

SABRAO Journal of Breeding and Genetics
 57 (1) 126-136, 2025
<http://doi.org/10.54910/sabrao2025.57.1.13>
<http://sabraojournal.org/>
 pISSN 1029-7073; eISSN 2224-8978



THE HISTORY OF THE DEVELOPMENT OF OLD-WORLD COTTON SPECIES

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SUMMARY

Several laws have reached creation for studying the world cotton diversity, with an enormous theoretical and practical importance. For practical selection, the characteristics of special value are the bush shape, its durability and non-recumbency, types of branching, and the branches' structure: the size, shape, and opening rates of the ripe bolls, quick entry into the crop, and quick ripening. Therefore, it is necessary to study its relationship with the day length and light period, to irrigation, soil fertility, characteristics of the saline soil, and the existence of other similar signs. From such diversity, it showed cotton is an extremely flexible crop with great opportunities for selection, including the selection of base material. Specifically, the diploid species, such as, *Gossypium herbaceum* and *Gossypium arboreum*, has a great significance to selection. These old world cotton species are the results of centuries of evolution. Concepts about the origin, botanical composition, relations, evolution, and geographical distribution of cultivated and wild cotton species have been inaccurate until now. Therefore, it is obligatory to revise and update, correct, and supplement the existing information.

Keywords: Old world cotton, *G. herbaceum*, *G. arboreum*, diploid cotton, cultivars, collection, wild and cultivated, landraces

Key findings: The present review focuses on the advisory information on the history, development, and genetic potential of the old world cotton species. The findings were contributions by the different scientists from the cotton-growing countries, including China, India, USA, Pakistan, Brazil, and Uzbekistan. The presented compilation of the worldwide past findings will serve as a base source and an opportunity for improving the future research on cotton.

Communicating Editor: Prof. Naqib Ullah Khan

Manuscript received: May 17, 2024; Accepted: August 30, 2024.

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Citation: Muminov KH, Amanov B, Buronov A, Tursunova N, Valiyev L, Omonov O, Kodirova S, Pirnazarov E, Iskandarov A (2025). The history of the development of old-world cotton species. *SABRAO J. Breed. Genet.* 57(1): 126-136. <http://doi.org/10.54910/sabrao2025.57.1.13>.

INTRODUCTION

The Malvales order contains the Malvaceae family, consisting of several genera, including the genus *Gossypium*. This genus includes more than 45 diploid and only five allotetraploid species used reached inclusion (Abdurakhmonov *et al.*, 2012). Crop plants' cultivation help meet the current requirements of the national economy. These plants served as food, fiber, fruits and vegetables, fodder, and raw material for various medicinal and aromatic products industries (Buronov *et al.*, 2023; Omonov *et al.*, 2023). In fulfilling community demands, scientists worked on the nature of plants by using different selection and agrotechnics to further enhance the productivity and improve the quality of crop plants. Plant growth conditions are the soil-climate conditions managed by humans to cultivate the soil in various ways, applying fertilizers, and improving planting technology through technological measures for higher yield.

With these unfavorable conditions, the crop plant yield and quality lower, eventually leading to death. The history of cultivated plants is developing in an integral connection with the history of mankind. The history also explored the connectivity of the origin and development of cultivated plants with human culture. The variations in the farming system, cultivation technology, and the plant growth conditions caused the beginning of new signs and varied characteristics in crop plants (Baboev *et al.*, 2017, 2021).

Gossypium arboreum L. and *G. herbaceum* L. are two diploid ($2n = 26$) cultivated cotton species popularly known as old world, Asiatic, and Desi cotton in India and Pakistan. The diploid cultivated cotton belongs to the A-genome (Fryxell, 1979). *Gossypium herbaceum* has contributed the cytoplasm and nuclear A-genome to tetraploid ($2n = 52$) cotton (Wendel *et al.*, 1989). Morphologically, the diploid and tetraploid cultivated cotton species differed in plant habit, leaf shape, flower, boll, seed, and fiber parameters. Although, the diploid cultivated cotton species have overlapping morphological characters, distinguishable, to some extent, based on plant

habit, leaves, bracteole, and boll features (Hutchinson *et al.*, 1947; Fryxell, 1992).

The cotton diploid species are annual sub-shrubs in habit with *G. arboreum*, which are taller and lankier than *G. herbaceum*. *G. arboreum* is common with long and narrow-lobed leaves, whereas a slightly constricted lobe base is generally visible in *G. herbaceum* leaves, making it a broad-lobed type. Bracteoles with fewer (3–4) teeth are closely invested to buds that are longer than broad found in *G. arboreum*, while *G. herbaceum* has more teeth (6–8), flaring widely from the buds. In *G. arboreum*, bolls are mostly round, with tapering points and a less smooth to deeply pitted rough boll surface. *G. herbaceum* can be noticeable with round bolls with less to no tapering beak and smooth to less pitted surfaces. Individually, such characters may not be helpful in unambiguous distinction between the two species; however, by taking as a group, reliable distinctions can often be prominent.

Genetic, cytogenetic, isozyme, and molecular investigations vividly suggested *G. herbaceum* and *G. arboreum* are two distinct species. These two species' crossing can also easily succeed to produce F_1 's that are fertile and vigorous, with pollen fertility of about 60%. With genetic incompatibility, in the F_2 and subsequent generations, higher frequencies of non-viable seeds, seedling mortality, and abnormal plant morphologies commonly occurred (Sanamyan *et al.*, 2016a; 2016b). Best plants' appearance in the segregating generations tends to resemble one of the parental species. Such observations propose these species differed distinctly (Sanamyan *et al.*, 2019; 2022). Cytogenetically, these two diploid cotton species differed by one reciprocal translocation (Gerstel, 1953; Gerstel and Sarvella, 1956; Phillips, 1961).

Isozyme variation at 40 loci among 103 *G. arboreum* and 31 *G. herbaceum* accessions provided additional evidence of species distinctness, as eight unique polymorphic loci in *G. herbaceum* appeared, with 13 in *G. arboreum* (Wendel *et al.*, 1989). Molecular evidence for species distinctness comes from diversity analysis using AFLP markers in

cultivated Indian diploid cotton, where *G. herbaceum* and *G. arboreum* formed two different clusters (Rana and Bhat, 2004). Based on RAPD markers in cluster analysis, the genotypes of the respective species also grouped into distinct clusters, providing additional support of species *G. arboreum* and *G. herbaceum* sharpness (Rana and Bhat, 2002).

Cotton breeders desired to use these diploid genetic resources to enhance the biotic and abiotic stress tolerance in cultivated tetraploid cotton genotypes. In the Indian subcontinent, efforts are in progress to genetically improve the cultivated diploids for desirable plant, boll, and fiber characteristics. Several cultivated diploid cotton landraces and improved lines are invaluable genetic resources for biotechnological studies (Amanov *et al.*, 2020, 2022). Accordingly, the presented research pursued to elucidate global diploid cultivated gene pools regarding their evolution, domestication, geographical distribution, available germplasm resources, their relationship with other species, breeding implications, and the future use of the diploid cotton species.

Taxonomy of old world cultivated cotton

The botanical names *G. herbaceum* L. and *G. arboreum* L. originated from Linnaeus (1753), who also named the two American cultivated cotton species, *G. hirsutum* L. and *G. barbadense* L. Parlatore (1866) published the first relatively advanced classification of *Gossypium*. Making the essential distinction between diploid and tetraploid species, Zaitzev (1928) and Hutchinson *et al.* (1947), considerably contributed to our understanding of the cultivated cottons, partitioning them into the currently recognized four species. This insight also gained support in all the succeeding research, including classical taxonomy (Hutchinson *et al.*, 1947; Fryxell, 1979) and molecular phylogenetic and genomic studies (Wendel *et al.*, 1989, 2010; Wendel and Albert, 1992; Wendel and Grover, 2015). Hutchinson *et al.* (1947) also defined the taxonomy for the two old world cultivated cotton species as:

A. *Gossypium arboreum* L., Sp. Pl. 693. 1753. 1. *G. arboreum* cv. *indicum*, 2. *G. arboreum* cv. *burmanicum*, 3. *G. arboreum* cv. *bengalense*, 4. *G. arboreum* cv. *cernuum*, 5. *G. arboreum* cv. *soudanense*, 6. *G. arboreum* cv. *sinense*

B. *Gossypium herbaceum* L., Sp. Pl. 693. 1753. 1. *G. herbaceum* L. var. *africanum* (Watt) Vollesen, 2. *G. herbaceum* L. var. *acerifolium* (Guill. et Perr.) (Chevalier, 1939). Intermediate types between this and var. *acerifolium* occur in the savannah regions of West and North Central Africa. Information about this had citations by Hutchinson *et al.* (1947).

Mauer (1954) defined the taxonomy for the two old world cultivated cotton species as: 1. *G. herbaceum* subsp. *africanum* (Watt) Mauer, 2. *G. herbaceum* subsp. *pseudoarboreum* Mauer, 3. *G. herbaceum* subsp. *frutescens* (Delile) Mauer, 4. *G. herbaceum* subsp. *euherbaceum* Mauer, 5. *G. arboreum* subsp. *obtusifolium* (Roxb.) Mauer, 6. *G. arboreum* subsp. *perenne* (Blanco) Mauer, 7. *G. arboreum* subsp. *neglectum* (Tod) Mauer, 8. *G. arboreum* subsp. *nanking* (Meyen) Mauer.

For *G. arboreum*, these authors also authenticated no neatly differentiated subspecies could be definite. They also rejected a taxonomic distinction between perennial and annual types and discussed the usefulness and practicability of the distinction among the geographical races, listing the six geographical landraces, as above. Fryxell (1979) cited one inferior subdivision, in one of the two species, as *G. herbaceum* var. *africanum*. Most of the modern germplasm banks follow the taxonomic concepts of Hutchinson *et al.* (1947) and Fryxell (1979), notwithstanding with the artificiality of the cultivar groups as meaningful biological and genetic entities (Wendel *et al.*, 1989).

G. herbaceum subsp. *africanum*, the wild, non-domesticated form in Southern Africa and possible ancestor of the domesticated variants; *G. herbaceum* subsp. *herbaceum*, the improved, hypothetically monophyletic group comprise the following four geographical cultivars, with the same also identified by Kulkarni *et al.* (2009): 1. *G. herbaceum* subsp.

Herbaceum cv. *acerifolium*, 2. *G. herbaceum* subsp. *Herbaceum* cv. *persicum*, 3. *G. herbaceum* subsp. *Herbaceum* cv. *kuljianum*, 4. *G. herbaceum* subsp. *Herbaceum* cv. *wightianum*.

G. herbaceum and G. arboreum use in polyploidy

Colchicine (C₂₂H₂₅O₆N), a product extracted from the seeds and bulbs of the autumn crocus (*Colchicum autumnale* L.), as well as, other anti-mitotic agents, such as, amiprophosmethyl oryzalin, and trifluralin, have long been functioning to induce polyploidy (Blakeslee and Avery, preventing the formation of microtubules, and consequently, spindle fibers during cell division (Petersen *et al.*, 2003).

Thus, colchicine can effectively arrest cell division at the early anaphase stage. At this phase, duplication of the chromosomes have materialized, but, mitosis has not yet taken place, and restriction of cell wall formation at this stage results in the polyploid cells. These cells, generally found larger than their diploid counterparts and frequently develop into thicker tissues, result in large-sized plant organs (Vainola, 2000). In addition, pollen grains' diameter, as well as, the size and number of stomata are typically broader in the polyploids (Blakeslee and Aery, 1937; De-Jesus-Gonzales and Weathers, 2003). The ploidy manipulation is a considered valuable tool in genetic improvement of various crop plants, including the *Solanum* spp. (Chauvin *et al.*, 2003), citrus (Wu and Mooney, 2002), pomegranate (Shao *et al.*, 2003), *Allium* spp. (Jakse *et al.*, 2003), and azaleas (De-Schepper *et al.*, 2004).

Past studies enunciated an attempt has surfaced to enhance the ploidy level, seeking different goals in various plants. In citrus, the production of tetraploid (4n) parents sought to develop seedless triploids by crossing (4n) and (2n) parents (Wu and Mooney, 2002). In medicinal plants, *Scutellaria* spp. (Gao *et al.*, 2002) and *Artemisia* spp. (De-Jesus-Gonzalez and Weathers, 2003), tetraploidy increases the amounts of the secondary metabolites, baicalin, and artemisinin. In azalea,

chromosome doubling has been applicable to obtain new ornamental characteristics (De-Schepper *et al.*, 2004).

Moreover, the polyploids provide a wider germplasm base for breeding aspects (Thao *et al.*, 2003). Cotton (*Gossypium* sp.) development has become a particularly useful group for studying the polyploidy (Adams and Wendel, 2004). The classification of diploid cottons attained eight genome groups (A-K) based initially on cytology and refined by molecular studies (Wendel and Cronn, 2003). The polyploidization between an A-genome and a D-genome of diploids approximately 1.5 million years ago developed the AD allotetraploid group of cotton (Senchina *et al.*, 2003).

Induction of polyploidy in interspecific and intergeneric hybrids results in duplicating the two genomes found in the hybrid, forming an allopolyploid. This further allows for continued introgression of the desired genes into the cultivated gene pools (Olsen *et al.*, 2006). In better understanding the fate of polyploidization in cultivated diploid cotton species, the phenotypical and cytological effects of various doses of colchicine underwent analysis in plants treated at various developmental stages and for different periods.

Morpho-biological characteristics of G. herbaceum and G. arboreum

The significance of the source material for selection lies in the presence of biological diversity of plant forms and their genetic identification based on a set of valuable traits. In this regard, the study and comprehensive assessment of germplasm based on morpho-biological and economically valuable properties determines its relevance. For studying the morphological variability of the cotton, an attempt continued to determine the adaptive significance of some traits, as well as, to compare the traits of wild and cultivated species, which should help to elucidate their family relationships.

The latter received much attention in connection with the misconceptions in the literature about the composition of the genus *Gossypium* L. As already mentioned, the

pertinent detailed research is of great interest, providing exhaustive characteristics of the variability in the morphology of vegetative and reproductive organs in the genus *Gossypium* L. Likewise, it will provide data demonstrating variations in some characters (for example, the nature of branching) under the influence of environmental conditions (Mauer, 1954; Konstantinov, 1967). However, this characteristic is far away from exhaustive (Muminov *et al.*, 2023). Therefore, it is necessary to continue the study of the genus *Gossypium* L. in this direction, both by summarizing the available genetic material and through experimental research observations on the living plants (Figures 1-4).

Morphological features of *G. herbaceum*

An annual herb, its stems and branches are round, faintly striated, bent slightly at the joints, and sparsely hairy. Leaves are leathery, prominently reticulated, deeply cordate, less than half cut into 5–7 broad ovate rotund, suddenly acute or apiculate lobes, below distinctly pilose, especially along the veins. Its bracteoles are large, green, broadly ovate rotund obtuse, only very slightly united at the bottom, but profoundly cordate, and gashed across the top into 7–9 fairly long teeth. The flowers are medium, yellow with purple claws, and rotating to the right; the calyx is large, loose, undulate, and with large glands. The capsule is small, round, pitted with 3–4 valves, with large seeds (40–62 g), angled beaked, coated with gray fuzz, and harsh grayish-white wool. Previous studies reported and confirmed similar results by comparing the morphological and economic characteristics of Afro-Asian cotton species (Mauer, 1954). Key characters for the *G. herbaceum*'s identification are bushy annual, bracteoles flaring widely from the flower bud, usually broader than long, an upper margin usually serrated into 6–8 teeth, small and round capsule, with 3–4 locules (www.cicr.org.in).

Morphological features of *G. arboreum*

A perennial, usually 1.82 to 3.05 meters tall, with long trailing thin branches, stems, and

particularly, young branches, its petioles, peduncles, and bracteoles have a deep glossy purple color, a peculiarity sometimes even possessed by young leaves, especially the under surface. Leaves are thick and leathery, with a dotted gland, sub-glabrous or having short, abortively stellate hairs on the blade, especially more under surface. It has few younger spreading hairs on the petiole and young shoots, with the leaf blade mostly five lobed. Flowers are yellow with purplish red petal spot, and capsules are round to tapering, with 3–4 loculi. Similar findings came from previous studies by comparing the morphological and economic characteristics of Indo-Chinese cotton species (Mauer, 1954) (Figures 1-4). A key feature for its identification are bracteoles closely investing the flower bud, entirely or with 3–4 coarse teeth near the apex, longer than broad, capsule, round to tapering, with 3–4 loculi (www.cicr.org.in).

Germplasm collection of *G. herbaceum* and *G. arboreum*

A global germplasm collection of the cultivated diploid cotton has been ongoing in the Central Institute of Cotton Research (CICR), Nagpur, India, which is the national center for cotton collection, conservation, evaluation, and documentation. It holds the highest number of collections belonging to the diploid species *G. arboreum* (1870) and *G. herbaceum* (530) (Table 1).

The Indian *G. arboreum* germplasm comprises native landraces, such as '*cernuum*,' '*indicum*,' and '*bengalense*,' and some collections from China, representing the race '*sinense*.' In addition to that, representative collection from Africa, probably belonging to the race '*soudanense*' and the '*comilla*' cotton of Bangladesh existed in the Indian collection. Most of the *G. herbaceum* collections belonged to the race '*wightianum*' and very few to the var. '*africanum*'. Systematic race-wise characterization of the cotton germplasm has been very difficult due to overlapping morphological traits and lack of race-specific phenotypic and molecular markers. However, race-wise classification is yet to proceed in

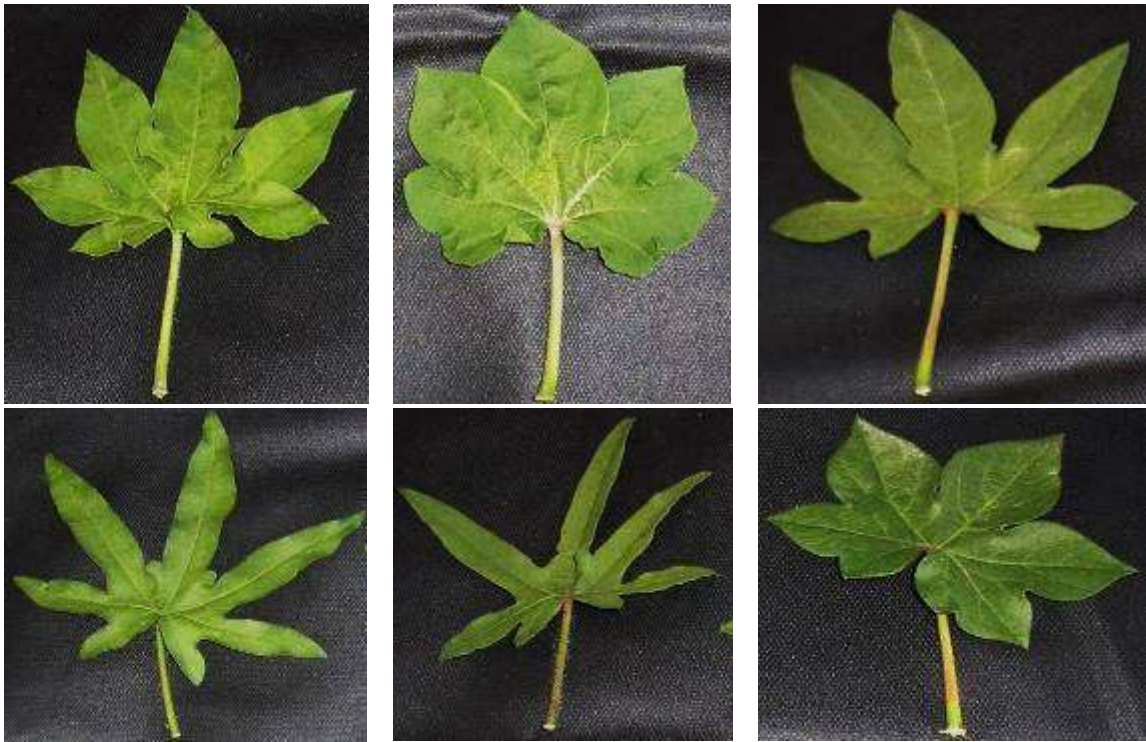


Figure 1. Diversity on leaf plate shape observed in *G. herbaceum* and *G. arboreum* germplasm. Source: Muminov (2017).



Figure 2. Diversity of color, height, and shape of *G. herbaceum* and *G. arboreum* germplasm. Source: Muminov (2017).



Figure 3. Diversity of structure style, stigma, filament, and anther of *G. herbaceum* and *G. arboreum* germplasm. Source: Muminov (2017).



Figure 4. Diversity of cotton boll stock structure of *G. herbaceum* and *G. arboreum* germplasm. Source: Muminov (2017).

Table 1. Gene banks of diploid cultivated cotton worldwide.

Country	Number of accessions		Location	Reference
	<i>G. arboreum</i>	<i>G. herbaceum</i>		
India	1870	530	Central Institute for Cotton Research, Nagpur, India	Anonymous (2005)
China	369	NA	Chinese Academy of Agricultural Science, Nanjing China	Liu <i>et al.</i> (2006)
USA	1730	194	Southern Plains Agricultural Research Center (SPARC), Crop Germplasm Research Unit, College Station, Texas, USA	Anonymous (2005)
Uzbekistan	1623	1292	Institute of Genetics and Plant Experimental Biology (IG&PEB), Academy of Sciences of Uzbekistan (ASUz), Uzbek Scientific Research Institute of Cotton Breeding and Seed Production (UzSRICBSP), Ministry of Agriculture and Water Resources (MAWR), Republic of Uzbekistan, Uzbek Research Institute of Plant Industry (UzRIPI), Ministry of Agriculture and Water Resources (MAWR), Republic of Uzbekistan	Abdurakhmonov <i>et al.</i> (2014)
Iran	NA	42	Iran National Gene Bank and Iran Cotton Research Institute, Gurgan, Iran	Sheidal and Alishah (1998)
Vietnam	45	1	Nha Ho Cotton Research Center, Vietnam	Le (1996)
France	69	50	CIRAD, Montpellier, France	Dessauw and Hau (2006)

India using morphological and molecular markers. Most accessions' characterization of both cotton species ensued for different agronomic and fiber properties, and said germplasm groupings may help future breeders (Singh *et al.*, 2001).

Elite types with specific traits, such as red plant body, brown lint, nectariless, spotless flower, big bolls, higher ginning outturn, early maturity, high seed oil, and longer staple have been prominent in the accessions (Singh *et al.*, 2001, 2004). Most diploid A-genome accessions of the USA were product imports from India and China during 1994–1995 (Anonymous, 2005). The French cotton germplasm collection, preserved in the Centre de Cooperation Internationale en Recherche Agronomique pour le Developpement (CIRAD) in Montpellier, France, acquired varying samples from eight expeditions in African countries and the Arabian Peninsula. The collections include *G. arboreum* race 'soudanense' (22), *G. herbaceum* var. *africanum* (2), cultivars of both species, and other ancestral forms (18 in *G. herbaceum* and 17 in *G. arboreum*) that are yet for characterization (Dessauw and Hau, 2006).

The *G. herbaceum* germplasm of Iran consists of 42 ecotypes collected at an altitude range of 10–500 m, and are well characterized morphologically and cytologically. Xiang (1988) collected 369 samples of *G. arboreum* with the race 'sinense' from 20 provinces. The study characterized samples using 72 attributes that showed a taller plant stature and extended growing periods in the Southern regions' accessions versus the short plant height and early-maturing landraces of the Chinese Northeastern zones. Vietnamese cotton collection is predominantly a *G. arboreum* race 'burmanicum.' Although, collection of wild and cultivated diploid cotton also exists with Sudan at Shambat, but the detailed information about this collection is unavailable (Ali *et al.*, 2003). In the presented study, Table 1 shows the germplasm status, which is also incomplete due to a paucity of information from Pakistan, Bangladesh, Thailand, and other South-East Asian countries, where domestication of *G. arboreum* occurred. Meanwhile, a similar case occurs with Russian republics adjacent to Western China, where domestication of *G. herbaceum* race 'kuljianum' took place.

The main cotton germplasm collection has its historical preservation at the research centers and institutions of the Academy of Sciences of Uzbekistan (ASUz), Ministry of Agriculture and Water Resources, Uzbekistan (MAWR). Table 1 also summarizes and highlights the general content and description of cotton germplasm resources of the chief collections made in different countries (Abdurakhmonov *et al.*, 2014). These collections maintain cultivars, wild and primitive, pre-domesticated landraces, hybrids representing the primary gene pool, and the two cultivated Asian diploids (*G. herbaceum* [1,292 samples] and *G. arboreum* [1,623 samples]), representing the secondary gene pool. However, some redundancy of the cotton accessions maintained by collections could be possible. Future comparative inventory work will tackle this because each collection has specificities formed according to distinctive research efforts conducted by these institutions' earlier scientists.

CONCLUSIONS

Nowadays, the phylogeny, evolution, geographical distribution, genetic possibilities of the cotton, including the cultural and wild representatives of the old world, undergo studies and put into practice modern methods of biology. They updated the overview of *Gossypium* L. taxonomy and its developmental history. The said data include more than 50 recognized species of *Gossypium* L., distributed in arid and semi-arid regions of the tropics and subtropics (Abdurakhmonov *et al.*, 2014; Wendel and Grover, 2015). This review provides information on the history, development, and genetic potential of the old world cotton species. The data also provide an opportunity to determine the development and evolution of the species *G. herbaceum* and *G. arboreum* diversity. In particular, the ideas on occurring cultural and wild representatives, botanical composition, kinship relations, evolution, and geographical distribution are still ambiguous. This work can serve as a source for revision, correction, completion, and the

use of genetic potential of existing genetic material.

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