Cotton Genomics and Genetics 2024, Vol.15, No.2, 81-92
http://cropscipublisher.com/index.php/cgg

Review Article Open Access

Taxonomic Classification of *Gossypium*: Historical Perspectives and Modern Advances

Xuanjun Fang
Hainan Institute of Tropical Agricultural Resources, Sanya, 572025, Hainan, China
Corresponding email: xuanjun.fang@hitar.org

Cotton Genomics and Genetics, 2024, Vol.15, No.2 doi: 10.5376/cgg.2024.15.0008
Received: 02 Feb., 2024
Accepted: 06 Mar., 2024
Published: 20 Mar., 2024

Preferred citation for this article:
Fang X.J., 2024, Taxonomic classification of *Gossypium*: historical perspectives and modern advances, Cotton Genomics and Genetics, 15(2): 81-92 (doi: 10.5376/cgg.2024.15.0008)

Abstract This study provides a comprehensive overview of the taxonomic classification of the genus *Gossypium*, tracing its historical development and highlighting modern advancements. It elucidates the evolution of classification methods and their impact on cotton breeding, conservation, and research. The findings reveal that the significant shift from traditional morphological classification to molecular phylogenetics and genomic sequencing technologies has improved species delineation and resolved taxonomic ambiguities. The integration of multi-omics approaches and bioinformatics tools has further enhanced the understanding of genetic relationships and evolutionary processes within the genus. Additionally, the application of CRISPR and genetic editing technologies has opened new avenues for functional genomics and trait manipulation in breeding programs. The advancements in *Gossypium* taxonomy have profound implications for the future of cotton breeding and conservation. Accurate classification and a deeper understanding of genetic diversity facilitate the development of improved cotton varieties and effective conservation strategies. Continued interdisciplinary collaboration and the adoption of cutting-edge technologies are essential for advancing *Gossypium* research and addressing global agricultural challenges.

Keywords *Gossypium*; Cotton taxonomy; Molecular phylogenetics; Genomic sequencing; Genetic diversity; Cotton breeding

◆

1 Introduction

The genus *Gossypium*, commonly known as cotton, belongs to the Malvaceae family and comprises approximately 50 species distributed across tropical and subtropical regions worldwide, excluding Europe (Viot and Wendel, 2023). *Gossypium* species are notable for their economic importance, particularly in the production of natural fibers. The genus includes both diploid and allotetraploid species, with the latter resulting from polyploidization events that have significantly influenced their evolutionary trajectory (Paterson et al., 2012; Hu et al., 2019). The evolutionary history of *Gossypium* is marked by rapid diversification and complex phylogenetic relationships, which have been elucidated through extensive molecular and genetic studies (Cronn et al., 2002; Wu et al., 2018).

Gossypium species are of immense agricultural and economic significance due to their role in the global textile industry. *Gossypium hirsutum* and *Gossypium barbadense* are the two primary species cultivated for their superior fiber qualities, with *G. hirsutum* being the most widely grown due to its high yield and adaptability, and *G. barbadense* valued for its superior fiber properties (Yuan et al., 2015; Wang et al., 2018; Hu et al., 2019). Beyond their economic value, *Gossypium* species also serve as a model for studying polyploidy and plant domestication, providing insights into the genetic and molecular mechanisms underlying fiber development and environmental resilience (Zhang et al., 2018; Yang et al., 2020). Additionally, the genus has ethnobotanical relevance, with various species used in traditional medicine for their antimicrobial properties (De Lima et al., 2021).

This study aims to provide a comprehensive overview of the classification of the *Gossypium* genus, tracing its historical perspective and highlighting modern advancements. By integrating data from phylogenetic studies, genomic analyses, and ethnobotanical research, the study elucidates the evolutionary relationships within the genus and the genetic basis of its domestication and diversification. This study will also explore the impact of recent genomic discoveries on cotton breeding and improvement, emphasizing the potential to enhance fiber quality and environmental adaptability. Through this integrated analysis, the study aspires to offer a detailed understanding of the complexity and evolutionary dynamics of *Gossypium* classification, contributing to the broad knowledge of plant evolution and agricultural biotechnology.

2 Historical Perspectives on *Gossypium* Classification

2.1 Early taxonomic efforts

The initial taxonomic efforts to classify the genus *Gossypium* were spearheaded by Todaro in the mid-19th century, with significant contributions in 1863 and 1877. These early studies provide a theoretical foundation for understanding the genus, which is economically important due to its cotton fiber production (Fryxell, 1969). Following Todaro, Watt's major treatise in 1907 further advanced the classification, providing a more detailed understanding of the genus (Fryxell, 1969).

2.2 Classical morphological studies

Classical morphological studies played a crucial role in the taxonomic classification of *Gossypium*. Botanists began to employ more rigorous morphological studies, examining various plant parts such as leaves, flowers, seeds, and fibers in detail. This period saw the publication of several monographs and floras that described and categorized *Gossypium* species based on their morphological traits. Notable contributions came from botanists such as Alphonse de Candolle and Asa Gray, who systematically documented the diversity within the genus (Hoquet, 2014; Haufler, 2015). These morphological studies provided a more structured framework for distinguishing between species, despite the limitations imposed by the lack of genetic and molecular tools. Furthermore, researchers like Zaitzev (1928) and Mauer (1930) made significant conceptual advances by focusing on the morphological characteristics of the species (Fryxell, 1969). These studies were instrumental in identifying and categorizing various species within the genus based on observable traits.

2.3 Contributions of Linnaean taxonomy

The advent of Linnaean taxonomy in the 18th century marked a pivotal moment in the classification of *Gossypium*. Carl Linnaeus, the father of modern taxonomy, introduced a binomial nomenclature system that brought uniformity and consistency to species classification (Zhang and Shea, 2007). Linnaeus himself classified several *Gossypium* species, providing a theoretical foundation for subsequent taxonomic work. The Linnaean system emphasized the importance of hierarchical classification and species naming conventions, which greatly influenced botanical taxonomy. Linnaeus's contributions were instrumental in organizing the existing knowledge of *Gossypium* species and facilitating further taxonomic research.

The Linnaean system of taxonomy, which classifies organisms based on a hierarchical structure, was applied to *Gossypium* by several researchers. Hutchinson's treatment in 1947 is perhaps the most widely accepted modern classification, despite some nomenclatural inadequacies (Fryxell, 1969). Prokhanov (1947) and Roberty (1942, 1946, 1950) also contributed to the Linnaean taxonomy of *Gossypium*, although their classifications were often considered chaotic and less useful (Fryxell, 1969).

2.4 Evolution of *Gossypium* classification over time

The classification of *Gossypium* has evolved significantly over time, incorporating new data from various scientific disciplines. Modern studies have integrated molecular genetics, biogeography, and phylogenetic analysis to provide a more comprehensive understanding of the genus (Huang et al., 2020; Viot and Wendel, 2023). For instance, the evolutionary history of *Gossypium* has been elucidated through the analysis of nuclear and chloroplast genes, revealing rapid diversification and complex hybridization events (Cronn et al., 2002). Additionally, the genome sequencing of *Gossypium* species has provided insights into the phylogenetic relationships and evolutionary history of cotton genomes (Hu et al., 2019; Huang et al., 2020).

3 Modern Advances in *Gossypium* Taxonomy

3.1 Molecular phylogenetics

Molecular phylogenetics has significantly advanced our understanding of the evolutionary relationships within the *Gossypium* genus. By employing phylogenomic methods, researchers have been able to reassess the phylogenetic history of *Gossypium*, providing a temporal framework for its diversification. For instance, whole genome resequencing data has revealed that the New World diploid cottons likely originated following transoceanic dispersal from Africa about 6.6 million years ago, with most biodiversity evolving during the mid-Pleistocene (Grover et al., 2019). Additionally, the evolutionary history of *Gossypium* has been clarified through the integration of data from molecular genetics and phylogenetic analysis, uncovering multiple previously cryptic interspecific hybridizations (Viot and Wendel, 2023).

3.2 Genomic sequencing technologies

The advent of advanced genomic sequencing technologies has revolutionized the study of *Gossypium*. High-quality genome sequences of various *Gossypium* species have been generated using techniques such as single-molecule real-time sequencing, BioNano optical mapping, and high-throughput chromosome conformation capture. These technologies have provided reference-grade genome assemblies for species like *Gossypium hirsutum* and *Gossypium barbadense*, which are crucial for understanding cotton evolution and improving fiber quality (Wang et al., 2019). Huang et al. (2020) assembled the genome of *Gossypium* herbaceum and improved the existing genomes of *Gossypium arboreum* and *Gossypium hirsutum*, providing insights into the phylogenetic relationships and origin history of the cotton A-genomes.

3.3 Comparative genomics

Comparative genomics has played a pivotal role in elucidating the structural variations and evolutionary processes within *Gossypium*. For example, comparative analyses of the genomes of *Gossypium raimondii* and *Gossypium arboreum* have identified genome-specific repetitive elements that contribute to genome variation between the A and D genomes (Lu et al., 2020). Additionally, the comparison of genome sequences of *Gossypioides kirkii* with those of *Gossypium* species has revealed structural rearrangements such as chromosome fusions and inversions, which are essential for understanding the evolutionary dynamics of chromosome number variation in plants (Udall et al., 2019).

3.4 Role of bioinformatics in modern taxonomy

Bioinformatics has become an indispensable tool in modern taxonomy, enabling the analysis and interpretation of large-scale genomic data. The integration of bioinformatics techniques has facilitated the identification of quantitative trait loci associated with superior fiber quality in *Gossypium* species, thereby accelerating breeding programs (Wang et al., 2019). Moreover, the use of bioinformatics in the study of genome-specific repetitive elements has promoted research on *Gossypium* genome evolution and subgenome identification (Lu et al., 2020). The inclusion of novel descriptors such as associated microorganisms and mitochondrial genomes in taxonomic studies has also provided a deeper understanding of the evolutionary and ecological dimensions of organisms (Serra et al., 2020).

Modern advances in molecular phylogenetics, genomic sequencing technologies, comparative genomics, and bioinformatics have significantly enhanced our understanding of *Gossypium* taxonomy, providing valuable insights into the evolutionary history and genetic improvement of this economically important genus.

4 Current Taxonomic Classification of *Gossypium*

4.1 Overview of current classification systems

The genus *Gossypium*, commonly known as cotton, comprises approximately 50 species distributed across tropical and subtropical regions worldwide, excluding Europe (Viot and Wendel, 2023). The classification of *Gossypium* has evolved significantly with advancements in molecular genetics, cytogenetics, and phylogenetic analysis. Modern classification systems integrate these diverse data sources to provide a comprehensive understanding of species relationships and diversification within the genus (Wang et al., 2018; Wang et al., 2019). The genus is divided into several genome groups, including one allotetraploid group (AD) and eight diploid genome groups (A-G and K) (Wu et al., 2018).

4.2 Species delineation and identification

Species delineation within *Gossypium* has been historically challenging due to the complexity of hybridization and polyploidization events. Traditional morphological methods have been supplemented with molecular markers and genomic tools to improve species identification and classification (Yin et al., 2020; Hörandl, 2022) For instance, the use of chloroplast genome sequences has provided insights into the phylogenetic relationships and repeat sequence variations among *Gossypium* species, aiding in more accurate species delineation (Wu et al., 2018). Additionally, the development of synthetic allotetraploids through distant hybridization has expanded the genetic resources available for species identification and breeding (Yin et al., 2020).

4.3 Subgenus and section level classifications

At the subgenus and section levels, *Gossypium* species are classified based on their genomic composition and evolutionary history. Comparative genomics and whole-genome sequencing have revealed significant structural variations and gene family expansions that contribute to the speciation and evolutionary history of *Gossypium* (Hu et al., 2019; Yang et al., 2020). Hu et al. (2019) studied the whole genome sequences of two cultivated species, *Gossypium barbadense* and *Gossypium hirsutum*. The study revealed species-specific changes in gene expression, structural variations, and gene family expansions through high-quality de novo assembly, which are key factors in species differentiation and evolution (Figure 1). Studies have identified distinct genetic clades within the genus, with the D-genome species forming a strong monophyletic clade, while C, G, and K-genome species exhibit more complex relationships due to recent radiation and hybridization events (Wu et al., 2018).

4.4 Hybridization and polyploidy in *Gossypium*

Hybridization and polyploidy are central to the evolution and diversification of *Gossypium*. The genus includes both diploid and allotetraploid species, with the latter resulting from hybridization events between A-genome and D-genome species (Hu et al., 2019; Anwar et al., 2022). Polyploidization has led to the formation of new species with unique genetic and phenotypic traits, contributing to the adaptability and economic importance of cotton (Mandák et al., 2018; Hörandl, 2022). Modern genomic tools have facilitated the identification of quantitative trait loci (QTLs) associated with desirable traits, such as fiber quality, in hybrid and polyploid cotton species (Wang et al., 2019; Anwar et al., 2022).

5 Challenges and Controversies in *Gossypium* Taxonomy

5.1 Issues with morphological variability

Morphological variability within the *Gossypium* genus presents significant challenges in taxonomic classification. The extensive diversity in physical traits such as plant architecture, leaf shape, and fiber characteristics complicates the identification and classification of species. For instance, the study of *Gossypium* populations in Amazonian Native Communities revealed substantial morphological diversity, which may result from spontaneous crosses and environmental adaptations, making it difficult to delineate clear taxonomic boundaries (Morales-Aranibar et al., 2023). Additionally, the variability in morphological traits can be influenced by both genetic and environmental factors, further complicating taxonomic efforts (Kushanov et al., 2022).

5.2 Genetic divergence and convergence

Genetic divergence and convergence within *Gossypium* species add another layer of complexity to taxonomy. The introgression from *Gossypium hirsutum* to *Gossypium barbadense* has significantly reorganized the genomic architecture of the latter, leading to increased genetic diversity and divergence (Wang et al., 2022). This genetic mixing can obscure species boundaries and create challenges in distinguishing between species based solely on genetic data. Moreover, the independent evolution of A-genomes in *Gossypium herbaceum* and *Gossypium arboreum*, despite their common ancestry, highlights the complexity of genetic divergence within the genus (Huang et al., 2020). The study shows that there is no ancestor-descendant relationship between the A_1 and A_2 genomes, and that the two A-genomes evolved independently (Figure 2). The research also found that multiple long terminal repeat (LTR) bursts contributed significantly to the size expansion, species formation, and evolution of the A-genomes. These findings clarify the controversy over the origin of the A-genomes, provide insights into the phylogenetic relationships and origin history of the cotton A-genomes, and offer valuable genetic resources for cotton improvement (Huang et al., 2020).

5.3 Discrepancies between classical and molecular data

Discrepancies between classical taxonomic methods and modern molecular data often lead to controversies in *Gossypium* taxonomy. Classical methods, which rely heavily on morphological traits, may not always align with molecular phylogenetic analyses. For example, the evolutionary history and domestication of *Gossypium* species, as revealed through molecular genetics and phylogenetic analysis, sometimes contradict traditional taxonomic classifications based on morphology (Viot and Wendel, 2023). These discrepancies necessitate a reevaluation of taxonomic frameworks to integrate both classical and molecular data for a more accurate classification.

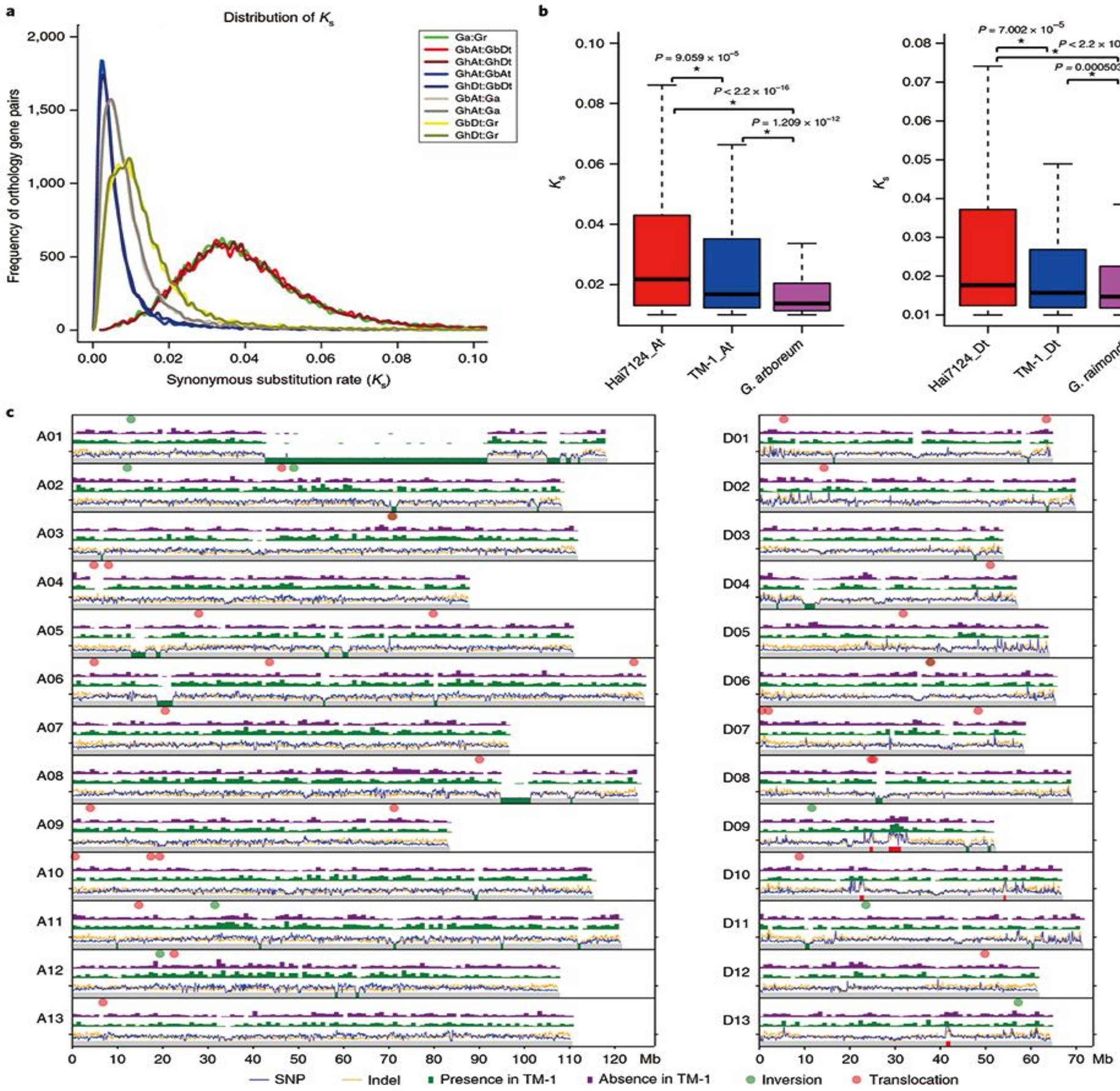

Figure 1 Evolution of the allopolyploid cotton genome (Adopted from Hu et al., 2019)

Image caption: (a) Evolutionary analysis of the *G. barbadense* and *G. hirsutum* genomes, showing the Ks distribution of orthologous genes, indicating that the divergence time of these species is between 0.4 and 0.6 million years ago. (b) Comparison of the codon substitution rate distribution between the two subgenomes of TM-1 and Hai7124 and their progenitors, revealing the accelerated evolution of the cotton genome. (c) Distribution of SNPs, indels, PAVs, inversions, and translocations in the TM-1 and Hai7124 genomes. This figure illustrates the genetic and structural variations in the cotton genome during evolution (Adapted from Hu et al., 2019)

5.4 Impact of hybridization events

Hybridization events within the *Gossypium* genus have a profound impact on taxonomy. The occurrence of interspecific hybridizations, both intentional and unintentional, has led to the creation of new genetic combinations and the blurring of species boundaries. The dual domestication and subsequent hybridization of *Gossypium barbadense* and *Gossypium hirsutum* exemplify how hybridization can complicate taxonomic classification (Viot and Wendel, 2023). Additionally, the identification of introgression events from *Gossypium* *hirsutum* to *Gossypium barbadense* underscores the role of hybridization in shaping the genetic landscape of the genus (Wang et al., 2022).

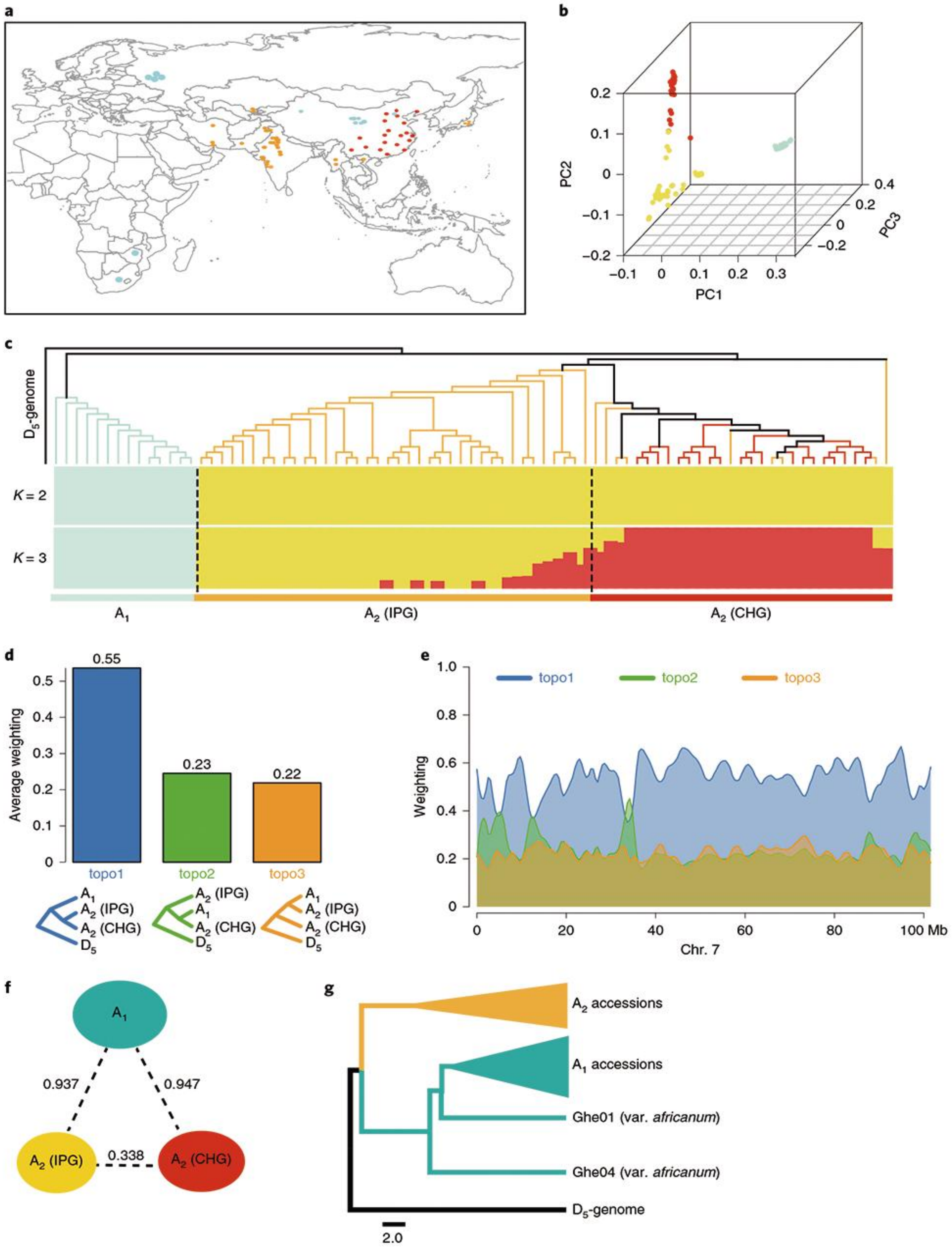

Figure 2 Geographic distribution and population analysis of the A_1 and A_2 accessions (Adopted from Huang et al., 2020)

Image caption: (a): Geographic distribution of the collected A_1 and A_2 genomes. Green dots represent the collection sites of A_1 genomes, red dots represent A2 genomes collected in China, and yellow dots represent A2 genomes collected outside of China. (b): Principal component analysis (PCA) based on whole-genome SNPs, showing the first three principal components of the A_1 and A_2 genomes. The green, red, and yellow dots are consistent with the colors in Figure 2a. PCA analysis shows that despite their geographic origins, these cotton genomes are divided into two independent groups, namely the A_1 group and the A_2 group. This indicates a significant genetic distinction between the A_1 and A_2 genomes. (c): Genetic relationships between all A_1 and A_2 genomes.

The upper panel shows the phylogenetic tree based on whole-genome SNPs, and the lower panel shows the population structure analysis based on different cluster numbers (K=2 and K=3). The branch colors are consistent with Figure 2a. The phylogenetic tree shows that A_1 and A_2 genomes cluster into two independent branches, validating their independent evolution and providing evidence for understanding the independent evolution of A_1 and A_2 genomes (Adapted from Huang et al., 2020)

5.5 Evolutionary dynamics and genome variation

The evolutionary dynamics and genome variation within *Gossypium* species pose significant challenges to taxonomy. The activity of genome-specific repetitive sequences, such as the ICRd motif in the D genome, contributes to genome variation and complicates the understanding of evolutionary relationships (Lu et al., 2020). The structural variations and gene expression changes observed in allotetraploid cotton species highlight the ongoing evolutionary processes that influence genome architecture and species differentiation (Hu et al., 2019). These dynamic evolutionary changes necessitate continuous updates to taxonomic classifications to reflect the current understanding of *Gossypium* genomics.

6 Applications of *Gossypium* Taxonomy in Breeding and Conservation

6.1 Implications for cotton breeding programs

The taxonomic classification of *Gossypium* has profound implications for cotton breeding programs. Understanding the genetic diversity and evolutionary history of *Gossypium* species allows breeders to identify and utilize favorable traits from wild and domesticated species. For instance, the reference genome sequences of *Gossypium hirsutum* and *Gossypium barbadense* have facilitated the identification of quantitative trait loci (QTLs) associated with superior fiber quality, which can be introgressed into breeding lines to improve cotton varieties (Hu et al., 2019; Wang et al., 2019). Additionally, the genetic analysis of mutagenesis in wild cotton species has identified candidate genes related to flowering traits, which can be used in marker-assisted selection to develop early-flowering and high-yielding cotton varieties (Kushanov et al., 2022).

6.2 Conservation strategies for wild *Gossypium* species

Conservation of wild *Gossypium* species is crucial for maintaining genetic diversity, which is essential for the long-term sustainability of cotton breeding programs. The genetic diversity of *Gossypium* populations in Amazonian native communities highlights the importance of preserving these genetic resources (Morales-Aranibar et al., 2023). Conservation strategies should focus on protecting natural habitats and promoting in situ conservation of wild species. Additionally, *ex situ* conservation methods, such as seed banks and botanical gardens, can be employed to safeguard genetic material for future use in breeding programs (Peng et al., 2022; Morales-Aranibar et al., 2023).

6.3 Utilization of genetic diversity

The genetic diversity within the *Gossypium* genus provides a valuable resource for improving cotton crops. Comparative genomics and phylogenetic studies have revealed extensive structural variations and gene family expansions that contribute to the adaptation and resilience of different *Gossypium* species (Wu et al., 2018; Hu et al., 2019). By leveraging this genetic diversity, breeders can introduce traits such as disease resistance, drought tolerance, and improved fiber quality into cultivated cotton varieties. The identification of divergence hotspot regions and site-specific selection in chloroplast genomes further aids in understanding the evolutionary relationships and potential for genetic improvement (Wu et al., 2018).

6.4 Case studies in breeding and conservation

Several case studies illustrate the successful application of *Gossypium* taxonomy in breeding and conservation efforts. For example, the introgression of favorable chromosome segments from *Gossypium barbadense* into *Gossypium hirsutum* has led to the development of cotton lines with enhanced fiber quality (Wang et al., 2019). Wang et al. (2019) conducted a detailed analysis of the reference genome sequences of two cultivated cotton species, *Gossypium hirsutum* and *Gossypium barbadense*. The study employed single-molecule real-time sequencing, optical mapping, and high-throughput chromosome conformation capture techniques to construct high-quality genome assemblies for both species. Comparative genomic analysis revealed multiple structural variations. Additionally, a backcross population incorporating the superior fiber traits of *G. barbadense* was constructed, leading to the identification of 13 quantitative trait loci (QTLs) related to fiber quality (Figure 3). These resources will enhance research on cotton evolution and functional genomics, providing a reference for future fiber improvement breeding programs.

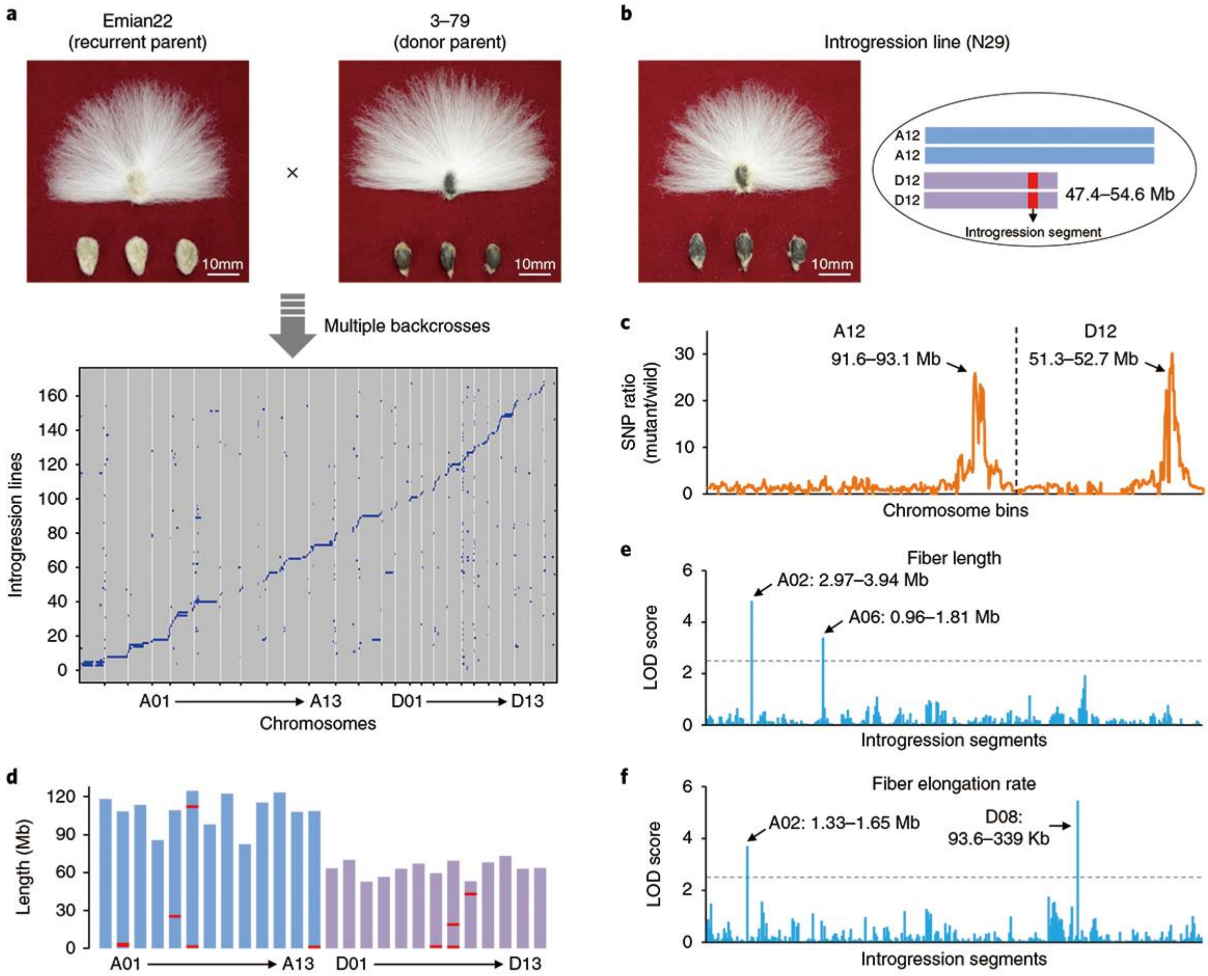

Figure 3 Identification of favorable chromosome segments controlling fiber quality by using introgression lines (Adopted from Wang et al., 2019)

Image caption: (a) A backcross population constructed using *Gossypium hirsutum* Emian22 (recurrent parent) and *Gossypium barbadense* 3-79 (donor parent), showing the fiber characteristics of both cotton species and the identified introgression segments across the 26 chromosomes; (b) The introgression segment on chromosome D12 and its fiber characteristics, particularly the segment containing limited fuzz fibers; (c) SNP ratio of Xuzhou142fl, with mapping results from sequencing two different pools in the F2 population; (d) Distribution of quantitative trait loci (QTLs) related to fiber quality on the chromosomes of *Gossypium hirsutum*, with each QTL indicated by a red box; (e, f) QTL mapping for fiber length and fiber elongation rate, respectively, showing the LOD scores and physical locations of different introgression segments. Figure 3 validates the identification and mapping of 13 important QTLs related to fiber quality through the backcross population, providing a foundation for further cotton improvement breeding programs (Adapted from Wang et al., 2019)

Another case study involves the genetic analysis of *Gossypium herbaceum* and *Gossypium arboreum*, which has provided insights into their independent domestication and interspecific gene flow, informing breeding strategies for these diploid species (Huang et al., 2020; Grover et al., 2022). These examples demonstrate the practical benefits of integrating taxonomic knowledge into breeding and conservation programs.

The taxonomic classification of *Gossypium* plays a critical role in advancing cotton breeding and conservation efforts. By understanding the genetic diversity and evolutionary history of *Gossypium* species, researchers and breeders can develop improved cotton varieties and implement effective conservation strategies to ensure the sustainability of this economically important crop.

7 Future Directions in *Gossypium* Taxonomic Research

7.1 Integration of multi-omics approaches

The integration of multi-omics approaches, including genomics, transcriptomics, proteomics, and metabolomics, holds significant promise for advancing the taxonomic classification of *Gossypium*. By leveraging these comprehensive datasets, researchers can gain deeper insights into the genetic and molecular underpinnings of species differentiation and evolutionary relationships. For instance, the assembly of high-quality reference genomes for *Gossypium hirsutum* and *Gossypium barbadense* has already provided valuable resources for comparative genomics and evolutionary studies (Wang et al., 2019). Additionally, the improved genome sequences of *Gossypium herbaceum* and *Gossypium arboreum* have shed light on the phylogenetic relationships and evolutionary history of cotton A-genomes (Huang et al., 2020). Future research should focus on integrating these multi-omics datasets to refine the taxonomic classification and uncover novel insights into the evolutionary dynamics of the *Gossypium* genus.

7.2 Advancements in computational methods

Advancements in computational methods, including machine learning and artificial intelligence, offer new opportunities for enhancing the accuracy and efficiency of taxonomic classification in *Gossypium*. These methods can be employed to analyze large-scale genomic and phenotypic datasets, identify patterns, and predict evolutionary relationships. For example, the use of high-throughput sequencing technologies and bioinformatics tools has enabled the construction of detailed phylogenetic trees and the identification of structural variations in cotton genomes (Wang et al., 2019). By incorporating advanced computational techniques, researchers can further refine these analyses and develop more robust taxonomic frameworks. Additionally, the application of computational methods to integrate and analyze multi-omics data will facilitate a more comprehensive understanding of the genetic and phenotypic diversity within the *Gossypium* genus.

7.3 Potential for CRISPR and genetic editing technologies

The advent of CRISPR and other genetic editing technologies has revolutionized the field of plant genetics and offers significant potential for advancing *Gossypium* taxonomic research. CRISPR/Cas9 and related systems have been successfully applied to create targeted gene mutations and study gene function in *Gossypium* species (Zhang et al., 2018; Qin et al., 2020; Li et al., 2021). For instance, the development of a CRISPR/Cas9 system for *Gossypium hirsutum* has enabled the generation of transgene-clean edited plants with enhanced disease resistance (Zhang et al., 2018). Similarly, the use of a modified CRISPR/Cas9 system for base editing in *Gossypium hirsutum* has demonstrated high specificity and accuracy for creating point mutations (Qin et al., 2020). Future research should explore the potential of these technologies to investigate the genetic basis of taxonomic traits, facilitate the creation of novel germplasm, and enhance our understanding of the evolutionary processes shaping the *Gossypium* genus.

7.4 Collaborative international research efforts

Collaborative international research efforts are essential for advancing *Gossypium* taxonomic research and addressing the complex challenges associated with the classification and conservation of cotton species. By fostering collaborations between researchers, institutions, and countries, it is possible to pool resources, share knowledge, and leverage diverse expertise. For example, the establishment of standardized cytogenetic and genomic nomenclature for *Gossypium* has facilitated comparative studies and breeding programs worldwide (Wang et al., 2018). Additionally, international collaborations have contributed to the assembly of high-quality reference genomes and the identification of genetic diversity in cotton populations (Wang et al., 2019; Morales-Aranibar et al., 2023). Future research should continue to promote collaborative efforts to enhance the taxonomic classification, conservation, and sustainable utilization of *Gossypium* species on a global scale.

8 Concluding Remarks

The taxonomic classification of the genus *Gossypium* has undergone significant advancements through historical and modern research. Early taxonomic investigations laid the groundwork for understanding the genus's diversity, which includes approximately 50 species distributed globally, except in Europe. Modern phylogenetic and genomic studies have provided deeper insights into the evolutionary history and domestication processes of key species such as *Gossypium barbadense* and *Gossypium hirsutum*. These studies have revealed the complex interplay of polyploidization, interspecific hybridization, and introgression events that have shaped the current genetic landscape of cotton. Additionally, the genetic diversity within native populations, particularly in regions like the Amazonian Native Communities, has been documented, highlighting the role of local cultivation practices in maintaining genetic variability.

These findings emphasize the importance of combining traditional taxonomic methods with modern genomic technologies to fully understand the evolutionary dynamics of the *Gossypium* genus. Future efforts should continue to focus on sequencing and annotating the genomes of more *Gossypium* species, providing a more comprehensive understanding of the genetic diversity and evolutionary history of the genus. Investigating the functional roles of specific genes and transposons in cotton adaptability and fiber quality is crucial for breeding programs aimed at improving crop resilience and productivity. Future research should also strive to preserve the genetic diversity in native populations, as these populations may harbor unique traits valuable for future breeding efforts. Additionally, further studies on the impact of polyploidy on gene expression and genome stability will enhance researchers' understanding of the success of polyploid species such as *G. hirsutum* and *G. barbadense*.

The taxonomic classification and evolutionary study of *Gossypium* have greatly benefited from the integration of historical perspectives and modern genomic advances. These efforts have not only clarified the complex evolutionary history of this economically important genus but also provided valuable resources for future research and breeding programs. By continuing to explore the genetic and functional diversity within *Gossypium*, researchers can develop more resilient and productive cotton varieties, ensuring the sustainability of this vital crop in the face of changing environmental conditions.

Acknowledgments

The CropSci Publisher appreciates the feedback from two anonymous peer reviewers on the manuscript of this study, whose careful evaluation and constructive suggestions have contributed to the improvement of the manuscript.

Conflict of Interest Disclosure

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

◆

References

Anwar M., Iqbal M.Z., Abro A.A., Memon S., Bhutto L.A., Memon S.A., and Peng Y., 2022, Inter-specific hybridization in cotton (*Gossypium hirsutum*) for crop improvement, Agronomy, 12(12): 3158.
https://doi.org/10.3390/agronomy12123158

Cronn R.C., Small R.L., Haselkorn T., and Wendel J.F., 2002, Rapid diversification of the cotton genus (*Gossypium*: Malvaceae) revealed by analysis of sixteen nuclear and chloroplast genes, American Journal of Botany, 89(4): 707-725.
https://doi.org/10.3732/ajb.89.4.707

De Lima L.F., de Oliveira J.O., Carneiro J.N.P., Lima C.N.F., Coutinho H.D.M., and Morais-Braga M.F.B., 2021, Ethnobotanical and antimicrobial activities of the *Gossypium* (Cotton) genus: a review, Journal of Ethnopharmacology, 279: 114363.
https://doi.org/10.1016/j.jep.2021.114363

Fryxell P.A., 1969, A classification of *Gossypium* L. (Malvaceae), Taxon, 18(5): 585-591.
https://doi.org/10.2307/1218405

Grover C.E., Arick M.A., Thrash A., Conover J.L., Sanders W.S., Peterson D.G., Frelichowski J., Scheffler J., Scheffler B., and Wendel J.F., 2019, Insights into the evolution of the new world diploid cottons (*Gossypium*, subgenus Houzingenia) based on genome sequencing, Genome Biology and Evolution, 11(1): 53-71.
https://doi.org/10.1093/gbe/evy256

Grover C.E., Arick M.A., Thrash A., Sharbrough J., Hu G., Yuan D., Yuan D., Miller E., Ramaraj T., Peterson D., Udall J., and Wendel J.F., 2022, Dual domestication, diversity, and differential introgression in Old World cotton diploids, Genome Biology and Evolution, 14(12): evac170.
https://doi.org/10.1093/gbe/evac170

Haufler C.H., 2015, Alan R. Smith: Recipient of the 2014 Asa Gray Award, American Society of Plant Taxonomists, Systematic Botany, 40(1): 2-3.
https://doi.org/10.1600/036364415X686279

Hoquet T., 2014, Botanical authority: Benjamin Delessert’s collections between travelers and Candolle’s natural method (1803-1847), Isis, 105(3): 508-539.
https://doi.org/10.1086/678169

Hörandl E., 2022, Novel approaches for species concepts and delimitation in polyploids and hybrids, Plants, 11(2): 204.
https://doi.org/10.3390/plants11020204

Hu Y., Chen J., Fang L., Zhang Z., Ma W., Niu Y., Ju L., Deng J., Zhao T., Lian J., Baruch K., Fang D., Liu X., Ruan Y., Rahman M., Han J., Wang K., Wang Q., Wu H., Mei G., Zang Y., Han Z., Xu C., Shen W., Yang D., Si Z., Dai F., Zou L., Huang F., Bai Y., Zhang Y., Brodt A., Ben-Hamo H., Zhu X., Zhou B., Guan X., Zhu S., Chen X., and Zhang T., 2019, *Gossypium barbadense* and *Gossypium hirsutum* genomes provide insights into the origin and evolution of allotetraploid cotton, Nature Genetics, 51(4): 739-748.
https://doi.org/10.1038/s41588-019-0371-5

Huang G., Wu Z., Percy R., Bai M., Li Y., Frelichowski J., Hu J., Wang K., Yu J., and Zhu Y., 2020, Genome sequence of *Gossypium herbaceum* and genome updates of *Gossypium arboreum* and *Gossypium hirsutum* provide insights into cotton A-genome evolution, Nature Genetics, 52(5): 516-524.
https://doi.org/10.1038/s41588-020-0607-4

Kushanov F.N., Komilov D.J., Turaev O.S., Ernazarova D.K., Amanboyeva R.S., Gapparov B.M., and Yu J.Z., 2022, Genetic analysis of mutagenesis that induces the photoperiod insensitivity of wild cotton *Gossypium hirsutum* subsp. *purpurascens*, Plants, 11(22): 3012.
https://doi.org/10.3390/plants11223012

Li B., Liang S., Alariqi M., Wang F., Wang G., Wang Q., Xu Z., Yu L., Zafar M., Sun L., Si H., Yuan D., Guo W., Wang Y., Lindsey K., Zhang X., and Jin S., 2021, The application of temperature sensitivity CRISPR/LbCpf1 (LbCas12a) mediated genome editing in allotetraploid cotton (*G. hirsutum*) and creation of nontransgenic, gossypol-free cotton, Plant Biotechnology Journal, 19(2): 221.
https://doi.org/10.1111/pbi.13470

Lu H., Cui X., Zhao Y., Magwanga R.O., Li P., Cai X., Zhou Z., Wang X., Liu Y., Xu Y., Hou Y., Peng R., Wang K., and Liu F., 2020, Identification of a genome-specific repetitive element in the *Gossypium* D genome, Peer J, 8: e8344.
https://doi.org/10.7717/peerj.8344

Mandák B., Krak K., Vít P., Lomonosova M.N., Belyayev A., Habibi F., Wang L., Douda J., and Štorchová H., 2018, Hybridization and polyploidization within the *Chenopodium album* aggregate analysed by means of cytological and molecular markers, Molecular Phylogenetics and Evolution, 129: 189-201.
https://doi.org/10.1016/j.ympev.2018.08.016

Morales-Aranibar L., Yucra F., Aranibar C., Saenz M., Gonzales H., Aguilera J., Álvarez J., Zuffo A., Steiner F., Ratke R., and Teodoro P.E., 2023, First report on the genetic diversity of populations of *Gossypium barbadense* L. and *Gossypium hirsutun* L. in the Amazonian native communities, Cusco-Peru, Plants, 12(4): 865.
https://doi.org/10.3390/plants12040865

Paterson A., Wendel J., Gundlach H., Guo H., Jenkins J., Jin D., Llewellyn D., Showmaker K., Shu S., Udall J., Yoo M., Byers R., Chen W., Doron-Faigenboim A., Duke M., Gong L., Grimwood J., Grover C., Grupp K., Hu G., Lee T., Li J., Lin L., Liu T., Marler B., Page J., Roberts A., Romanel E., Sanders W., Szadkowski E., Tan X., Tang H., Xu C., Wang J., Wang Z., Zhang D., Zhang L., Ashrafi H., Bedon F., Bowers J., Brubaker C., Chee P., Das S., Gingle A., Haigler C., Harker D., Hoffmann L., Hovav R., Jones D., Lemke C., Mansoor S., Rahman M., Rainville L., Rambani A., Reddy U., Rong J., Saranga Y., Scheffler B., Scheffler J., Stelly D., Triplett B., Deynze A., Vaslin M., Waghmare V., Walford S., Wright R., Zaki E., Zhang T., Dennis E., Mayer K., Peterson D., Rokhsar D., Wang X., and Schmutz J., 2012, Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibres, Nature, 492(7429): 423-427.
https://doi.org/10.1038/nature11798

Peng R., Xu Y., Tian S., Unver T., Liu Z., Zhou Z., Cai X., Wang K., Wei Y., Liu Y., Wang H., Hu G., Zhang Z., Grover C., Hou Y., Wang Y., Li P., Wang T., Lu Q., Wang Y., Conover J., Ghazal H., Wang Q., Zhang B., Montagu M., Peer Y., Wendel J., and Liu F., 2022, Evolutionary divergence of duplicated genomes in newly described allotetraploid cottons, Proceedings of the National Academy of Sciences, 119(39): e2208496119.
https://doi.org/10.1073/pnas.2208496119

Qin L., Li J., Wang Q., Xu Z., Sun L., Alariqi M., Manghwar H., Wang G., Li B., Ding X., Rui H., Huang H., Lu T., Lindsey K., Daniell H., Zhang X., and Jin S., 2020, High-efficient and precise base editing of C• G to T• A in the allotetraploid cotton (*Gossypium hirsutum*) genome using a modified CRISPR/Cas9 system, Plant Biotechnology Journal, 18(1): 45-56.
https://doi.org/10.1111/pbi.13168

Serra V., Gammuto L., Nitla V., Castelli M., Lanzoni O., Sassera D., Bandi C., Sandeep B., Verni F., Modeo L., and Petroni G., 2020, Morphology, ultrastructure, genomics, and phylogeny of *Euplotes vanleeuwenhoeki* sp. nov. and its ultra-reduced endosymbiont "*Candidatus* Pinguicoccus supinus" sp. nov., Scientific Reports, 10(1): 20311.
https://doi.org/10.1038/s41598-020-76348-z

Udall J.A., Long E., Ramaraj T., Conover J.L., Yuan D., Grover C.E., Gong L., Arick M., Masonbrink R., Peterson D., and Wendel J.F., 2019, The genome sequence of *Gossypioides kirkii* illustrates a descending dysploidy in plants, Frontiers in Plant Science, 10: 1541.
https://doi.org/10.3389/fpls.2019.01541

Viot C.R., and Wendel J.F., 2023, Evolution of the cotton genus, *Gossypium*, and its domestication in the Americas, Critical Reviews in Plant Sciences, 42(1): 1-33.
https://doi.org/10.1080/07352689.2022.2156061

Wang K., Wendel J.F., and Hua J., 2018, Designations for individual genomes and chromosomes in *Gossypium*, Journal of Cotton Research, 1(1): 1-5.
https://doi.org/10.1186/s42397-018-0002-1

Wang M., Tu L., Yuan D., Zhu D., Shen C., Li J., Liu F., Pei L., Wang P., Zhao G., Ye Z., Huang H., Yan F., Ma Y., Zhang L., Liu M., You J., Yang Y., Liu Z., Huang F., Li B., Qiu P., Zhang Q., Zhu L., Jin S., Yang X., Min L., Li G., Chen L., Zheng H., Lindsey K., Lin Z., Udall J., and Zhang X., 2019, Reference genome sequences of two cultivated allotetraploid cottons, *Gossypium hirsutum* and *Gossypium barbadense*, Nature Genetics, 51(2): 224-229.
https://doi.org/10.1038/s41588-018-0282-x

Wang P., Wang M., Dong N., Sun G., Jia Y., Geng X., Liu M., Wang W., Pan Z., Yang Q., Li H., Wei C., Wang L., Zheng H., He S., Zhang X., Wang Q., and Du X., 2022, Introgression from *Gossypium hirsutum* is a driver for population divergence and genetic diversity in *Gossypium barbadense*, The Plant Journal, 110(3): 764-780.
https://doi.org/10.1111/tpj.15702

Wu Y., Liu F., Yang D., Li W., Zhou X., Pei X., Liu Y., He K., Zhang W., Ren Z., Zhou K., Ma X., and Li Z.H., 2018, Comparative chloroplast genomics of *Gossypium* species: insights into repeat sequence variations and phylogeny, Frontiers in Plant Science, 9: 376.
https://doi.org/10.3389/fpls.2018.00376

Yang Z., Qanmber G., Wang Z., Yang Z., and Li F., 2020, *Gossypium* genomics: trends, scope, and utilization for cotton improvement, Trends in Plant Science, 25(5): 488-500.
https://doi.org/10.1016/j.tplants.2019.12.011

Yin X., Zhan R., He Y., Song S., Wang L., Ge Y., and Chen D., 2020, Morphological description of a novel synthetic allotetraploid (A1A1G3G3) of *Gossypium herbaceum* L. and *G. nelsonii* Fryx. suitable for disease-resistant breeding applications, PLoS One, 15(12): e0242620.
https://doi.org/10.1371/journal.pone.0242620

Yuan D., Tang Z., Wang M., Gao W., Tu L., Jin X., Chen L., He Y., Zhang L., Zhu L., Li Y., Liang Q., Lin Z., Yang X., Liu N., Jin S., Lei Y., Ding Y., Li G., Ruan X., Ruan Y., and Zhang X., 2015, The genome sequence of Sea-Island cotton (*Gossypium barbadense*) provides insights into the allopolyploidization and development of superior spinnable fibres, Scientific Reports, 5(1): 17662.
https://doi.org/10.1038/srep17662

Zhang J., Huang G.Q., Zou D., Yan J.Q., Li Y., Hu S., and Li X.B., 2018, The cotton (*Gossypium hirsutum*) NAC transcription factor (FSN1) as a positive regulator participates in controlling secondary cell wall biosynthesis and modification of fibers, New Phytologist, 217(2): 625-640.
https://doi.org/10.1111/nph.14864

Zhang Z.Q., and Shear W.A., 2007, Linnaeus tercentenary and invertebrate taxonomy: an introduction, Zootaxa, 1668(1): 7-10.
https://doi.org/10.11646/zootaxa.1668.1.2