

# Genomics Approaches for Enhancing Abiotic Stress Tolerance in Groundnut: A Pathway to Crop Improvement

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**Abstract:-** Genomics approaches have revolutionized crop improvement by providing insights into the genetic basis of abiotic stress tolerance in groundnut (*Arachis hypogaea* L.). Abiotic stresses such as drought, heat, salinity, and nutrient deficiencies pose significant challenges to groundnut production and global food security. This review highlights the key genomics approaches employed in groundnut research to enhance abiotic stress tolerance. Transcriptomics, including RNA sequencing (RNA-Seq), has enabled the identification of stress-responsive genes and regulatory networks. Marker-assisted selection (MAS) and quantitative trait loci (QTL) mapping have facilitated the identification of molecular markers and genomic regions associated with stress tolerance traits. Genomic selection integrates genomic information and phenotypic data for the prediction and selection of stress-tolerant individuals. Gene editing technologies, particularly CRISPR-Cas9, offer precise modification of stress-related genes. Comparative genomics has revealed conserved regions and genes associated with stress tolerance across species. Genomic resources and databases specific to groundnut aid in the identification of candidate genes and the design of molecular markers. These genomics approaches offer great potential for developing stress-tolerant groundnut varieties, ensuring sustainable agriculture, and addressing global food security challenges.

**Keywords:-** Abiotic Stress, Genomics, Groundnut, MAS, Transcriptomics.

## I. INTRODUCTION

Genomics approaches have revolutionized the field of crop improvement by providing valuable insights into the genetic basis of complex traits, including abiotic stress tolerance[1]. Among the various crops under investigation, groundnut (*Arachis hypogaea* L.), commonly known as peanut, plays a crucial role in global food security and economic stability[2]. However, groundnut production is severely affected by abiotic stresses such as drought, heat, salinity, and nutrient deficiencies[3]. These stresses not only limit crop productivity but also contribute to yield instability and reduced quality. Therefore, enhancing the abiotic stress tolerance of groundnut is of utmost importance for sustainable agriculture and food

production[4]. In recent years, genomics-based research has significantly contributed to our understanding of the molecular mechanisms underlying abiotic stress tolerance in groundnut[5]. The availability of the groundnut genome sequence has opened up new avenues for investigating stress-responsive genes, regulatory elements, and genetic variations associated with stress tolerance traits[6]. This wealth of genomic information, coupled with advanced molecular tools and techniques, has enabled scientists to design targeted strategies for improving groundnut crops[7].

## II. KEY GENOMICS APPROACHES

One of the key genomics approaches employed in groundnut research is transcriptomics, which involves studying the patterns of gene expression in response to abiotic stresses. High-throughput RNA sequencing (RNA-Seq) has allowed researchers to identify differentially expressed genes under stress conditions and gain insights into the regulatory networks involved in stress tolerance[8, 9]. For instance, a study by [10] used RNA-Seq to analyze the gene expression profiles of drought-tolerant and drought-sensitive groundnut genotypes, leading to the identification of stress-responsive genes involved in signaling, transcriptional regulation, osmotic adjustment, and antioxidant defense.

## III. MARKER-ASSISTED SELECTION (MAS)

Marker-assisted selection (MAS) is another genomics-based approach widely used in groundnut breeding programs to select plants with desirable abiotic stress tolerance traits. Molecular markers associated with stress tolerance have been identified through quantitative trait loci (QTL) mapping studies. For instance, [11] conducted a QTL mapping study for drought tolerance in groundnut and identified several genomic regions associated with this trait. The identified QTLs serve as valuable targets for marker-assisted breeding [12], enabling breeders to select and combine stress-tolerant alleles in elite groundnut varieties[1]. Genomic selection, an emerging breeding strategy, integrates genomic information and phenotypic data to predict the performance of individuals based on their genomic estimated breeding values (GEBVs)[13]. This approach has been successfully applied in groundnut breeding for stress tolerance traits. For instance, [14]

utilized genomic selection to improve drought tolerance in groundnut, resulting in the development of lines with improved productivity under water-limited conditions. Genomic selection offers the advantage of predicting performance at early stages, enabling breeders to make informed decisions and accelerate the development of stress-tolerant varieties[15].

Furthermore, advances in gene editing technologies, particularly CRISPR-Cas9, have opened up new possibilities for precisely modifying specific genes associated with abiotic stress tolerance in groundnut. Gene editing allows researchers to validate the function of candidate genes by creating targeted mutations and assessing the resulting phenotypic changes. This technology holds great promise for developing groundnut varieties with enhanced stress tolerance. For example, [16] used CRISPR-Cas9 to modify a key gene involved in drought response in groundnut, resulting in improved drought tolerance in the edited plants.

The integration of omics data from genomics, transcriptomics, proteomics, and metabolomics provides a comprehensive understanding of the molecular networks and regulatory mechanisms involved in abiotic stress responses in groundnut. This integrative approach helps unravel complex interactions and identify key genes and pathways associated with stress tolerance in groundnut. For instance, [17] employed an integrated transcriptomic and metabolomic analysis to elucidate the molecular mechanisms underlying heat stress tolerance in groundnut. They identified several key genes and metabolites involved in heat stress response, including those related to heat shock proteins, antioxidant defense, and osmotic adjustment.

#### IV. COMPARATIVE GENOMICS

Comparative genomics is another powerful tool that leverages the availability of genome sequences from different plant species to identify conserved regions and genes associated with abiotic stress tolerance. By comparing the groundnut genome with well-studied crops such as soybean and common bean, researchers can identify candidate genes for stress tolerance. Comparative genomics studies have revealed the existence of orthologous genes and gene families involved in stress responses across different species, providing valuable targets for further investigation in groundnut. The generation and utilization of genomic resources and databases specific to groundnut have also facilitated research and breeding efforts. Genomic databases, such as PeanutBase [18], provide a centralized repository of genomic information, genetic maps, and marker resources, enabling efficient data storage, retrieval, and analysis. These resources aid in the identification of candidate genes, the design of molecular markers, and the selection of breeding populations with desirable traits. Furthermore, germplasm collections, such as the International Peanut Germplasm Collection (IPGC), serve as a valuable resource for studying genetic diversity and identifying stress-tolerant accessions for breeding

programs. Genomics approaches have revolutionized the study of abiotic stress tolerance in groundnut, providing valuable insights into the genetic basis of stress response and tolerance mechanisms. Transcriptomics, marker-assisted selection, genomic selection, gene editing, comparative genomics, and integrative omics analyses have greatly advanced our understanding of the complex traits associated with abiotic stress tolerance in groundnut[19]. These genomics-based strategies offer tremendous potential for the development of stress-tolerant groundnut varieties with enhanced productivity and stability under adverse environmental conditions. By harnessing the power of genomics, groundnut breeders can accelerate the crop improvement process and contribute to global food security in the face of changing climatic conditions and growing agricultural challenges.

Here are some key aspects of groundnut genomics research for crop improvement in terms of abiotic stress tolerance:

- **Genomic sequencing:** The availability of the groundnut genome sequence provides a valuable resource for studying the genes and genetic pathways associated with abiotic stress tolerance. The genome sequencing enables the identification of stress-responsive genes and their regulatory elements.
- **Transcriptomics and gene expression profiling:** Transcriptomic studies, such as RNA sequencing (RNA-Seq), help in understanding the changes in gene expression patterns under different abiotic stress conditions. By comparing gene expression profiles of tolerant and susceptible groundnut varieties, researchers can identify genes and molecular pathways involved in stress response.
- **Marker-assisted selection (MAS):** Groundnut genomics research has facilitated the development of molecular markers associated with abiotic stress tolerance traits. MAS allows breeders to select plants with desirable traits at early stages, based on marker profiles. This expedites the breeding process for developing stress-tolerant groundnut varieties.
- **Quantitative trait loci (QTL) mapping:** QTL mapping involves identifying specific genomic regions associated with abiotic stress tolerance traits. Groundnut genomics studies have identified QTLs linked to drought, heat, salinity, and other stress-related traits. These QTLs serve as valuable targets for marker-assisted breeding programs aimed at improving stress tolerance.
- **Genomic selection:** Genomic selection integrates genomic information and phenotypic data to predict the performance of groundnut plants. This approach enables breeders to select individuals with superior stress tolerance based on their genomic estimated breeding values (GEBVs), even before they are subjected to stress trials.
- **Genetic transformation and gene editing:** Genomic tools also facilitate genetic transformation and gene editing techniques in groundnut. Researchers can introduce or modify specific genes associated with

abiotic stress tolerance to enhance groundnut's resilience to adverse environmental conditions.

By employing these genomics approaches, researchers aim to identify key genes, genetic markers, and molecular mechanisms involved in abiotic stress tolerance in groundnut[20]. The knowledge gained from genomics research can then be utilized in breeding programs to develop improved groundnut varieties with enhanced stress resilience, higher yields, and improved agricultural sustainability.

## V. CONCLUSION

In conclusion, genomics approaches have greatly advanced our understanding of abiotic stress tolerance in groundnut and provided valuable tools for crop improvement. Transcriptomics, marker-assisted selection, genomic selection, gene editing, comparative genomics, and integrative omics analyses have shed light on the genetic basis of stress tolerance and facilitated the development of stress-tolerant groundnut varieties. These genomics-based strategies offer tremendous potential for enhancing crop productivity, stability, and sustainability under adverse environmental conditions. By harnessing the power of genomics, groundnut breeders can expedite the development of stress-tolerant varieties, contributing to global food security and addressing the challenges posed by abiotic stresses. Continued research and integration of genomics approaches hold promise for further advancements in groundnut crop improvement.

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## Conflict of Interest

The authors declare no conflict of interest regarding the publication of this article.

## REFERENCES

- [1]. Thudi, M., et al., *Genomic resources in plant breeding for sustainable agriculture*. 2021. **257**: p. 153351.
- [2]. Akram, N.A., et al., *Peanut (Arachis hypogaea L.): A prospective legume crop to offer multiple health benefits under changing climate*. 2018. **17**(5): p. 1325-1338.
- [3]. Ojiewo, C.O., et al., *Advances in crop improvement and delivery research for nutritional quality and health benefits of groundnut (Arachis hypogaea L.)*. 2020. **11**: p. 29.
- [4]. de Andrade, L.A., et al., *Plant Growth-Promoting Rhizobacteria for Sustainable Agricultural Production*. 2023. **11**(4): p. 1088.
- [5]. Vala, A.K.G., et al., *Transcriptome analysis identifies novel gene (s) and pathways for salt stress responses in Dandi cultivar*. 2022: p. 1-15.
- [6]. Puppala, N., et al., *Sustaining yield and nutritional quality of peanuts in harsh environments: Physiological and molecular basis of drought and heat stress tolerance*. 2023. **14**.
- [7]. Thomson, M.J., et al., *Functional allele validation by gene editing to leverage the wealth of genetic resources for crop improvement*. 2022. **23**(12): p. 6565.
- [8]. Jacob, F., et al., *Altered expression levels of transcripts of GNAC TFs during drought stress in susceptible and tolerant cultivars of groundnut*. 2022. **3**: p. 100062.
- [9]. Thoppurathu, F.J., et al., *Unravelling the treasure trove of drought-responsive genes in wild-type peanut through transcriptomics and physiological analyses of root*. 2022. **22**(2): p. 215-233.
- [10]. Fracasso, A., L.M. Trindade, and S.J.B.P.B. Amaducci, *Drought stress tolerance strategies revealed by RNA-Seq in two sorghum genotypes with contrasting WUE*. 2016. **16**(1): p. 1-18.
- [11]. Pandey, M.K., et al., *Improved genetic map identified major QTLs for drought tolerance-and iron deficiency tolerance-related traits in groundnut*. 2020. **12**(1): p. 37.
- [12]. Sapre, S.S., et al., *Biochemical traits in pearl millet (Pennisetum glaucum) against downy mildew disease*. 2013. **83**(12): p. 1411-1415.
- [13]. Jonas, E. and D.-J.J.T.i.b. de Koning, *Does genomic selection have a future in plant breeding?* 2013. **31**(9): p. 497-504.
- [14]. Gautami, B., et al., *Quantitative trait locus analysis and construction of consensus genetic map for drought tolerance traits based on three recombinant inbred line populations in cultivated groundnut (Arachis hypogaea L.)*. 2012. **30**: p. 757-772.
- [15]. Derbyshire, M.C., J. Batley, and D.J.C.P.B. Edwards, *Use of multiple 'omics techniques to accelerate the breeding of abiotic stress tolerant crops*. 2022: p. 100262.
- [16]. Li, R., et al., *CRISPR/Cas9-Mediated SINPR1 mutagenesis reduces tomato plant drought tolerance*. 2019. **19**(1): p. 1-13.
- [17]. Shinwari, Z.K., et al., *Genetic engineering approaches to understanding drought tolerance in plants*. 2020. **14**: p. 151-162.
- [18]. Berendzen, J., et al., *The legume information system and associated online genomic resources*. 2021. **3**(3): p. e74.
- [19]. Chaudhary, J., et al., *Advances in omics approaches for abiotic stress tolerance in tomato*. 2019. **8**(4): p. 90.
- [20]. Anwar, A. and J.-K.J.I.j.o.m.s. Kim, *Transgenic breeding approaches for improving abiotic stress tolerance: recent progress and future perspectives*. 2020. **21**(8): p. 2695.