Agri Articles
(e-Magazine for Agricultural Articles)
Volume: 06, Issue: 06 (NOV-DEC, 2026)
Available online at http://www.agriarticles.com
©Agri Articles, ISSN: 2582-9882

Genomic Assisted Breeding in Groundnut

*Narendra Kumar, Sheetal Gupta, Raja Ram Choudhary and Lokesh Kumar Thawait
ICAR-Indian Institute of Groundnut Research, Regional Research Station,
Bikaner-334006, Rajasthan, India
*Corresponding Author's email: narendrapb09@gmail.com

Groundnut is a vital oilseed and legume, but various environmental challenges and pests can hinder its productivity. Traditional breeding has significantly contributed to developing improved groundnut varieties with higher yields, better adaptability, and resistance to various stresses Advancements in genomics are opening up new pathways for improvement through techniques like genomics-assisted selection (GAS). Genomics-assisted selection integrates molecular information with traditional breeding, enhancing the accuracy and efficiency of selecting desirable genotypes. This approach allows breeders to identify favourable genomic regions and predict the breeding value of genotypes earlier.

Introduction

Groundnut (*Arachis hypogaea* L.) is an important oilseed and legume crop valued for its nutritional and economic importance. It is a rich source of oil, protein, and essential nutrients, supporting food security and farmers' livelihoods. It contains range of essential minerals and vitamins which play vital roles in various bodily functions. Besides kernel, their shells are used in the animal feed, fuel, and fertilizer industries. Haulm is very nutritious, palatable utilized for animal feed. Despite its economic importance, groundnut production is frequently affected by several biotic and abiotic stresses, including foliar diseases, aflatoxin contamination, drought, high temperature, and soil salinity. These constraints often reduce crop productivity and affect the quality of the produce. Conventional breeding has improved groundnut varieties, though its progress is often slow due to its complex allotetraploid genome and long breeding cycles. Recent advances in genomics-assisted selection (GAS) approaches *viz*., MAS, QTL mapping, GWAS, and genomic selection, have made crop improvement more efficient by helping develop high-yielding varieties with better stress resistance and nutritional quality. These approaches can help accelerate the development of varieties with improved disease resistance, drought tolerance, higher yield, and better nutritional quality, particularly in terms of oil composition.

Major Genomics-Assisted Breeding Approaches

Genomics-assisted selection involves the application of molecular and genomic information to identify and select superior genotypes carrying favourable alleles for desirable traits. Several approaches have been developed to facilitate the genetic improvement of groundnut.

- **Marker-assisted selection (MAS):** Marker-assisted selection is one of the most widely established applications of molecular breeding. It involves the use of DNA markers closely linked to genes or QTLs controlling important traits to identify desirable plants during the breeding process. Unlike conventional phenotypic selection, MAS allows the selection of plants based on their genetic constitution, irrespective of environmental conditions or developmental stages. The major advantage of MAS is that it allows the selection of desirable plants at early growth stages, reducing dependence on repeated phenotypic screening.

- **Marker-Assisted Backcrossing (MABC):** MABC is used primarily used to transfer specific desirable genes or QTLs from donor parents into popular cultivated varieties. The main objective is to introduce the target trait while retaining most of the genetic background and desirable agronomic characteristics of the recurrent parent.
- **Quantitative trait loci (QTL) mapping selection:** QTL mapping is an important approach for identifying genomic regions associated with quantitative traits such as pod yield, drought tolerance, disease resistance, seed size, and oil content. It involves the development of mapping populations from genetically contrasting parents, followed by phenotypic evaluation and molecular marker analysis. The identification of stable QTLs across different environments is particularly important for their application in breeding programmes. Once validated, closely linked markers can be used for marker-assisted selection and gene pyramiding. Combining multiple favourable QTLs into a single genetic background can help develop groundnut cultivars with improved resistance to multiple stresses and enhanced productivity.
- **Genomic Selection (GS):** While MABC excels for traits controlled by a few major genes, polygenic traits like pod yield are governed by numerous loci with small individual effects. Genomic selection addresses this by utilizing genome-wide markers to estimate Genomic Estimated Breeding Values (GEBVs) for all candidate lines in a population, enabling selection even without prior knowledge of individual gene locations. It can facilitate early-generation selection, reduce the need for extensive phenotyping, and increase the efficiency of recurrent selection programs.
- **Genome-wide association studies (GWAS):** Genome-wide association studies are increasingly being used to identify marker–trait associations in diverse germplasm collections. Unlike conventional QTL mapping, which generally uses biparental populations, GWAS utilizes natural genetic diversity and historical recombination events to identify genomic regions associated with important traits. GWAS is particularly useful for identifying candidate genes and favourable alleles present in different genetic backgrounds.
- **Haplotype-Based Selection:** Uses combinations of linked markers (haplotypes) rather than individual markers. Improves precision in selecting favourable genomic regions.
- **Genomic Prediction and Selection Models:** Employ statistical and machine-learning approaches to predict phenotypic performance from genomic data. Widely used in modern plant and animal breeding.
- **Genome editing:** Genome editing is a powerful approach that enables precise modification of specific DNA sequences that are associated with desirable traits. Technologies such as CRISPR/Cas9, TALENs, and zinc-finger nucleases (ZFNs) are used to introduce targeted changes in the genome, including gene knockouts, insertions, deletions, and nucleotide substitutions. This method has the potential to boost key traits, such as making the plants more resistant to diseases, helping them withstand drought conditions, and ultimately increasing their yield.

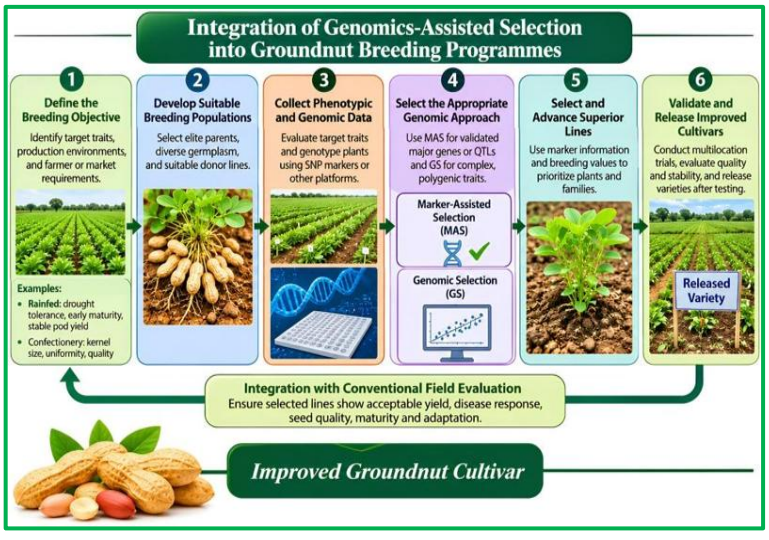
Main feature of Genomic assisted approaches

Genomic Selection Approach	Main Feature	Best Suited For
Marker-assisted selection	Selection using linked markers	Major genes/simple traits
Marker-Assisted Backcrossing	Introgression of specific genes	Disease resistance, quality traits
Genomic Selection	Genome-wide prediction	Complex traits, yield
Genome-wide association studies	Uses marker-trait associations	Trait discovery and breeding
QTL mapping selection	Selection based on mapped QTLs	Traits with known QTLs
Haplotype-based selection	Uses marker combinations	Fine-scale selection
Genomic prediction	Predictive modelling	High-throughput breeding

Applications of Genomics-Assisted Selection in Groundnut Improvement

Genomics-assisted selection (GAS) has become an important tool in groundnut improvement. Its major applications include improving disease resistance, drought tolerance, aflatoxin resistance, oil quality, and yield potential.

- **Biotic Stress Resistance (Disease and Pest Management):** Foliar fungal diseases, notably Late Leaf Spot (LLS), collar rot, stem rot and rust, along with insect pests like white grub, jassids, aphids, and tobacco caterpillar routinely devastate groundnut yields. Genomics-assisted breeding helps identify resistance-associated QTLs and transfer them into popular cultivars using marker-assisted selection (MAS) and marker-assisted backcrossing (MABC). Rust resistance from GPBD 4 has been introgressed into popular cultivars such as ICGV 91114, JL 24, and TAG 24 using MABC.
- **Abiotic Stress Tolerance:** Climate change has led to more frequent droughts and heat waves, which can affect flowering, pegging, pod development, and overall yield in groundnut. QTL mapping and genomic selection help identify important genomic regions linked to drought tolerance, root development, and efficient water use. These regions can be used in breeding programmes to develop drought-tolerant varieties. Early-maturing genotypes are also useful in escaping terminal drought. For example, QTLs such as qHW-A05.4 (haulm weight), qPW-A03.2 (pod weight), qSW-A03.1 (100-seed weight), and qTR-A09.1 (transpiration rate) have been identified as potential genomic regions for improving drought tolerance and yield-related traits in groundnut (Pandey *et al.* (2021).
- **Oil Quality Enhancement:** Improvement in fatty acid composition is an important objective of groundnut breeding. By utilizing molecular markers to target mutations in the fatty acid desaturase genes (*FAD2A* and *FAD2B*), breeders have created lines with high oleic-to-linoleic acid ratios. These varieties exhibit extended shelf-life, improved resistance to oxidative rancidity, and superior cardiovascular health benefits for consumers. In India, ICAR-IIGR, Junagadh released two high-oleic groundnut varieties *viz*., Girnar 4 and Girnar 5 through molecular breeding approaches.
- **Improvement of yield and yield-related traits:** Pod yield is a complex quantitative trait influenced by pod number per plant, seed weight, shelling percentage, harvest index, and reproductive efficiency, controlled by multiple genes and are strongly influenced by environmental conditions. QTL mapping and GWAS help identify favourable alleles, while genomic selection can capture the combined effects of numerous loci contributing to yield performance. Genomic studies using diverse groundnut germplasm have identified genomic regions associated with pod yield, 100-seed weight, flowering, and other yield-related characteristics. These markers can be used to select promising breeding lines and improve yield potential. Genomic regions associated with fresh seed dormancy (qfsd-1 and qfsd-2) (Bommireddy *et al.,* 2024) and seed size (major QTL on B07 and BIG SEED locus on B09) (Gangurde *et al.*, 2023) have been identified in groundnut. These QTLs and associated markers offer opportunities for marker-assisted selection to improve seed dormancy and develop large-seeded varieties.



Advantages and Limitations of Major Genomics-Assisted Selection Approaches

Approach	Advantages	Limitations
Marker-Assisted Selection (MAS)	• Faster than phenotypic selection • Can select plants at seedling stage • Useful for traits with high heritability and major genes • Reduces environmental effects on selection	• Less effective for complex quantitative traits • Requires tightly linked markers • Marker-trait association may break due to recombination
Marker-Assisted Backcrossing (MABC)	• Rapid transfer of desirable genes into elite cultivars • Reduces linkage drag • Accelerates recurrent parent genome recovery	• Requires reliable markers for foreground and background selection • Costly and labor-intensive • Best suited for traits controlled by major genes
Genomic Selection	• Captures effects of both major and minor genes • Highly effective for complex traits • Shortens breeding cycle • Increases genetic gain per unit time	• High initial genotyping and computational costs • Requires large training populations • Prediction accuracy may decrease across populations or environments
GWAS	• Identifies novel genes and QTLs • High mapping resolution • Utilizes natural genetic diversity	• Population structure can cause false associations • Requires large and diverse populations • Significant markers may not always be useful in breeding
QTL-Mapping Selection	• Identifies genomic regions controlling traits • Useful for marker development and gene discovery	• Many QTLs have small effects • QTL effects vary across environments • Mapping populations are expensive to develop
Haplotype-Based Selection	• More precise than single-marker selection • Captures linkage information among genes	• Requires dense genomic data • Data analysis is computationally demanding
Genomic prediction	• Can predict breeding values before phenotyping • Handles large genomic datasets • Enhances selection efficiency	• Requires advanced statistical expertise • Prediction accuracy depends on quality of training data

Conclusion

Genomics-Assisted Selection has fundamentally transformed groundnut improvement from an empirical art into a precise, predictive science. By unlocking the genetic potential hidden within wild progenitors and elite germplasm alike, GAS provides breeders with the tools necessary to develop climate-resilient, disease-resistant, and nutrient-dense varieties. Continued investment in genomic technologies, bioinformatics, and global partnerships will be essential to ensure that groundnut cultivation remains productive and sustainable in the face of evolving environmental and market demands.

References

1. Bomireddy, D., Sharma, V., Gangurde, S. S., Mohinuddin, D. K., Kumar, R., Senthil, Reddisekar, M., Bera, S. K. and Pandey, M. K. (2024). Multi-locus genome wide association study uncovers genetics of fresh seed dormancy in groundnut. *BMC Plant Biology*, *24*(1), 1258.

2. Desmae, H., Jordan, D. R., & Varshney, R. K. (2019). Genetics, genomics and breeding of groundnut (*Arachis hypogaea* L.). *Plant Breeding*, 138.
3. Gangurde, S. S., Pasupuleti, J., Parmar, S., Variath, M. T., Bomireddy, D., Manohar, S. S., Varshney, R. K., Singam, P., Guo, B., & Pandey, M. K. (2023). Genetic mapping identifies genomic regions and candidate genes for seed weight and shelling percentage in groundnut. *Frontiers in Genetics,* 14, Article 1128182.
4. Janila, P., Variath, M. T., Pandey, M. K., Desmae, H., Motagi, B. N., Okori, P, Manohar, S. S., Rathnakumar, A. L., Radhakrishnan, T., Liao, B., and Varshney, R. K. (2016). Genomic tools in groundnut breeding program: status and perspectives. *Frontiers in Plant Science*, *7*, 289.
5. Pandey, M. K., Gangurde, S. S., Sharma, V., Pattanashetti, S. K., Naidu, G. K., Faye, I., Hamidou, F., Desmae, H., Kane, N. A., Yuan, M., Vadez, V., Nigam, S. N., & Varshney, R. K. (2021). Improved genetic map identified major QTLs for drought tolerance- and iron deficiency tolerance-related traits in groundnut. *Genes*, 12(1), 37.
6. Ravi, K., Vadez, V., Isobe, S., Mir, R. R., Guo, Y., Nigam, S. N., Gowda, M. V. C., Radhakrishnan, T., Bertioli, D. J., Knapp, S. J., and Varshney, R. K. (2011). Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (*Arachis hypogaea* L.). Theoretical and Applied Genetics, 122, 1119–1132.
7. Varshney, R. K., Pandey, M. K., Janila, P., Nigam, S. N., Sudini, H., Gowda, M. V. C., Sriswathi, M., Radhakrishnan, T., Manohar, S. S., and Nagesh, P. (2014). Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut (*Arachis hypogaea* L.). Theoretical and Applied Genetics, 127, 1771–1781.
8. Varshney, R. K., Mohan, S. M., Gaur, P. M., Gangarao, N. V. P. R., Pandey, M. K., Bohra, A., Sawargaonkar, S. L., Chitikineni, A., Kimurto, P. K., Janila, P., Saxena, K. B., Fikre, A., Sharma, M., Rathore, A., Pratap, A., Tripathi, S., Datta, S., Chaturvedi, S. K., Mallikarjuna, N., and Gowda, C. L. L. (2013). Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. *Biotechnology Advances, 31*(8), 1120–1134.