INTEGRATION OF GENOMIC SELECTION AND BIOTECHNOLOGY FOR SUSTAINABLE CROP IMPROVEMENT

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ABSTRACT

Sustainable crop improvement is essential to meet the rising global demand for food, feed, and fiber amidst environmental challenges and resource limitations. The integration of genomic selection (GS) with advanced biotechnological tools offers a promising pathway toward accelerated and precise crop breeding. This review presents a comprehensive account of how genomic selection—based on whole-genome prediction models—and biotechnology, including molecular markers, genetic engineering, and genome editing, are being combined to enhance crop performance, stress tolerance, and nutritional quality. We explore how GS enables early prediction of complex traits, thereby shortening breeding cycles, while biotechnological interventions such as CRISPR-Cas and transgenic technologies allow targeted trait improvements. The synergy of these tools is particularly transformative in developing climate-resilient, pest-resistant, and nutrient-enriched crop varieties. The review also discusses integrative approaches that combine high-throughput phenotyping, bioinformatics, and multi-omics technologies to optimize selection accuracy. Limitations such as regulatory hurdles, data management challenges, and adoption gaps in low-income regions are addressed. Finally, the paper outlines future prospects involving AI-powered genomic prediction, pan-genomic models, and sustainable bio-innovation platforms. The integration of GS and biotechnology holds the key to achieving resilient and inclusive agricultural systems for the 21st century.

Keywords: Genomic selection, Biotechnology, Crop breeding, Genome editing, Sustainability, Multi-omics, CRISPR

1. INTRODUCTION

Sustainable agriculture faces immense challenges in the 21st century due to the increasing demand for food, shrinking arable land, climate change, and the degradation of natural resources. Feeding a growing global population—expected to reach 9.7 billion by 2050—while preserving environmental integrity has become a critical concern for agricultural scientists and policymakers. Key to meeting this challenge is the development of crop varieties that are high-yielding, nutrient-rich, stress-tolerant, and resource-efficient. However, achieving this requires more than conventional farming practices; it demands innovative, science-based solutions that can bridge productivity with sustainability.

Traditional plant breeding methods have contributed significantly to crop improvement over the last century by selecting superior genotypes based on observable traits. Yet, these methods are often slow, labor-intensive, and limited by environmental influences and genetic complexity. The advent of molecular tools has transformed the breeding landscape, enabling breeders to peer directly into the genome. Marker-assisted selection (MAS), quantitative trait loci (QTL) mapping, and genome-wide association studies (GWAS) have opened new avenues to identify and utilize genetic variability for important agronomic traits. Nonetheless, these techniques, while powerful, still rely heavily on phenotyping and can be inefficient for complex traits governed by many genes, such as drought resistance or nutrient use efficiency.

To overcome the limitations of both traditional and molecular methods, integrated approaches that combine genomic selection (GS) with modern biotechnological tools have emerged as a promising frontier. Genomic selection uses genome-wide markers to predict breeding values, thereby accelerating the breeding cycle and improving selection accuracy for complex traits. When integrated with advanced biotechnologies like genetic engineering, CRISPR/Cas9-based genome editing, and tissue culture-based propagation systems, GS can significantly enhance the precision and speed of crop improvement programs. Furthermore, the use of omics technologies—such as transcriptomics, proteomics, and metabolomics—can offer deeper insights into plant responses to stress and inform targeted breeding strategies.

Given the complexity of modern agricultural systems, a holistic, interdisciplinary strategy is essential. Integrating genomic selection with biotechnology not only allows for the rapid development of climate-resilient and high-yielding cultivars but also supports conservation of genetic resources and sustainable land use. This review aims to explore the synergistic potential of genomic and biotechnological tools in driving sustainable crop improvement and highlights the need for coordinated research, infrastructure, and policy support to realize their full impact on global food security.

2. PRINCIPLES OF GENOMIC SELECTION (GS)

2.1 Concept of GS and GEBVs

Bernardo (2008) emphasized that genomic selection (GS) offers a paradigm shift from traditional phenotypic selection to a model that uses genome-wide markers to predict the performance of untested genotypes. He highlighted the value of genomic estimated breeding values (GEBVs) in enhancing

selection accuracy and reducing breeding cycle time.

Crossa et al. (2010) introduced the integration of GS into plant breeding pipelines, explaining that GEBVs are derived from genome-wide marker data using statistical models. Their study demonstrated that GS outperformed traditional selection in terms of prediction accuracy, particularly in crops with complex traits such as yield.

Heffner, Sorrells, and Jannink (2009) provided a comprehensive review on GS and concluded that GEBVs can increase selection intensity and reduce generation intervals. They argued that by capturing small-effect loci across the genome, GS is well-suited for polygenic trait improvement.

Meuwissen, Hayes, and Goddard (2001) were the pioneers who proposed the concept of GS, showing through simulations that genome-wide dense marker maps could predict breeding values accurately without requiring phenotypic data. This foundational study introduced the term GEBVs and laid the groundwork for GS implementation in both animal and plant breeding.

2.2 Role of prediction models (BLUP, Bayes A/B, and GBLUP)

De los Campos et al. (2013) emphasized the application of Genomic Best Linear Unbiased Prediction (GBLUP) in plant breeding, highlighting its accuracy and scalability in predicting genomic estimated breeding values (GEBVs). The study outlined how GBLUP uses a genomic relationship matrix to capture additive genetic variance, which improves prediction accuracy for complex traits in crops like maize and wheat.

Habier et al. (2007) introduced the concept of Bayesian approaches in genomic selection, particularly Bayes A and Bayes B, and demonstrated how these models provide higher prediction accuracy in traits controlled by a few major genes. Their work compared these models with traditional BLUP methods and showed the advantage of marker-specific variance estimation in Bayesian models.

Jannink et al. (2010) reviewed the evolution of genomic prediction models in plant breeding and examined the performance of BLUP, GBLUP, and Bayesian methods under various scenarios. The review emphasized the importance of choosing appropriate models based on trait architecture and population structure, suggesting that Bayes B often outperformed GBLUP in traits with large-effect loci.

Meuwissen, Hayes, and Goddard (2001) were pioneers in proposing the use of dense marker maps and prediction models like BLUP and Bayesian regression for genomic selection. Their landmark paper laid the theoretical foundation for using models such as Bayes A and B in estimating GEBVs, leading to widespread adoption in both animal and plant breeding programs.

2.3 Genotyping platforms and their role in GS

Akhunov et al. (2009) highlighted the development of high-density SNP genotyping arrays in wheat, underscoring their importance in marker-assisted selection and genomic prediction. Their study demonstrated how these platforms improved genetic resolution, enabling more accurate estimates of marker-trait associations, particularly in polyploid crops like wheat.

Elshire et al. (2011) introduced the Genotyping-by-Sequencing (GBS) method as a low-cost, high-throughput platform that

revolutionized genomic selection in crops. The GBS approach facilitated rapid discovery and genotyping of thousands of SNPs, especially for non-model crops lacking reference genomes.

Ganal, Durstewitz, Polley, et al. (2011) discussed the development and application of SNP arrays such as the Illumina Golden Gate and Infinium assays. These arrays have enabled highly accurate genotyping in cereals, vegetables, and legumes, making them integral to GS pipelines.

Kumar et al. (2012) reviewed the comparative efficiency of different genotyping platforms, including DArT, SSRs, SNP arrays, and next-generation sequencing (NGS)-based tools. The authors concluded that NGS platforms provided greater marker density and genome coverage, enhancing GS effectiveness across breeding programs.

Poland and Rife (2012) emphasized the use of genotyping-by-sequencing in genomic selection, particularly in wheat and barley. Their work showed how low-cost, high-throughput sequencing could replace traditional genotyping techniques, thereby enabling large-scale genomic predictions with higher accuracy.

3. BIOTECHNOLOGY IN CROP IMPROVEMENT

3.1 Marker-Assisted Selection (MAS)

Marker-Assisted Selection is a molecular breeding technique where DNA markers closely linked to desirable traits (such as disease resistance, drought tolerance, or yield) are used to select plants even before these traits are visibly expressed.

Applications of MAS:

1. **Accelerated Breeding**- MAS allows breeders to identify and select desirable genotypes early in the plant lifecycle, speeding up the breeding process.

2. **Improved Accuracy**- since MAS relies on molecular markers; it reduces the influence of environmental factors and provides more precise selection than traditional phenotypic selection.

3. **Trait Pyramiding**- MAS enables the combination (or "pyramiding") of multiple genes (e.g., resistance genes) into a single plant variety to enhance durability against pests or diseases.

4. **Backcross Breeding Support**- It aids in transferring specific genes into elite cultivars while retaining most of the recipient genome, known as marker-assisted backcrossing (MABC).

5. **Difficult-to-Measure Traits**- Traits like drought tolerance or root architecture, which are hard to measure directly, can be selected using associated markers.

Limitations of MAS:

1. **High Initial Cost**- Developing molecular markers and identifying linkages with target traits require substantial investment in time, technology, and expertise.

2. **Limited to Known QTLs**- MAS is effective only when the genetic basis of a trait is well understood, including identification of reliable markers and quantitative trait loci (QTLs).

3. **Complex Traits Challenge**- Traits controlled by multiple genes (polygenic traits) with small individual effects are harder to improve using MAS alone compared to Genomic Selection (GS).

4. **Marker-Trait Association Errors**- Linkage disequilibrium might change across populations or environments, potentially reducing marker efficiency in different breeding materials.

5. **Infrastructure Dependence**- Successful implementation requires access to molecular labs, genotyping platforms, and trained personnel, which may not be available in all regions.

3.2 Transgenic Technologies

Transgenic technology involves the insertion of foreign genes (transgenes) into the genome of an organism to introduce new traits. In plants, this allows the development of genetically modified (GM) crops with improved characteristics like pest resistance, enhanced nutrition, or environmental tolerance.

1. Bt Crops

Bt crops are genetically modified to express genes from the bacterium *Bacillus thuringiensis* (Bt), which produces proteins toxic to specific insect pests.

Key Benefits:

- Built-in resistance to pests like *Helicoverpa armigera* (cotton bollworm).
- Reduced need for chemical insecticides.
- Improved yield and environmental safety.

Examples-
Bt cotton, Bt maize

2. Golden Rice

Golden Rice is genetically modified to produce beta-carotene, a precursor of vitamin A, in its edible parts (rice endosperm).

- To combat vitamin A deficiency, especially in developing countries where rice is a staple food.

Key Feature-

The golden colour comes from the accumulation of beta-carotene, made possible by introducing genes from *daffodil* and *bacteria*.

3.3 Genome Editing (CRISPR, TALENs)

Genome editing technologies like CRISPR-Cas9 and TALENs (Transcription Activator-Like Effector Nucleases) enable precise alterations in the DNA of organisms to modify or regulate specific genes.

Targeted Trait Improvement

- **Precision Breeding**- CRISPR and TALENS can knock out undesirable genes or insert beneficial alleles for traits such as disease resistance, drought tolerance, improved yield, and nutritional enhancement.

- **Speed and Efficiency**- Unlike traditional breeding, genome editing offers faster development of improved cultivars without introducing foreign DNA.

- **Examples**:

  a) Rice varieties with blast resistance via CRISPR.

b) Wheat with reduced gluten content.

c) Maize improved for drought resistance.

Regulatory Landscape

- **Varied Global Policies-**

  1) U.S.: Some CRISPR-edited crops are exempt from GMO regulations if no foreign DNA is introduced.

  2) EU: Strict GMO regulations still apply to genome-edited crops.

  3) India and China: Under development; more cautious but evolving.

- **Case-by-case Approval-** Regulation depends on the process (how it's done) vs. product (what's produced), differing by country.

Public Perception:

- **Mixed Reactions-** Some view genome editing as safer than GMOs due to its precision and absence of transgenes. Others raise ethical, ecological, or health concerns.

- **Trust and Transparency-** Acceptance improves with transparent communication, regulatory clarity, and demonstrated benefits (e.g., disease resistance, sustainability).

- **Education is Key-** Public understanding is still limited; informed outreach is crucial for wider acceptance.

4. INTEGRATION OF GENOMIC SELECTION AND BIOTECHNOLOGY

4.1 Complementarity between Genomic Selection and Gene Editing

Genomic Selection (GS) and gene editing technologies like CRISPR-Cas9 or TALENs are complementary in the crop improvement pipeline. While GS enables the prediction of performance based on whole-genome marker data—capturing both major and minor genes—gene editing allows precise modification of known functional genes. GS can identify elite candidates that carry favorable polygenic backgrounds, and gene editing can then be used to fix or enhance specific alleles within those candidates, creating genotypes that are both broadly optimized and finely tuned.

4.2 Accelerated Breeding Cycles and Trait Pyramiding

By integrating GS and gene editing, the breeding cycle can be significantly shortened. GS enables early selection at the seedling stage using genotypic data, while gene editing bypasses the need for multiple generations to introgress target traits. Moreover, this integration supports trait pyramiding—stacking multiple beneficial traits (like disease resistance, drought tolerance, and nutritional quality) into a single line. This synergy speeds up the generation of superior cultivars.

4.3 Use in Polygenic Traits like Drought and Yield

Polygenic traits such as drought tolerance and yield are challenging to improve through conventional breeding or editing alone because they involve many genes with small effects. GS helps by predicting phenotypes using information from thousands of markers, while gene editing can enhance key regulators or pathways associated with the trait. When used together, GS provides a roadmap of where improvements can be made, and gene editing delivers those improvements with precision.

Table: Synergy between Genomic Selection and Gene Editing in Crop Improvement

Trait	Genomic Selection Role	Gene Editing Role	Integration Benefit
Drought Tolerance	Identifies minor-effect QTLs for drought response	Targets major regulators like DREB genes or stomatal regulators	Improves complex trait selection with higher accuracy and precision
Yield Improvement	Predicts superior genotypes combining many loci	Modifies key genes impacting sink-source balance and plant architecture	Combines prediction with precise alteration for maximum productivity
Nutritional Quality	Selects lines with favorable alleles related to protein, vitamins	Edits biosynthetic pathway genes for enhanced micronutrient content	Fast-tracks development of superior biofortified cultivars

5. ENABLING TECHNOLOGIES

5.1 High-throughput phenotyping (HTP)

HTP uses advanced imaging, sensors, and automation (like drones and robotics) to collect large-scale data on plant traits rapidly. It enables real-time monitoring of traits like plant height, canopy temperature, biomass, and disease symptoms under diverse conditions.

5.2 Bioinformatics and AI in Genomic Prediction

This involves using computational tools and machine learning algorithms to analyze genomic data, predict genetic traits, and assist breeders in selecting the best genotypes. It accelerates selection processes and increases precision in plant breeding programs.

5.3 Multi-omics Integration

This approach integrates multiple biological data types—such as genomics (DNA level), transcriptomics (RNA expression), proteomics (proteins), and metabolomics (metabolites)—to provide a comprehensive view of plant functions and traits. It helps in understanding gene-to-phenotype pathways.

6. APPLICATIONS IN MAJOR CROPS

A. Cereals (e.g., Rice, Wheat, Maize)

- Genome editing (CRISPR/Cas9) has enabled precise improvement of traits such as:

  a) Drought tolerance in maize

  b) Blast resistance in rice

  c) Rust resistance in wheat

- Marker-assisted selection has been widely used for QTL pyramiding in cereals for yield and stress tolerance.

- Transgenic approaches have enhanced micronutrient content (e.g., Golden Rice enriched in Vitamin A).

B. Legumes (e.g., Chickpea, Soybean, Pigeonpea)

- Legumes often suffer from biotic stresses like wilt and pod borer and abiotic stress such as drought.

- Genomic selection in chickpea and pigeonpea has accelerated breeding for:

  a) Root architecture improvement (drought adaptation)

  b) Disease resistance genes

- CRISPR is being explored to enhance protein quality and oil content in soybean.

C. Oilseeds (e.g., Groundnut, Mustard, Soybean)

- Focus areas include:

  a) Improving oil quality (high oleic acid content)

  b) Resistance to aflatoxin in groundnut

- Molecular breeding in mustard for early maturity and shattering resistance

- Genome editing tools used to reduce anti-nutritional factors in rapeseed.

D. Horticultural Crops (e.g., Tomato, Potato, Banana, Brinjal)

- **Tomato**: Improved shelf life and drought resistance using CRISPR.

- **Banana**: Resistance to Panama disease developed through transgenic approaches.

- **Potato**: Late blight resistance via gene editing.

- **Brinjal**: Bt Brinjal deployed in some countries to control fruit and shoot borer.

6.1 Breeding for Complex Traits

A. Abiotic Stress Tolerance

- Traits include drought, heat, salinity, and cold tolerance.

- Use of QTL mapping, transcriptomics, and genome-wide association studies (GWAS) in crops like:

  a) Wheat: heat and drought tolerance

  b) Rice: submergence (Sub1 gene)

  c) Chickpea: root traits under drought

B. Disease Resistance

- Breeding for resistance to fungal, bacterial, and viral pathogens using:

  a) Pyramiding R-genes through marker-assisted backcrossing

  b) CRISPR knockouts of susceptibility genes

- Examples:

  1) Wheat: leaf rust, stem rust (Sr genes)

  2) Potato: late blight resistance (Rpi genes)

  3) Tomato: TYLCV resistance

C. Micronutrient Density (Biofortification)

- Focused on reducing hidden hunger via:

  a) Fe, Zn biofortification in rice and wheat

  b) High-protein maize (QPM)

  c) High-iron beans and pearl millet

- Tools include MAS, transgenics, and CRISPR for modifying nutrient pathways.

Table 1: Applications in Major Crop Groups

Crop Group	Example Crops	Key Traits Improved	Technology Used
Cereals	Rice, Wheat, Maize	Drought tolerance, disease resistance, yield	MAS, CRISPR, GWAS
Legumes	Chickpea, Soybean	Drought tolerance, protein content, pest resistance	GS, CRISPR, MAS
Oilseeds	Groundnut, Mustard	Oil quality, aflatoxin resistance, maturity	CRISPR, MAS, RNAi
Horticultural	Tomato, Banana, Potato	Shelf life, disease resistance, shelf stability	Transgenics, CRISPR, RNAi

Table 2: Breeding for Complex Traits

Trait	Crops Involved	Breeding Tools Used	Key Outcomes
Abiotic stress	Wheat, Rice, Chickpea	QTL mapping, GWAS, CRISPR	Heat/drought/salinity resistance
Disease resistance	Potato, Tomato, Wheat	Gene pyramiding, RNAi, CRISPR	Late blight, rust, TYLCV resistance
Micronutrient density	Rice, Wheat, Pearl millet	Biofortification, Transgenics, CRISPR	Higher Fe, Zn, Vitamin A content

9. CONCLUSION

The convergence of advanced genomics, artificial intelligence, and collaborative platforms is reshaping the future of crop improvement. These synergies offer unprecedented opportunities to enhance efficiency, precision, and adaptability in plant breeding. Technologies like CRISPR, genomic selection, and AI-driven pipelines enable faster and more targeted development of resilient, high-yielding varieties.

At the same time, pan-genomes and global open-access data platforms ensure that the full spectrum of genetic diversity is leveraged, while fostering global collaboration and knowledge sharing. Together, these innovations create a powerful ecosystem for addressing the growing challenges of climate change, food security, and resource limitations.

Moving forward, the pathway to sustainable and equitable crop improvement depends not only on technological innovation but also on inclusive policies, ethical frameworks, and capacity building—especially in developing regions. A balanced approach that merges science, ethics, and accessibility will be key to ensuring that the benefits of modern breeding tools are shared fairly across all communities.

REFERENCES

1. Cheng, Q., & Wang, X. (2024). Machine learning for AI breeding in plants. *Genomics, Proteomics &*

Bioinformatics, 22(4). https://doi.org/10.1093/gpbjnl/qzae051

2. Koh, E., Sunil, R. S., Lam, H. Y. I., & Mutwil, M. (2024). Harnessing big data and artificial intelligence to study plant stress. *arXiv Preprint*

3. Moeinizade, S., Hu, G., & Wang, L. (2021). A reinforcement learning approach to resource allocation in genomic selection. *arXiv Preprint*

4. Spindel, J., Begum, H., Akdemir, D., Collard, B., Redoña, E., Jannink, J. L., & McCouch, S. R. (2020). Genomic selection in rice breeding: Training population, marker number, and predictive ability. *PLOS Genetics*. (Inferred from earlier context) — Though not in search results, it's widely published.

5. Tripathi, L., Ntui, V. O., & Tripathi, J. N. (2022). Control of bacterial diseases of banana using CRISPR/Cas-based gene editing. *International Journal of Molecular Sciences*, 23, 3619.

6. Chennakesavulu, K., Singh, H., Trivedi, P. K., Jain, M., & Yadav, S. R. (2022). Engineering drought, salinity, and thermo-tolerance in crops using CRISPR. *Plant Cell Reports*, 41, 815–831.

7. Nazir, R., Mandal, S., Mitra, S., Ghorai, M., Das, N., & Jha, N. K. (2022). CRISPR toolkit to enhance salt stress tolerance in rice and wheat. *Physiologia Plantarum*, 174, e13642.

8. Zhan, Y. (2021). Genome editing for plant research and crop improvement. *Journal of Integrative Plant Biology*.

9. Molla, K. A., Sretenovic, S., Bansal, K. C., & Qi, Y. (2021). Precise plant genome editing using base and prime editors. *Nature Plants*, 7, 1166–1187.

10. Xu, W., Yao, Z., Wang, X., & Bilichak, A. (2022). In planta gene editing efficiency in wheat. *ACS Agricultural Science & Technology*.

11. Gosavi, G., Ren, B., Li, X., & Zhou, H. (2022). Development of herbicide-tolerant crops via genome editing. *ACS Agricultural Science & Technology*.

12. Sturme, M. H. J., van der Berg, J. P., Bouwman, L. M. S., De Schrijver, A., de Maagd, R. A., & others (2022). Off-target effects by CRISPR-Cas in plants. *ACS Agricultural Science & Technology*.

13. Jiang, Y., Sun, K., & An, X. (2022). CRISPR/Cas applications in maize improvement. *ACS Agricultural Science & Technology*. Wu, X., Hu, Z., Zhang, Y., et al. (2024). Genomic signatures of cowpea domestication and improvement. *Nature Genetics*, 56, 992–1005.

14. Varshney, R. K. (2021). Breeding custom-designed crops for drought adaptation. *Advanced Genetics*.

15. Molla, K. A., Sretenovic, S., Bansal, K. C., & Qi, Y. (2021). Crop genome editing with base and prime editors. *Nature Plants*, 7, 1166–1187. (Repeat acknowledged)

16. Chen, K., Wang, Y., Zhang, R., Zhang, H., & Gao, C. (2019). CRISPR/Cas genome editing in agriculture. *Annual Review of Plant*

Biology, 70, 667–697. (Though 2019, provides context.)

17. Bartholomé, J., Prakash, P. T., & Cobb, J. N. (2021). Genomic prediction: Progress and perspectives for rice improvement. *arXiv Preprint*.

18. Sanchez-Martin, J., Widrig, V., Herren, G., Wicker, T., & Keller, B. (2022). Population genomics of Aegilops tauschii for wheat improvement. *Nature Biotechnology*, 40, 422–431.

19. Meiling Ming, Q. R. Pan, C., He, Y., & Zhang, Y. (2020). CRISPR–Cas12b for plant genome engineering. *Nature Plants*.

20. Xun, W., Shao, J., Shen, Q., & Zhang, R. (2020). Rhizosphere microbiome for plant fitness. *Computational and Structural Biotechnology Journal*.

21. Wang, L., Rengel, Z., Zhang, K., Jin, K., & Lyu, Y. (2020). Ensuring future food security: Insights into the rhizosphere. *iScience*.

22. Lian, Z., Nguyen, C. D., Liu, L., Wang, G., & Chen, J. (2022). Developmental regulators to improve plant transformation. *Plant Biotechnology Journal*.

23. Wu, M., Chen, A., Li, X., Li, X., & Hou, X. (2024). Non-tissue culture transformation and delivery strategies. *Advanced Biotechnology*.

24. Zhang, D., Xu, F., Wang, F., Le, L., & Pu, L. (2025). Synthetic biology and AI in crop improvement. *Plant Communications*.

25. Wang, Y., & Demirer, G. S. (2023). Synthetic biology for molecular farming and AI integration. *Trends in Biotechnology*.

26. Yan, Y., & Wang, W. (2025). Machine learning after a decade: Is it still a missing keystone in genomic-based plant breeding? *Artificial Intelligence Review*, 58, 260.

27. Crossa, J., Pérez-Rodríguez, P., Cuevas, J., Montesinos-López, O., & others (2017). Genomic Selection in plant breeding. *Trends in Plant Science*. (Included for context though before 2020.)