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Review Paper on Genetic Diversity and Domestication of Cotton (*Gossypium* spp. L) Crop

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Abstract

Cotton (*Gossypium* spp. L.) has been cultivated in tropical and sub-tropical climates of the world. Although the wild species are often woody perennials, ranging from shrubs to trees, the domesticated species are generally cultivated as herbaceous row crops or, in a few areas of the world by ratooning. In addition to being the world's most important textile fiber crop, cotton is the world's second-most important oil seed crop after Soybean. The level of genetic diversity of crop species is an essential element of sustainable crop production in agriculture, including cotton. The genetic diversity of *Gossypium* species is exclusively wide, encompassing wide geographic and ecological niches.

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Introduction

Cotton (*Gossypium* spp. L.) has been cultivated in tropical and sub-tropical climates of the world. Although the wild species are often woody perennials, ranging from shrubs to trees, the domesticated species are generally cultivated as herbaceous row crops or, in a few areas of the world by ratooning. In addition to being the world's most important textile fiber crop, cotton is the world's second-most important oil seed crop after Soybean (Efe *et al.*, 2013). All species of cotton are propagated by sexually produced seeds, where it has orthodox type of seed storage system. Cotton has bisexual flowers and is basically a self-pollinated crop. Cotton out crosses freely, the out crossing being the result of insect pollination (Poehlman and Sleper, 1995). Natural cross-pollination varies from nil to 60% depending upon the climatic conditions and honey bee activity; cotton pollen being sticky and heavy doesn't allow wind pollination (Singh, 1998).

Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology. Information on genetic diversity within and among closely related crop varieties is essential for a rational use of genetic resources.

The level of genetic diversity of crop species is an essential element of sustainable crop production in agriculture, including cotton. The genetic diversity of *Gossypium* species is exclusively wide, encompassing wide geographic and ecological niches. It is conserved *in situ* at centers for cotton origin (Ulloa *et al.*, 2006) and preserved *ex situ* within worldwide cotton germplasm collections and materials of breeding programs. Cotton productivity and the future of cotton breeding efforts tightly depend on the level of the genetic diversity of cotton gene pools and its effective exploitation in cotton breeding programs. Therefore, the objective of this review paper is to understand the diversity, distribution,

domestication and utilization of cotton crop throughout the world.

Review of literature

Origin and economic importance of the cotton crop

The place of origin of the *Gossypium* genus is not known, however the primary centers of diversity for the genus are west-central and southern Mexico (18 species), north-east Africa and Arabia (14 species) and Australia (17 species).

Archaeological records indicate that *Gossypium* fiber has been used since 6000 BC. A *Gossypium* thread, used to string copper beads, from Mehrgarh in Pakistan has been dated at 6th millennium BC (Moulherat *et al.*, 2002). It is unknown whether this is from a domesticated cotton species, but it suggests that cotton fiber was known and used at this time. Cotton was probably used as wadding, packing or for dressing wounds prior to being used for spinning into yarn (Smith, 1995). *Gossypium* remains in the form of cloth, string, assorted bits of fiber and boll fragments were found in different layers of deposits in caves in Tehuacan Valley in Mexico (Smith Jr. and MacNeish, 1964). These have been identified as being from tetraploid *Gossypium*, with the earliest bolls dating from approximately 5800 BC. Archaeological remains of scraps of fabrics and cords, unprocessed fibers formed into plugs and cotton boll segments from a site in Peru are thought to be the earliest forms of domesticated *G. barbadense*. The findings show a continuum of increasing seed size and fiber diameter from the earlier (2500 BC) to later (1000 BC) levels (Stephens and Moseley, 1973).

The geographic center of origin for *G. hirsutum* is North and Central America and Mexico, and for *G. barbadense* is South America (Jenkins, 2003). *G. hirsutum* was probably first domesticated by pre-Columbian people of the Yucatan peninsula (Brubaker and Wendel, 1994). These early semi-domesticated forms dispersed into the rest of Mesoamerica as well as northern South America and into the Caribbean (Iqbal *et al.*, 2001). Selection then occurred for reduced seed dormancy, annualized growth habit and photoperiod independent flowering creating genotypes more similar to modern cultivars. Interestingly, modern North American *G. hirsutum* has a very limited genetic diversity, thought to be due to a genetic bottleneck resulting from the selection pressure of domestication (Iqbal *et al.*, 2001). This is hypothesized to partly result from the Kekchi Indians of

Guatemala intercropping cotton with capsicums and harvesting the cotton as soon as the first bolls developed to prevent competition with the capsicums, thus rigorously selecting for early maturity along with reduced seed dormancy and annual growth. Data suggests that a doubling of seed size has led to a three-fold increase in lint index (g lint/100 seed) and an 80% increase in mean fiber length during domestication (Stephens, 1965). This increased fiber length has been achieved by a prolonging of the fiber elongation period and greater growth rate early in fiber development in modern cultivars compared to wild *G. hirsutum* (Applequist *et al.*, 2001).

Economic Importance of cotton

The cotton plant is mainly cultivated for its lint (fiber). Cotton is a multipurpose crop that supplies five basic products: Lint, oil, meal, seed hulls, and linters. In World, cotton plays an important role in the economic development. The lint provides high quality fiber for textiles and the cottage industries and hence, cotton is a key commodity for import substitution and saving of foreign currency. Cotton offers employment opportunity on farms and in textile factories. The above ground parts of the plant also provide various uses. The seed is used for oil production by oil mills while the cake is used for animal feed. The stalk is a good source of fuel wood (Niles and Feaster, 1984).

Taxonomy of cotton crop

Cotton, a woody perennial shrub, is taxonomically classified within the family Malvaceae and genus *Gossypium*. The family Malvaceae comprises about 100 genera and 1500 species. The genus *Gossypium* includes approximately 50 species split across two ploidy levels, 45 diploid ($2n=2x=26$) and at least five allotetraploid ($2n=4x=52$) (Fryxell, 1992; Brubaker *et al.*, 1999), whose aggregate geographic ranges encompasses most tropical and subtropical regions of the world (Sauer, 1993).

Description of cotton gene pools and worldwide germplasm collections

Although wild cottons (*Gossypium* spp) are perennial shrubs and trees, the domesticated cottons are tropic and sub-tropic annual crops cultivated since prehistoric times of the development of human civilization. The *Gossypium* genus of the *Malvaceae* family contains more than 45 diploid species and 5 allotetraploid species

(Fryxell *et al.*, 1992; Percival *et al.*, 1999; Ulloa *et al.*, 2007). These species are grouped into nine genomic types ($x = 2n = 26$, or $n = 13$) with designations: AD, A, B, C, D, E, F, G, and K (Percival *et al.*, 1999). The species are largely spread throughout the diverse geographic regions of the world.

Diploid cottons, referred as Old World cottons, are classified into eight (A-G to K) cytogenetically defined genome groups that have African/Asian, American, and Australian origin (Endrizzi *et al.*, 1985). Two of these Old World cottons from Asian origin, *G. arboretum* L. and *G. herbaceum* L., with a spinnable seed fiber, were originally cultivated in Asian continent.

The New World allotetraploid cottons include the commercially important species, *G. hirsutum* and *G. barbadense*, which are extensively cultivated worldwide (Abdurakhmonov, 2007; Campbell *et al.*, 2010). *G. hirsutum* (also called Acala or Upland, short stapled, Mocó, and Cambodia cotton) is the most widely cultivated (90%) and industrial cotton among all *Gossypium* species. It includes the Upland cotton cultivars and other early maturing, annually grown herbal bushes. The center of origin for *G. hirsutum* is Mesoamerica (Mexico and Guatemala), but it spread throughout Central America and Caribbean. Two centers of genetic diversity exist within *G. hirsutum*: Southern Mexico-Guatemala and Caribbean (Brubaker *et al.*, 1999); Mexico-Guatemala gene pool is considered the site of original domestication and primary center of diversity. Within this range, *G. hirsutum* exhibits diverse types of morphological forms, including wild, primitive to domesticated accessions.

G. barbadense (also called as long staple fibered Pima, Sea Island or Egyptian cotton), accounting for about 9% of world cotton production, was originally cultivated in coastal islands and lowland of the USA and became known as Sea Island cotton. Sea Island cottons, then, were introduced into Nile Valley of Egypt and widely grown as Egyptian cotton to produce long staple fine fibers (Abdalla *et al.*, 2001). The wide-distribution of *G. barbadense* included mostly South America, southern Mesoamerica and the Caribbean basin (Fryxell, 1979).

Domestication and early cultivation

The domesticated diploid and tetraploid cottons appeared in Indus valley and New World by 3500-2300 B.C., respectively (Hutchinson *et al.*, 1947; Jiang *et al.*, 1998). The four cultivated species are divided into two

groups, the old world or Asiatic cottons including diploid species, *Gossypium herbaceum* L. and *Gossypium arboretum* L., and new world cotton comprising tetraploid species *Gossypium hirsutum* L. (American or Upland cottons) and *Gossypium barbadense* L. (Pima, Sea Island, Egyptian cottons). Upland cotton, representing 95% of the global cotton crop, predominates other species in terms of cultivated area, production and bulk of trade around the world. It can be found as far north as 37°N in the United States, and as far south as the 32°S in Australia. Pima cotton is prized for its superior fiber quality, however, it accounts for less than 2% of the world cotton crop and cultivation is confined mostly to the Nile valley of Egypt, and California and Arizona states of USA due to narrow adaptation.

The domestication of the wild /non feral/ of the *G. africanum* occurs naturally in the savanna across the southern Africa (Vollesen, 1987) whereas the domesticated *G. herbaceum* (AA diploid cultivated species) was found to be at northeast being grown mainly from Ethiopia to Central Asia, northwestern China, and India (Guo *et al.*, 2006). Similarly, *G. herbaceum* might be from Southwest Asia (Abedin, 1979). The *G. arboreum* (AA diploid cultivated species) is primarily grown across east Asia from India to Korea (Guo *et al.*, 2006). Both the diploid cultivated species (*G. herbaceum*, and *G. arboreum*) of Africa, and Asia are short staple cotton with fiber length of less than 23 mm where studied using morphological, cytogenetic, genetic, and molecular revealed biologically distinct (Desai *et al.*, 2006). Therefore, these two species with *G. arboretum* now provide only about 4% of world production. On the other hand the *G. hirsutum* (tetraploid cultivated species) where they are from Mesoamerica prevalent in south eastern part of U.S.A at middle of 18th century (Phillips, 1976; Smith *et al.*, 1999). Later at 1785 *G. barbadense* (tetraploid cultivated species) was widely grown in U.S.A of Georgia, and South Carolina /South America/ (Brown, and Ware, 1958; Smith *et al.*, 1999). Sea Island cotton was cultivated in lowland whereas green seed cotton was inland consequently known as upland cotton (Smith *et al.*, 1999). Therefore, these upland types with their derived varieties are the main stay of worldwide industry (May and Lege, 1999). Most commercially cultivated cottons are derived from two species namely *G. hirsutum* (90% of world planting), and *G. barbadense* (Long staple and quality fiber). Therefore, the early utilization, and cultivation of the crop have been reported from Pakistan before around 5000 B.C, and North Arabia at 4450 to 3000 B.C (Moulherat *et al.*, 2002). Therefore, the cotton lint was

spun, and woven for cloth making before 3000 B.C. (McGregor, 1976).

Cotton distribution/expansion

The subgenus *Gossypium* having 14 species are naturally distributed in Africa, Arabian Peninsula, Pakistan, and eastward (Vollesen, 1987). However, the first cotton seed arriving U.S.A was Georgia green seed (Hutchinson *et al.*, 1947). Similarly, in the 19th century the Mexican green seeds also introduced into U.S.A where known as varieties of upland cotton (Smith *et al.*, 1999). Cotton was introduced into tropics, subtropics, and Australia during U.S.A civil war of 1861 to 1865 (Constable *et al.*, 2001). At the same time, both *G. hirsutum*, and *G. barbadense* were also introduced into Australia as source of textile fibers from the Mexico where they are native, and domesticated originally (Brubaker *et al.*, 1999).

The genetic diversity of cotton (*Gossypium* spp), including all its morphological, physiological and agronomic properties, is exclusively wide (Mauer, 1954). There is a great deal of genetic diversity in the *Gossypium* genus with characteristics such as:-

- plant architecture
- stem pubescence and color
- leaf plate shape
- flower color
- pollen color
- boll shape
- fiber quality
- yield potential
- early maturity
- photoperiod dependency and
- Resistance to multi-adversity environmental stresses that is important for the applied breeding of cotton.

Besides morphological diversity in *Gossypium* genus, representatives of different genomic groups have diverse characteristics in many agronomically useful traits. Considering only *G. hirsutum* accessions, exotic and cultivar germplasm represent a wide range of genetic diversity in yield and fiber quality parameters.

For example, in the analyses of ~1000 *G. hirsutum* exotic and cultivated accessions in the two different environments, Mexico and Uzbekistan, we found a wide range of useful agronomic diversities (Abdurakhmonov *et al.*, 2004, 2006, 2008, 2009).

In one or two environments, the cotton

- Boll mass varies in a range of 1-9 grams per boll
- 1000 seed mass varies in a range of 50-170 grams
- Lint percentage varies in a range of 0-45%
- Micronaire varies in a range of 3-7 mic
- Fiber length varies in a range of 1-1.28 inch, and
- Fiber strength varies in a range of 26-36 g/tex.

There was also a wide range of variation in photoperiodic flowering (day neutral, weak to strong photoperiodic dependency) and maturity (Abdurakhmonov, 2007). This wide phenotypic diversity of cotton shows the extensive plasticity of cotton plants and potential of their wide utilization in the breeding programs as an initial material.

Some examples of exploiting genetic diversity through traditional breeding

There are numerous examples on the utilization of such genetic variations in solving many fundamental problems in cotton breeding and production (Abdurakhmonov, 2007). For instance, the exploration for genetic diversity for *Verticillium* wilt fungi from the exotic *G. hirsutum* ssp *mexicanum* var *nervosum* germplasm and its on-time mobilization into the elite cultivars solved wilt epidemics (Abdullaev *et al.*, 2009). As a result, the wilt resistant variety series named as “Tashkent” were developed (Abdakarimov *et al.*, 2003; Abdurakhmonov, 2007). Later, salt tolerant genotype AN-Boyovut- 2 was selected from Tashkent cultivar biotypes demonstrating a continuation of a 'genetic diversity imprint' introgressed from the wild landrace stock (Abdakarimov *et al.*, 2003). This is one of the success stories on exploiting genetic diversity and its impact from the single landrace stock germplasm, *G. hirsutum* ssp. *mexicanum* (Abdurakhmonov, 2007). A number of other examples on the creation of natural defoliation, disease and pest resistance, tolerance to multi-adversity stresses, improved seed oil content and fiber quality parameters, utilizing the exotic germplasm genetic diversity have been well documented (Abdakarimov *et al.*, 2003; Abdurakhmonov *et al.*, 2005, 2007).

Challenges and perspectives of exploiting diversity of different gene pools

The introduction of genetic diversity into elite cotton germplasm is difficult and the breeding process is slow. When breeders use new and exotic germplasm sources,

which possess desirable genes for crop trait improvements, large blocks of undesirable genes are also introgressed during the recombination between the two parental lines (linkage drag). This linkage drag has limited the use of such germplasm. Therefore, the utilization of useful genetic diversity of the wild germplasm using traditional breeding efforts is challenging due to:

1. Hybridization issues between various cotton genomes
2. Sterility issues of interspecific multi-genome hybrids
3. Segregation distortion
4. Photoperiodic flowering of wild cottons and
5. Long timescale (10-12 years of efforts) required for successful introgression and recovering superior quality homozygous genotypes using traditional breeding approaches (Abdurakhmonov, 2007).

This underlies necessity for the development of new innovative genomics approaches to support and accelerate the traditional efforts of exploiting the genetic diversity in cotton breeding. Continuing the introduction of genetic diversity into cultivated plants is important for reducing crop vulnerability and improving important traits such as yield, fiber quality traits, and disease and pest resistance of the cotton crop. The most effective utilization of the genetic diversity of *Gossypium* species further requires

1. Characterization of candidate gene(s) underlying the phenotypic and agronomic diversities based on genomic information in other species.
2. Estimation of molecular diversity, genetic distances, genealogy and phylogeny of gene pools and germplasm groups.
3. Acceleration of linkage mapping and marker-assisted selection.
4. Development of efficient cotton transgenomics.
5. Sequencing cotton genome(s) (Abdurakhmonov, 2007).

Summary and conclusions of the study are as follows:

By having a wide geographic and ecological dispersal, the *Gossypium* genus represents and preserves large amplitude of morphobiological and genetic diversity within its *ex situ* worldwide germplasm collections and *in situ* occupation sites.

Further, the narrowness of genetic diversity in cultivar germplasm was associated with recent and possibly future declines in cotton production and its quality, which was a timely warning to accelerate efforts on broadening the genetic base of cultivar germplasm resource. Traditional efforts have succeeded in introgressing many new genetic variations into cultivar germplasm from other gene pools, but it is still challenging and the breeding process is slow due to a number of genetic barriers and obstacles to accomplish the goal. This underlies the importance of development of innovative tools to exploit the biologically meaningful genetic variations, existing in *Gossypium* genus. The most effective utilization of genetic diversity of *Gossypium* species further requires characterization of candidate gene(s) underlying the phenotypic and agronomic diversities, acceleration of linkage mapping, map-based cloning and marker assisted selection that underlie development of modern genomics technologies such as high-resolution, cost effective LD-based association mapping.

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