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Combining Genomic Selection (GS) with Marker-Assisted Selection (MAS)

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1. Introduction:

Molecular breeding represents a modern approach to crop improvement that integrates molecular biology tools with conventional breeding techniques to enhance selection efficiency and precision. It relies on DNA markers and genomic information to identify desirable traits at an early stage, thereby reducing dependence on phenotypic selection alone. Among the most important strategies in molecular breeding are Genomic Selection (GS) and Marker-Assisted Selection (MAS). Marker-Assisted Selection involves the use of specific DNA markers linked to genes or quantitative trait loci (QTLs) to select individuals carrying desirable traits. In contrast, Genomic Selection uses genome-wide markers to predict the breeding value of individuals, capturing the cumulative effect of both major and minor genes.

The integration of GS and MAS has become increasingly important due to their complementary nature. MAS is highly effective for traits controlled by a few major genes, while GS is better suited for complex polygenic traits governed by many genes with small effects. Combining these approaches enables breeders to achieve higher accuracy in selection, improve genetic gain, and accelerate breeding cycles. This integrated strategy is particularly valuable in addressing current agricultural challenges such as improving yield, enhancing tolerance to abiotic stresses like drought and heat, and improving quality traits in crops.

2. Overview of Marker-Assisted Selection (MAS)

Marker-Assisted Selection is a molecular breeding technique that uses DNA markers linked to specific genes or QTLs to facilitate indirect selection of desirable traits. The fundamental principle of MAS is that markers closely associated with target genes can reliably indicate the presence of those genes, allowing selection to be performed at the DNA level rather than relying solely on phenotype. This approach increases efficiency, especially for traits that are difficult, time-consuming, or expensive to measure.

MAS can be broadly categorized into different types, including Marker-Assisted Backcrossing (MABC) and Marker-Assisted Recurrent Selection (MARS). In MABC,

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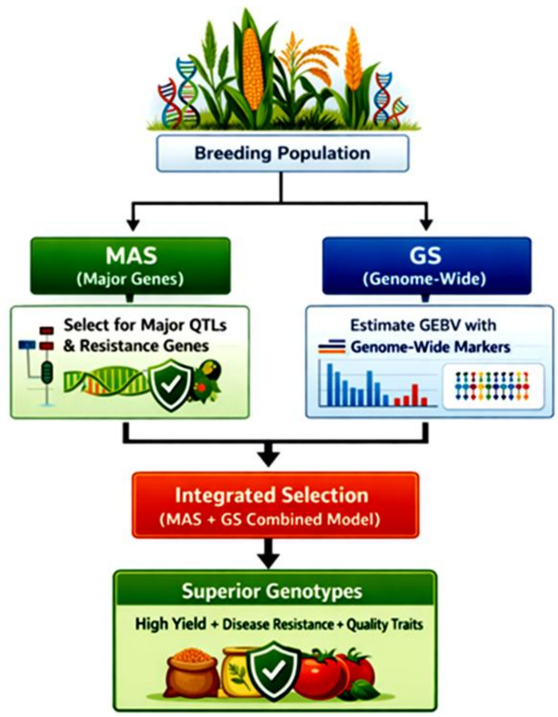
markers are used to introgress a specific gene or QTL from a donor parent into a superior recurrent parent while minimizing the transfer of unwanted genomic regions. In contrast, MARS focuses on accumulating favorable alleles from multiple loci over successive generations, thereby improving quantitative traits.

The applications of MAS are particularly prominent in the introgression of major genes or QTLs, especially for disease resistance breeding, where resistance genes can be transferred efficiently into elite cultivars. One of the major advantages of MAS is its high precision in selecting for traits controlled by major genes, as it allows accurate identification of individuals carrying the desired alleles. However, MAS has certain limitations. It is less effective for polygenic traits controlled by many genes with small effects, as it typically targets only a limited number of markers. Additionally, its efficiency depends on the availability of well-validated markers linked to target traits.

3. Overview of Genomic Selection (GS)

Genomic Selection is an advanced breeding approach that uses genome-wide molecular markers to predict the genetic potential of individuals. Unlike MAS, which focuses on specific markers associated with known QTLs, GS considers all markers across the genome simultaneously, thereby capturing both major and minor gene effects. The core concept of GS lies in estimating the Genomic Estimated Breeding Value (GEBV) of individuals, which represents their predicted genetic merit based on marker information.



Several statistical models are used in GS to estimate GEBVs, including Genomic Best Linear Unbiased Prediction (GBLUP) and various Bayesian models. GBLUP assumes equal variance across markers and is widely used due to its simplicity and efficiency, whereas Bayesian models allow for variable marker effects and are particularly useful when some markers have larger effects than others.

GS has wide applications in improving complex traits such as yield, drought tolerance, and other quantitative traits that are controlled by many genes. One of its major advantages is its ability to capture the effects of small-effect QTLs distributed across the genome, leading to higher prediction accuracy for complex traits. Additionally, GS enables faster breeding cycles by allowing early selection without extensive phenotyping in each generation.

Despite its advantages, GS also has limitations. It requires large training populations with both genotypic and phenotypic data to build accurate prediction models. Furthermore, the approach involves high computational costs and requires advanced statistical expertise and infrastructure. These challenges can limit its application in resource-constrained breeding programs.

4. Rationale for Combining Genomic Selection (GS) and Marker-Assisted Selection (MAS)

The integration of Genomic Selection (GS) and Marker-Assisted Selection (MAS) is driven by their complementary strengths in crop improvement programs. MAS is highly effective for traits controlled by major genes or large-effect quantitative trait loci (QTLs), enabling precise introgression and selection of these key loci. In contrast, GS is designed to capture the cumulative effects of numerous minor genes distributed across the genome, making it more suitable for complex polygenic traits. By combining these two approaches, breeders can simultaneously exploit both major and minor genetic effects, leading to more comprehensive genetic improvement.

Another important rationale for integration is the need to improve selection accuracy. While MAS provides high precision for specific loci, it does not account for the background genetic variation. GS addresses this limitation by incorporating genome-wide marker information, thereby increasing the accuracy of predicting breeding values. Additionally, integrating GS and MAS allows for more efficient utilization of genomic resources, including high-density marker data and validated QTL information. This combined approach helps bridge the gap between selection for simple traits (controlled by few genes) and complex traits (controlled by many genes), ultimately enhancing breeding efficiency and genetic gain.

5. Strategies for Integration of GS and MAS

Several strategies have been developed to effectively integrate GS and MAS in breeding programs. One common approach is the sequential strategy, where MAS is first used to select individuals carrying desirable major QTLs, followed by GS to improve the genetic background by selecting for polygenic traits. This approach ensures that key genes are fixed early, while overall genetic performance is optimized through genomic prediction.

Another strategy is the simultaneous approach, in which known major markers are incorporated as fixed effects within GS models. This allows breeders to explicitly account for large-effect QTLs while still utilizing genome-wide marker information for predicting minor gene effects. A related approach is weighted genomic selection, where markers associated with important QTLs are assigned higher weights in the prediction model, thereby increasing their influence on selection decisions.

Hybrid breeding pipelines also play a significant role in integration. In such pipelines, early generations are screened using MAS to eliminate undesirable genotypes, and advanced generations are subjected to GS for selection based on overall genetic merit. Furthermore, multi-trait selection models enable the simultaneous improvement of qualitative traits (e.g., disease resistance) and quantitative traits (e.g., yield), making the breeding process more efficient and balanced.

6.Statistical and Computational Approaches

The integration of GS and MAS relies heavily on advanced statistical and computational methods. Mixed linear models are widely used, as they can incorporate both fixed effects (for major QTLs identified through MAS) and random effects (for genome-wide markers used in GS). These models provide a flexible framework for combining different sources of genetic information.

Bayesian models are also extensively used in genomic prediction, particularly when prior information about QTLs is available. These models allow breeders to assign different levels of importance to markers based on prior knowledge, making them highly suitable for integrating MAS-derived information into GS frameworks. In recent years, machine learning approaches such as Random Forest and Deep Learning have gained popularity due to their ability to model complex, non-linear relationships between genotype and phenotype.

Several software tools have been developed to facilitate these analyses, including rrBLUP, GAPIT, and BGLR. These tools provide user-friendly platforms for implementing genomic prediction models and integrating marker information, making them accessible to plant breeders and researchers.

7. Applications in Crop Improvement

The combined use of GS and MAS has wide-ranging applications in crop improvement across different crop groups. In cereals such as rice, wheat, and maize, this integrated approach is used to simultaneously improve disease resistance and yield, which are often controlled by different genetic mechanisms. MAS helps in the precise introgression of resistance genes, while GS enhances yield potential by capturing polygenic effects.

In legumes such as soybean and pigeon pea, the integration of GS and MAS is applied to improve protein content and stress tolerance. These traits are critical for both nutritional quality and adaptability to changing environmental conditions. Similarly, in horticultural crops like banana and tomato, the combined approach is used to enhance quality traits such as fruit size, taste, and shelf life, along with resistance to diseases.

Moreover, this integrated strategy plays a crucial role in climate-resilient breeding by enabling the development of crop varieties that can withstand abiotic stresses such as drought, heat, and salinity, while maintaining high productivity.

8. Case Studies

Several case studies highlight the effectiveness of combining GS and MAS in practical breeding programs. In rice, breeders have successfully combined blast resistance genes identified through MAS with GS-based selection for yield, resulting in varieties that are both high-yielding and disease-resistant. In maize, GS has been used to predict hybrid performance, while MAS ensures the presence of key genes controlling important traits, thereby improving hybrid breeding efficiency.

In wheat, the integration of MAS for rust resistance genes with GS for yield and other agronomic traits has led to the development of improved varieties with enhanced resistance and productivity. Similarly, in soybean, the combined approach has been used to improve oil content and yield by targeting both major genes and polygenic traits, demonstrating the versatility and effectiveness of integrating GS and MAS in modern breeding programs.

References

1. Alemu, A. A., et al. (2024). Genomic selection in plant breeding: Key factors shaping two decades of progress. *Molecular Plant*, *17*(4), 552–578.
2. Bernardo, R., & Yu, J. (2007). Prospects for genomewide selection for quantitative traits in maize. *Crop Science*, *47*(3), 1082–1090.
3. Bhat, J. A., Ali, S., Salgotra, R. K., Mir, Z. A., Dutta, S., Jadon, V., Tyagi, A., Mushtaq, M., Jain, N., Singh, P. K., Singh, G. P., & Prabhu, K. V. (2016). Genomic selection in the era of next-generation sequencing. *Plant Cell Reports*, *35*, 173–186.
4. Crossa, J., Pérez-Rodríguez, P., Cuevas, J., Montesinos-López, O., Jarquín, D., de Los Campos, G., Burgueño, J., González-Camacho, J. M., Pérez-Elizalde, S., Beyene, Y., Dreisigacker, S., Singh, R., Zhang, X., Gowda, M., Roorkiwal, M., & Varshney, R. K. (2017). Genomic selection in plant breeding: Methods,

models, and perspectives. *Trends in Plant Science, 22*(11), 961–975.

5. Desta, Z. A., & Ortiz, R. (2014). Genomic selection: Genome-wide prediction in plant improvement. *Trends in Plant Science, 19*(9), 592–601.
6. Escamilla, D. M., et al. (2025). Genomic selection: Essence, applications, and prospects. *The Plant Genome*.
7. Heffner, E. L., Sorrells, M. E., & Jannink, J. L. (2009). Genomic selection for crop improvement. *Crop Science, 49*(1), 1–12.
8. Jannink, J. L., Lorenz, A. J., & Iwata, H. (2010). Genomic selection in plant breeding: From theory to practice. *Briefings in Functional Genomics, 9*(2), 166–177.
9. Larkin, D. L., & Yu, X. (2019). Genomic selection: Considerations for successful implementation. *Agronomy, 9*(9), 479.
10. Merrick, L. F., Carter, A. H., & Wang, J. (2021). Breeding with major and minor genes: Genomic selection for disease resistance. *Frontiers in Plant Science, 12*, 713829.
11. Meuwissen, T. H. E., Hayes, B. J., & Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics, 157*(4), 1819–1829.
12. Spindel, J., & McCouch, S. (2016). When more is better: How data sharing would accelerate genomic selection. *Theoretical and Applied Genetics, 129*, 1617–1623.
13. Varshney, R. K., Terauchi, R., & McCouch, S. R. (2014). Harvesting the promising fruits of genomics: Applying genome sequencing technologies to crop breeding. *Trends in Plant Science, 19*(10), 631–643.
14. Verma, S., et al. (2025). Integrating marker-assisted selection (MAS) and genomic selection (GS) for plant functional trait improvement. In *Advances in plant breeding research* (Book chapter). Springer.
15. Xu, Y., Li, P., Zou, C., Lu, Y., Xie, C., Zhang, X., Prasanna, B. M., & Olsen, M. S. (2020). Enhancing genetic gain in the era of molecular breeding. *Plant Communications, 1*(3), 100005.