IRSTI 34.31.21

https://doi.org/10.70264/jbr.v1.1.2025.5

COTTON (GOSSYPIUM L.) GLOBAL DISTRIBUTION AND ADAPTATION TO DIFFERENT GEOGRAPHIC REGIONS

Orken Aisulu^{1,3}, Manabayeva Shuga^{1,3}, Makhmadjanov Sabir², Ramazanova Malika¹, Kali Balnur¹, Rakhimzhanova Aizhan¹, Tussipkan Dilnur¹*

¹National center for biotechnology, Korgalzhyn hwy. 13/5, Astana, 010000, Kazakhstan ²Agricultural Experimental Station of Cotton and Melon Growing, Atakent, 160525 Kazakhstan ³L.N. Gumilyov Eurasian National University, Satpayev st. 2, Astana, 010000, Kazakhstan

*Corresponding author: Tussipkan Dilnur tdilnur@mail.ru

ABSTRACT

Cotton (*Gossypium* L.) is one of the most economically significant crops globally, with its cultivation spanning diverse geographic regions. The genus *Gossypium* comprises over 50 species, four of which are widely cultivated for their superior fiber quality. First, this review provides a summary of the phylogey of *Gossypium*, including genomic features of diploid and allotetraploid species. Second, we detail the origin of all *Gossypium* species and the human-mediated introduction of *Gossypium* arboreum, *Gossypiumherbaceum*, *Gossypium barbadense*, *Gossypium hirsutum*, and *Gossypium harknessii* species into new areas. This review highlights the need for continued research into the genetic diversity and adaptive mechanisms of cotton to enhance its sustainable production worldwide.

Key words: Cotton (Gossypium L.), phylogenesis, evolutionary origin, geographic distribution

Received: February 21, 2025 / Accepted: March 31, 2025 / Published: 31 March, 2025

© The Author(s) 2025.

Citation: Orken, A., Manabayeva, Sh., Makhmadjanov, S., Ramazanova, M., Kali, B., Aizhan, R., Tussipkan, D. (2025). Cotton (Gossypium L.) global distribution and adaptetion to different geografic region. Journal of Biological Research, 1(1), 43-55. https://doi.org/10.70264/jbr.v1.1.2025.5.

1 INTRODUCTION

Cotton (*Gossypium* L.) is one of the most important fiber crops in the world, with significant economic value [1]. The extensive distribution and adaptation of *Gossypium* species to five continents and multiple cropping zones can be attributed to its distinct evolutionary history [2]. The geographic distribution of cotton cultivation reflects its ability to adapt to different topographies, soil types, and climatic conditions. This adaptability underscores the importance of site-specific management practices to optimize yield, quality, and sustainability. These practices include soil and water management, pest control, and mechanized farming techniques to ensure environmental sustainability and maximize economic returns [3].

Four of the approximatelly 55 species in the genus *Gossypium* have been domesticated [4], including two diploid and two allotetraploid species. The diploid species are *G. arboreum*, native to the Indian subcontinent and widely cultivated in South Asia, while *G. herbaceum*, native to southern Africa and cultivated in parts of Africa and the Middle East. The allotetraploid species is *G. hirsutum*, known as upland cotton, which accounts for about 90% of world cotton production [5]. It is native to Mexico and Central America. *G. barbadense*, known for its superior fiber quality and is native to the coastal regions of Colombia, Peru, and Ecuador. These species are

central to the global textile industry and remain a focus of research to improve fiber properties, disease resistance, and environmental adaptability. While *G. hirsutum* dominates in many regions due to its robust adaptability, other species, such as *G. barbadense* and *G. arboreum*, are predominantly grown in parts of Asia and Africa due to their localized genetic traits and environmental suitability [6].

Environmental factors influence the growth and productivity of cotton, with high temperatures often leading to sterility and boll shedding in certion regions [7]. In this literature review, we aim to highlight the most relevant information on the economically important crop of cotton, which requires sunlight and heat.

2 MATERIALS AND METHOD

2.1 Materials

This reviw focus on different *Gossypium* species as a research material.

2.2 Data Sources and Search Strategy

Web of Science Core Collection, PubMed and Google scholar containing over 47 articles are published which the most impactful international and local journals including articles, reviews, book and book chapter. The literature search covered forthe period from 2003 to 2024. Additionally, we utilized resources such as Plants of the World Online and various legal websites.

2.3 Research Tools and Visualization Methods

The strategies used to retrieve were as follows: topical subject as Cotton (*Gossypium* L.), phylogenesis, evolutionary origin, geographic distribution.

Map was made by using Mapchart (<u>https://www.mapchart.</u> <u>net/</u>). Microsoft Office Excel 2021 was used for quantitative analysis of the literature and made table.

3 PHYLOGENESIS

The genus *Gossypium* L. is recognized for its central role in global textile production and for its significant contribution to basic and applied plant sciences. Its unique genomic architecture and evolutionary history make it a valuable model for taxonomy, polyploidy, and cytogenetic studies.

Taxonomically, *Gossypium* L. belongs to the tribe Gossypieae, the family Malvaceae, and the order Malvales [8]. The genus comprises more than 50 species, which are broadly divided into diploid (2n = 2x = 26) and allopolyploid (2n = 4x = 52) species [9]. Based on chromosomal features and interspecific hybridization studies, these species are assigned to eight diploid genome groups (A to G and K) and one allopolyploid group (AD) [10].

3.1 Genomes of diploid species

Diploid species exhibit significant diversity in their chromosome morphology, genome structure, and adaptation to distinct ecological niches. For example, A-genome diploids, such as *G. arboreum*, are native to Asia, while D-genome species are primarily found in arid regions of the Americas.

According to genetic studies based on molecular markers, the primary diploid cotton lineages bedun to diverge approximatelly 7–11 million years ago [11]. Transoceanic migration and hybridization of the Afro-Asian A genome species with a New World representative possessing the D genome is thought to have produced polyploid species (AD genome) about 1–2 million years ago [4]. The ancestral group of allotetraploid cotton (AD genome) is divided into seven allotetraploid species.

The classification of *Gossypium* species into genome groups (A to G, K) is based on their evolutionary history, chromosome structure, and geographical distribution. Diploid *Gossypium* species (2n = 2x = 26) have different genomic architectures. These genomes are categorized into groups A, B, C, D, E, F, G, and K based on evolutionary divergence and adaptations to different ecological niches.

Differences in chromosome morphology, DNA content, and molecular phylogenetics support the division into genome groups. Chromosome size, shape, and DNA composition vary widely among species, reflecting their evolutionary adaptations to different environments. Molecular phylogenetic studies have further validated these classifications, revealing distinct evolutionary lineages within *Gossypium* [13].

The whole genome sequence of the diploid species *G. arboreum* cotton was made publicly available for the first time in 2022 [14]. The whole genome sequences of the diploid species of the genus *Gossypium*. L have undergone several up-

dates and refinements since that work [14-16].

3.2 Genomes of allotetraploid species

Hybridization between ancestral A- and D-genome species approximately 1-2 million years ago led to the formation of allopolyploid cotton species, including the commercially important G. hirsutum and G. barbadense [9]. This polyploidization event conferred increased genetic plasticity, contributing to their superior agronomic traits and environmental adaptability. Recent genomic studies have further refined our understanding of the evolutionary history and genome organization of Gossypium. Advances in high-throughput sequencing technologies have facilitated the assembly of reference genomes for several diploid and polyploid species, revealing extensive structural variation and gene duplication events underlying their phenotypic diversity [10]. Comparative cytogenetic analyses have identified conserved chromosomal rearrangements and provided insights into genome evolution within the genus [9]. These findings underscore the importance of Gossypium as a model system for studying polyploidization processes and genome stability, with implications for crop improvement and breeding programs.

Several new cotton species have been identified and categorized in recent years [17-18]. For instance, *Gossypium stephensii*, discovered by Gallagher et al. (2017) on Wake Atoll in the Pacific Ocean, is characterized by its distinct morphological features and genetic profile. Similarly, *Gossypium ekmanianum* was recognized as a separate allopolyploid species during phylogenetic studies by Grover et al. (2015). These species have provided valuable insights into the evolutionary pathways and diversification expanding our understanding the genetic complexity and adaptive strategies of *Gossypium*.

Allopolyploid cotton species, such as *Gossypium tomentosum* (Hawaii) and *Gossypiumdarwinii* (Galápagos), are frequently found in remote areas. According to Wendel and Grover (2015), these isolated populations demonstrate that cotton has undergone substantial geographic diversification and adaptation to various ecological circumstances. Through phylogenetic studies employing NJ and ML techniques, stable sibling relationships were found between *G. barbadense* and *G. darwinii* and *G. hirsutum* and *G. ekmanianum*. In addition to confirming prior findings, new relationships were revealed that had not been considered before [19]. Possible occurrences such as paralogy and homoplasy cause high sequence identity and inadequate phylogenetic resolution, making it difficult to identify reliable evolutionary relationships [20-21].

The advantages of genome sequencing and resequencing data allow the study of the genetic basis of the genus *Gossypium* L. For the first time, the complete genome sequence of *G. hirsutum* cotton was developed in 2015 [22]. Following this study, the complete genome sequences of allotetraploid species in the genus *Gossypium* L have been updated and refined multiple times [22-29]. These genome sequences provide a platform for all molecular genetic improvement research.

Thus, cotton genome research highlights its ability to adapt and evolve under the influence of geographic and climatic factors. This makes cotton a unique model system for studying the mechanisms of adaptation and diversification in crop plants.

4 THE ORIGIN OF *GOSSYPIUM* SPECIES

The regions with the highest diversity include Australia, Mexico, and Africa, reflecting the evolutionary adaptation of cotton species to different environments (Table 1).

Pacific Islands and Galápagos

Several island species are of special conservation interest [30].

Hawaiian Islands: G. tomentosum.

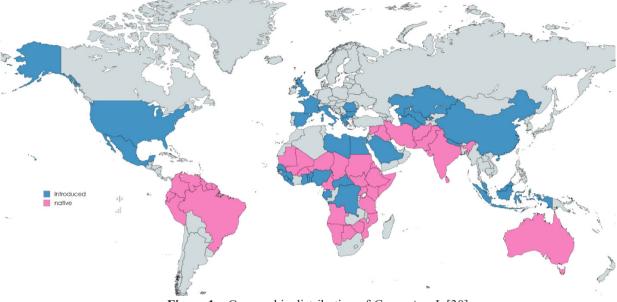


Figure 1 – Geographic distribution of Gossypium L [30].

Australia

Australia has many *Gossypium* species, particularly in the western and northern regions [30].

Western Australia (11 species): Gossypium anapoides, Gossypium costulatum, Gossypium enthyle, Gossypium exiguum, Gossypium londonderriense, Gossypium marchantii, Gossypium nobile, Gossypium pilosum, Gossypium populifolium, Gossypium pulchellum, Gossypium robinsonii.

Northern Australia (2 species): Gossypium cunninghamii, Gossypium nelsonii.

North and Central America

Mexico is a center of diversity for diploid and polyploid *Gossypium* species [30].

Northwest Mexico (6 species): Gossypium californicum, Gossypium contextum, Gossypium dicladum, G. harknessii, Gossypium hypadenum, Gossypium turneri.

Southwest Mexico (4 species): Gossypium laxum, Gossypium lobatum, Gossypium patens, Gossypium schwendimanii.

Central Mexico (3 species): Gossypium aridum, Gossypium gossypioides, Gossypium trilobum.

Africa

Numerous species of *Gossypium* are native to various African regions, particularly in arid and semi-arid environments [30].

Widespread African species: Gossypium anomalum (Angola, Burkina Faso, Cameroon, Cape Verde, Chad, Eritrea, Mali, Mauritania, Namibia, Niger, Somalia, Sudan), G. herbaceum (Botswana, Mozambique, Namibia, Swaziland, Zimbabwe), Gossypium longicalyx (Sudan, Tanzania, Uganda), Gossypium triphyllum (Angola, Botswana, Namibia), Gossypium somalense (Chad, Ethiopia, Kenya, Niger, Somalia, Sudan, Uganda). Galápagos Islands: G. darwinii, Gossypium klotzschianum.

Wake Island: G. stephensii.

South America

South America has a smaller but significant number of native species [30].

Brazil and surrounding areas: *Gossypium mustelinum* (northeast Brazil), *G. nobile* (north Brazil), *G. barbadense* (Colombia, Ecuador, Peru), *Gossypium raimondii* (Peru).

The distribution of *Gossypium* species highlights the remarkable adaptability and ecological specialization of the genus, providing valuable insights for evolutionary and conservation studies.

Asia

Asia is home to several *Gossypium* species, predominantly on the Indian subcontinent, the Arabian Peninsula, and surrounding regions [30].

Indian subcontinent (2 species): *G. arboreum* (India, Sri Lanka), *G. herbaceum* (Afghanistan, Iran, Iraq).

Arabian Peninsula (4 species): Gossypium areysianum (Yemen), Gossypium incanum (Yemen), Gossypium stocksii (India, Oman, Pakistan, Somalia, Yemen).

Central Asia (1 species): *G. herbaceum* is also found in regions extending into Afghanistan and Iran.

Southeast Asia (1 species): *Gossypium timorense* is native to the Lesser Sunda Islands in modern Indonesia.

5 SUCCESSFUL INTRODUCTION AND DISTRI-BUTION OF *GOSSYPIUM* SPECIES IN THE WORLD

The genus *Gossypium* has a broad geographical distribution, with several species introduced into different regions for agricultural cultivation and genetic research. Below is a comprehensive overview of key species and their regional introductions (Table 1).

G. arboreum

Asia: Widely introduced in Bangladesh, India, China, Pakistan, and Vietnam, *G. arboreum* has played a critical role in traditional textile production and breeding for stress tolerance.

Africa: Successful introductions have been observed in Ethiopia, Ghana, Mali, Nigeria, and Sudan, where the species has adapted to diverse agroclimatic conditions.

G. herbaceum

Asia: This species has also been introduced into Bangladesh, India, China, Pakistan, and Vietnam, where it complements *G. arboreum* in traditional cotton farming systems.

Africa: Due to its adaptability, *G. herbaceum* cultivation has been established in Ethiopia, Ghana, Mali, Nigeria, and Sudan.

Europe: Mediterranean countries such as Greece, Italy, Spain, and Romania have adopted this species for cotton production.

Middle East and Central Asia: *G. herbaceum* has become an important part of the cotton industry in Iran, Iraq, Tajikistan, Turkmenistan, and Uzbekistan.

G. barbadense

Asia: Regions such as Bangladesh, Thailand, and Vietnam have successfully adopted *G. barbadense* for its superior fiber quality.

Africa: The species has been introduced into Angola, Benin, Chad, and Tanzania, where it supports the production of high quality cotton fiber.

The Americas: Countries such as Brazil, Belize, Honduras, and the Caribbean nations (Bahamas, Dominican Republic, and Jamaica) have established large-scale cultivation of this species, which contributes significantly to cotton production.

Middle East and Central Asia: *G. barbadense* is widely grown in Iran, Iraq, Tajikistan, Turkmenistan, and Uzbekistan to support fiber-intensive industries.

G. hirsutum

Asia: Bangladesh, Thailand, and Vietnam have adopted this species for its high yield potential and adaptability to different environmental conditions.

Africa: *G. hirsutum* is grown extensively in Angola, Benin, Chad, and Tanzania.

Americas: Brazil, the Caribbean (Bahamas, Dominican Republic, Jamaica), Belize, and Honduras are significant producers.

Europe: The Mediterranean climate has enabled the successful introduction of *G. hirsutum* in Greece, Italy, Spain, and Romania.

Middle East and Central Asia: Iran, Iraq, Kazakhstan, Tajikistan, Turkmenistan, and Uzbekistan have included *G. hirsutum* in extensive breeding programs due to its agronomic advantages.

G. harknessii

California

Despite the successful introduction of domesticated Gos-

sypium species, the expansion of wild species remains limited due to several biological, ecological, and economic factors. Only four domesticated species (G. hirsutum, G. barbadense, G. arboreum, and G. herbaceum) produce high-quality, economically viable fiber, while wild species often produce inferior or non-fibrous materials [31]. Many wild species are highly specialized and adapted to specific ecological niches, such as G. darwinii from the Galapagos Islands and G. sturtianum from Australia, limiting their adaptability to other regions. Conservation efforts prioritize rare and endemic species, such as G. klotzschianum and G. stephensii, to preserve genetic diversity and ecological roles [32]. Agronomic limitations, such as low yield, disease susceptibility, and poor fiber characteristics, reduce their utility in commercial agriculture. Interspecific hybridization is challenging due to differences in ploidy level, chromosomal incompatibility, and genetic divergence, making it difficult to transfer desirable traits [33]. Limited research on wild species has further restricted their adoptation and use, although G. aridum and G. tomentosum have shown potential for drought tolerance and disease resistance, indicating promise for future breeding programs [34].

To provide a comprehensive understanding of global cotton cultivation, it is essential to examine both the worldwide distribution of *Gossypium* species and their significance in specific regions, including Kazakhstan. While cotton has been successfully introduced and cultivated across various continents, Kazakhstan's cotton industry remains a key component of its agricultural sector, particularly in the Turkestan region.

In terms of cotton varieties, Kazakhstan has made significant progress in breeding and selecting high-yield, pest-resistant cultivars. Out of the 13 cotton varieties developed by the «Agricultural Experimental Station of Cotton and Melon Growing» LLP, 9 have been included in the Register of Breeding Achievements Recommended for use in the Republic of Kazakhstan. These include Bereke-07, Maktaaral-4005, Maktaaral-4007, Maktaaral-4011, Myrzashol-80, Pakhtaaral-3031, Pakhtaaral-3044, Maktaaral-4017, and Maktaaral-5027. These varieties have been widely adopted and now cover more than 90% of the total cotton-growing area in the Turkestan region. Additionally, all 13 varieties have received patents for breeding achievements, with the most recent addition being the promising Maktaaral-5027 variety, which was patented in 2021 and exhibits strong resistance to key cotton pests such as the cotton bollworm (Helicoverpa armigera) and Spodoptera species [48].

Despite advancements in breeding and cultivation, several challenges persist in Kazakhstan's cotton farming sector. These include soil salinization, water shortages, climate change, pest infestations, and soil depletion. To address these issues, breeding programs have prioritized the development of cotton varieties with early maturation (105–110 days), high salt and drought tolerance, and resistance to diseases and pests. These efforts aim to enhance productivity while maintaining soil fertility in crop rotation systems.

	1	1			1	Individual	1	1	1	First
Species names	Synonyms	Description	Geographic de native to	stribution [30] introduced into	Individual genome [43]	chromosome [43]	Whole genome sequence	Chl	mit	published in
Gossypium anapoides	N/A	With many unbranched stems emerging from the top of a woody lignotuber, the species is erect [40].	Western Australia	N/A	K ₁₂	K ₁₂ 01-K ₁₂ 13	N/A	N/A	N/A	Novon 23: 448 (2014 publ. 2015)
Gossypium anomalum	Cienfuegosia anomala, Hibiscus anomalus	It is resistant to aphids, springtails, cotton wilt, angular leaf spot, and drought and possesses high- quality fiber and cytoplasmic male sterility [41]	Angola, Burkina, Cameroon, Cape Verde, Chad, Eritrea, Mali, Mauritania, Namibia, Niger, Somalia, Sudan	N/A	Bl	B101-B113	GCA_025698475.1 [44]	N/A	N/A	Sert. Benguel.: 21 (1859)
Gossypium arboreum L.	Gossypium arboreum f. indicum	It is among the few species of cotton that are grown. Black root rot, reniform nematodes, spider mites, hoppers, white files, aphids, leaf curl virus, thrips, and drought tolerance [41].	India, Sri Lanka	Angola, Bangladesh, Benin, Chad, China, Cuba, Ethiopia, Gabon, Ghana, Mali, Nigeria, Sudan, Tanzania, Thailand, Togo, Trinidad and Tobago, Uganda, Vietnam, Yemen.	A ₂	A201-A213	GCA_025698485.2 [45]	HQ325740.1 [45]	KR736342 [45]	Sp. Pl.: 693 (1753)
Gossypium areysianum	Gossypium anomalum subsp.	The desert or arid shrubland biomes are where it grows most commonly [42].	Yemen	N/A	E3	E ₃ 01-E ₃ 13	N/A	N/A	N/A	Esq. Geogr. Bot.: 49 (1895)
Gossypium aridum	areysianum Erioxylum aridum	It is a tree that grows mostly in the seasonally dry tropical habitat. It is resistant to reniform nematodes and can withstand salinity [42].	Mexico Central, Mexico Gulf, Mexico Northeast, Mexico Northwest, Mexico Southwest	N/A	D_4	D ₄ 01-D ₄ 13	GCA_013487665.1 [44]	N/A	N/A	J. Genet. 28: 422 (1934)
Gossypium armourianum	N/A	It resists bacterial blight, jassids, and white flies [41].	Mexico	N/A	D ₂₋₁	D _{2a} 01-D _{2a} 13	GCA_013677265.1 [44]	N/A	N/A	J. Washington Acad. Sci. 23: 558 (1933)
Gossypium australe	Cienfuegosia australis, Fugosia australis, Hibiscus australis, Notoxylinon australe	This woody shrub is native to northwest. Averaging two or three feet in height, it prefers sandy soils close to watercourses. It has glanded plants and glandless seeds and is resistant to aphids, spider mites, Fusarium, and Verticillium wilts. It can also withstand drought [41].	Northern Territory, Queensland, Western Australia	N/A	G ₂	G ₂ 01-G ₂ 13	N/A	N/A	N/A	(1933) Fragm. 1: 46 (1858)
Gossypium barbadense L.	Gossypium barbadense var. eubarbadense, Gossypium barbadense subsp. typicum, Hibiscus barbadensis (L.), Neogossypium barbadense (L.)	This tropical cotton grows to the size of a small tree. It is long, high- quality, and extensively grown lint that is resistant to Verticillium with [41]. This shrub grows most commonly in the seasonally dry tropical habitat. It is utilized for food and fuel, as well as for medicinal and environmental purposes.	Colombia, Ecuador, Peru	Angola, Bahamas, Bangladesh, Belize, Benin, Bolivia, Brazil, Cambodia, Cameroon, Chad, Chile, China, Cuba, Dominican Republic, Egypt, Ethiopia, French Guinan, Gabon, Gambia, Ghana, Guinea, Guyana, Haiti, Honduras, Jamaica, Kenya, Laos, Liberia, Maldives, Mexico, Nepal, Niger, Nigeria, Senegal, Sierra Leone, Sri Lanka, Sudan, Suriname, Tanzania, Thailand, Togo, Turkmenistan, Uganda, Uzbekistan, Venezuela, Vietnam,	(AD) ₂	A ₁ 01-A ₂ 13; D ₂ 01-D ₂ 13	GCA_018997955.1 [26]	N/A	N/A	Sp. PL: 693 (1753)
Gossypium bickii	Cienfuegosia pedata, Fugosia pedata, Notoxylinon pedatum	It is a shrub that grows mainly in the tropical biome that experiences seasonal dryness. Both glanded- plant and landless-seed are present [41].	Northern Territory, Queensland	N/A	G	G ₁ 01-G ₁ 13	GCA_025503065.1 [14]	N/A	N/A	Bot. Zhurn. S.S.S.R. 32: 65 (1947)
Gossypium bricchettii	Cienfuegosia bricchettii	It is a shrub and grows primarily in the desert or dry shrubland biome.	Ethiopia, Kenya, Somalia	N/A	Е	N/A	N/A	N/A	N/A	Kew Bull. 42: 349 (1987) Trudý
Gossypium californicum	N/A	It grows primarily in the desert or dry shrubland biome.	Mexico Northwest	N/A	N/A	N/A	N/A	N/A	N/A	Trudý Sredne- Aziatsk. Gosud. Univ. Lenina, n.s., 28: 21 (1950)
Gossypium contextum	N/A	It is a shrub and grows primarily in the desert or dry shrubland biome.	Mexico Northwest	N/A	N/A	N/A	N/A	N/A	N/A	J. Washington Acad. Sci. 16: 337 (1926)
Gossypium costulatum	Cienfuegosia latifolia, Fugosia latifolia, Hibiscus latifolius, Notoxylinon latifolium Cienfuegosia	It grows primarily in the desert or dry shrubland biome.	Western Australia	N/A	K8	K801-K813	N/A	N/A	N/A	Relaz. Cult. Coton.: 109 (1877)
Gossypium cunninghamii	Cienfuegosia benthamii, Cienfuegosia punctata, Fugosia punctata	It is a shrub and grows primarily in the desert or dry shrubland biome.	Northern Australia	N/A	К9	K901-K913	N/A	N/A	N/A	Relaz. Cult. Coton.: 110 (1877)

Table 1 – Global distribution and genomic characteristics of Gossypium L species.

Type: Review. https://doi.org/10.70264/jbr.v1.1.2025.5

		It many seture at 1				1		1	1	I I W I
Gossypium hypadenum	N/A	It grows primarily in the desert or dry shrubland biome.	Mexico Northwest	N/A	N/A	N/A	N/A	N/A	N/A	J. Washington Acad. Sci. 16: 336 (1926) Empire
Gossypium incanum	Cienfuegosia incana	It grows primarily in the desert or dry shrubland biome.	Yemen	N/A	E_4	E ₄ 01-E ₄ 13	N/A	N/A	N/A	Cotton Growing Rev. 36: 165 (1959)
Gossypium irenaeum	N/A	It grows primarily in the wet tropical biome.	Guatemala	N/A	N/A	N/A	N/A	N/A	N/A	Smithsonian Misc. Collect. 60(4): 1 (1912)
Gossypium klotzschianum	Hibiscus barbadensis var. klotzschianus	It has salinity tolerance [41].	Galápagos, Mexico Northwest	N/A	D _{3-k}	D _{3k} 01-D _{3k} 13	GCA_013677235.1 [44]	N/A	N/A	(1912) Kongl. Vetensk. Acad. Handl. 1853; 228
Gossypium Iaxum	N/A	It grows primarily in the seasonally dry tropical biome.	Mexico Southwest	N/A	D ₉	D ₉ 01-D ₉ 13	GCA_013511315.1 [44]	N/A	N/A	Madroño 21: 265 (1972)
Gossypium lobatum	N/A	It has resistance to Verticillium wilt [41]It is a tree and grows primarily in the seasonally dry tropical biome	Mexico Southwest	N/A	D ₇	D ₇ 01-D ₇ 13	GCA_013467485.1 [44]	N/A	N/A	Madroño 13: 261 (1956)
Gossypium londonderriense	N/A	biome. It is a subshrub and grows primarily in the seasonally dry tropical biome. It is characterized by	Western Australia	N/A	К ₆	K ₆ 01-K ₆ 13	N/A	N/A	N/A	Syst. Bot. 17: 100 (1992)
Gossypium longicalyx	N/A	scandent growth, gland- dotted stems, and petiolate ovate leaves with acuminate tips. Its yellow flowers feature gland-dotted petals and a deeply divided calyx, while the fruit consists of ovoid, 3-locular capsules containing densely pubescent seeds. This species is typically found in seasonally wet Acacia bushlands and scrub vegetation at elevations of 800–900 meters. It has Resistance to reniform nematode [41]	Sudan, Tanzania, Uganda	N/A	F ₁	F ₁ 01-F ₁ 13	GCA_025698465.1 [14]	N/A	N/A	Kew Bull. 13: 221 (1958)
Gossypium marchantii	N/A	It is a subshrub and grows primarily in the seasonally dry tropical biome.	Western Australia	N/A	K ₅	K ₅ 01-K ₅ 13	N/A	N/A	N/A	Syst. Bot. 17: 103 (1992)
Gossypium morrilli	N/A	It grows primarily in the desert or dry shrubland biome.	Mexico Northwest	N/A	N/A	N/A	N/A	N/A	N/A	J. Washington Acad. Sci. 16: 339 (1926)
Gossypium mustelinum	G. hirsutum f. mustelinum, G. hirsutum subsp. mustelinum	It has longer fibers [41]. It is a shrub and grows primarily in the seasonally dry tropical biome.	Brazil Northeast	N/A	(AD) ₄	A _m 01-A _m 13; D _m 01-D _m 13	GCA_017165895.1 [26]	N/A	N/A	Wild Cult. Cotton: 167 (1907
Gossypium nelsonii	N/A	It grows primarily in the seasonally dry tropical biome.	Northern Australia	N/A	G3	G ₃ 01-G ₃ 13	N/A	N/A	N/A	Austral. J. Bot. 22: 184 (1974)
Gossypium nobile	N/A	It is a shrub and grows primarily in the seasonally dry tropical biome.	Brazil North, Western Australia	N/A	К ₁₁	K ₁₁ 01-K ₁₁ 13	N/A	N/A	N/A	Syst. Bot. 17: 103 (1992)
Gossypium patens	N/A	It grows primarily in the seasonally dry tropical biome. It is a perennial or subshrub	Mexico Southwest	N/A	N/A	N/A	N/A	N/A	N/A	J. Washington Acad. Sci. 16: 337 (1926)
Gossypium pilosum	N/A	It is a perennial or subshrub and grows primarily in the seasonally dry tropical biome.	Western Australia	N/A	K4	K ₄ 01-K ₄ 13	N/A	N/A	N/A	Austral. J. Bot. 22: 183 (1974)
Gossypium populifolium	Cienfuegosia populifolia, Fugosia populifolia, Hibiscus populifolius, Notoxylinon populifolium	It is a shrub and grows primarily in the seasonally dry tropical biome.	Western Australia	N/A	K3	K ₃ 01-K ₃ 13	N/A	N/A	N/A	Relaz. Cult. Coton.: 107 (1877)
Gossypium pulchellum	Cienfuegosia pulchella, Fugosia pulchella	This herb or shrub has hairy stems and ovate leaves with stellate hairs. Its pink flowers bloom from June to September, featuring a stellate-hairy calyx, glabrous corolla, and numerous stamens united by a staminal tube.	Western Australia	N/A	K ₁₀	K ₁₀ 01-K ₁₀ 13	N/A	N/A	N/A	Austral. J. Bot. 13: 92 (1965)
Gossypium raimondii	Gossypium klotzschianum subsp. raimondii	It has resistance to jassids [41]. Its genome has been sequenced in order to improve the productivity and fiber quality of other <i>Gossypium</i> species.	Peru	N/A	D ₅	D ₅ 01-D ₅ 13	GCA_025698545.1 [14]	KU317325.1	HQ325744.1	Notizbl. Bot. Gart. Berlin- Dahlem 11: 548 (1932)
Gossypium robinsonii	Gossypium sturtii subsp. robinsonii, Hibiscus robinsonii	Gossypium robinsonii is a glabrous herb or shrub with palmately lobed leaves, persistent stipules, and pink, blue, or purple flowers measuring 40-60 mm, featuring stellate hairs on the corolla. It produces dehiscent capsules with 2-4 seede per loculus	Western Australia	N/A	C ₂	C ₂ 01-C ₂ 13	N/A	N/A	N/A	Fragm. 9: 126 (1875)
Gossypium rotundifolium	N/A	seeds per loculus It is a perennial or subshrub and grows primarily in the seasonally dry tropical	Western Australia	N/A	К ₂	K ₂ 01-K ₂ 13	GCA_025506655.1 [44]	N/A	N/A	Syst. Bot. 17: 111 (1992)

Journal of Biological Research 1 (1), 2025: pp. 43-55.

Gossypium schwendimanii	N/A	It grows primarily in the seasonally dry tropical biome. It has Resistance to	Mexico Southwest	N/A	D ₁₁	D ₁₁ 01-D ₁₁ 13	GCA_013677275.1 [44]	N/A	N/A	Aliso 11: 54 (1987)
Gossypium somalense	Cienfuegosia somalensis	reniform nematode, Extra fiber strength, resistance to Egyptian bollworm and pink bollworm, arid tolerance	Chad, Ethiopia, Kenya, Niger, Somalia, Sudan, Uganda	N/A	E2	E ₂ 01-E ₂ 13	N/A	N/A	N/A	Evol. Gossypium 31 (1947)
Gossypium stephensii	N/A	[41]. It is a shrub and grows primarily in the wet tropical biome. It has strong fibers,	Wake I.	N/A	(AD) ₇	A _s 01-A _s 13; D _s 01-D _s 13	GCA_024704795.1 [29]	N/A	N/A	Syst. Bot. 42 119 (2017)
Gossypium stocksii	N/A	It has strong fibers, resistance to leaf curl virus, resistance to reniform nematode. [41]. It is a shrub and grows primarily in the desert or dry shrubland biome.	India, Oman, Pakistan, Somalia, Yemen	N/A	E ₁	E ₁ 01-E ₁ 13	GCA_020496765.1 [46]	N/A	N/A	J.D.Hooker Fl. Brit. India 1: 34 (1874)
Gossypium sturtianum	Cienfuegosia gossypioides, G, australiense, Gossypium gossypioides, G, sturtii, Hibiscus gossypiodes, Sturtia gossypioides	It has glandless-seed and glanded-plant, Resistance to Fusarium wilt [41].	New South Wales, Northern Territory, Queensland, South Australia, Victoria, Western Australia	N/A	C ₁	C ₁ 01-C ₁ 13	GCA_025698515.1 [26]	N/A	N/A	Vict. Naturalist 6 9 (1947)
Gossypium thurberi	Thurberia thespesioides	It has tolerance to mild frost via defoliation, high resistance to Verticillium dahliae test [41].	Arizona, Mexico Northeast, Mexico Northwest, New Mexico	N/A	D ₁	D ₁ 01-D ₁ 13	GCA_004027125.1 [44]	N/A	N/A	Relaz. Cult Coton.: 7 (1877)
Gossypium timorense	Gossypium javanicum	It grows primarily in the seasonally dry tropical biome. It has tolerance to heat,	Lesser Sunda Is.	N/A	N/A	N/A	N/A	N/A	N/A	Bot. Zhurr S.S.S.R. 32 64 (1947)
Gossypium tomentosum	Gossypium hirsutum f. tomentosum, Hibiscus tomentosus	It has tolerance to heat, source of the nectariless trait for resistance against tarnished plant bug, fleahop- pers, boll rot and bollworm, resistance to jassids and thrips, high fiber quality, fiber length and fiber <u>fineness [41]</u> . It is a shrub and grows	Hawaii	N/A	(AD) ₃	A _u 01-A _u 13; D _u 01-D _u 13	GCA_018144435.1 [47]	N/A	N/A	Fl. Vit.: 22 (1865)
Gossypium trifurcatum	N/A	It is a shrub and grows primarily in the desert or dry shrubland biome.	Somalia	N/A	E / B		N/A	N/A	N/A	Kew Bull 42: 342 (1987)
Gossypium trilobum	Hibiscus ingenhousii, Ingenhouzia triloba, Thurberia triloba	Cytoplasmic male sterility and restorer factor. Drought tolerance, resistance to bollworm, pink worm, boll rot, Verticillium and Fusarium wilt [41].	Mexico Central, Mexico Northeast, Mexico Northwest, Mexico Southwest	N/A	D ₈	D ₈ 01-D ₈ 13	GCA_013467465.1 [44]	N/A	N/A	J. Genet. 31 288 (1935)
Gossypium triphyllum	Cienfuegosia triphylla, Fugosia triphylla, Gossypium anomalum subsp. triphyllum	It is a shrub and grows primarily in the desert or dry shrubland biome. Flower color range from blue to purple.	Angola, Botswana, Namibia	N/A	B ₂	B ₂ 01-B ₂ 13	N/A	N/A	N/A	Bull. Herb Boissier, sé 2, 2: 1004 (1902)
Gossypium turneri	N/A	It has caduceus involucels [41]. It grows primarily in the desert or dry shrubland biome. It is a shrub and grows	Mexico Northwest	N/A	D ₁₀	D ₁₀ 01-D ₁₀ 13	GCA_008044935.1 [16]	N/A	N/A	Madroño 2 155 (1978
Gossypium vollesenii	N/A	It is a shrub and grows primarily in the desert or dry shrubland biome.	Somalia	N/A	Е	N/A	N/A	N/A	N/A	Rheedea 2 154 (1992)

*The table is organized alphabetically by species names

DISCUSSION

Whole genome sequencing has been conducted for 29 species of the genus *Gossypium*, providing critical insights into their evolutionary relationships, genetic diversity, and potential for breeding improvement. However, the mitochondrial and chloroplast genomes have only been sequenced for a limited number of species, indicating a significiant gap in the holistic genomic understanding of this genus. Despite this progress, whole genome sequencing has been performed for only 29 out of the 55 recognized *Gossypium* species, underscoring the complexity and challenges of achieving comprehensive genomic coverage across of this diverse genus. Further efforts are needed to expand genomic resources, particularly for less studied species, to improve our understanding of their evolutionary and ecological significance.

The United States, China, and Australia have been at the

forefront of whole-genome sequencing (WGS) efforts in Gossypium species. These countries have advanced research facilities and substantial funding for agricultural genomics, enabling them to undertake comprehensive sequencing projects. For instance, the U.S. Department of Agriculture's Agricultural Research Service has been actively involved in cotton genomics research. Similarly, China's Nanjing Agricultural University and the Chinese Academy of Sciences have made significant contributions to cotton genome sequencing. Australia's Commonwealth Scientific and Industrial Research Organisation (CSIRO) has also played a key role in sequencing efforts, with a particular focus on wild cotton species native to Australia. [35] These nations prioritize the sequencing of species with notable agronomic importance or unique genetic traits that can enhance breeding programs. For example, sequencing of G. australe, a wild Australian species, has provided insights into disease resistance and gland morphogenesis, traits valuable for cotton improvement.

The limited number of sequenced *Gossypium* species can be attributed to several factors. First, despite advances in sequencing technologies, whole genome sequencing (WGS) remains financially demanding, especially for large-scale projects. While the cost of sequencing a human genome has decreased to approximately \$600, this figure primarily reflects human genomics and may not be directly aplicable to plant genomes, which often present unique challenges. [36]

Plant genomes, including those of *Gossypium* species, often exhibit large sizes, high levels of repetitive sequences, and polyploidy, complicating sequencing and assembly processes. These complexity requires advanced technologies and substantial computational resources, which further increases costs. [37] Consequently, research efforts have prioritized economically significant species to maximize the return on investment. This strategic focus ensures that resources are allocated to species with the greatest potential impact on agriculture and industry. [38] In summary, the combination of financial costs, technological demands, and strategic prioritization of economically important species contributes to the limited number of *Gossypium* species that have undergone whole genome sequencing [39].

Table 1 provides valuable information regarding the first formal descriptions and publications of various *Gossypium* species. Historical records indicate that basic species such as *G. arboreum*, *G. barbadense*, and *G. herbaceum*. were first described in *Species Plantarum*: 693 (Linnaeus, 1753), marking an important milestone in botanical taxonomy. Subsequently, *G. hirsutum*, the most widely cultivated cotton species today, was described in the second edition of *Species Plantarum*: 975 (Linnaeus, 1763).

The most recent discovery in the genus is *G. stephensii*, described in *Systematic Botany* 42: 119 (2017). This discovery underscores the continued botanical exploration and genetic characterization of cotton species, which is essential for understanding their evolutionary relationships and potential for crop improvement.

Sequencing of cotton varieties and lines from developing countries remains underexplored at the molecular level. Advancing research in this area holds great potential, as local cultivars may contain loci responsible for valuable traits. Uncovering these genetic resources could make significant contribution to the global advancement of cotton production.

AUTHOR CONTRIBUTIONS

OA: Data curation, formal analysis, software, and writingoriginal draft. MSA: writing-review and editing, conceptualization, supervision. MSP: data resources, data curation, formal analysis, visualization. RMB: data curation, Software. KB: Data curation, software. AR: data curation, software. TD: Data curation, writing, review and editing, conceptualization, formal analysis, investigation, supervision.

FUNDING

This study was funded by the grant, titled « Creation of drought tolerance classification for Kazakhstan cotton-collection and identification of SNP markers associated with drought tolerance traits» (AP23489921).

ACKNOWLEDGMENTS

We thank the Ministry of Science and Higher Education of the Republic of Kazakhstan for providing financial support.

COMPETING INTERESTS

The authors declare that the research was conducted in the absence of any commercial or financial relationship that could be construed as a potential conflict of interest.

OPEN ACCESS

This article is licensed under a Creative Commons Attribution-NonCommercial 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. To view a copy of this licence, visit https://creativecommons.org/licenses/by-nc/4.0/.

LITERATURE

1. Ruan Y. L., Llewellyn D. J., Furbank R. T. Suppression of sucrose synthase gene expression represses cotton fiber cell initiation, elongation, and seed development // The Plant Cell. – 2003. – Vol. 15(4) – P. 952-964. <u>https://doi.org/%20</u>10.1105/tpc.010108

2. Chen Y., Dong H. Mechanisms and regulation of senescence and maturity performance in cotton // Field Crops Research. – 2016. – Vol. 189. – P. 1-9. <u>https://doi.org/10.1016/j.</u> <u>fcr.2016.02.003</u>

3. Ahmad S., Iqbal M., Muhammad T., Mehmood A., Ahmad S., Hasanuzzaman M. Cotton productivity enhanced through transplanting and early sowing // Acta Scientiarum. Biological Sciences. – 2018. – Vol. 40. – P. 1-7. <u>https://doi. org/10.4025/actascibiolsci.v40i1.34610</u>

4. Wendel J. F., Grover C. E. Taxonomy and evolution of the cotton genus, Gossypium // Cotton. – 2015. – Vol. 57. – P. 25-44. https://doi.org/10.2134/agronmonogr57.2013.0020

5. Ma Z., Zhang Y., Wu L., Zhang G., Sun Z., Li Z., Jiang Y., Ke H., Chen B., Liu Z., Gu Q., Wang Z., Wang G., Yang J., Wu J., Yan Y., Meng C., Li L., Li X., Mo S., ... Wang X. High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement // Nature Genetics. – 2021. – Vol. 53(9). – P. 1385-1391. <u>https://doi.org/10.5281/zenodo.4851529</u>.

6. Wu K. M., Guo Y. Y. The evolution of cotton pest management practices in China // Annu. Rev. Entomol. – 2005. – Vol. 50(1). – P. 31-52. <u>https://doi.org/10.1146/annurev.</u> ento.50.071803.130.349

7. Amin A., Nasim W., Mubeen M., Ahmad A., Nadeem M., Urich P., Fahad Sh., Ahmad Sh., Wajid A., Tabassum F., Hammad H.M., Sultana S.R., Anwar S., Baloch Sh.Kh., Wahid A., Wilkerson C.J., Hoogenboom G. Simulated CSM-CROPGRO-cotton yield under projected future climate by SimCLIM for southern Punjab, Pakistan // Agricultural Systems. – 2018. – Vol. 167. – P. 213-222. <u>https://doi. org/10.1016/j.agsy.2017.05.010</u>

8. Kushanov F. N. et al. Genetic analysis of mutagenesis that induces the photoperiod insensitivity of wild cotton Gossypium hirsutum subsp. purpurascens // Plants. – 2022. – Vol. 11(22) – P. 3012. <u>https://doi.org/10.3390/plants11223012</u>

9. Grover C. E. et al. Re-evaluating the phylogeny of allopolyploid Gossypium L // Molecular Phylogenetics and Evolution. – 2015. – Vol. 92. – P. 45-52. <u>https://doi.org/10.1016/j.</u> <u>ympev.2015.05.023</u>

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

11. Chen X. et al. Targeted mutagenesis in cotton (Gossypium hirsutum L.) using the CRISPR/Cas9 system //Scientific reports. – 2017. – Vol. 7(1). – P. 44304. <u>https://doi.org/10.1038/srep44304</u>

12. Hawkins J. S. et al. Differential lineage-specific amplification of transposable elements is responsible for genome size variation in Gossypium //Genome research. – 2006. – Vol. 16(10). – P. 1252-1261. <u>http://www.genome.org/cgi/doi/10.1101/gr.5282906</u>.

13. Grover C. E. et al. Genetic analysis of the transition from wild to domesticated cotton (Gossypium hirsutum L.) //G3: Genes, Genomes, Genetics. – 2020. – Vol. 10(2). – P. 731-754. <u>https://doi.org/10.1534/g3.119.400909</u>

14. Wang M. et al. Genomic innovation and regulatory rewiring during evolution of the cotton genus Gossypium //Nature Genetics. – 2022. – Vol. 54(12). – P. 1959-1971. <u>https://</u> doi.org/10.1038/s41588-022-01237-2

15. Grover C. E. et al. Insights into the evolution of the New World diploid cottons (Gossypium, subgenus Houzingenia) based on genome sequencing //Genome Biology and Evolution. – 2019. – Vol. 11(1). – P. 53-71. <u>https://doi.org/10.1093/gbe/evy256</u>

16. Udall J. A. et al. De novo genome sequence assemblies of Gossypium raimondii and Gossypium turneri //G3: Genes, Genomes, Genetics. – 2019. – Vol. 9(10). – P. 3079-3085. <u>https://doi.org/10.1534/g3.119.400392</u>

17. Stewart J. M. D. Gossypium anapoides (Malvaceae), a new species from western Australia //Novon: A Journal for Botanical Nomenclature. – 2015. – Vol. 23(4). – P. 447-451. https://doi.org/10.3417/2007140

18. Gallagher J. P. et al. A new species of cotton from Wake Atoll, Gossypium stephensii (Malvaceae) //Systematic Botany. – 2017. – Vol. 42(1) – P. 115-123. <u>https://doi.org/10.1600/036364417X694593</u>

19. Grover C. E. et al. A high-resolution model of gene expression during Gossypium hirsutum (cotton) fiber development //bioRxiv. – 2024. – P. 2024.07. 20.604417. <u>https://doi.org/10.1101/2024.07.20.604417</u>

20. Flagel L. E., Wendel J. F., Udall J. A. Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton //BMC genomics. – 2012. – Vol. 13. – P. 1-13. <u>https://doi.org/10.1186/1471-2164-13-302</u>

21. Min W. et al. Root distribution and growth of cotton as affected by drip irrigation with saline water //Field Crops Research. – 2014. – Vol. 169. – P. 1-10. <u>https://doi.org/10.1016/j.fcr.2014.09.002</u>

22. Li F. et al. Genome sequence of cultivated Upland cot-

ton (Gossypium hirsutum TM-1) provides insights into genome evolution //Nature biotechnology. – 2015. – Vol. 33(5). – P. 524-530. <u>https://doi.org/10.1038/nbt.3208</u>

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

24. Ning W. et al. Origin and diversity of the wild cottons (Gossypium hirsutum) of Mound Key, Florida //Scientific Reports. – 2024. – Vol. 14(1). – P. 14046. <u>https://doi.org/10.1038/s41598-024-64887-8</u>

25. Wang M. et al. Reference genome sequences of two cultivated allotetraploid cottons, Gossypium hirsutum and Gossypium barbadense //Nature genetics. – 2019. – Vol. 51(2). – P. 224-229. <u>https://doi.org/10.1038/s41588-018-0282-x</u>

26. Chen Z. J. et al. Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement //Nature genetics. – 2020. – Vol. 52(5). – P. 525-533. https://doi.org/10.1038/s41588-020-0614-5

27. De Lima L. F. et al. Ethnobotanical and antimicrobial activities of the Gossypium (Cotton) genus: A review //Journal of Ethnopharmacology. – 2021. – Vol. 279. – P. 114363. https://doi.org/10.1016/j.jep.2021.114363

28. Gallagher, J., Grover, C., Rex, K., Moran, M., Wendel, J. A new species of cotton from Wake Atoll, Gossypium stephensii (Malvaceae) // Systematic Botany. – 2017. – Vol. 42. – P. 115–123. <u>https://doi.org/10.1600/036364417X694593</u>

29. 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.E., Hou, Y., Wang, Y., Li, P., Wang, T., Lu, Q., Wang, Y., Conover, J.L., Ghazal, H., Wang, Q., Zhang, B., Van Montagu, M., Van de Peer, Y., Wendel, J.F., Liu, F. Evolutionary divergence of duplicated genomes in newly described allotetraploid cottons // Proceedings of the National Academy of Sciences of the United States of America. – 2022. – Vol. 119(39). – e2208496119. <u>https://doi.org/10.1186/s12870-024-05262-7</u>

30. https://powo.science.kew.org/

31. Hu G. et al. Evolution and diversity of the cotton genome //Cotton precision breeding. – Cham : Springer International Publishing, 2021. – P. 25-78. <u>https://doi.org/10.1007/978-3-030-64504-5_18</u>

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

33. Maryum Z. et al. An overview of salinity stress, mechanism of salinity tolerance and strategies for its management in cotton //Frontiers in Plant Science. – 2022. – Vol. 13. – P. 907937. https://doi.org/10.3389/fpls.2022.907937

34. Aslam S. et al. The tale of cotton plant: From wild type to domestication, leading to its improvement by genetic transformation //American Journal of Molecular Biology. – 2020. – Vol. 10(2). – P. 91-127. <u>https://doi.org/10.4236/ajmb.2020.102008</u>

35. Chen Z. J. et al. Toward sequencing cotton (Gossypium) genomes //Plant physiology. -2007. - Vol. 145(4). -.

1303-1310. https://doi.org/10.1104/pp.107.107672

36. https://www.genome.gov/about-genomics/fact-sheets/ Sequencing-Human-Genome-cost

37. Schatz M. C., Witkowski J., McCombie W. R. Current challenges in de novo plant genome sequencing and assembly //Genome biology. – 2012. – Vol. 13. – P. 1-7. <u>https://doi.org/10.1186/gb-2012-13-4-243</u>

38. Claros M. G. et al. Why assembling plant genome sequences is so challenging //Biology. – 2012. – Vol. 1(2). – P. 439-459. <u>https://doi.org/10.3390/biology1020439</u>

39. Wu Y. et al. Comparative chloroplast genomics of Gossypium species: insights into repeat sequence variations and phylogeny //Frontiers in Plant Science. – 2018. – Vol. 9. – P. 376. <u>https://doi.org/10.3389/fpls.2018.00376</u>

40. Stewart J, Craven L, Brubaker C, Wendel J. Gossypium anapoides (Malvaceae), a new species from Western Australia. Novon: a journal for botanical nomenclature. 2015. 23(4):447-451 <u>https://doi.org/10.3417/2007140</u>

41. Shim J., Mangat P. K., Angeles-Shim R. B. Natural variation in wild Gossypium species as a tool to broaden the genetic base of cultivated cotton //J. Plant Sci. Curr. Res. – 2018. – Vol. 2. – №. 005. <u>https://doi.org/10.24966/PSCR-3743/100005</u>

42. Govaerts R. et al. The World Checklist of Vascular Plants, a continuously updated resource for exploring global plant diversity //Scientific data. – 2021. – Vol. 8(1). – P. 215. https://doi.org/10.1038/s41597-021-00997-6

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

44. Grover C. E. et al. The Gossypium anomalum genome as a resource for cotton improvement and evolutionary analysis of hybrid incompatibility //G3. – 2021. – Vol. 11(11). – P. 319. <u>https://doi.org/10.1093/g3journal/jkab319</u>

45. Chen Z. et al. Entire nucleotide sequences of Gossypium raimondii and G. arboreum mitochondrial genomes revealed A-genome species as cytoplasmic donor of the allotetraploid species //Plant Biology. – 2017. – Vol. 19(3). – P. 484-493. <u>https://doi.org/10.1111/plb.12536</u>

46. Yu D. et al. Multi-omics assisted identification of the key and species-specific regulatory components of drought-tolerant mechanisms in Gossypium stocksii //Plant Biotechnology Journal. – 2021. – Vol. 19(9). – P. 1690. <u>https://doi.org/10.1111/pbi.13655</u>

47. Shen C. et al. Gossypium tomentosum genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton //Genomics. – 2021. – Vol. 113.(4). – P. 1999-2009. https://doi.org/10.1016/j.ygeno.2021.04.036

48. Makhmadjanov S. P. et al. Cotton advanced lines assessment in the southern region of Kazakhstan. -2023 http://doi.org/10.54910/sabrao2023.55.2.1.

49. Rakhimov A. A. Development of the basics of mutational selection of cotton for quantitative traits: dissertation. – Tashkent, 2018. – 185 p.

50. Saidov R. K. Improvement of industrial cotton variet-

ies (*Gossypium hirsutum L*.) under the influence of ionizing radiation: dissertation. – Tashkent, 2020. – 210 p.

51. Mamatov K. S., Karimov T. I. New mutant cotton varieties // CyberLeninka Electronic Scientific Library. – 2021. – No. 4. – P. 45–52.

52. Rasulov U. B., Yuldashev K. M. Genetics, selection, and seed production of cotton. – Tashkent: UzAgroPress, 2019. - 312 p.

53. Kasimov A. T., Tursunov N. O. The gene pool of world cotton diversity – the basis of fundamental and applied research // ResearchGate. -2018. - Vol. 6. - P. 12-20.

REFERENCES

1. Ruan Y. L., Llewellyn D. J., Furbank R. T. Suppression of sucrose synthase gene expression represses cotton fiber cell initiation, elongation, and seed development // The Plant Cell. – 2003. – Vol. 15(4) – P. 952-964. <u>https://doi.org/%20</u>10.1105/tpc.010108

2. Chen Y., Dong H. Mechanisms and regulation of senescence and maturity performance in cotton // Field Crops Research. – 2016. – Vol. 189. – P. 1-9. <u>https://doi.org/10.1016/j.</u> <u>fcr.2016.02.003</u>

3. Ahmad S., Iqbal M., Muhammad T., Mehmood A., Ahmad S., Hasanuzzaman M. Cotton productivity enhanced through transplanting and early sowing // Acta Scientiarum. Biological Sciences. – 2018. – Vol. 40. – P. 1-7. <u>https://doi.org/10.4025/actascibiolsci.v40i1.34610</u>

4. Wendel J. F., Grover C. E. Taxonomy and evolution of the cotton genus, Gossypium // Cotton. – 2015. – Vol. 57. – P. 25-44. <u>https://doi.org/10.2134/agronmonogr57.2013.0020</u>

5. Ma Z., Zhang Y., Wu L., Zhang G., Sun Z., Li Z., Jiang Y., Ke H., Chen B., Liu Z., Gu Q., Wang Z., Wang G., Yang J., Wu J., Yan Y., Meng C., Li L., Li X., Mo S., ... Wang X. High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement // Nature Genetics. – 2021. – Vol. 53(9). – P. 1385-1391. <u>https://doi.org/10.5281/zenodo.4851529</u>.

6. Wu K. M., Guo Y. Y. The evolution of cotton pest management practices in China // Annu. Rev. Entomol. – 2005. – Vol. 50(1). – P. 31-52. <u>https://doi.org/10.1146/annurev.</u> ento.50.071803.130.349

7. Amin A., Nasim W., Mubeen M., Ahmad A., Nadeem M., Urich P., Fahad Sh., Ahmad Sh., Wajid A., Tabassum F., Hammad H.M., Sultana S.R., Anwar S., Baloch Sh.Kh., Wahid A., Wilkerson C.J., Hoogenboom G. Simulated CSM-CROPGRO-cotton yield under projected future climate by SimCLIM for southern Punjab, Pakistan // Agricultural Systems. – 2018. – Vol. 167. – P. 213-222. <u>https://doi. org/10.1016/j.agsy.2017.05.010</u>

8. Kushanov F. N. et al. Genetic analysis of mutagenesis that induces the photoperiod insensitivity of wild cotton Gossypium hirsutum subsp. purpurascens //Plants. – 2022. – Vol. 11(22) – P. 3012. <u>https://doi.org/10.3390/plants11223012</u>

9. Grover C. E. et al. Re-evaluating the phylogeny of allopolyploid Gossypium L //Molecular Phylogenetics and Evolution. – 2015. – Vol. 92. – P. 45-52. <u>https://doi.org/10.1016/j.</u> <u>ympev.2015.05.023</u>

10. Wang K., Wendel J. F., Hua J. Designations for indi-

vidual genomes and chromosomes in Gossypium //Journal of Cotton Research. – 2018. – Vol. 1(1) – P. 1-5. <u>https://doi.org/10.1186/s42397-018-0002-1</u>

11. Chen X. et al. Targeted mutagenesis in cotton (Gossypium hirsutum L.) using the CRISPR/Cas9 system //Scientific reports. – 2017. – Vol. 7(1). – P. 44304. <u>https://doi.org/10.1038/srep44304</u>

12. Hawkins J. S. et al. Differential lineage-specific amplification of transposable elements is responsible for genome size variation in Gossypium //Genome research. – 2006. – Vol. 16(10). – P. 1252-1261. <u>http://www.genome.org/cgi/doi/10.1101/gr.5282906</u>.

13. Grover C. E. et al. Genetic analysis of the transition from wild to domesticated cotton (Gossypium hirsutum L.) //G3: Genes, Genomes, Genetics. – 2020. – Vol. 10(2). – P. 731-754. <u>https://doi.org/10.1534/g3.119.400909</u>

14. Wang M. et al. Genomic innovation and regulatory rewiring during evolution of the cotton genus Gossypium //Nature Genetics. – 2022. – Vol. 54(12). – P. 1959-1971. <u>https://</u> doi.org/10.1038/s41588-022-01237-2

15. Grover C. E. et al. Insights into the evolution of the New World diploid cottons (Gossypium, subgenus Houzingenia) based on genome sequencing //Genome Biology and Evolution. – 2019. – Vol. 11(1). – P. 53-71. <u>https://doi.org/10.1093/gbe/evy256</u>

16. Udall J. A. et al. De novo genome sequence assemblies of Gossypium raimondii and Gossypium turneri //G3: Genes, Genomes, Genetics. – 2019. – Vol. 9(10). – P. 3079-3085. <u>https://doi.org/10.1534/g3.119.400392</u>

17. Stewart J. M. D. Gossypium anapoides (Malvaceae), a new species from western Australia //Novon: A Journal for Botanical Nomenclature. – 2015. – Vol. 23(4). – P. 447-451. https://doi.org/10.3417/2007140

18. Gallagher J. P. et al. A new species of cotton from Wake Atoll, Gossypium stephensii (Malvaceae) //Systematic Botany. – 2017. – Vol. 42(1) – P. 115-123. <u>https://doi.org/10.1600/036364417X694593</u>

19. Grover C. E. et al. A high-resolution model of gene expression during Gossypium hirsutum (cotton) fiber development //bioRxiv. – 2024. – P. 2024.07. 20.604417. <u>https://doi.org/10.1101/2024.07.20.604417</u>

20. Flagel L. E., Wendel J. F., Udall J. A. Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton //BMC genomics. – 2012. – Vol. 13. – P. 1-13. <u>https://doi.org/10.1186/1471-2164-13-302</u>

21. Min W. et al. Root distribution and growth of cotton as affected by drip irrigation with saline water //Field Crops Research. – 2014. – Vol. 169. – P. 1-10. <u>https://doi.org/10.1016/j.fcr.2014.09.002</u>

22. Li F. et al. Genome sequence of cultivated Upland cotton (Gossypium hirsutum TM-1) provides insights into genome evolution //Nature biotechnology. – 2015. – Vol. 33(5). – P. 524-530. https://doi.org/10.1038/nbt.3208

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

24. Ning W. et al. Origin and diversity of the wild cottons (Gossypium hirsutum) of Mound Key, Florida //Scientific Reports. – 2024. – Vol. 14(1). – P. 14046. <u>https://doi.org/10.1038/s41598-024-64887-8</u>

25. Wang M. et al. Reference genome sequences of two cultivated allotetraploid cottons, Gossypium hirsutum and Gossypium barbadense //Nature genetics. – 2019. – Vol. 51(2). – P. 224-229. <u>https://doi.org/10.1038/s41588-018-0282-x</u>

26. Chen Z. J. et al. Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement //Nature genetics. – 2020. – Vol. 52(5). – P. 525-533. <u>https://doi.org/10.1038/s41588-020-0614-5</u>

27. De Lima L. F. et al. Ethnobotanical and antimicrobial activities of the Gossypium (Cotton) genus: A review //Journal of Ethnopharmacology. – 2021. – Vol. 279. – P. 114363. https://doi.org/10.1016/j.jep.2021.114363

28. Gallagher, J., Grover, C., Rex, K., Moran, M., Wendel, J. A new species of cotton from Wake Atoll, Gossypium stephensii (Malvaceae) // Systematic Botany. – 2017. – Vol. 42. – P. 115–123. <u>https://doi.org/10.1600/036364417X694593</u>

29. 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.E., Hou, Y., Wang, Y., Li, P., Wang, T., Lu, Q., Wang, Y., Conover, J.L., Ghazal, H., Wang, Q., Zhang, B., Van Montagu, M., Van de Peer, Y., Wendel, J.F., Liu, F. Evolutionary divergence of duplicated genomes in newly described allotetraploid cottons // Proceedings of the National Academy of Sciences of the United States of America. – 2022. – Vol. 119(39). – e2208496119. <u>https://doi.org/10.1186/s12870-024-05262-7</u>

30. https://powo.science.kew.org/

31. Hu G. et al. Evolution and diversity of the cotton genome //Cotton precision breeding. – Cham : Springer International Publishing, 2021. – P. 25-78. <u>https://doi.org/10.1007/978-3-030-64504-5_18</u>

32. Viot C. R., Wendel J. F. Evolution of the cotton genus, Gossypium, and its domestication in the Americas //Critical Reviews in Plant Sciences. – 2023. – Vol. 2(1). – P. 1-33. https://doi.org/10.1080/07352689.2022.2156061

33. Maryum Z. et al. An overview of salinity stress, mechanism of salinity tolerance and strategies for its management in cotton //Frontiers in Plant Science. – 2022. – Vol. 13. – P. 907937. <u>https://doi.org/10.3389/fpls.2022.907937</u>

34. Aslam S. et al. The tale of cotton plant: From wild type to domestication, leading to its improvement by genetic transformation //American Journal of Molecular Biology. – 2020. – Vol. 10(2). – P. 91-127. <u>https://doi.org/10.4236/ajmb.2020.102008</u>

35. Chen Z. J. et al. Toward sequencing cotton (Gossypium) genomes //Plant physiology. – 2007. – Vol. 145(4). – . 1303-1310. <u>https://doi.org/10.1104/pp.107.107672</u>

36. https://www.genome.gov/about-genomics/fact-sheets/ Sequencing-Human-Genome-cost

37. Schatz M. C., Witkowski J., McCombie W. R. Current challenges in de novo plant genome sequencing and assembly //Genome biology. – 2012. – Vol. 13. – P. 1-7. <u>https://doi.org/10.1186/gb-2012-13-4-243</u>

38. Claros M. G. et al. Why assembling plant genome sequences is so challenging //Biology. – 2012. – Vol. 1(2). – P. 439-459. <u>https://doi.org/10.3390/biology1020439</u>

39. Wu Y. et al. Comparative chloroplast genomics of Gossypium species: insights into repeat sequence variations and phylogeny //Frontiers in Plant Science. – 2018. – Vol. 9. – P. 376. https://doi.org/10.3389/fpls.2018.00376

40. Stewart J, Craven L, Brubaker C, Wendel J. Gossypium anapoides (Malvaceae), a new species from Western Australia. Novon: a journal for botanical nomenclature. 2015. 23(4):447-451 <u>https://doi.org/10.3417/2007140</u>

41. Shim J., Mangat P. K., Angeles-Shim R. B. Natural variation in wild Gossypium species as a tool to broaden the genetic base of cultivated cotton //J. Plant Sci. Curr. Res. – 2018. – Vol. 2. – №. 005. <u>https://doi.org/10.24966/PSCR-3743/100005</u>

42. Govaerts R. et al. The World Checklist of Vascular Plants, a continuously updated resource for exploring global plant diversity //Scientific data. – 2021. – Vol. 8(1). – P. 215. https://doi.org/10.1038/s41597-021-00997-6

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

44. Grover C. E. et al. The Gossypium anomalum genome as a resource for cotton improvement and evolutionary analysis of hybrid incompatibility //G3. – 2021. – Vol. 11(11). – P. 319. <u>https://doi.org/10.1093/g3journal/jkab319</u>

45. Chen Z. et al. Entire nucleotide sequences of Gossypium raimondii and G. arboreum mitochondrial genomes revealed A-genome species as cytoplasmic donor of the allotetraploid species //Plant Biology. – 2017. – Vol. 19(3). – P. 484-493. <u>https://doi.org/10.1111/plb.12536</u>

46. Yu D. et al. Multi-omics assisted identification of the key and species-specific regulatory components of drought-tolerant mechanisms in Gossypium stocksii //Plant Biotechnology Journal. – 2021. – Vol. 19(9). – P. 1690. <u>https://doi.org/10.1111/pbi.13655</u>

47. Shen C. et al. Gossypium tomentosum genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton //Genomics. – 2021. – Vol. 113.(4). – P. 1999-2009. https://doi.org/10.1016/j.ygeno.2021.04.036

48. Makhmadjanov S. P. et al. Cotton advanced lines assessment in the southern region of Kazakhstan. – 2023 http://doi.org/10.54910/sabrao2023.55.2.1.

49. Rakhimov A. A. Development of the basics of mutational selection of cotton for quantitative traits: dissertation. – Tashkent, 2018. – 185 p.

50. Saidov R. K. Improvement of industrial cotton varieties (*Gossypium hirsutum L.*) under the influence of ionizing radiation: dissertation. – Tashkent, 2020. – 210 p.

51. Mamatov K. S., Karimov T. I. New mutant cotton varieties // CyberLeninka Electronic Scientific Library. – 2021. – No. 4. – P. 45–52.

52. Rasulov U. B., Yuldashev K. M. Genetics, selection, and seed production of cotton. – Tashkent: UzAgroPress, 2019. - 312 p.

53. Kasimov A. T., Tursunov N. O. The gene pool of world cotton diversity – the basis of fundamental and applied research // ResearchGate. -2018. - Vol. 6. - P. 12-20.

МАҚТАНЫҢ (*GOSSYPIUM* L.) ЖАҺАНДЫҚ ТАРАЛУЫ ЖӘНЕ ӘРТҮРЛІ ГЕОГРАФИЯЛЫҚ АЙМАҚТАРҒА БЕЙІМДЕЛУІ

Өркен Айсулу^{1,3}, Манабаева Шуга^{1,3}, Махмаджанов Сабир², Рамазанова Малика¹, Қали Балнұр¹, Рахимжанова Айжан², Түсіпқан Ділнұр^{1*}

¹Ұлттық биотехнология орталығы, Қорғалжын тас жолы 13/5, Астана, 010000, Қазақстан ²Мақта және бақша ауыл шаруашылығы тәжірбие станциясы, Атакент, 160525 Қазақстан ³Л.Н.Гумилев атындағы Еуразия Ұлттық Университеті, Сатпаев к-сі. 2, Астана, 010000, Қазақстан

* Корреспондент-автор: Түсіпқан Ділнұр tdilnur@mail.ru

АҢДАТПА

Мақта (Gossypium L.) - әлемдегі ең маңызды экономикалық дақылдардың бірі, оны өсіру әр түрлі географиялық аймақтарды қамтиды. Gossypium тұқымдасының 50-ден астам түрі бар, олардың төртеуі талшықтың жоғары сапасы үшін кеңінен өсіріледі. Бұл шолуда, біріншіден, біз диплоидты және аллотетраплоидты түрлердің геномдық ерекшеліктерін қоса алғанда, Gossypium филогенезінің қысқаша мазмұнын ұсындық. Екіншіден, біз Gossypium барлық түрлерінің шығу тегін және G. arboreum, G. herbaceum, G. barbadense, G. hirsutum, және G. harknessii түрлерінің адамның делдалдығымен жаңа аумақтарға таралуын қамтыдық. Бұл шолу мақтаның генетикалық әртүрлілігі мен бейімделу механизмдері бойынша зерттеулерді жалғастыру қажеттілігін көрсетеді, бұл оның бүкіл әлем бойынша тұрақты өндірісін арттырады.

Кілт сөздер: Мақта (Gossypium L.), филогенетика, эволюциялық шығу тегі, географиялық таралуы.

ГЛОБАЛЬНОЕ РАСПРОСТРАНЕНИЕ И АДАПТАЦИЯ К РАЗЛИЧНЫМ ГЕОГРАФИЧЕСКИМ РЕГИОНАМ ХЛОПКА (GOSSYPIUM L.)

Өркен Айсулу^{1,3}, Манабаева Шуга^{1,3}, Махмаджанов Сабир², Рамазанова Малика¹, Қали Балнұр¹, Рахимжанова Айжан², Түсіпқан Ділнұр^{1*}

¹Национальный центр биотехнологии, Коргалжынское шоссе 13/5, Астана, 010000, Казахстан ²Сельскохозяйственная опытная станция хлопководства и бахчеводства, Атакент, 160525 Казахстан 3Евразийский национальный университет им. Л.Н.Гумилева, ул. Сатпаева. 2. Астана, 010000, Казахстан

* Автор-корреспондент: Түсіпқан Ділнұр tdilnur@mail.ru

АННОТАЦИЯ

Хлопчатник (Gossypium L.) - одна из наиболее экономически значимых культур в мире, выращиваемая в различных географических регионах. Род Gossypium включает более 50 видов, четыре из которых широко культивируются из-за их превосходного качества волокна. В этом обзоре, во-первых, мы представили краткое изложение филогенеза Gossypium, включая особенности геномов диплоидных и аллотетраплоидных видов. Во-вторых, мы представили происхождение всех видов Gossypium и описали интродукцию G. arboreum, G. herbaceum, G. barbadense, G. hirsutum, и Gossypium harknessii на новых территориях. В этом обзоре подчеркивается необходимость продолжения исследований генетического разнообразия и адаптивных механизмов хлопчатника для повышения устойчивости его производства во всем мире.

Ключевые слова: *Хлопчатник (Gossypium L.), филогенетика, эволюционное происхождение, географическое рас*пространение.