

Research Report

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## Harnessing Genetic Diversity in Peanut for Enhanced Crop Performance

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Legume Genomics and Genetics, 2024 Vol.15, No.5 doi: [10.5376/lgg.2024.15.0023](https://doi.org/10.5376/lgg.2024.15.0023)

Received: 06 Sep., 2024

Accepted: 07 Oct., 2024

Published: 18 Oct., 2024

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**Preferred citation for this article:**

Yu D.M., and Chen S.Y., 2024, Harnessing genetic diversity in peanut for enhanced crop performance, Legume Genomics and Genetics, 15(5): 232-243 ([10.5376/lgg.2024.15.0023](https://doi.org/10.5376/lgg.2024.15.0023))

**Abstract** Peanuts are a critical global crop, providing essential nutrients and serving as a key agricultural commodity. However, peanut cultivation faces numerous challenges, including susceptibility to drought, pests, diseases, and declining genetic diversity. To address these issues, genetic improvement of peanuts is vital. This study reviews the current status of genetic diversity in peanuts, emphasizing the importance of wild relatives, landraces, and advanced breeding lines as sources of valuable genetic variation. We also explore peanut germplasm collections, phenotypic and molecular characterization methods, and pre-breeding strategies to harness genetic resources. Additionally, we highlight breeding efforts for key traits, including yield, drought tolerance, disease resistance, and nutritional quality. The utilization of modern breeding tools, such as marker-assisted selection, genomic selection, and CRISPR/Cas9 gene editing, is discussed in the context of accelerating genetic gains. A case study on breeding for aflatoxin resistance in peanuts demonstrates successful genetic interventions and future prospects. The integration of genomics, transcriptomics, and high-throughput technologies is critical for further advancing peanut breeding. Ultimately, developing climate-resilient and sustainably cultivated peanut varieties requires enhanced genetic diversity, strong policy support, and the involvement of key stakeholders.

**Keywords** Peanut breeding; Genetic diversity; Drought tolerance; Aflatoxin resistance; CRISPR/Cas9 gene editing

### 1 Introduction

Peanut (*Arachis hypogaea* L.) is a vital crop globally, serving as a significant source of edible oil and protein. It is cultivated extensively in regions such as Asia, Africa, and America, contributing to both agricultural economies and food security (Chen et al., 2019). Peanuts are not only economically important but also offer multiple health benefits due to their rich content of bioactive components like phenolics, flavonoids, polyphenols, and resveratrol. Additionally, peanuts play a crucial role in improving soil quality through biological nitrogen fixation, making them an essential crop in sustainable agricultural practices (Akram et al., 2018). Despite its importance, peanut cultivation faces several challenges. The crop is susceptible to various abiotic stresses, including drought, salinity, and heat stress, which can significantly impact yield and quality. Moreover, the genetic bottlenecks resulting from its polyploid nature limit the genetic diversity available for breeding programs, making it difficult to develop stress-tolerant and high-yielding varieties (Burow et al., 2001). The limited molecular variations recorded in cultivated peanuts further complicate efforts to enhance genetic diversity and improve crop performance (Krishna et al., 2004).

To address these challenges, there is a pressing need for genetic improvement in peanuts. Advances in genomic research have provided valuable insights into the complex genome architecture of peanuts, identifying key genes involved in oil metabolism and stress responses (Chen et al., 2019; Song et al., 2022). The identification and utilization of genetic loci, such as AhVt1, which controls variegated testa color, can aid in marker-assisted selection and the development of new peanut varieties with desirable traits (Chen et al., 2023). Additionally, the introduction of variability from wild species into cultivated peanuts through synthetic amphidiploids has shown promise in broadening the gene pool and enhancing genetic diversity (Burow et al., 2001).

This study reviews the current status of genetic diversity in cultivated peanuts and identifies key genetic loci associated with desirable traits. It evaluates the potential of genomic tools and marker-assisted selection in peanut breeding programs, emphasizing their role in accelerating genetic improvement. The study focuses on the role of

wild species and synthetic polyploids in introducing genetic variation and enhancing peanut stress resistance, highlighting the promising prospects of these resources in improving the resilience of peanut crops to environmental challenges.

## 2 Genetic Diversity in Peanuts

### 2.1 Understanding genetic diversity

Genetic diversity refers to the total number of genetic characteristics in the genetic makeup of a species. In peanuts (*Arachis hypogaea* L.), genetic diversity is crucial for breeding programs aimed at improving crop performance, disease resistance, and adaptability to various environmental conditions. The genetic architecture of peanuts, including its polyploid nature and self-pollination tendencies, has historically limited the genetic diversity within cultivated varieties (Pandey et al., 2012; Tawanna, 2024).

### 2.2 Sources of genetic variation in peanuts

Wild relatives of peanuts, such as *Arachis cardenasii* and other species within the genus *Arachis*, are invaluable sources of genetic variation. These wild species harbor alleles that can confer resistance to biotic and abiotic stresses, which are often absent in cultivated varieties. For instance, the introduction of *A. cardenasii* into peanut breeding programs has led to the development of disease-resistant cultivars that have significantly improved food security and reduced fungicide use globally (Figure 1) (Bertioli et al., 2021). Additionally, wild species-derived induced allotetraploids have been used to introduce new traits, such as disease resistance and improved agronomic characteristics, into cultivated peanuts (Suassuna et al., 2020; Ballén-Taborda et al., 2023).

Induced mutations and the development of advanced breeding lines are other critical sources of genetic variation. Techniques such as genotyping-by-sequencing (GBS) and the use of molecular markers have facilitated the identification of single nucleotide polymorphisms (SNPs) and quantitative trait loci (QTLs) associated with desirable traits. For example, advanced backcross populations have been used to map QTLs for traits like pod constriction and yield components, revealing the potential of wild alleles to enhance peanut productivity and adaptation (Fonceka et al., 2012; Brown et al., 2021; Yang, 2024).

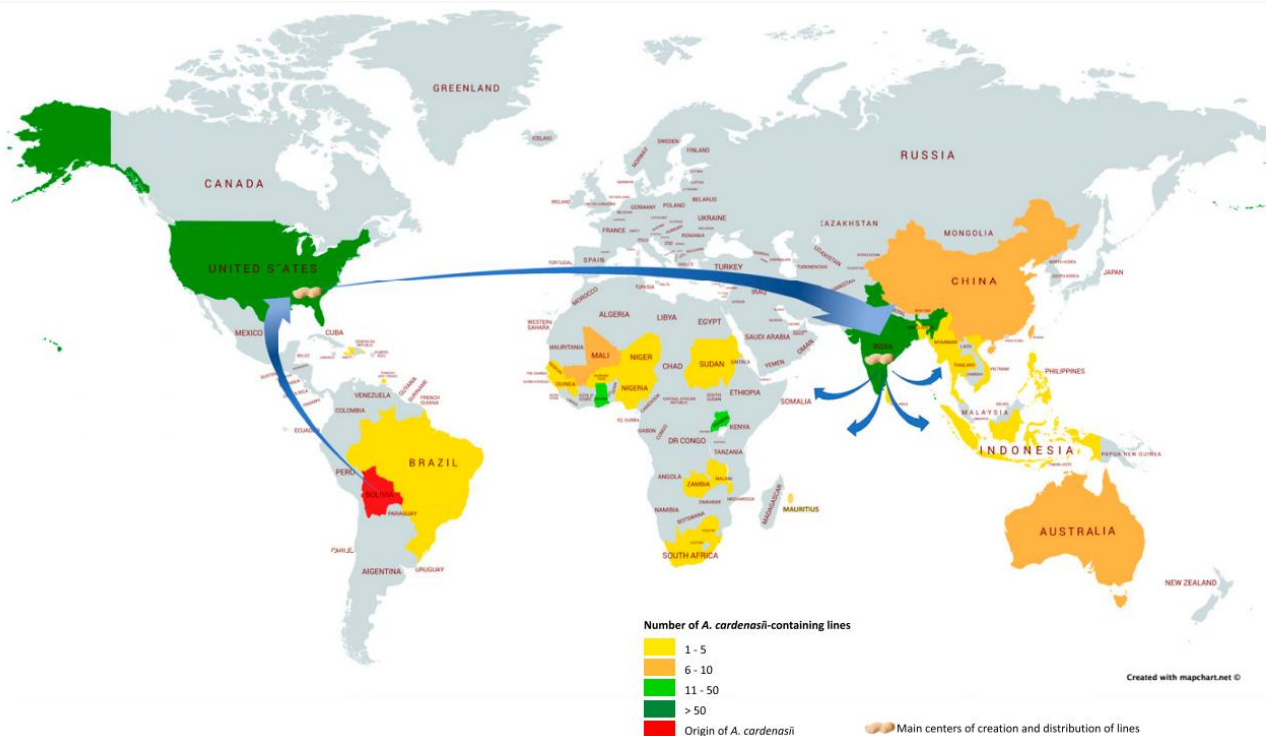


Figure 1 Global dispersal of *A. cardenasii* GKP 10017 and its genetic contribution to the peanut crop (Adopted from Bertioli et al., 2021)

Image caption: Counts are of cultivars and lines, which are registered and/or publicly available and do not include lineages that are confined to a single breeding program or lineages from segregating populations (Adopted from Bertioli et al., 2021)

### 2.3 Importance of genetic diversity for crop improvement

Genetic diversity is essential for the long-term improvement and sustainability of peanut crops. It allows breeders to develop cultivars with enhanced resistance to diseases, pests, and environmental stresses. The incorporation of diverse genetic material can lead to the development of superior genotypes with improved yield, quality, and adaptability. For instance, the use of wild species and advanced breeding techniques has led to the identification of introgression lines with high levels of resistance to late leaf spot and rust, as well as significant genetic variability for agronomic traits (Sharma et al., 2017).

### 2.4 Current status of genetic diversity in peanut breeding programs

Despite the recognized importance of genetic diversity, peanut breeding programs have historically relied on a narrow genetic base, primarily using elite breeding lines and cultivars. This has resulted in limited genetic variation within cultivated peanuts. However, recent efforts have focused on broadening the genetic base by incorporating wild relatives and developing core and mini core collections to represent the genetic variability of entire germplasm collections (Upadhyaya et al., 2002). Advances in peanut genomics, such as the development of molecular markers and genetic maps, have also accelerated the identification and utilization of beneficial alleles for crop improvement (Pandey et al., 2012).

In summary, harnessing genetic diversity from wild relatives, induced mutations, and advanced breeding lines is crucial for enhancing peanut crop performance. Continued efforts to broaden the genetic base and utilize modern genomic tools will be essential for the sustainable improvement of peanut cultivars.

## 3 Exploration and Utilization of Genetic Resources

### 3.1 Germplasm collection and conservation

Germplasm collection and conservation are fundamental to preserving the genetic diversity necessary for crop improvement. Large germplasm collections, such as those held in genebanks, contain a wide array of genetic material that can be used to enhance the genetic base of breeding programs. For instance, the Chinese Academy of Agricultural Sciences has developed a core collection of 576 accessions and a primary mini core collection of 298 accessions from a larger collection of 6 839 cultivated peanut lines (Jiang et al., 2012). Similarly, the U.S. has established a core collection of 831 accessions to represent its *Arachis hypogaea* L. germplasm collection (Holbrook and Dong, 2005).

### 3.2 Characterization of peanut germplasm

Phenotypic characterization involves evaluating germplasm for various morphological, agronomic, and quality traits. For example, the U.S. mini-core collection has been assessed for traits such as plant height, lateral branch growth, and pod yield using both traditional and high-throughput phenotyping methods (Sarkar et al., 2022). In China, a mini-mini core collection of 99 accessions was developed and evaluated for 21 morphological traits, capturing the range of traits displayed in the larger core collection (Jiang et al., 2012).

Molecular characterization uses genetic markers to assess the genetic diversity and relationships within germplasm collections. The U.S. peanut mini core collection was characterized using 73 SSR markers, revealing moderate levels of genetic variation and distinct groupings based on subspecies and botanical types (Kottapalli et al., 2007). In China, a mini-core collection was genotyped using 109 SSR markers, identifying 554 SSR alleles and demonstrating abundant genetic diversity (Jiang et al., 2014).

### 3.3 Core and mini-core collections

Core and mini-core collections are subsets of larger germplasm collections that represent the genetic diversity of the entire collection. These collections are designed to improve the efficiency of germplasm utilization in breeding programs. For instance, a mini core subset of 184 accessions was developed from a larger peanut core collection, preserving the genetic variation available in the core collection (Upadhyaya et al., 2002). Similarly, a mini core collection of 112 accessions was established in the U.S., capturing the majority of genetic variation expressed in the core collection (Holbrook and Dong, 2005).

### 3.4 Pre-breeding and introgression strategies

Pre-breeding and introgression strategies involve the incorporation of desirable traits from wild or exotic germplasm into cultivated varieties. These strategies are essential for enhancing the genetic base and improving the performance of crop cultivars. For example, the U.S. mini-core collection has been used to identify sources of resistance to late leaf spot, improving the efficiency of identifying resistant accessions in the entire collection (Holbrook and Dong, 2005). Additionally, the Chinese mini-core collection has been evaluated for resistance to bacterial wilt, identifying accessions with high levels of resistance (Jiang et al., 2012).

### 3.5 Case study: utilization of wild arachis species for disease resistance

Wild *Arachis* species are valuable sources of disease resistance genes that can be introgressed into cultivated peanut varieties. The development of core and mini-core collections facilitates the identification and utilization of these valuable genetic resources. For instance, the Chinese mini-core collection has been used to identify accessions with high oleic acid content, which is associated with improved disease resistance and agronomic traits (Yong et al., 2008). Similarly, the U.S. mini-core collection has been characterized for seed quality traits, providing information for further breeding and genetic research (Wang et al., 2011).

## 4 Breeding for Enhanced Crop Performance

### 4.1 Key traits for peanut improvement

Yield potential is a critical trait for peanut improvement, as it directly impacts the economic viability of the crop. Studies have shown that plant height-related traits are closely associated with yield, and understanding the genetic basis of these traits can help in better controlling crop yield. For instance, a meta-analysis identified numerous genomic regions associated with plant height and first branch length, which are crucial for peanut development and growth (Wang et al., 2021). Additionally, introgression of wild alleles has been shown to improve photosynthetic traits and yield in peanut lines, demonstrating the potential of utilizing wild species for yield enhancement. Drought and heat tolerance are essential for peanut cultivation, especially in semi-arid regions. Research has highlighted the importance of developing peanut cultivars with enhanced drought tolerance through physiological and yield trait assessments. For example, certain peanut lines have shown improved drought tolerance and yield stability under water stress conditions, making them suitable for semi-arid environments (Pereira et al., 2016). Moreover, the introgression of wild alleles has been effective in improving water use efficiency and drought tolerance in peanut (Dutra et al., 2018).

Disease and pest resistance are vital for maintaining peanut crop health and productivity. Genetic engineering techniques have been employed to introduce resistance to various fungal, viral, and insect pests in peanut. These techniques include the use of genes coding for pathogenesis-related proteins, RNA interference, and crystal proteins, among others (Krishna et al., 2015). Additionally, the development of introgression lines with high levels of resistance to late leaf spot and rust has been achieved through the use of wild species, providing valuable genetic resources for peanut improvement (Sharma et al., 2017). Improving the nutritional quality and oil content of peanut is another key breeding objective. Association mapping has been used to identify genetic markers linked to important traits such as protein and oil content, oleic acid, and linoleic acid. These markers facilitate marker-assisted selection for enhancing the nutritional quality of peanut (Zhang et al., 2018). Furthermore, genomic studies have identified significant marker-trait associations for oil and seed quality traits, which can be utilized in breeding programs to develop nutritionally superior peanut cultivars (Pandey et al., 2014).

### 4.2 Traditional breeding approaches

Hybridization is a traditional breeding approach that involves crossing different peanut lines to combine desirable traits. This method has been used to develop peanut cultivars with improved agronomic and quality traits. For instance, the development of a mini core subset of peanut has facilitated the utilization of genetic resources in breeding programs, enhancing the diversity of cultivars (Upadhyaya et al., 2002). Backcrossing is another traditional breeding technique used to introduce specific traits from a donor parent into a recurrent parent. This approach has been employed to introgress wild alleles into cultivated peanut, resulting in improved traits such as

drought tolerance and yield (Dutra et al., 2018). Backcrossing helps in retaining the desirable traits of the recurrent parent while incorporating new traits from the donor parent.

#### 4.3 Modern breeding techniques

Marker-assisted selection (MAS) is a modern breeding technique that uses genetic markers to select for desirable traits. MAS has been successfully applied in peanut breeding to improve traits such as disease resistance, oil content, and drought tolerance. For example, significant marker-trait associations have been identified for various agronomic traits, which can be used in MAS to accelerate the development of improved peanut cultivars (Pandey et al., 2014; Zhang et al., 2018). Genomic selection (GS) involves using genome-wide markers to predict the breeding value of individuals. This technique has been shown to enhance crop productivity and resilience by improving multiple traits simultaneously. GS can harness allelic diversity and increase selection efficiency, making it a valuable tool for peanut improvement (Dwivedi et al., 2017).

Genome-wide association studies (GWAS) are used to identify genetic variants associated with specific traits. GWAS has been employed in peanut to study traits such as yield, disease resistance, and nutritional quality. For instance, a GWAS study identified numerous genomic regions associated with plant height-related traits, providing insights into the genetic basis of these traits (Wang et al., 2021). Additionally, GWAS has been used to identify marker-trait associations for various agronomic traits in peanut (Figure 2) (Pandey et al., 2014). CRISPR/Cas9 and other gene editing technologies offer precise tools for modifying specific genes in peanut. These technologies have the potential to introduce or enhance traits such as disease resistance, drought tolerance, and nutritional quality. Genetic engineering techniques, including CRISPR/Cas9, have been used to develop transgenic peanut plants with improved resistance to biotic and abiotic stresses (Krishna et al., 2015). The continued development and application of gene editing technologies will further accelerate peanut improvement efforts.

### 5 Case Study: Breeding for Aflatoxin Resistance in Peanut

#### 5.1 Background on aflatoxin contamination and its impact

Aflatoxin contamination in peanuts, primarily caused by the fungus *Aspergillus flavus*, poses a significant threat to food safety and public health due to its toxic, carcinogenic, and immunosuppressive properties (Bhatnagar-Mathur et al., 2015; Yu et al., 2020; Jiang et al., 2021). This contamination can occur at various stages, including pre-harvest, post-harvest, and during storage, severely affecting the quality and marketability of peanuts (Nigam et al., 2009). The presence of aflatoxins in peanuts not only hampers international trade but also poses serious health risks to consumers, making it a critical issue for the peanut industry worldwide (Njoki et al., 2023).

#### 5.2 Genetic resources for aflatoxin resistance

Efforts to combat aflatoxin contamination have led to the identification of several genetic resources and resistance-associated genes in peanuts. For instance, quantitative trait loci (QTL) mapping has identified six novel resistant QTLs in the peanut variety J11, which significantly improve resistance to *A. flavus* infection (Jiang et al., 2021). Additionally, two peanut genotypes, Zh.h0551 and Zh.h2150, have been identified with significantly lower aflatoxin production, and 60 single nucleotide polymorphism (SNP) markers associated with this resistance have been detected (Yu et al., 2020). The AhRAF4 gene family, induced by *A. flavus* inoculation, has also been characterized, providing insights into the genetic basis of resistance (Deng et al., 2018).

#### 5.3 Breeding approaches and achievements

Breeding for aflatoxin resistance in peanuts has employed various approaches, including traditional breeding, molecular breeding, and biotechnological advancements. At ICRISAT, efforts have focused on identifying and utilizing genetic resistance to pre-harvest seed infection and aflatoxin production, although progress has been limited due to the complex nature of resistance and high genotype-environment interactions (Nigam et al., 2009). Transcriptome analyses have identified differentially expressed genes and pathways associated with resistance, such as those involved in disease resistance, hormone biosynthesis, and reactive oxygen species detoxification (Figure 3) (Wang et al., 2013; Soni et al., 2020). Gene co-expression network analysis has further revealed key hub genes that play major roles in resistance to *A. flavus* (Cui et al., 2022).

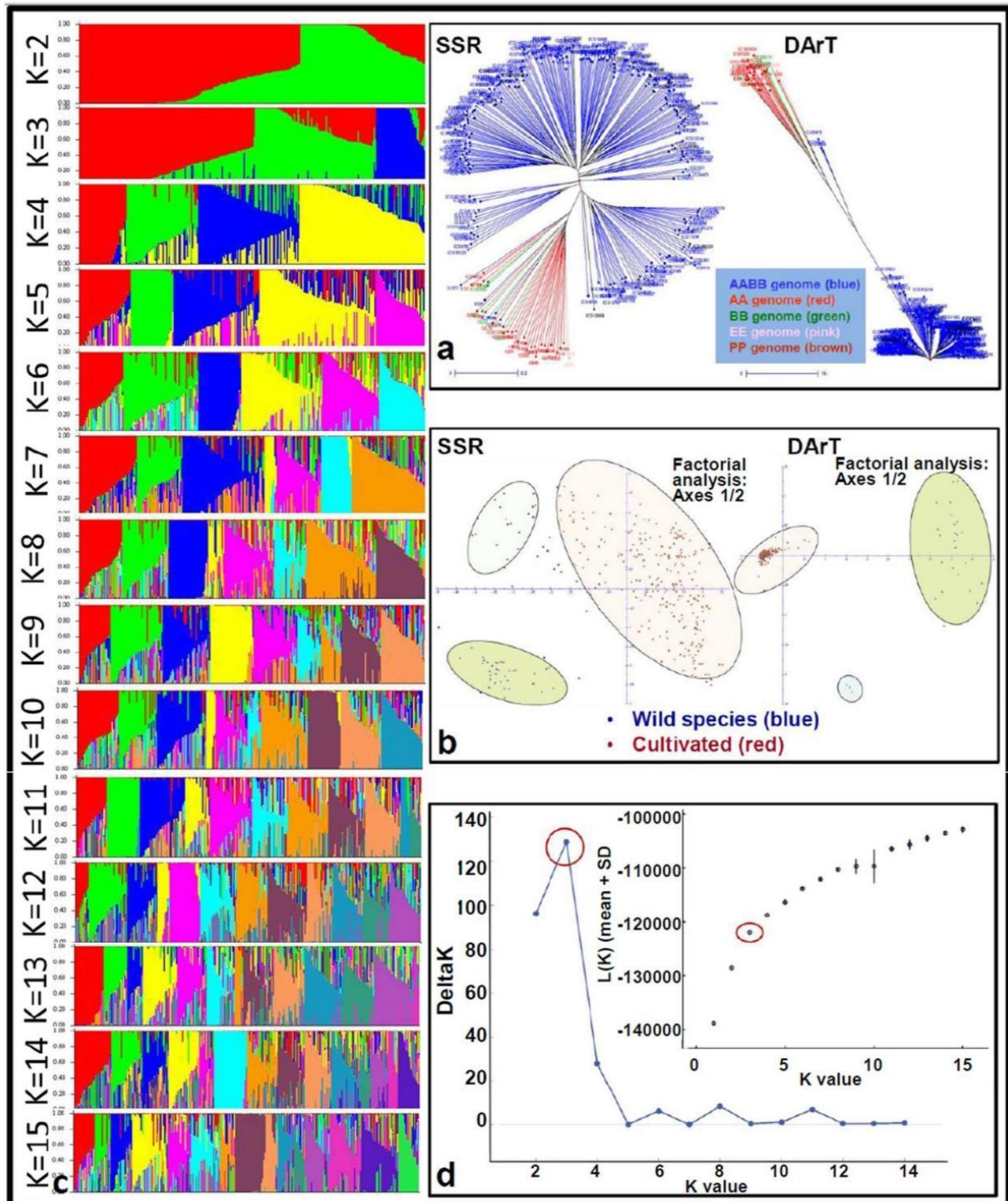


Figure 2 Genetic and population structure of the peanut 'reference set' (Adopted from Pandey et al., 2014)

Image caption: This figure shows (a) grouping of genotypes based on SSR and DARt marker genotyping data, (b) principle co-ordinate analysis (PCoA) based on SSR and DARt marker genotyping data. In the case of SSR as well as DARt based PCoA, cultivated genotypes are clustered in two groups and the wild species genotypes are clustered in one group. (c) the population structure in the reference set at different values of K (K = 1 to K = 15), and (d) presence of three subgroups based on mean Fst values (Adopted from Pandey et al., 2014)

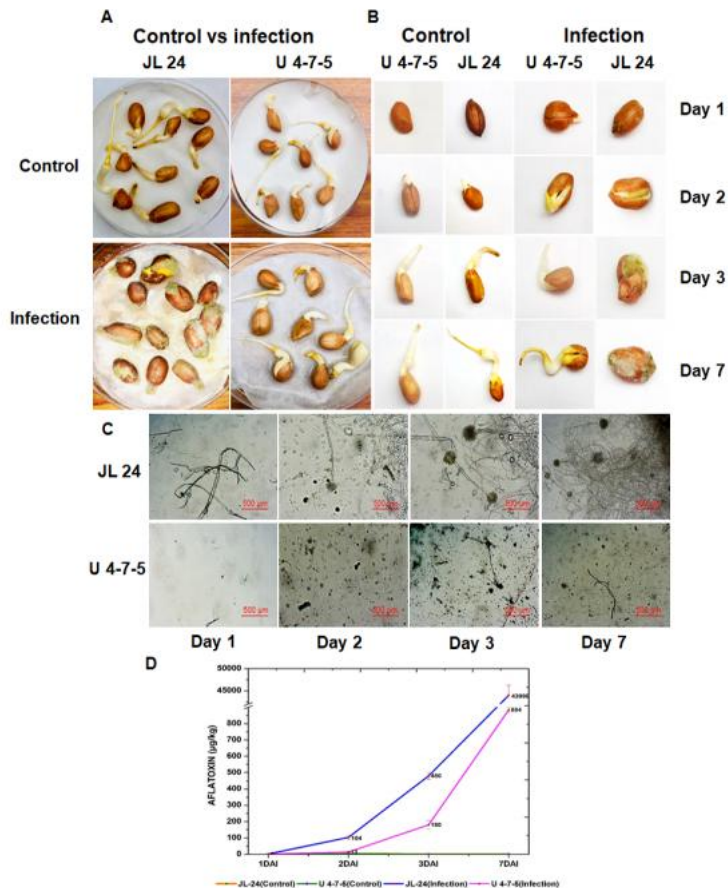


Figure 3 Phenotypic observations for seeds of U 4-7-5 and JL 24 during aflatoxin production (AP) by *A. flavus* at different time points along with microscopic observation and aflatoxin estimation (Adopted Soni et al., 2020)

Image caption: This figure shows the diagrammatic representation of phenotypic observations for seeds of JL 24 and U 4-7-5 at different time points (A,B), microscopic observation during AP at different time points (C) and graphical representation of AP estimation at different time points under control and infection conditions clearly showing the presence of highest amount of toxin at Day 7 after inoculation (D) (Adopted Soni et al., 2020)

#### 5.4 Future directions and challenges

Future breeding efforts should focus on integrating advanced molecular techniques with traditional breeding to enhance resistance to aflatoxin contamination. The development of transgenic peanuts with genes that inhibit aflatoxin biosynthesis or enhance antifungal properties appears promising (Nigam et al., 2009). Additionally, a deeper understanding of the genetic and molecular mechanisms underlying resistance, coupled with effective phenotyping strategies, will be crucial for developing durable resistance in commercial peanut varieties (Bhatnagar-Mathur et al., 2015; Korani et al., 2018). However, challenges such as the complexity of resistance traits, environmental interactions, and the need for reliable screening protocols must be addressed to achieve significant progress in breeding aflatoxin-resistant peanuts.

### 6 Integrative Approaches for Peanut Improvement

#### 6.1 Genomics and transcriptomics in peanut breeding

Genomics and transcriptomics have become pivotal in peanut breeding, offering insights into the genetic architecture and expression profiles of peanut plants. Recent advancements have led to the development of molecular markers, genetic and physical maps, and functional genomics platforms that facilitate the identification of quantitative trait loci (QTLs) and genes associated with tolerance to abiotic and biotic stresses, as well as agronomic traits (Pandey et al., 2012). Genome-wide association studies (GWAS) have been particularly useful, identifying significant marker-trait associations (MTAs) for various traits, which can be leveraged to improve

biotic resistance, nutritional quality, and yield components (Pandey et al., 2014). The integration of these genomic tools with traditional breeding methods accelerates the development of superior peanut cultivars.

### **6.2 Integrating omics data for trait improvement**

The integration of multi-omics data, including genomics, transcriptomics, proteomics, metabolomics, and phenomics, provides a comprehensive understanding of the biological processes underlying peanut traits. This holistic approach allows for the elucidation of growth, senescence, yield, and stress responses in peanuts (Yang et al., 2021; Huang et al., 2023). By combining data from different omics layers, researchers can construct models to predict complex traits and identify key regulatory networks. This integration is crucial for developing peanut varieties with enhanced traits such as disease resistance, drought tolerance, and improved nutritional content (Mahmood et al., 2022; Chao et al., 2023).

### **6.3 High-throughput phenotyping and genotyping**

High-throughput phenotyping and genotyping technologies are revolutionizing peanut breeding by enabling the rapid and accurate collection of large-scale data. These technologies facilitate the identification of phenotypic traits through various sensors and imaging techniques, which are then correlated with genotypic data to uncover the genetic basis of important agronomic traits (Zhao et al., 2019). The use of high-throughput genotyping, such as single nucleotide polymorphism (SNP) arrays and sequencing technologies, allows for the precise mapping of genetic variations and the identification of candidate genes for targeted breeding (Pandey et al., 2014; Tong and Nikoloski, 2020). This approach significantly shortens the breeding cycle and enhances the efficiency of selecting elite genotypes.

### **6.4 Role of bioinformatics and data management**

Bioinformatics plays a critical role in managing and analyzing the vast amounts of data generated from high-throughput phenotyping and genotyping. Advanced bioinformatics tools and platforms are essential for integrating and interpreting multi-omics data, enabling researchers to identify key genetic markers and regulatory networks associated with desirable traits (Marsh et al., 2021). Effective data management systems are necessary to store, retrieve, and analyze large datasets, facilitating the translation of research findings into practical breeding applications. The development of comprehensive databases and user-friendly tools ensures that breeders can access and utilize this information to develop climate-resilient and high-yielding peanut varieties (Naqvi et al., 2022; Chao et al., 2023).

## **7 Future Perspectives in Peanut Genetic Improvement**

### **7.1 Climate-resilient peanut varieties**

The development of climate-resilient peanut varieties is crucial to ensure food security in the face of changing environmental conditions. Recent advancements in peanut genomics have enabled the identification of genes associated with tolerance to abiotic stresses such as drought and salinity. For instance, the integration of genomic selection and speed breeding techniques holds promise for the rapid development of climate-smart peanut varieties (Pandey et al., 2020). Additionally, the utilization of wild *Arachis* species, which possess significant variability for stress resistance, can be instrumental in breeding programs aimed at enhancing climate resilience (Sharma et al., 2017).

### **7.2 Sustainable peanut farming practices**

Sustainable farming practices are essential to minimize the environmental impact of peanut cultivation. The introduction of disease-resistant cultivars, such as those enhanced with genetics from *Arachis cardenasii*, has already demonstrated reduced fungicide use and improved food security (Bertioli et al., 2021). Furthermore, the development of core and mini core collections can facilitate the use of diverse genetic resources, promoting sustainable agricultural practices by reducing the reliance on a narrow genetic base (Upadhyaya et al., 2002). The adoption of molecular breeding techniques, including marker-assisted selection, can also contribute to the development of high-yielding, disease-resistant varieties, thereby supporting sustainable farming (Holbrook et al., 2011).



### 7.3 Integrating farmer and stakeholder preferences in breeding programs

Incorporating the preferences of farmers and other stakeholders into breeding programs is vital for the successful adoption of new peanut varieties. Understanding the genetic diversity and population structure of peanut cultivars from different regions can help tailor breeding programs to meet local needs (Wang et al., 2016). Additionally, the assessment of genetic diversity among elite cultivars can provide insights into the breeding history and guide the development of varieties that align with farmer preferences (Brown et al., 2021). Engaging with farmers and stakeholders throughout the breeding process ensures that the developed varieties are well-suited to the specific agronomic and market conditions.

### 7.4 Policy and funding support for peanut genetic research

Policy and funding support are critical to advancing peanut genetic research and ensuring the long-term resilience of peanut crops. The reduction in botanical collections and seed exchanges due to restrictive national laws highlights the need for supportive policies that facilitate international collaboration and germplasm access (Bertioli et al., 2021). Increased investment in molecular genetic technology and genomic research can accelerate the development of superior peanut cultivars (Krishna et al., 2015). Moreover, funding for translational genomics and the deployment of new technologies will be essential to achieve higher genetic gains and develop climate-smart, high-yielding peanut varieties (Pandey et al., 2020). By addressing these future perspectives, the peanut research community can enhance crop performance and contribute to global food security in a sustainable manner.

## 8 Concluding Remarks

The research on harnessing genetic diversity in peanut has highlighted several critical findings. Firstly, the development of a mini core subset of peanut germplasm has preserved the genetic variability necessary for crop improvement, facilitating the exploitation of peanut genetic resources. The introduction of wild species, such as *Arachis cardenasii*, into peanut breeding programs has significantly enhanced disease resistance and food security globally. Advances in peanut genomics, including the development of molecular markers and genetic maps, have accelerated the identification of genes associated with stress tolerance and agronomic traits, thus aiding molecular breeding efforts. The use of wild species-derived induced allotetraploids has broadened the genetic variability available for peanut breeding, introducing novel phenotypes and improving disease resistance. Additionally, segmental allopolyploidy and homoeologous recombination have been shown to increase genetic diversity in peanut, resulting in new genome structure variations.

Genetic diversity is paramount for the resilience and adaptability of peanut crops. The narrow genetic base of cultivated peanut poses a significant vulnerability to evolving pests, pathogens, and changing climatic conditions. Utilizing wild species and creating synthetic allotetraploids have proven effective in introducing new traits and enhancing resistance to biotic and abiotic stresses. Molecular genetic research has provided tools such as marker-assisted selection (MAS) and single nucleotide polymorphisms (SNPs) that enable precise breeding strategies and the development of superior genotypes. The integration of diverse genetic resources into breeding programs is essential for sustaining long-term crop improvement and ensuring food security.

Enhancing peanut crop performance through genetic diversity requires a multifaceted approach that includes the conservation and utilization of wild germplasm, the application of advanced genomic tools, and international collaboration for germplasm exchange. The studies reviewed underscore the importance of maintaining and expanding genetic diversity to develop peanut cultivars that are resilient, high-yielding, and capable of withstanding various environmental stresses. Future breeding efforts should focus on integrating diverse genetic resources, employing modern biotechnological approaches, and fostering global cooperation to achieve sustainable improvements in peanut crop performance.

### Acknowledgments

We are grateful to Dr. Zhang for critically reading the manuscript and providing valuable feedback that improved the clarity of the text. We express our heartfelt gratitude to the two anonymous reviewers for their valuable comments on the manuscript.

## Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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