

**EVALUATION OF *G. HIRSUTUM* EXOTIC ACCESSIONS FROM UZBEK COTTON
GERMPLASM COLLECTION FOR FURTHER MOLECULAR MAPPING PURPOSES**

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Abstract

An extensive selection of cotton accessions (*G. hirsutum* L) from Uzbek cotton germplasm resources with genetic diversity has been carried out. A total of 1086 *G. hirsutum* accessions, including 228 wild *G. hirsutum* races (ssp. *palmeri*, ssp. *richmondi*, ssp. *morilli*, ssp. *mexicanum*, ssp. *latifolium*, ssp. *malum*, ssp. *yucatanense*, ssp. *punctatum*, ssp. *purpurascens* and ect.), and 858 *G. hirsutum* accessions belonging to ssp. *euirsutum* (according to Mauer) that represent a wide range of ecological niche such as Central Asian, Asian, European, American, African Mexican, and Australian ecotypes have been selected. 724 accessions out of 1086 selected were grown and phenotypically evaluated in greenhouse and field stations of the Institute of Genetics and Plants Experimental Biology (IG&PEB) in 2003. Morphobiological diversity within these evaluated cotton accessions has been discussed. Moreover, cataloguing of these selected cotton accessions according to international plant cataloguing standards are in progress that describes each accession in detail. Furthermore, these selected accessions will be used to tag new potential genes for fiber quality and agronomic traits using linkage-disequilibrium (LD) mapping technology.

Introduction

The genus *Gossypium* includes approximately 46 diploid and 5 allotetraploid species (Percival et al, 1999) that are mostly spread in tropical and subtropical regions of the world. There are two agronomically very important allotetraploid species, New World cottons - *G. hirsutum* and *G. barbadense*, which are widely cultivated worldwide. *G. hirsutum* is the most widely cultivated and industrial cotton among all *Gossypium* species. *G. hirsutum* includes itself upland cotton and other early-ripening, annually grown herbal bushes. Origin of the *G. hirsutum* is Guatemala, but it spread throughout Mesoamerica; its a large indigenous range encompassed most of Mesoamerica and Caribbean. Within this range *G. hirsutum* exhibits a diverse types of morphological forms, including wild to domesticated accessions.

According to Mauer, there are four groups of sub-species of *G. hirsutum*: 1) *G. hirsutum* ssp. *mexicanum*, 2) *G. hirsutum* ssp. *paniculatum*, 3) *G. hirsutum* ssp. *punctatum*, 4) *G. hirsutum* ssp. *euirsutum*. These four groups of sub-species include themselves a number of wild races such as *yucatanense*, *richmondi*, *punctatum*, *latifolium*, *palmeri*, *morilli*, *purpurascens* and their accessions as well as a number of domesticated variety accessions from American, African, Asian, Central Asian, European, Australian and Mexican ecotypes. These cotton accessions represent a wide range of morphological and genetic diversity, and can be used for mining new potential genes of fiber quality and other agronomic traits for future breeding programs.

Fiber yield and qualities are two most important goals of cotton breeding programs worldwide. The application of molecular genetics and marker-assisted breeding in the incorporation of superior fiber quality genes into adapted high-yielding cultivars is essential for development of new cultivars adapted for different growing conditions. Hence, finding molecular markers that are closely associated with yield and fiber quality genes using molecular mapping techniques will help cotton breeders to improve cotton varieties. However, the narrow genetic base of currently available cotton cultivars (Iqbal et al. 2001; Abdalla, 2001) makes it difficult to map agronomically important traits using molecular markers; therefore, there is a need to explore novel germplasm resources and identify candidate genetic resources for important agronomic traits including fiber quality and yield.

In Uzbekistan we have nearly 17,000 cotton germplasm accessions including isogenic, inbred lines, elite AD allotetraploid varieties (*G. hirsutum* and *G. barbadense*), monosomic and translocation lines (A. Abdullaev, personal communication; Musaev et al., 2000) along with wild, primitive and extant representatives of the A to G genome groups that have been developed in the Cotton Research Institutes of the Republic of Uzbekistan and collected over the world for the past 9-10 decades. Within the Institute of Genetics and Plant Experimental Biology (IG&PEB), we have a collection nearly 5,500 cotton accessions, including a large number of unique and “exotic” *G. hirsutum* accessions that were developed at the Institute or collected by Institute scientists from around the world. This germplasm constitute a vast potential resource of genes for agronomically important traits, such as insect and pathogen resistance, tolerance to environmental stresses, fiber quality (length, strength and lint yield) and yield potential.

The main goal of this work was to evaluate exotic cotton accessions developed and maintained at IG&PEB, Uzbekistan, for fiber quality and yield traits. Ultimately, these accessions will be further analyzed using DNA marker technology (Vos et al., 1995; McCough et al., 1997; Neff et al., 1998; Yu et al., 1998; Reddy et al., 2001; Abdalla et al., 2001; Kohel et al., 2001; Yu and Kohel, 2002; Ulloa et al., 2002) to identify candidate cotton accessions with new agronomically important genes. An “association-genetics” approach (Terwilliger et al., 1998; Bull et al., 2001; Tabor et al., 2002; Weiss and Clark., 2002; Schulze and McMahon, 2002.), based on linkage disequilibrium to identify DNA markers linked to genetic loci conditioning superior fiber yield and quality will be used. Below we discuss morphobiological diversity of studied cotton accessions based on phenotypic analyses in 2003.

Materials and Methods

Accessions were selected according to their genetic diversity and potential to contribute new genes from Uzbek cotton germplasm collection. Biological peculiarities of the selected accessions (germination and seed energy, budding and flowering time) were studied in the germplasm Unit of the IG&PEB and field stations, recording germination time and a number of seeds that were germinated in thermostats, and budding & flowering times in the field and greenhouse. Standard plant growing and agronomic technologies were used in growing of accessions. Seeds of wild species were germinated in thermostat; then, seedlings transferred to special paper pots with the cultivation soil, and after emerging two to three real leaves seedlings were planted in open filed or in Wagner pots. Morphological traits of each grown accessions were recorded periodically - in the first decade of August, in second decade of September and in third decade of October 2003 in field stations of the IG&PEB.

Results and Discussion

Selection of Cotton Accessions from Uzbek Germplasm

As a first step, an extensive selection of *G. hirsutum* accessions from Uzbek cotton germplasm collection based on genetic diversity and geographical origin has been carried out. A total of 1086 *G. hirsutum* accessions, including 228 wild *G. hirsutum* races (ssp. palmeri, ssp. richmondi, ssp. morilli, ssp. mexicanum, ssp. latifolium, ssp. malum, ssp. yucatanense, ssp. punctatum, ssp. purpurascens and ect.) and 858 *G. hirsutum* accessions belonging to ssp. euhirsutum (according to Mauer) that represent a wide range of ecological niche such as Central Asian, Asian, European, American, African Mexican, and Australian ecotypes have been selected (Figure 1).

The selected wild *G. hirsutum* accessions represent of both genetic diversity centers of *G. hirsutum*: Southern Mexico-Guatemala and Caribbean gene pools (Brubaker et al., 1999); These wild cotton accessions mostly were collected in field expeditions during past 50 years and deposited to the collection; some of them were obtained through cotton germplasm exchange programs. The selected variety accessions of *G. hirsutum* were from diverse ecological niche that represent Central Asian (Uzbekistan, Kazakhstan, Tajikistan, Turkmenistan), Asian (India, Pakistan, China, Turkey and ect.), American (USA, Argentine, Brazil), African (Tanzania, Sudan, South Africa and ect.), European (Bulgaria, Czechoslovakia, Ukraine, and ect.), Mexican and Australian ecotypes (Figure 1).

Biological Peculiarities of Selected Cotton Accessions

Studies on biological peculiarities of cotton accessions such as seed energy, seed germination ability, budding and flowering time were the initial step to describe accessions and to get preliminary information about biodiversity between sub-species. Seed energy and seed germination of the accessions depended on type of species, geographical origin of the accession, reproduction year and seed maturity. The results showed that seed germination ability and seed energy of wild, cultural-tropical, half-wild, and cultivated varieties of *G. hirsutum* were different.

Sub-species mexicanum is one of the wild races of *G. hirsutum*, a perennial monopodium bush with small and medium size leaf, almost naked short monopodium fruit branches with intensive antocyanin and dense gossypol glands. Seed energy and seed germination ability were low (12.5-20.0%). In some cases, seed germination of these wild accessions was very low in the thermostat, or sometime seeds did not germinate at all. However, energy of plant growth was very high (40-70%). Perhaps, the reason for low germination was stony nature of the seed, causing insufficient humidity access to the embryo. It also should be noted that the development of wild accessions grown in Wagner pots was late than those grown in the field condition. For in-

stance, the period from germination to budding phase of plants in Wagner pots was 104 -107 days while in the field stations it was equal to 45-50 days. Moreover, some accessions from ssp. *mexicanum* did not go to budding phase till July 20, 2003.

Sub-species ssp. *punctatum* (Schum. et Thonn) Mauer is one of the primitive cultivated and half-wild races of *G.hirsutum* L., that spread out as wild and half-wild races in tropical regions. Representatives of this sub-group are the most agronomically primitive cottons, having slender-stemmed shrubs with three lobbed leaves and carrying a large number of small cotton bolls with a small to medium seeds, bearing short fibers. Seed germination and seed energy were comparatively higher than the other wild races (50-100%), yet at the same time, there were races with very low seed germination ability (8.3-33.3%). Energy of plant growth was high and varied in a range of 50% to 90%. The period from seed germination to budding-time was 44 to 62 days. There were some accessions that did not go to budding phase till July 20, 2003 among representatives of ssp. *punctatum*.

Representatives of the sub-species *paniculatum* (Blanco Mauer) are the cultivated-tropical races of *G.hirsutum*, ancestors of modern sub-tropic ssp. *euirsutum* cottons. They are semi-sympodium and sympodium bushes with long branches and large leaves. These races are very variable with type of branching, early maturity, leaf shape and level of the seed fuzziness; gossypol glands are comparatively sparse. Seed germination was low (20%); energy of plant growth was 10%. The period from germination to budding was 73 days.

Representatives of ssp. *purpurascens* (*G. tricuspidatum*) of *G. hirsutum* are tree-like plants, with more or less big and small monopodium and sympodium branches. They are naked, sometimes more or less fuzzy-stem plants, having dense and very notable gossypol glands with antocyanin colored or completely red branches. Leaves are in medium to large size, three-, five-, and sometimes seven-lobbed. Seed energy and germination varied in a range of 30 to 100%. In plants grown in Wagner pots, period from germination to budding phase was 96-103 days while plants grown in the field condition it was equal to 45-57 days.

The remaining wild accessions of *G.hirsutum* also had the similar data on studied traits. Furthermore, it should be noted that most wild races of *G. hirsutum*, excluding some accessions, flowering phase was not observed till July 20, 2003. Perhaps, the reason for this might be photoperiod dependence of the wild cottons.

Representatives of ssp. *euirsutum* (Mauer) sympodium semi-herbal bushes with a large leaves, and strongly developed sympodium branches (monopodium ones are relatively few); leaf size, shape, seed fuzziness, fiber quality are very variable. Biological peculiarities of number of representatives of ssp. *euirsutum* from different ecological-geographical group have also been studied. American accessions have showed high variability on seed germination (41.6-100%) and seed germination energy (50-100%). The period of seed germination to budding was 79-85 days; period from seed germination to flowering-time was 103-121 days. Also it should be noted that among these American cottons there were non-flowering, photoperiodic accessions which failed to flower in long day conditions in Uzbekistan.

The remaining cotton accessions from Central Asian, Asian, European, American, Mexican, and Australian were grown in field stations of the Institute. The period of seed germination of these accessions was 11 to 21 days. This long and variable germination period might be due to unfavorable weather conditions (continual cold weather and heavy rainfalls) in Uzbekistan in 2003. In these accessions seed germination and seed energy studies were not carried out. The period from seed germination to budding phase varied in a range of 27-45 days; the period from seed germination to flowering phase varied in a range of 55-80 days.

Thus, preliminary data obtained on seed germination, seed energy, budding and flowering time revealed wide spectra of variations within each cotton ecotypes as well as within wild accessions of *G. hirsutum*.

Phenotypic Evaluation of Cotton Accessions

The amplitude of phenotypic diversity of cotton, including all its morphological, physiological and agronomic properties is exclusively wide (Mauer, 1954). Therefore, it is difficult to describe variation of traits that are important for applied breeding of cotton such as shape of cotton bush, its resistance and lodging properties, types of branching, structure of fruit branches, yield potential and early maturity, photoperiod dependency, and resistance to multi-adversity environmental stresses. This wide phenotypic diversity of cotton shows exclusive plasticity of cotton plants and possibility of their wide application in breeding programs as an initial material. Furthermore, diverse representatives of widely cultivated tetraploid cottons - *G.hirsutum*. L, one of the well-domesticated varieties and forms of multi-centurial public breeding efforts, has a particular value for both theoretical and applied cotton research programs.

Out of selected 1086 cotton accessions 724 accessions were planted in the greenhouse and experimental field stations of the Institute. Out of 724 accessions 706 accessions grew well, and further they were phenotypically evaluated (Figure 2).

223 wild cotton accessions were planted in specific photoperiod regulated greenhouse and wagons since most wild cotton accessions are photoperiodic and fail to flower in long day summer conditions of Uzbekistan. At the same time, these 223 wild accessions also were planted in the field stations to identify level of photoperiodic dependence, and evaluate them in the same

condition as the other grown accessions. 120 Central Asian, 188 American, 39 Asian, 45 European, 28 Mexican, 54 African, and 27 Australian *G. hirsutum* accessions have been planted in the field stations IG&PEB (Figure 2). We have studied following morphobiological and physiological properties of selected cotton accession in field conditions:

1. Shape of cotton bush
2. Existence of antocyanin color
3. Level of stem fuzziness
4. Structure of flower
5. Height of major stem
6. Height of stem node for the first fruit branch
7. Total number of stem nodes
8. Number of sympodium branches
9. Number of monopodium branches
10. Number and shape of cotton boll
11. Photoperiod sensitivity
12. Phenological observation (germination, flowering and maturity)

Phenotypic analyses of cultivated and wild cotton accessions of *G. hirsutum* have been carried out stage by stage –in the first decade of August, in second decade of September and in third decade of October 2003.

First decade of August, we have studied flowering properties of grown accessions, including morphology of leaf plates and structure of flowering organs. We determined that most of wild *G. hirsutum* accessions (223 wild accessions were grown) are strictly photoperiodic and did not go to flowering phase until August 20, 2003. At the same time, we also found some non-flowering, photoperiodic accessions among cultivated accessions with monopodium type of branching (Figure 3).

There were some similarities and differences in morphological description of flowering organs and leaf plates between wild, half-wild, cultural-tropical and cultivated accessions of cotton. Wild accessions of *G. hirsutum* L. mostly were characterized with five-cleft leaves, light-yellow or cream color pestle, and absence of antocyanin spots at flower basis, and light-cream color or light-yellow color pollens. Cotton accessions from mexicanum microcarpum palmeri sub-species had palmatisected leaves. Accession from Yucatan of Mexico (A-4722) was different from the others with palmately divided leaves, yellow color pestle with antocyanin spot at flower basis, and bright-yellow color pollen.

Cultivated variety accessions of *G. hirsutum* L. mostly were characterized with five-cleft leaves, light-cream color pestle without antocyanin spot, and yellow or cream color pollen. Only some accessions from South Africa (A-2615, A29-38, A2940) had palmately divided leaves, one accession of Uzbekistan (A-726) had palmatisected leaves and some accessions of Sudan (A-2622 and A-2623) had bright-yellow color pollen. Currently, phenotypic analyses and morphobiological description of wild cotton accessions that maintained in greenhouse are being continued.

In second decade of September, phenotypic analyses of grown accessions were continued and 355 cultivated variety accessions of *G. hirsutum* L. from different ecotypes were analyzed. Accessions from Central Asia included 110 accessions from Uzbekistan, one accession from Tajikistan, 6 accessions from Karakalpakstan, and two accessions from Kazakhstan. These group accessions, mostly from Uzbekistan, are basically uniform with exception of some accessions such as A-1711, AN316, A-1661, Kosonsoy, A726, Okra-3, A-1032, G-22) and had mostly compact or branched bushes with a fuzzy stem and strong to weak antocyanin spots. Plant height was 70-80 cm, the first fruit branches began at 5-6 or 7-10 stem nodes, a number of monopodium branches were less, a number of sympodium branches were varied from 16 to 25 or more, a total number of stem nodes were 20-30, a number of cotton bolls varied from 8-10 to 15-30, and boll shape was mostly egg-shaped or cone-shaped.

Flowering phase observation showed that Central Asian accessions are mostly middle maturing with vegetation period of 120-135 days. Among them, we found early maturing (A-3842 and C-4862) as well as late maturing accessions (A-3922 and hybrid from Artunov) with 118 and 145 days vegetation period respectively. It should be noted that accessions from Tajikistan, Kazakhstan and Karakalpakstan were similar on studied morphobiological characteristics. Among Karakalpakstan accessions, ultra-early maturing types were revealed with vegetation period of 112-125 days (A-1013, KK1086, A-1638, KK-1543).

Asian ecotype included one accessions from Afghanistan, one accessions from Iraq, two accessions from Syria, three accessions from Turkey, nine accessions from China, 12 accessions from India, 10 accessions from Pakistan, and two accessions from Korea. These accessions were different on studied trait characteristics. Accessions from India and Pakistan were uniform with branchy bushes, middle type of fuzzy stems and antocyanin color, egg-shaped and spherical bolls. A number of cotton bolls per plant were from 12 to 21. Accessions of Pakistan were middle and late maturing with vegetation period of 128-145 days. Among accessions of India, very early maturing accessions (A-3397 and B147) with vegetation period 113 days were determined. Accessions from Afghanistan, Iraq, Syria, Turkey, China and Korea showed average indices on studied morphobiological characteristics.

European ecotype included two accessions from Hungary, seven accessions from Bulgaria, twenty accessions from Ukraine, one accessions from Yugoslavia, and six accessions from Azerbaijan. Ukrainian cotton accessions were very different with homogeneity, and compact type of the bush structures. The level of antocyanin color and stem fuzziness varied from strong to weak. Plant height of this ecotype was average (60-80 cm), the first fruit containing branches were at 5-7 stem nodes, and total numbers of stem nodes were varied from 18 to 25, monopodium branches were few and weak, a number of sympodium branches were 13-20. Oval, spherical and cone-shaped cotton bolls were characteristic for these accessions. These accessions were relatively early maturing with vegetation period of 115-124 days.

American ecotype included 50 accessions from the USA, 10 accessions from Argentine, 31 accessions from Mexico, 2 accessions from Colombia and 2 accessions from Brazil. Mexican accessions were different with their uniformity, branchy bushes, level of antocyanin and stem fuzziness varied from strong to weak. Plant height varied from 70 to 120 cm, the first fruit branch began from 6-8 stem nodes, number of monopodium varied from 1 to 5, number of sympodium varied from 17 to 21, a total number of stem nodes were 22-27, a number of bolls were 17-22 per each plant. These accessions had oval, spherical and cone-shaped cotton bolls. Vegetation period was varied from 122 to 149. The remaining accessions from this ecotype had similar characteristics as Mexican cottons.

African ecotype included 2 accessions from Western Africa, 3 accessions from South Africa, 2 accessions from Ecuador, 3 accessions from Senegal, 9 accessions from Tanzania, 15 accessions from Sudan and 13 accessions from Algeria. African ecotype accessions were relatively similar to each other having branchy bushes, average level of antocyanin color and stem fuzziness. Plant height was 70-100 cm, the first fruit branch was at 6-8 stem nodes, all accessions had strong 24 monopodium branches and 17-20 sympodium branches, a number of stem nodes were 18-26, a number of cotton bolls were 14-23 with spherical shape. Phenological observations revealed that there are wide variations in vegetation period of Tanzanian and Algerian accessions (116-150 days). It also should be noted that South African accessions (A-2938, 4154, A2940, Pika7215) were late maturing (135-140 days). Accessions from Senegal and Sudan were relatively middle maturing with vegetation period of 126-135 days.

Most of accessions from Australian ecotypes were not homogenous and very different on bush type, stem fuzziness, leaf plate structure and branching type. In brief, plant height was middle-70-80 cm, the first fruit branch was at 5-8 stem nodes, a number of monopodium branches were 1-2, a number of sympodium branches were 16-21, and stem nodes number was 20-27. Yield potential of these accessions was average; a number of bolls were 15-20 per plant. These accessions were middle maturing with 121-131 days of vegetation.

In the third decade of October 2003, full morphological analyses of 129 cultivated variety accessions of the USA and 18 accessions from Australia, Tanzania, South African, Thailand, Republic of Chad and Uganda were carried out. These accessions were grown and analyzed in Uzbekistan for the first time. The results of analyses showed that accessions of the USA were morphologically similar (homogenous), excluding accessions A-4548, "S918-12302 resell" from California. Level of antocyanin color and stem fuzziness varied from strong to weak. Plant height also widely varied from 31 to 81 cm, the first fruit branch was at 8-12 stem nodes, a number of monopodium were 1-6, a number of sympodium 9-19. A total number of stem nodes were 15-30; leaf size was middle with five-cleft structure, flowers were middle size having cream color or sometimes red color pestle, without antocyanin spot on the basis; pollen and ovule were cream color or light-yellow. Most accessions had egg-shaped cotton bolls. Vegetation period varied from 153 to 178 days. One of the reasons for late maturity of accessions from the USA might be due to cold weather conditions (-3°C; +5-10°C) in the beginning of vegetative period of this year.

Cotton accessions from Australia, Tanzania, South African, Thailand, Republic of Chad and Uganda were morphologically similar with exception of Australian accessions. Australian accessions widely varied on plant height (46-74 cm), the first fruit branch was at 5-6 stem nodes, monopodium branches were few (1-2), a number of sympodium branches varied from 11 to 17, stem node numbers were 17-22. African accessions were middle height plants (90-117 cm) and showed average morphological indices (Table 3). Vegetation period varied 160 to 178 days.

In total 706 *G. hirsutum* accessions from Uzbek cotton germplasm were analyzed phenotypically stage by stage, recording the most important morphological characteristics. We determined that out of 706 analyzed, 555 accessions were day-neutral plants, 6 accessions were weakly photoperiodic, 57 accessions were photoperiodic and 88 accessions, including mostly wild races were strictly photoperiodic (Figure 3). There were also wide morphological diversity on pollen color (Figure 4), pestle color and pestle spot (Figure 5&6), boll shape, leaf shape, branching type, and vegetation period. Phenotypic analyses of greenhouse grown accessions and those wild accessions transferred to greenhouse from field station are being continued.

Cataloging of Selected Accessions

One of the long-term aims of the current research project was to create hard copy catalogue of selected cotton accessions on the basis of international plant cataloguing system. The detail cataloguing of phenotypic and molecular-genetic data for each selected accession obtained through this project is very important in future access to project results by world cotton research

community interested in using potential ‘candidate’ accessions for breeding purposes. Extensive studies on creation of plant cataloguing rules (Descriptor for Groundnuts 1992, Descriptor for Pistachio-2002, and Descriptor for Cotton 1885) were conducted and “Descriptor for Cotton” which was developed and approved by IPGRI in 1985 (<http://www/ipgri.cgiar.org>) was chosen for creation a catalogue of selected accessions. According introduction to this descriptor, IPGRI requires mandatory record accession data for the first four categories of the descriptor 1) Accession data; 2) Collection data; 3) Characterization; and 4) Preliminary information. The remaining categories describe the accession traits more detail, yet require periodically repeated experiments at collection site, and therefore, these categories can be used optionally. Since we doing on site experiments we will also use the remaining categories and add information for each accession as much as available. Furthermore, chosen descriptor was developed 15 years ago; it was analyzed in detail, considering recommendations from more recent descriptors (Descriptors for groundnuts-1992; and Descriptors for Pistachio-2002) and considering our germplasm curators’ suggestions, some corrections have been made to the “Descriptor for the cotton-1985”. In particular, two categories – “Characterization and preliminary evaluation” and “Further characterization and evaluation” were combined in one category “Characterization and evaluation” in our descriptor because of lack of primary information for accessions that were brought from abroad to our collection. We introduced new sub-categories, such as 1) cotton boll size, and 2) natural leaf defoliation properties; in “Susceptibility to biotic stresses” we introduced those diseases and disease sources that were specific to Uzbekistan.

At present 501 cotton accessions out of 724 grown were fully described till section of ‘4.6-SEEDS’ of “Descriptor for cotton” while 223 wild accessions were described till section of ‘4.2 –INFLORESCENCE AND FRUIT”. Inputting data in remaining categories will be carried out consequently with obtaining data in future.

Perspectives

“Association-Genetics” Studies or Linkage Disequilibrium among Upland Cotton Accessions

QTL mapping is a now-classical approach to identify molecular markers linked to complex traits that are segregating in specific populations. This approach requires specific mapping populations, usually consisting of several hundred F_2 or recombinant inbred (RI) progeny, be developed from each germplasm accession to be examined for important genes effecting fiber quality and yield. Each population must be genotyped using hundreds, perhaps thousands of molecular markers. This population development and marker screening are extremely time-consuming, high-risk and expensive work — prohibitively expensive if dozens, let alone hundreds or thousands, of germplasm accessions are to be examined. However, geneticists mapping complex traits in the human genome have circumvented the need for large F_2 or RI mapping populations (which not available in humans) by making use of information contained within the genetic recombinations that have occurred in typical human populations during the course of recent evolution. DNA markers linked to a specific disease caused by a mutation in a particular gene will show a low level of recombination with that trait within human population groups. This “linkage disequilibrium” can be detected statistically, and has been used to map and eventually clone a number of genes underlying complex genetic traits in humans (Weiss and Clark, 2002; Schulze and McMahon, 2002). By this method, certain alleles at a marker locus are “associated” with alleles at a linked locus affecting a trait of interest.

The genetics of cotton (*G. hirsutum*) germplasm is in many ways quite similar to the genetics of human populations. Both have undergone relatively recent population bottlenecks, and both show evidence of significant horizontal gene flow among various population groups. Both of these attributes are useful to the linkage disequilibrium or "association genetics" approach. Although novel to cotton research, the association genetics strategy is, in fact, highly applicable to the identification of markers linked to fiber quality and yield through the examination of linkage disequilibrium of DNA-based markers with fiber quality and yield traits in a large germplasm collection. This approach will be enhanced through the use of gene-specific CAPS markers derived from “candidate genes” that may actually underlie the phenotypic diversity in fiber quality and yield traits.

Although some association genetics studies in humans have been biased for false-positive correlations (Terwilliger and Weiss, 1998; Weiss and Clark, 2002), this pitfall can be overcome through elements of improved experimental design, such as the inclusion of a larger sampling base, that are readily applicable in cotton. Furthermore, association genetic studies are likely to be more effective and powerful tools than QTL linkage analysis for studying complex traits because they can have greater statistical power to detect several genes of small effect (Tabor et al., 2002). This approach searches for differences in allele frequency between individuals with a particular phenotype and unrelated control individuals (Mauricio, 2001).

Currently, analyses of fiber data of evaluated cotton accessions from Uzbek germplasm in progress. In future, these selected accessions of *G. hirsutum* further will be evaluated in Winter Nursery of USDA-ARS at Mexico for agronomic performance; the fiber quality traits will also be studied. Ultimately, the recorded fiber quality and agronomic trait data in both locations along with above-given morphological traits will be correlated with DNA markers (LD-mapping) that showed genetic linkage to fiber quality and yield properties to identify new potential agronomically important genes. Future LD-mapping efforts using these genetically diverse Upland cotton accessions will reveal unique alleles of fiber quality genes that are specific to each ecotypes or wild gene pool as well as determine ‘candidate’ cotton accessions with unique genes/alleles that will be useful for future cotton breeding programs.

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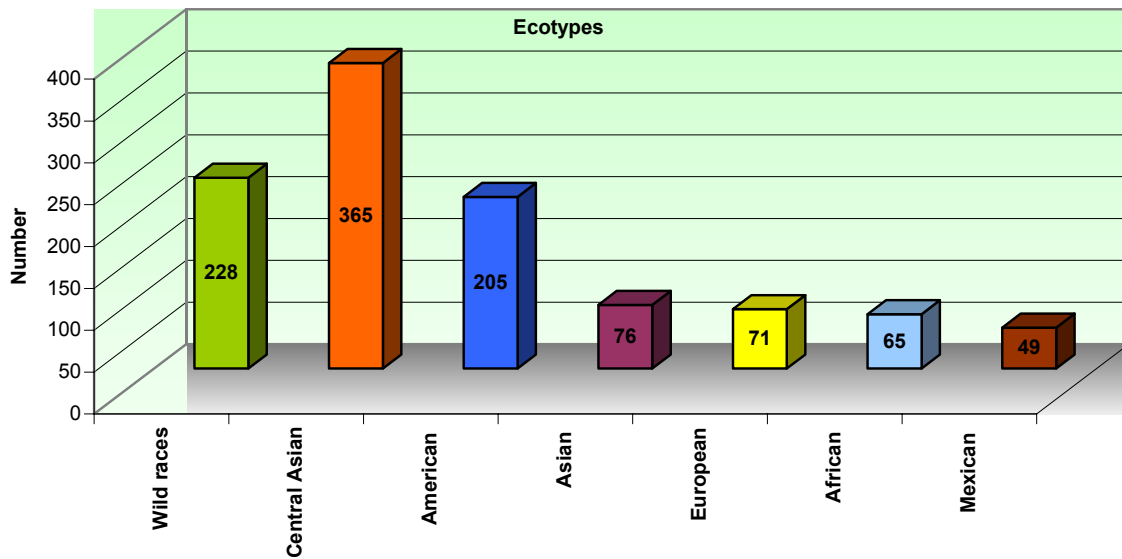


Figure 1. Selected *G. hirsutum* accessions from Uzbek cotton germplasm collection.

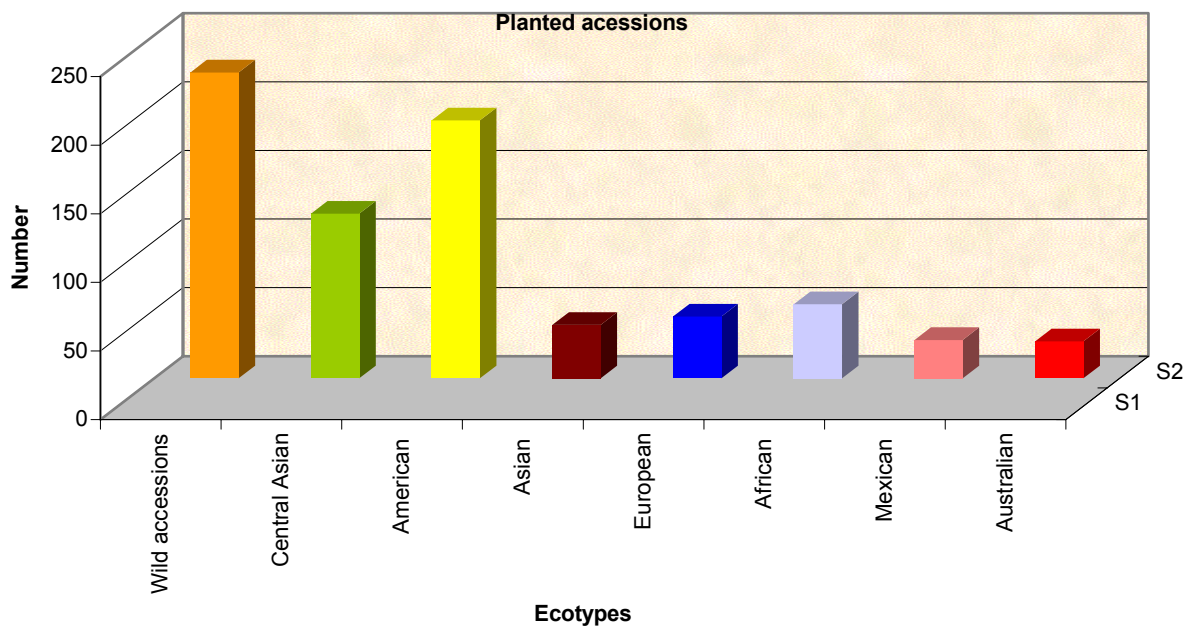


Figure 2. Grown cotton accessions from Uzbek cotton germplasm in 2003.

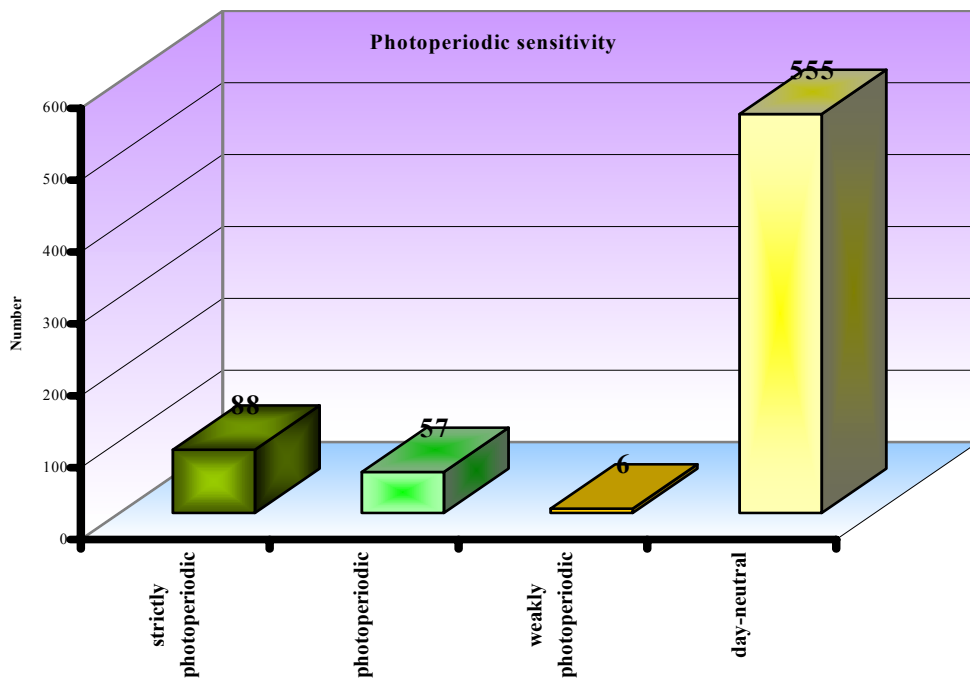


Figure 3. Photoperiodic dependency of evaluated accessions from Uzbek cotton germplasm.

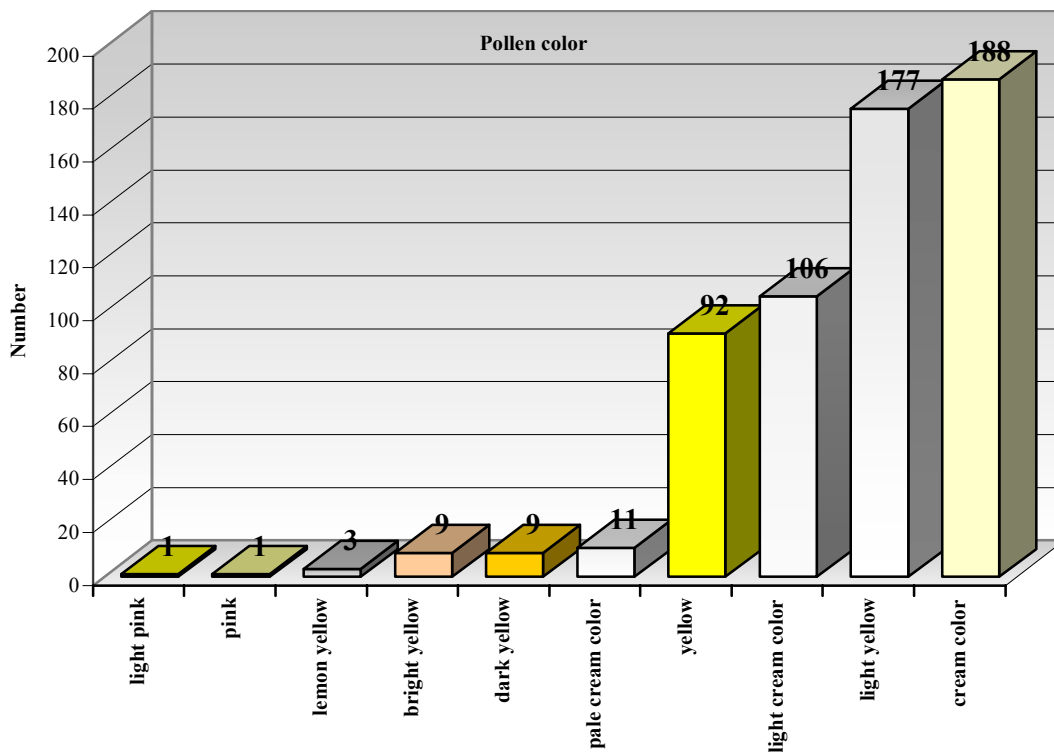


Figure 4. Diversity of evaluated variety accessions on pollen color.

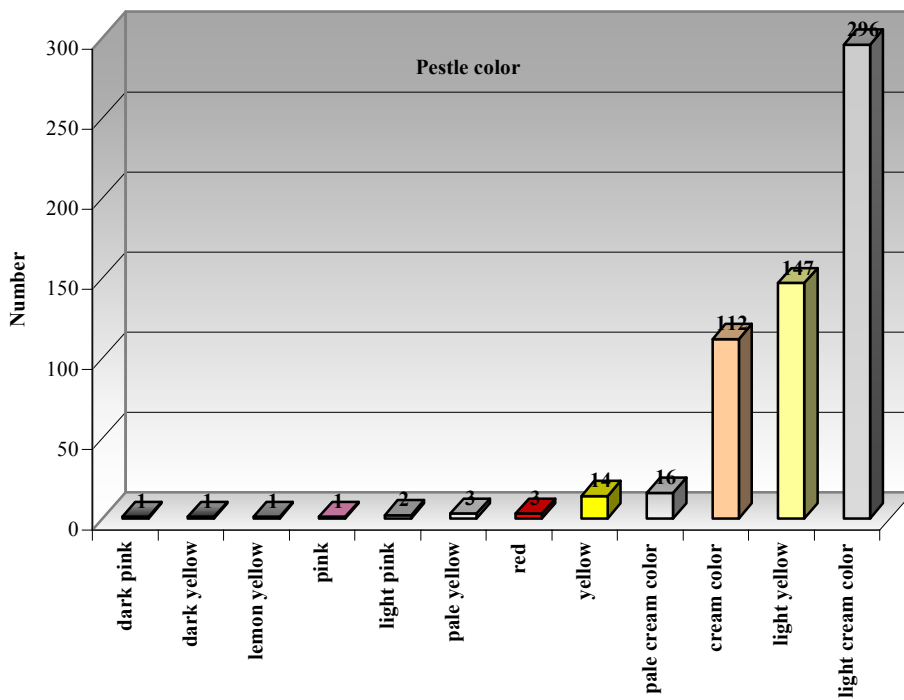


Figure 5. Diversity of evaluated variety accessions on pestle color.

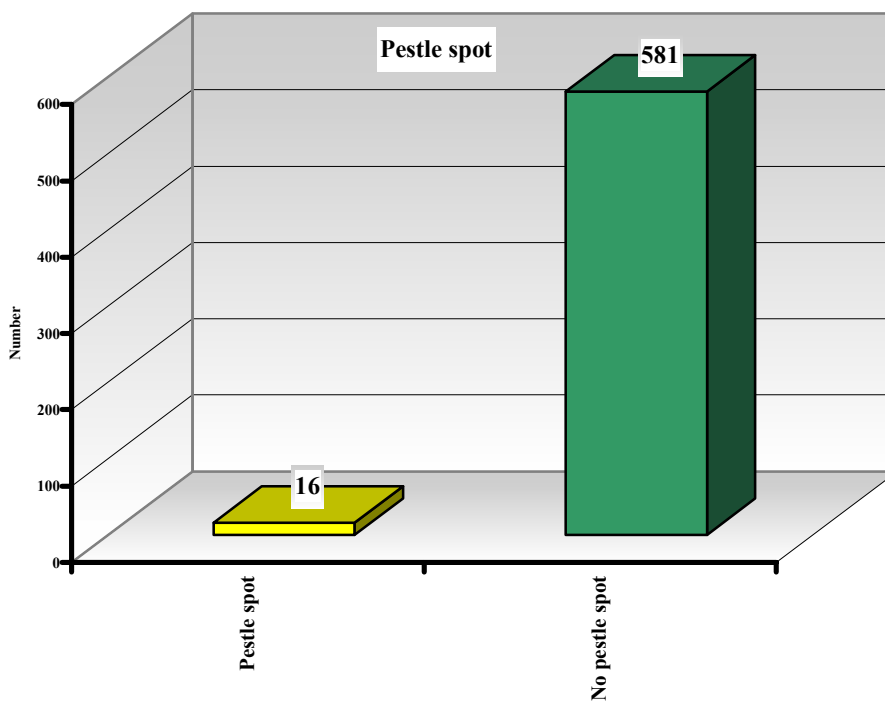


Figure 6. Diversity of evaluated variety accessions on pestle spot.