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Global Distribution of *Gossypium* Species and Its Agricultural Implications

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Abstract *Gossypium*, commonly known as cotton, includes approximately 50 species distributed across tropical and subtropical regions worldwide, excluding Europe. Among these, *Gossypium hirsutum* and *Gossypium* barbadense are the most widely cultivated, significantly contributing to global cotton production. The evolutionary history of *Gossypium* is marked by complex processes such as polyploidization and domestication, which have led to the development of species with superior fiber quality and resilience to environmental stresses. The primary objective of this study is to provide a comprehensive analysis of the global distribution of *Gossypium* species and their agricultural implications. It aims to summarize current knowledge on the biogeography and evolutionary history of *Gossypium* species; investigate the genetic and molecular mechanisms underlying fiber quality and environmental resilience in different *Gossypium* species; discuss the agricultural implications of these findings, particularly in the context of breeding strategies for improved cotton varieties; and identify gaps in the current research to suggest future directions for studies on *Gossypium* species. By synthesizing information from multiple studies, this research provides important theoretical foundations for a holistic understanding of the global distribution of *Gossypium* species and their agricultural significance.

Keywords *Gossypium*; Cotton cultivation; Agricultural implications; Global distribution; Genetic diversity

1 Introduction

Gossypium, commonly known as cotton, is a genus that includes approximately 50 species distributed across tropical and subtropical regions worldwide, excluding Europe (Viot and Wendel, 2023). The genus is of immense agricultural importance due to its role as the primary source of natural fiber for the textile industry. Among these species, *Gossypium hirsutum* and *Gossypium barbadense* are the most widely cultivated, contributing significantly to global cotton production (Wang et al., 2018; Han et al., 2019). The evolutionary history of *Gossypium* is marked by complex processes such as polyploidization and domestication, which have led to the development of species with superior fiber qualities and resilience to environmental stresses (Wu et al., 2018; Yang et al., 2020). Understanding the genetic and molecular bases of these traits is crucial for improving cotton breeding programs and ensuring sustainable cotton production (Zhang et al., 2018).

The primary objective of this systematic review is to provide a comprehensive analysis of the global distribution of *Gossypium* species and their agricultural implications. This review aims to summarize current knowledge on the biogeography and evolutionary history of *Gossypium* species; examine the genetic and molecular mechanisms underlying fiber quality and environmental resilience in different *Gossypium* species; discuss the agricultural implications of these findings, particularly in the context of breeding strategies for improved cotton varieties; and identify gaps in the current research and suggest future directions for studies on *Gossypium* species.

This paper is structured as follows: it provides an overview of the biogeography and evolutionary history of *Gossypium* species, highlighting key events such as polyploidization and domestication; delves into the genetic and molecular bases of fiber quality and environmental resilience, drawing on recent advances in genomics and comparative analyses; discusses the agricultural implications of these findings, focusing on breeding strategies and the potential for genetic improvement of cotton crops; identifies gaps in the current research and proposes future directions for studies on *Gossypium* species, aiming to enhance our understanding and utilization of this vital genus.

2 Taxonomy and Phylogeny of *Gossypium*

2.1 Classification of *Gossypium* species

The genus *Gossypium*, commonly known as cotton, comprises over 50 recognized species distributed across tropical and subtropical regions worldwide, excluding Europe. These species are classified into eight diploid genome groups (A through G, and K) based on cytogenetic and genomic diversity. The genus includes both diploid (2n=26) and allotetraploid (2n=52) species, with four species independently domesticated for their fiber: G. arboreum and *G. herbaceum* from Africa-Asia, and *G. hirsutum* and *G. barbadense* from the Americas. The morphological diversity within *Gossypium* is extensive, ranging from herbaceous perennials to tall trees, each exhibiting a variety of reproductive and vegetative traits (Wendel and Grover, 2015).

2.2 Phylogenetic relationships among *Gossypium* species

Phylogenetic studies have provided deeper insights into the relationships among *Gossypium* species. Early molecular phylogenetic analyses using nuclear and chloroplast DNA sequences revealed rapid radiation events within the genus, complicating the resolution of branching orders among major lineages. Subsequent studies employing multiple nuclear genes and chloroplast genomes have helped clarify these relationships, although some incongruences remain, particularly regarding the basal divergences and interrelationships among African cottons (Cronn et al., 2002; Viot and Wendel, 2023). For instance, the D-genome species form a monophyletic group, while the C, G, and K-genome species exhibit more complex relationships, likely due to recent radiation and hybridization events (Viot and Wendel, 2023). Comparative genomics of allotetraploid species, such as *G. hirsutum* and *G. barbadense*, has further elucidated the structural variations and gene expression changes that underpin their evolutionary divergence (Wang et al., 2018; Fang et al., 2019).

2.3 Evolutionary history and domestication

The evolutionary history of *Gossypium* is marked by significant events of polyploidization and domestication. The genus originated from a common ancestor shared with the genera Kokia and Gossypioides, with subsequent rapid radiation leading to the diversification of diploid and tetraploid species (Cronn et al., 2002; Viot and Wendel, 2023). The domestication of *Gossypium* species in the Americas is particularly noteworthy, with *G. barbadense* and *G. hirsutum* undergoing parallel domestication processes in Mesoamerica and South America, respectively (Viot and Wendel, 2023). These domestication events, dating back 8 000 years for *G. barbadense* and 5 500 years for *G. hirsutum*, transformed wild perennial shrubs into annual crops with desirable fiber traits (Viot and Wendel, 2023). The introgression of favorable traits between these species has further enhanced their agricultural value (Wang et al., 2018; Fang et al., 2019). Understanding the evolutionary and domestication history of *Gossypium* is crucial for improving cotton breeding programs and ensuring the sustainability of this vital crop (Fang et al., 2019; Viot and Wendel, 2023).

3 Geographical Distribution of *Gossypium* Species

3.1 Global distribution patterns

Gossypium species, commonly known as cotton, are distributed across tropical and subtropical regions worldwide, with the exception of Europe. The genus includes approximately 50 species, which are found in diverse habitats ranging from arid deserts to humid tropical forests (Cronn et al., 2002). The two most economically significant species, *Gossypium hirsutum* and *Gossypium barbadense*, are cultivated globally for their superior fiber qualities. *G. hirsutum*, also known as Upland cotton, accounts for about 90% of the world's cotton production and is grown in over 40 countries, including the United States, China, and India (Small and Wendel, 2000). *G. barbadense*, known for its extra-long staple fibers, is cultivated in regions such as Egypt, Peru, and the southwestern United States (Small and Wendel, 2000; Wang et al., 2018).

3.2 Centers of Diversity and Origin

The centers of diversity for *Gossypium* species are primarily located in the Americas, Africa, and Australia. *G. hirsutum* and *G. barbadense* originated and were domesticated in the Americas, with *G. hirsutum* being native to Mesoamerica and the Caribbean, and *G. barbadense* to the coastal regions of South America (Cronn et al., 2002; Lima et al., 2021). The wild progenitors of these species exhibit a wide range of genetic diversity, which has been shaped by both natural selection and human cultivation practices. For instance, *G. hirsutum* has a significant genetic pool in northern Yucatán and the Caribbean, where it has diversified into several races through introgression with *G. barbadense* (Lima et al., 2021). Similarly, *G. barbadense* has undergone extensive genetic changes due to its domestication and subsequent cultivation in diverse environments (Small and Wendel, 2000; Cronn et al., 2002).

3.3 Factors Influencing Distribution

The distribution of *Gossypium* species is influenced by a variety of environmental and anthropogenic factors. Climate plays a crucial role, with temperature, precipitation, and soil water availability being key determinants of habitat suitability. For example, *G. aridum*, a wild cotton species in Mexico, is highly sensitive to flowering growing degree days and annual available soil water, which dictate its distribution (Báez-González et al., 2022b). Similarly, G. thurberi, another wild species, is projected to lose a significant portion of its habitat due to climate change, highlighting the importance of environmental factors in shaping species distribution (Figure 1) (Báez-González et al., 2022b). Human activities, such as agricultural practices and breeding programs, have also significantly impacted the distribution of cultivated *Gossypium* species. The introduction of genetically modified cotton and the subsequent gene flow into wild populations have further complicated the genetic landscape of these species (Wu et al., 2018). Understanding these factors is essential for the conservation and sustainable use of *Gossypium* genetic resources.

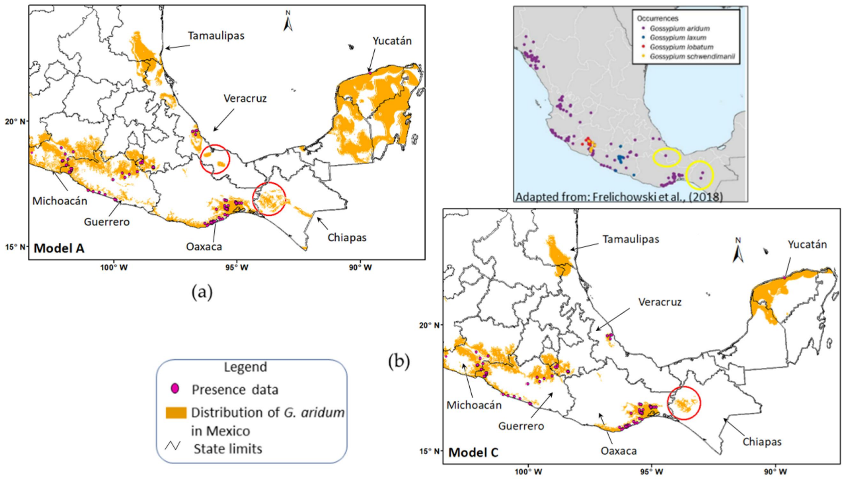

Figure 1 *Gossypium* aridum Models A (a) and C (b) showing presence data and potential distribution of *G. aridum* in the states of Michoacan, Guerrero, Oaxaca, Veracruz and Yucatan in Mexico. Areas encircled in red in Model A and Model C are areas overpredicted by the models (Adopted from Báez-González et al., 2022b)

Image caption: Represents the Global Crop Wild Relatives Occurrence Database, Global Biodiversity Information Facility, and National Cotton Germplasm Conservation Center reports for the states of Veracruz and Chiapas. This performance helps study the habitat and range of cotton in Africa, which is critical for conservation and agricultural research efforts (Adopted from Báez-González et al., 2022b)

4 Ecological and Environmental Adaptations

4.1 Adaptation to different climates and soils

Gossypium species exhibit remarkable adaptability to a variety of climates and soil types, which has facilitated their widespread distribution across tropical and subtropical regions. For instance, *Gossypium* thurberi, a wild cotton species native to northern Mexico and southwestern USA, thrives in areas with specific environmental conditions such as Annual Available Soil Water (AASW), Flowering Growing Degree Days (FGDD), and altitude (ALT). Similarly, *Gossypium* aridum, another wild cotton species in Mexico, has shown a preference for habitats characterized by specific ranges of FGDD and AASW, indicating that these variables significantly influence its distribution. The ability of *Gossypium* species to adapt to diverse soil types, including gypsum soils, further underscores their ecological versatility. Gypsum soils, which are chemically restrictive, host a variety of plant species that have developed unique physiological and morphological adaptations to thrive in such environments.

4.2 Role of ecological factors in species distribution

Ecological factors play a crucial role in the distribution of *Gossypium* species. The distribution of *Gossypium* thurberi, for example, is influenced by a combination of AASW, FGDD, and ALT, with AASW being the dominant factor under future climate scenarios. In the case of *Gossypium* aridum, FGDD has a greater influence on its distribution compared to AASW, highlighting the importance of temperature-related variables in determining habitat suitability (Báez-González et al., 2022a). Additionally, the genetic diversity and distribution of *Gossypium* species in specific regions, such as the Amazonian Native Communities in Peru, are shaped by both ecological and anthropogenic factors. The presence of *Gossypium* barbadense and *Gossypium* hirsutum in these communities is influenced by altitude and the association with other economic crops, indicating that both natural and human-mediated ecological factors contribute to their distribution (Dai et al., 2020).

4.3 Impact of climate change on distribution

Climate change poses significant challenges to the distribution of *Gossypium* species. Studies have projected drastic reductions in the potential distribution of *Gossypium thurberi* in northern Mexico due to increases in temperature and reductions in annual precipitation (Báez-González et al., 2022a). These changes are expected to lead to a 77-86% reduction in the species' current potential distribution area by the mid-21st century. Similarly, the distribution of *Gossypium aridum* is likely to be affected by climate change, as shifts in temperature and precipitation patterns alter the suitability of its habitat (Viot and Wendel, 2023). The impact of climate change on *Gossypium* species is not limited to wild populations; cultivated species such as *Gossypium hirsutum* also face challenges. The genetic basis of environmental adaptability in *Gossypium hirsutum* has been linked to specific haplotypes that confer resilience to varying environmental conditions, suggesting that breeding programs need to focus on these genetic traits to ensure the sustainability of cotton production under changing climatic conditions (Dai et al., 2020). The ecological and environmental adaptations of *Gossypium* species are multifaceted, involving a complex interplay of climatic, soil, and ecological factors. Understanding these adaptations is crucial for developing conservation strategies and improving agricultural practices to mitigate the impacts of climate change on cotton production.

5 Agricultural Implications of *Gossypium* Species

5.1 Importance of *Gossypium* in agriculture

Gossypium species, commonly known as cotton, play a pivotal role in global agriculture due to their significant contribution to the textile industry. Cotton is the most important natural fiber crop worldwide, providing essential raw materials for textile production (Yang et al., 2020). The two primary cultivated species, *Gossypium hirsutum* and *Gossypium barbadense*, are particularly valued for their fiber properties. *G. hirsutum*, also known as Upland cotton, is renowned for its high fiber yield and adaptability to various environmental conditions, making it the most widely grown cotton species globally (Hu et al., 2019; Wang et al., 2018). On the other hand, *G. barbadense*, or Sea-Island cotton, is prized for its superior fiber quality, including fineness and strength, which are highly sought after in the textile industry (Yuan et al., 2015). The economic importance of cotton extends beyond fiber production, as it supports millions of farmers and workers worldwide, particularly in developing countries where it is a major cash crop (Boblina et al., 2023).

5.2 Cultivation practices and regional differences

The cultivation practices of *Gossypium* species vary significantly across different regions, influenced by climatic conditions, soil types, and local agricultural practices. In tropical and subtropical regions, where cotton is predominantly grown, the choice of species and cultivation techniques are tailored to optimize yield and fiber quality. For instance, G. hirsutum is extensively cultivated in regions with diverse environmental conditions due to its resilience and high yield potential (Wang et al., 2018). In contrast, *G. barbadense* is often grown in areas with specific climatic conditions that favor the production of high-quality fibers (Figure 2) (Yuan et al., 2015). Advanced genomic and breeding techniques have been employed to enhance the fiber quality and environmental resilience of these species, enabling their cultivation in a broader range of environments (Wang et al., 2018; Yang et al., 2020). Additionally, the integration of modern technologies such as high-throughput sequencing and bioinformatics has facilitated the development of improved cotton varieties with desirable traits, including disease resistance and stress tolerance (Yang et al., 2020).

5.3 Challenges in *Gossypium* cultivation

Despite the advancements in cotton breeding and genomics, several challenges persist in the cultivation of *Gossypium* species. One of the primary challenges is the susceptibility of cotton plants to various pests and diseases, which can significantly impact yield and fiber quality. For example, grey mildew disease caused by Ramularia areola poses a substantial threat to cotton production in certain regions, necessitating the development of resistant cultivars (Boblina et al., 2023). Additionally, the complex and large genome of cotton presents challenges in genomic research and breeding efforts, although recent technological advancements have begun to address these issues (Yang et al., 2020). Environmental factors such as climate change and soil degradation also pose significant challenges, requiring ongoing research and innovation to develop cotton varieties that can withstand these stresses (Wang et al., 2018; Hu et al., 2019). Furthermore, the need for sustainable cultivation practices is increasingly recognized, as traditional methods often involve high water usage and chemical inputs, which can have adverse environmental impacts. Efforts to improve the sustainability of cotton production include the development of genetically modified varieties with enhanced water-use efficiency and reduced reliance on chemical pesticides (Mehetre, 2010; Zhou et al., 2022).

The global distribution and agricultural implications of *Gossypium* species underscore their critical role in the textile industry and the livelihoods of millions of people worldwide. Continued research and innovation in cotton genomics and breeding are essential to address the challenges faced in cultivation and to ensure the sustainable production of high-quality cotton fibers.

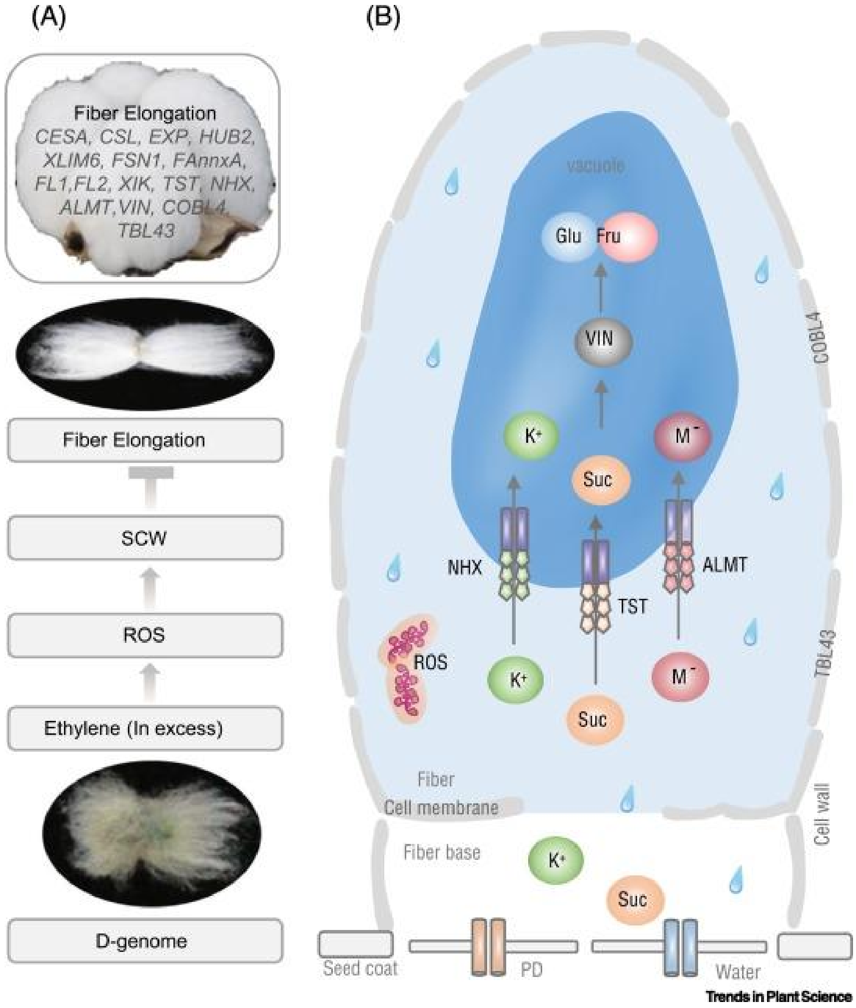

Figure 2 The Molecular Mechanism of Fiber Elongation (Adopted Yuan et al., 2015)

Image caption: This image collectively represents a comprehensive view of the molecular, genetic, and cellular processes involved in cotton fiber elongation (Adopted from Yuan et al., 2015)

6 Genetic Diversity and Breeding

6.1 Genetic variation among *Gossypium* species

The genus *Gossypium*, which includes approximately 50 species, exhibits significant genetic diversity that is crucial for cotton breeding programs. The genetic variation within and between species such as *Gossypium hirsutum* and *Gossypium* barbadense has been extensively studied. For instance, whole-genome resequencing of 240 *G. barbadense* accessions revealed substantial genetic polymorphisms, including over 3.6 million single-nucleotide polymorphisms (SNPs) and 221 354 insertion-deletions (indels), which are associated with important traits like fiber strength and lint percentage (Zhang et al., 2018). Similarly, *G. hirsutum*, which accounts for about 90% of global cotton production, shows a diverse array of morphological forms and genetic variation, as evidenced by studies analyzing allozyme variation across 538 accessions (Yuan et al., 2015). Comparative genomics has further elucidated the evolutionary history and speciation events that have shaped the genetic landscape of these species, highlighting species-specific alterations in gene expression and structural variations (Hu et al., 2019).

6.2 Breeding strategies for improving cotton crops

Breeding strategies for cotton improvement have leveraged the genetic diversity within *Gossypium* species to enhance fiber quality, yield, and environmental resilience. Modern breeding programs often utilize genome-wide association studies (GWAS) to identify candidate genes linked to desirable traits. For example, a GWAS on *G. hirsutum* identified significant SNPs associated with fiber quality traits, involving genes related to polysaccharide biosynthesis and signal transduction (Mehetre, 2010). Introgression lines, which incorporate favorable chromosome segments from *G. barbadense* into *G. hirsutum*, have been developed to combine superior fiber quality with higher yield (Viot and Wendel, 2023). Additionally, the use of high-throughput sequencing and bioinformatics has facilitated the construction of high-density genome variation maps, which are instrumental in accelerating the breeding process (Boblina et al., 2023).

6.3 Utilization of wild species in breeding programs

Wild *Gossypium* species represent a valuable genetic reservoir for cotton improvement. These species often possess traits such as disease resistance and environmental tolerance that are not present in cultivated varieties. The introgression of genes from wild species into cultivated cotton has been a key strategy in breeding programs. For instance, the genetic diversity found in Amazonian native communities, where *G. barbadense* var. *brasiliensis* and other variations are maintained, provides a rich source of genetic material for breeding (Yang et al., 2020). Moreover, the evolutionary history of *Gossypium*, which includes multiple instances of interspecific hybridization and polyploid formation, underscores the potential of wild species to contribute to the genetic improvement of cotton (Zhang et al., 2018). The integration of wild species into breeding programs not only enhances genetic diversity but also helps in developing cotton varieties that are more resilient to biotic and abiotic stresses (Boblina et al., 2023).

7 Pest and Disease Management

7.1 Major pests and diseases affecting *Gossypium*

Gossypium species, particularly *Gossypium hirsutum*, are significantly impacted by various pests and diseases, with the cotton bollworm (*Helicoverpa armigera*) being one of the most destructive pests globally. This pest is known for its high fecundity, strong migratory abilities, and polyphagous nature, affecting not only cotton but also other crops like tomato, soybean, and chickpea (Riaz et al., 2021). The cotton bollworm has developed resistance to multiple classes of insecticides, making its management particularly challenging (Ahmad et al., 2019). Additionally, climate change and cropping patterns have been shown to influence the population dynamics of *H. armigera*, further complicating pest management strategies (Huang and Hao, 2020).

7.2 Integrated pest management strategies

Integrated Pest Management (IPM) strategies are essential for controlling pests in *Gossypium* species. These strategies combine biological, chemical, and physical control measures to achieve effective pest management. The use of transgenic Bt cotton, which expresses Bacillus thuringiensis toxins, has been a significant advancement in controlling *H. armigera*. However, the development of resistance to Bt toxins necessitates the use of refuges and other IPM practices to delay resistance (Addison, 2010; Baker and Tann, 2017). Biological control agents, such as parasitoids and entomopathogenic fungi like Beauveria bassiana and Purpureocillium lilacinum, have also shown promise in reducing pest populations and enhancing plant growth (Lopez and Sword, 2015). Additionally, insect growth regulators (IGRs) like lufenuron have been effective against *H. armigera* while being relatively safe for non-target arthropod predators (Gogi et al., 2006).

7.3 Advances in disease resistance breeding

Advances in breeding for disease resistance in *Gossypium* species have focused on developing varieties that can withstand both biotic and abiotic stresses. The use of genetic modification to introduce resistance traits, such as Bt toxins, has been a cornerstone in managing pest populations (Baker and Tann, 2017). Additionally, breeding programs are increasingly incorporating traits that enhance resistance to fungal pathogens and other diseases. The integration of endophytic fungi, which can enhance plant growth and provide resistance to pests, represents a novel approach in disease resistance breeding (Lopez and Sword, 2015). Continuous monitoring and rotation of insecticides with novel modes of action are also recommended to manage resistance and ensure the long-term sustainability of pest control measures (Ahmad et al., 2019).

8 Biotechnological Advances

8.1 Genetic engineering in *Gossypium*

Genetic engineering has significantly advanced the cultivation and resilience of *Gossypium* species. One notable achievement is the sequencing of the *Gossypium* australe genome, which has revealed multiple genes associated with disease resistance and gland morphogenesis. This genome sequencing has facilitated the incorporation of disease resistance traits into domesticated cotton varieties, enhancing their resilience against pathogens like Verticillium dahliae (Cai et al., 2019). Additionally, the cloning and characterization of the *Gossypium* universal stress protein-2 (GUSP-2) gene have demonstrated its role in conferring resistance to various abiotic stresses, such as salt and drought, in both E. coli and *Gossypium* hirsutum (Hafeez et al., 2021). These genetic modifications are crucial for developing cotton varieties that can withstand environmental stresses and improve crop yields.

8.2 Biotechnological tools for crop improvement

Biotechnological tools have been instrumental in overcoming the genetic limitations of *Gossypium* species. The creation of synthetic amphiploids, such as the hybrid between *Gossypium hirsutum* and *G. arboreum*, has enabled the transfer of valuable traits like Verticillium and drought resistance into Upland cotton (Chen et al., 2015). Similarly, the development of a high-density SSR genetic map from a *Gossypium hirsutum* and *Gossypium darwinii* F_2 population has enriched the genetic diversity of cultivated cotton, providing a foundation for future breeding programs aimed at improving fiber quality and stress resistance (Chen et al., 2015). Furthermore, the synthesis of allotetraploids between *Gossypium* herbaceum and *G. australe* has facilitated the transfer of favorable genes, such as drought tolerance and resistance to sucking insects, into cultivated tetraploid cotton (Liu et al., 2015). These biotechnological advancements are pivotal for enhancing the genetic pool and resilience of cotton crops.

8.3 Future prospects of biotechnology in cotton production

The future of biotechnology in cotton production holds promising prospects for further improving crop resilience and quality. Advances in high-throughput sequencing and bioinformatics have opened new avenues for cotton genomics, enabling the identification and manipulation of genes responsible for fiber biogenesis and environmental resilience (Yang et al., 2020). The integration of biotechnological tools, such as genetic engineering and synthetic hybridization, will continue to play a crucial role in developing cotton varieties with superior traits. For instance, the utilization of wild *Gossypium* species, like *Gossypium anomalum*, which possesses excellent fiber strength and fineness, can be harnessed to enhance the quality of cultivated cotton (Mehetre, 2010). Additionally, the engineering of insect-resistant cotton varieties, such as those resistant to lepidopteran larvae, has already demonstrated significant success and will likely continue to be a focus of future biotechnological efforts (Boblina et al., 2023). These advancements will contribute to sustainable cotton production, ensuring high yields and quality in the face of environmental challenges.

9 Economic and Social Impact

9.1 Economic significance of cotton production

Cotton, particularly species like *Gossypium* hirsutum and *Gossypium* barbadense, plays a crucial role in the global economy. It is the most important natural fiber crop worldwide, covering over 33 million hectares in 77 countries and supporting millions of livelihoods (Boblina et al., 2023). The economic significance of cotton production is underscored by its contribution to the textile industry, which relies heavily on the high-quality fibers produced by these species. Advances in genomics and breeding have further enhanced cotton's economic value by improving fiber quality and yield, making it a more resilient crop against environmental stresses (Hu et al., 2019; Yang et al., 2020; Wang et al., 2018). The genetic diversity within *Gossypium* species also provides a rich resource for breeding programs aimed at enhancing fiber traits and disease resistance, thereby ensuring the sustainability and profitability of cotton farming (Viot and Wendel, 2023).

9.2 Social and cultural aspects of cotton farming

Cotton farming has profound social and cultural implications, particularly in regions where it is a major agricultural activity. In India, for instance, cotton supports over 60 million people, including 6 million small and marginal farmers (Boblina et al., 2023). The cultivation of cotton is deeply embedded in the cultural fabric of many communities, influencing social structures and local economies. The domestication and cultivation of cotton have also led to significant cultural exchanges and technological advancements over millennia, as evidenced by the parallel domestication events in Mesoamerica and South America (Viot and Wendel, 2023). These historical processes have not only shaped the genetic makeup of modern cotton species but also the cultural practices surrounding their cultivation and use (Morales-Aranibar et al., 2023).

9.3 Policy and trade issues affecting *Gossypium*

The global cotton industry is influenced by a complex web of policy and trade issues. Trade policies, subsidies, and international agreements play significant roles in shaping the cotton market. For example, the introduction of genetically modified (GM) cotton has had both positive and negative impacts on trade and local economies. While GM cotton has increased yields and reduced pesticide use, it has also led to concerns about gene flow into wild populations and the potential loss of genetic diversity. Additionally, policies aimed at supporting smallholder farmers and promoting sustainable practices are crucial for the long-term viability of cotton farming. The genetic resources and breeding advancements in *Gossypium* species provide opportunities to address these challenges by developing more resilient and high-yielding cotton varieties (Wang et al., 2018; Hu et al., 2019; Grover et al., 2020). Effective policy frameworks that balance economic growth with environmental sustainability and social equity are essential for the future of the cotton industry.

10 Conservation and Sustainability

10.1 Conservation of *Gossypium* genetic resources

The conservation of *Gossypium* genetic resources is crucial for maintaining the genetic diversity necessary for future breeding and adaptation to changing environmental conditions. *Gossypium* species, particularly G. hirsutum and G. barbadense, have undergone significant domestication and genetic modification, which has led to a reduction in genetic diversity among cultivated varieties (Hu et al., 2019; Viot and Wendel, 2023). Conservation efforts must focus on both in situ and ex situ strategies to preserve wild and semi-wild populations, which harbor valuable genetic traits that can be used to improve cultivated cotton (Wegier et al., 2011; Alacez et al., 2021). In situ conservation involves protecting natural habitats and wild populations, as seen in Mexico, the center of origin for *G. hirsutum*, where gene flow between wild and domesticated populations has been documented (Wegier et al., 2011; Alacez et al., 2021). Ex situ conservation, on the other hand, includes the collection and storage of seeds in gene banks, which ensures the availability of genetic material for future research and breeding programs (Zuffo et al., 2023).

10.2 Sustainable farming practices

Sustainable farming practices are essential for the long-term viability of cotton production. These practices include crop rotation, integrated pest management, and the use of organic fertilizers, which help maintain soil health and reduce the environmental impact of cotton farming (Yang et al., 2020). Advances in genomics have provided insights into the genetic basis of traits such as fiber quality and environmental resilience, enabling the development of cotton varieties that require fewer inputs and are more resistant to pests and diseases (Hu et al., 2019; Yang et al., 2020). For instance, the introgression of favorable genes from wild relatives into cultivated cotton has been shown to enhance resilience to environmental stresses, thereby supporting more sustainable farming practices Wang et al., 2018; Peng et al., 2022). Additionally, understanding the ecological niche and distribution of feral cotton can inform management practices that minimize gene flow from genetically modified (GM) varieties to wild populations, thereby protecting genetic diversity (Alacez et al., 2021).

10.3 Role of conservation in future agriculture

The role of conservation in future agriculture cannot be overstated. As climate change and other environmental pressures continue to impact agricultural systems, the genetic diversity preserved through conservation efforts will be invaluable for developing new cotton varieties that can withstand these challenges (Yang et al., 2020). The evolutionary history and genetic relationships among *Gossypium* species provide a foundation for identifying and utilizing beneficial traits from wild and semi-wild populations. For example, the genetic diversity found in Amazonian native communities highlights the potential for discovering new genetic variations that can be used to improve cultivated cotton. Furthermore, the integration of modern genomic tools with traditional conservation methods can accelerate the identification and incorporation of desirable traits into breeding programs, ensuring the sustainability and productivity of cotton agriculture in the future (Wang et al., 2018; Yang et al., 2020; Peng et al., 2022).

11 Conclusion

The systematic review on the global distribution of *Gossypium* species and its agricultural implications has revealed several critical insights. The genus *Gossypium*, comprising approximately 50 species, is widely distributed across tropical and subtropical regions, with significant genetic diversity and evolutionary history. The domestication of *Gossypium hirsutum* and *Gossypium barbadense* has been pivotal in the development of cotton as a major global crop, with advancements in genome sequencing providing deeper understanding of their genetic makeup and evolutionary divergence. Studies have highlighted the genetic diversity within native populations, particularly in regions like the Amazon and Mesoamerica, which are crucial for conservation and breeding programs. Additionally, the potential impacts of climate change on the distribution of wild cotton species, such as *Gossypium thurberi* and *Gossypium aridum*, underscore the need for adaptive conservation strategies.

Future research should focus on several key areas to further enhance our understanding and utilization of *Gossypium* species. Firstly, there is a need for comprehensive studies on the genetic diversity and adaptive traits of wild and feral cotton populations, which can provide valuable genetic resources for breeding programs aimed at improving fiber quality and stress resilience. Secondly, the impact of climate change on the distribution and survival of wild cotton species necessitates the development of predictive models and conservation strategies to safeguard these genetic resources. Additionally, exploring the coexpression networks and gene regulatory mechanisms in cotton seeds can offer insights into the phenotypic diversification and domestication processes, aiding in the development of superior cotton varieties. Finally, the ethnobotanical and antimicrobial properties of *Gossypium* species present an untapped potential for pharmaceutical applications, warranting further investigation.

The global distribution and genetic diversity of *Gossypium* species hold significant agricultural and ecological importance. The integration of advanced genomic tools and ecological modeling can enhance our understanding of cotton evolution, domestication, and adaptation to changing environments. It is imperative to prioritize the conservation of wild cotton species and their habitats to maintain genetic diversity and support sustainable cotton production. Collaborative efforts between researchers, breeders, and conservationists are essential to address the challenges posed by climate change and to harness the full potential of *Gossypium* species for agricultural and medicinal applications. Continued investment in research and development will be crucial in ensuring the resilience and productivity of cotton crops in the face of global environmental changes.

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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.

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