

Genomics beyond Heterotic Boundaries: Hybrid Breeding Under Weak Heterotic Structure.

Prof. Amritendu Misra

Suresh Gyan Vihar University, Jaipur, Rajasthan, India

Abstract

Heterotic grouping has historically underpinned the success of hybrid breeding programs, particularly in crops such as maize. However, in many crop species and modern breeding populations, heterotic structure is weak, overlapping, or poorly defined, limiting the efficiency of conventional group-based hybrid development strategies. Advances in genomics have enabled a paradigm shift from reliance on discrete heterotic pools to genome-wide prediction of hybrid performance. This manuscript reviews current genomic approaches for hybrid breeding under weak heterotic structure, including genomic relationship matrices, genomic prediction models incorporating additive and non-additive effects, and optimization of crossing strategies. We discuss training population design, prediction of combining ability, and practical applications across crops lacking strong heterotic patterns. The genomic framework offers a robust alternative to classical heterotic grouping, enabling data-driven hybrid prediction, enhanced genetic gain, and improved utilization of genetic diversity.

Keywords: Genomic selection, heterotic groups, hybrid breeding, combining ability, genomic prediction, $G \times E$ interaction

How to cite this article: Misra A. Genomics beyond Heterotic Boundaries: Hybrid Breeding Under Weak Heterotic Structure. *Int J Drug Deliv Technol.* 2026;16(59s): 1600-1602. DOI: 10.25258/ijddt.16.59s.179

Source of support: Nil

Conflict of interest: None

1. Introduction

Hybrid breeding has been one of the most successful strategies for increasing crop productivity worldwide. The foundation of this success lies in the exploitation of heterosis, typically achieved by crossing genetically divergent parents belonging to well-defined heterotic groups. Classical breeding programs, particularly in maize, have relied heavily on the existence of stable and predictable heterotic patterns.

However, in many crops and breeding populations, heterotic grouping structure is weak, inconsistent, or absent. The lack of clear divergence between parental pools reduces the predictability of hybrid performance and complicates the identification of superior cross combinations. This challenge is increasingly observed due to germplasm exchange, genetic recycling, and the narrowing of elite breeding pools.

The advent of high-density molecular markers and high-throughput genotyping platforms has enabled the application of genomic prediction approaches that bypass the need for rigid heterotic grouping. These approaches allow breeders to predict hybrid performance directly from genome-wide marker information, providing a powerful alternative to traditional methods.

This manuscript synthesizes current genomic strategies used in hybrid breeding systems where heterotic structure is weak and discusses their implications for future breeding programs.

2. Limitations of Classical Heterotic Grouping under Weak Structure

The effectiveness of heterotic grouping depends on clear genetic divergence between pools and consistent

expression of heterosis across environments. When these conditions are not met, several limitations arise:

- Reduced predictability of hybrid performance

- Overlap between heterotic groups

- Low correlation between group identity and combining ability

- Inefficient allocation of field testing resources

In such systems, group-based crossing schemes fail to capture the true genetic architecture of hybrid performance.

3. Genomic Relationship-Based Breeding Framework

3.1 Genomic Relationship Matrices (GRM)

Genomic relationship matrices quantify realized genetic similarity among individuals using genome-wide marker data. Unlike pedigree-based relationships, GRMs capture both recent and historical recombination events.

GRMs enable:

- Estimation of general combining ability (GCA)

- Prediction of hybrid performance for untested crosses

- Identification of complementary parental lines

This framework removes the dependence on discrete heterotic groups and replaces it with continuous genomic relatedness.

4. Genomic Prediction Models for Hybrid Performance

Hybrid performance is influenced by multiple genetic components:

- Additive effects

- Dominance effects

- Epistatic interactions

Modern genomic prediction models incorporate these components using:

Genomic Best Linear Unbiased Prediction (GBLUP)

Additive–dominance models

Bayesian regression approaches

Machine learning algorithms

These models estimate marker effects across the genome and predict the performance of both tested and untested hybrid combinations with high accuracy.

5. Training Population Design Under Weak Heterotic Structure

In the absence of strong heterotic grouping, the design of the training population becomes critical for model performance.

Key considerations include:

Representation of the full genetic diversity of the breeding population

Inclusion of diverse parental combinations

Balanced sampling of crosses

Multi-environment phenotyping

Well-designed training populations ensure that genomic models capture the relevant genetic variance components influencing hybrid performance.

6. Prediction of Combining Ability

Genomic approaches allow direct prediction of:

General Combining Ability (GCA) based on additive genomic effects

Specific Combining Ability (SCA) based on dominance and interaction effects

This enables breeders to identify superior parental combinations without extensive field testing, particularly in crops lacking established heterotic pools.

7. Optimization of Crossing Strategies

Genomic information can be integrated into optimization algorithms to:

Select optimal parental combinations

Maximize expected genetic gain

Maintain long-term genetic diversity

Reduce breeding cycle time

Such approaches transform hybrid breeding into a predictive and optimization-driven system.

8. Applications across Crops

The genomic framework is particularly valuable in crops where heterotic patterns are weak or inconsistent, including:

Hybrid wheat

Rice

Sorghum

Pearl millet

Vegetable crops

In these systems, genomic prediction has significantly improved hybrid identification and breeding efficiency.

9. Implications for Future Breeding

The shift from heterotic grouping to genomic prediction represents a major paradigm shift in plant breeding:

Classical Approach/

Genomic Approach

Fixed heterotic groups/

Continuous genomic relationships

Rule-based crossing//

Data-driven prediction

Limited hybrid exploration/

Genome-wide cross prediction

Moderate genetic gain/

Accelerated genetic gain

This transformation enhances the ability of breeding programs to respond to climate change, resource constraints, and increasing food demand.

10. Conclusion

When heterotic structure is weak, reliance on classical group-based breeding becomes inefficient. Genomic approaches provide a robust alternative by enabling accurate prediction of hybrid performance using genome-wide marker information.

The integration of genomic prediction, optimized training populations, and data-driven crossing strategies allows breeders to transcend heterotic boundaries and achieve sustained genetic gain.

Acknowledgment

The author acknowledges the contributions of plant breeding and genomics communities in advancing hybrid breeding methodologies.

“Weak heterotic groups, strong genomic answers.”

References:

1. Chen, S.P., Tung, C.W., Wang, P.H., et al. (2023). Statistical package for evaluation of hybrid performance via genomic selection. *Scientific Reports*, 13, 12204.
2. Cuevas, J., Crossa, J., Montesinos-López, A., et al. (2025). Enhancing wheat genomic prediction by a hybrid kernel approach. *Frontiers in Plant Science*, 16:1605202.
3. Fritsche-Neto, R., Ali, J., De Asis, E.J., et al. (2023). Improving hybrid rice breeding programs via genomic prediction. *Theoretical and Applied Genetics*, 137:3.
4. Gu, Z., et al. (2023). Structure and function of rice hybrid genomes reveal genetic basis of heterosis. *Nature Genetics*, 55:1619–1620.
5. Li, C., et al. (2022). Genomic insights into improvement of heterotic groups in maize breeding. *Nature Plants*, 8:971–984.
6. Sun, J., et al. (2026). Heterotic group classification and heterosis prediction in recombinant maize lines. *Journal of the Science of Food and Agriculture*.
7. Zhang, H., et al. (2025). Whole-genome resequencing-based classification of heterotic

- groups in sorghum. *International Journal of Molecular Sciences*, 26:7950.
8. Zhang, X.L., Zhu, Q., Li, J.Q., et al. (2024). Maximizing rice yields through heterosis and genomic breeding strategies. *Rice Genomics and Genetics*, 15(4):190–202.
 9. Abdullah, M., et al. (2025). Hybrid wheat development and heterosis exploitation strategies. *Rice* 18