



## Marker-Assisted Selection and Genomic Selection in Plants

(\*Rahul Choudhary)

M.Sc. Scholar, Department of Genetics and Plant Breeding, SHUATS, Prayagraj

\*Corresponding Author's email: [rahulchoudhary6188@gmail.com](mailto:rahulchoudhary6188@gmail.com)

Advancements in plant breeding and genetics have revolutionized the way we develop and improve crops. Two key methodologies that have emerged as powerful tools in modern plant breeding are Marker-Assisted Selection (MAS) and Genomic Selection (GS). Both approaches utilize genetic information to enhance plant breeding efficiency and accuracy, but they operate on different principles and scales. This chapter provides a detailed exploration of Marker-Assisted Selection and Genomic Selection, highlighting their methodologies, applications, advantages, limitations, and future directions.

### Marker-Assisted Selection (MAS)

Marker-Assisted Selection (MAS) leverages molecular markers linked to specific traits of interest to facilitate the selection of desirable genotypes. Molecular markers are DNA sequences with known locations in the genome that are associated with particular traits, such as disease resistance, yield, or quality.

#### Types of Molecular Markers

- Simple Sequence Repeats (SSRs) : Also known as microsatellites, SSRs are repeating sequences of 1-6 base pairs in length. They are highly polymorphic and useful for gene mapping and linkage studies.
- Single Nucleotide Polymorphisms (SNPs) : SNPs are variations at a single nucleotide position in the genome. They are abundant and provide high-resolution genetic information.
- Random Amplified Polymorphic DNA (RAPD) : RAPD markers are generated by amplifying random segments of the genome. They are useful for generating genetic fingerprints but are less precise than SSRs or SNPs.
- AFLP (Amplified Fragment Length Polymorphism) : AFLP involves the restriction of DNA followed by selective amplification. It provides a large number of markers and is useful for genetic mapping and diversity studies.

#### Identification of Markers

- Trait Mapping : The first step involves identifying genetic markers linked to the trait of interest through linkage mapping or quantitative trait locus (QTL) mapping. This requires creating a mapping population (e.g., F<sub>2</sub>, backcross) and using markers to associate with trait variations.
- Marker Validation : Validating markers involves ensuring their consistent association with the trait across different populations and environments.

#### Marker-Assisted Breeding

- Selection of Parents: Use markers to select parental lines that possess the desired trait-linked markers.

- Segregation Analysis: In the breeding population, use markers to select progeny that carry the desirable alleles for the target trait.
- Backcrossing: Employ markers to track the presence of desirable alleles in backcross populations, improving the precision of trait introgression.

### Applications of MAS

**Disease and Pest Resistance:** MAS is widely used to develop crops with resistance to diseases and pests. For example, markers linked to rust resistance in wheat or blight resistance in potatoes help breeders develop resistant varieties more efficiently.

MAS facilitates the selection of traits related to crop quality, such as improved nutritional content, taste, or texture. For instance, markers linked to high oil content in oilseed crops can be used to enhance oil yield.

Markers associated with abiotic stress tolerance (e.g., drought, salinity) help develop varieties that can withstand challenging environmental conditions, crucial for maintaining productivity in adverse climates.

### Advantages and Limitations of MAS

- Increased Precision: MAS provides a more precise method of selection compared to traditional phenotypic selection.
- Time Efficiency: MAS accelerates the breeding process by allowing early selection of desirable traits in seedlings.
- Reduced Environmental Impact: By selecting for traits such as disease resistance, MAS can reduce the need for chemical inputs.
- Marker Availability : Effective MAS requires the availability of validated markers for the traits of interest.
- Cost : The initial setup for MAS can be expensive due to the need for molecular biology tools and expertise.
- Linkage Drag: Unwanted genetic regions linked to the desired trait may be inherited along with the trait, potentially affecting plant performance.

### Genomic Selection (GS)

Genomic Selection (GS) involves predicting the performance of plants based on their entire genomic profile rather than specific markers linked to traits. GS uses high-density genomic data to estimate the breeding value of individuals, enabling selection of superior genotypes with high accuracy.

- High-Density Genotyping : GS relies on high-density genotyping platforms, such as SNP arrays or next-generation sequencing (NGS), to obtain comprehensive genomic information.
- Phenotypic Data : Phenotypic data are collected to develop predictive models that relate genetic information to trait performance.
- Training Population : A training population with both genotypic and phenotypic data is used to develop predictive models. The model estimates the relationship between genetic markers and trait performance.
- Validation Population : A separate validation population is used to test the accuracy of the predictive model and ensure its robustness.
- Breeding Value Prediction : The developed model is used to predict the breeding values of new genotypes based on their genomic data.
- Selection of Superior Genotypes : Genotypes with high predicted breeding values are selected for further breeding or production.

## Applications of GS

**Yield Improvement:** GS is used to enhance crop yield by selecting genotypes with superior performance based on comprehensive genomic data. This approach accelerates the development of high-yielding varieties.

### Complex Traits

GS is particularly effective for selecting complex traits controlled by multiple genes, such as drought tolerance or disease resistance, where traditional MAS may be less effective.

### Accelerated Breeding

By providing accurate predictions of plant performance early in the breeding process, GS accelerates the overall breeding cycle, allowing for quicker development of improved varieties.

## Advantages and Limitations of GS

- **Broad Trait Coverage** : GS can be applied to traits controlled by multiple genes, including complex and polygenic traits.
- **Increased Selection Accuracy** : Provides higher accuracy in predicting breeding values compared to traditional selection methods.
- **Efficiency** : Reduces the time and cost associated with phenotypic evaluations by focusing on genomic data.
- **Data Requirements** : Requires extensive genotypic and phenotypic data, which can be resource-intensive to collect.
- **Model Dependence** : The accuracy of GS depends on the quality of the predictive models and the training population.
- **Complexity** : The implementation of GS involves complex statistical and computational methods, which may require specialized expertise.

## Conclusion

Marker-Assisted Selection (MAS) and Genomic Selection (GS) represent significant advancements in plant breeding, offering powerful tools for improving crop traits and accelerating the development of new varieties. MAS focuses on the use of specific molecular markers linked to desired traits, while GS utilizes comprehensive genomic data to predict breeding values and select superior genotypes. Both approaches have unique advantages and limitations, and their integration can provide a more robust and efficient breeding strategy. As technology continues to evolve, the applications and effectiveness of MAS and GS are expected to expand, contributing to more sustainable and productive agricultural systems.

## References

1. Arruda, M. P., Lipka, A. E., Brown, P. J., Krill, A. M., Thurber, C., Brown-Guedira, G., ... & Kolb, F. L. (2016). Comparing genomic selection and marker-assisted selection for Fusarium head blight resistance in wheat (*Triticum aestivum* L.). *Molecular Breeding*, 36, 1-11.
2. Zhao, Y., Mette, M. F., Gowda, M., Longin, C. F. H., & Reif, J. (2014). Bridging the gap between marker-assisted and genomic selection of heading time and plant height in hybrid wheat. *Heredity*, 112(6), 638-645.
3. Cerrudo, D., Cao, S., Yuan, Y., Martinez, C., Suarez, E. A., Babu, R., ... & Trachsel, S. (2018). Genomic selection outperforms marker assisted selection for grain yield and physiological traits in a maize doubled haploid population across water treatments. *Frontiers in plant science*, 9, 366.