection for complex traits in cereals. Plant Biotechnology Journal, 21(3), 456–468.

IPCC. (2022). Climate Change 2022: Impacts, Adaptation, and Vulnerability. Cambridge University Press.

Meuwissen, T. H. E., et al. (2001). Prediction of total genetic value using genome-wide dense marker maps. Genetics, 157(4), 1819–1829.

Yabe S, Yoshida H, Kajiya-Kanegae H, Yamasaki M, Iwata H, Ebana K, et al. (2018) Description of grain weight distribution leading to genomic selection for grain-filling characteristics in rice. PLoS ONE 13(11): e0207627. https://doi.org/10.1371/journal.pone.0207627