

**O‘ZBEKISTON
BIOLOGIYA
JURNALI**

**Узбекский
Биологический
Журнал**



**Uzbek
Biological
Journal**

3–2017

**O'ZBEKISTON RESPUBLIKASI FANLAR AKADEMIYASI
АКАДЕМИЯ НАУК РЕСПУБЛИКИ УЗБЕКИСТАН**

**O'ZBEKISTON
BIOLOGIYA
JURNALI**

3

2017

**УЗБЕКСКИЙ
БИОЛОГИЧЕСКИЙ
ЖУРНАЛ**

Издается с января 1957 г. по 6 номеров в год

**ТАШКЕНТ, ИЗДАТЕЛЬСТВО "ФАН" АКАДЕМИИ НАУК
РЕСПУБЛИКИ УЗБЕКИСТАН, 2017**

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Журнал зарегистрирован Агентством по печати и информации Республики Узбекистан 22.12.2006
Регистрационный номер 0052.

Изд. № 3-22. Сдано на верстку 10.10.2017. Подписано в печать 21.11.2017.
Формат 60x84¹/₈. Гарнитура Cambria. Бумага офсетная.
Уч.-изд. л. 8,0. Усл.-печ. л. 8,83. Тираж 112 экз.
Цена договорная.

Издательство "Фан" АН РУз
100047, Ташкент, ул. Я. Гулямова, 70

Отпечатано в типографском отделе Издательства "Фан" АН РУз. Заказ №16.
100047, Ташкент, ул. Я. Гулямова, 70

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UDC 575.113; 575.116

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SUCCESSES AND PERSPECTIVES OF GENOMICS IN UZBEKISTAN

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To timely address current and projected issues in cotton farming, and for boosting its cotton production, Uzbekistan has paid a particular attention to develop "omics" science based cotton programs, established modern research facilities, prepared new generation of biotechnologists and molecular breeders, and enhanced global collaborations with advanced centres worldwide. Scientists have concentrated and significantly advanced on molecular marker technologies, genetic mapping of important loci conditioning complex agronomic traits, cloning and characterization of important cotton genes and sequence signatures, application of marker-assisted selection (MAS) and genetic engineering technologies that resulted in development of Uzbekistan's own 'biotech' and MAS-derived novel cotton cultivars, which are being commercialized in near future. Here the key achievements, current developments, and future perspectives were revisited.

Cotton research is one of the priorities of Uzbekistan that concentrated on improvement of cotton fibre quality and lint yield, productivity, maturity, resistance to various diseases and abiotic stresses. Uzbekistan roughly produces about 5% of world fibre production and exports 10% of world fibre that puts Uzbekistan in the rank of sixth largest cotton producer and the second largest cotton exporter in the world [7]. Cotton farming occupies around 30% of all lands available for cultivation in the country, which produces 0.85-1.0 million metric tons of fibre valued at ~US\$0.9 to 1.2 billion [20, 32].

Uzbekistan cotton production is affected by reduction in area engaged for growing the cotton, policy environment (e.g., food security), the bio-security issues threatening cotton, and environmental stress factors such as shortages in irrigation and water deficiencies as well as soil salinization issues [6, 7, 33]. These are gradually influencing the fibre quality and productivity of cotton. Uzbekistan's cotton lint fibre yield was 753 kg/ha in 2010/11 and estimated at 804 kg/ha in 2012/13 or 812 kg/ha in 2013/14, which is close to the world average [7, 33, 34].

To address issues standing in cotton production, during past century cotton farming, Uzbekistan, being the northernmost cotton growing region, has built a sustainable agricultural system for cotton production, gained sufficient expertise, collected the richest cotton germplasm resources, bred highly adapted, early maturing cotton cultivars suitable to be grown in the northern latitudes and arid zones, and promoted cotton science through its multiple research institutions, centres and associations devoted to cotton growing, research, fibre preparation and its export [3, 4, 20, 32, 42].

Further, to address current and projected issues in cotton production, along with contemporary cotton breeding programs and institutions in the country, Uzbekistan paid a particular attention to develop its own "omics" science based scientific programs. A stepping stone into this development was Uzbekistan President's personal attention and government's significant investment during the past 22-years of independence of the country. This resulted in development of effective research environment, building a well-equipped modern laboratories for genomics and biotechnology research, and training of qualified scientists in this direction [7, 9]. Researchers developed strong international collaborations with leading cotton genomics and biotechnology laboratories worldwide to shape up the world science level cotton research program in Uzbekistan [9].

These collaborations accelerated the cotton genomics and biotechnology of Uzbekistan, enhanced

the development of genetically engineered cotton varieties, promoted technology transfer, and resulted in jointly patenting of newly developed products [28]. Achievements and perspectives of Uzbekistan's "omics" science programs related to cotton was highlighted by Abdurakhmonov in detail [7]. Here, the most important achievements on this direction were briefly revisited and some ongoing efforts and the future perspectives of scientific development were discussed.

Molecular marker development and genetic mapping.

A large number of cotton microsatellites and candidate gene-specific markers were developed [21, 27, 56]. Several agronomically important quantitative trait loci (QTLs), controlling the fibre length, lint yield and natural leaf defoliation traits were mapped [22, 25, 27]. To study photoperiodic flowering in cotton, a collection of photoperiod-converted radiomutants (32P) including their wild-type parental lines was investigated using SSR markers [23]. Further using bi-parental mapping populations developed via crossing the photoperiod-converted, day-neutral flowering radiomutants to the original photoperiodic wild parents, QTL regions responsible for photoperiodic conversions and causing the day-neutral flowering after the mutation were mapped. These QTL regions were localized on chromosome 5 of cotton [7, 49].

To address emerging threats of Fusarium wilt disease in Uzbekistan, a race/genotype distribution of FOV fungi in Uzbekistan was studied and most frequently occurring FOV races and their pathogenicity were identified [38, 51]. Several QTL loci contributing to FOV resistance in cotton were mapped using SSR markers [4, 5, 7].

Molecular tagging of major QTLs conditioning salt, drought and heat tolerance in cotton is in progress to apply modern molecular breeding tools in the development of abiotic-stress tolerant cotton cultivars. These ongoing efforts will address current needs of cotton farming in the event of projected climate change and water deficiency as well as land salinization increase in the region [64, 67].

According to reports, the chromosome substitution (CS-B) lines are effective way in enhancing fibre quality because one of the chromosome or chromosome arm of CS-Bs was replaced with Pima 3-79 line (*G. barbadense* L.), which have superior fibre quality [60]. The direct comparative analysis of CS-B lines showed that CS-B25 had significantly lower micronaire than TM-1 and seven CS-B lines (2, 6, 16, 18, 5Lo, 22Lo, 22sh) had greater lint percentage than 3-79 or TM-1 [61]. In addition, CS-B lines showed positive additive effect associated with fibre traits when these lines were crossed to five US cultivars [61].

To conduct fine QTL-mapping of fibre quality genes and further release of improved germplasm resources bearing Pima fibre quality loci in Upland cotton background, Uzbekistan cotton cultivar specific chromosome substituted recombinant inbred line (UzCS-RIL) mapping populations have been developed. For this purpose, within the frame of USDA/ARS-Uzbekistan cooperation programs, a set of CS-B lines developed by USDA/ARS scientists was obtained, and sexual crosses between several improved Uzbek cultivars and CS-B lines for chromosomes 16, 22, and 25 were performed [59, 62]. At present fifth generation of UzCS-RIL mapping populations have been developed and they are being phenotypically evaluated in multi-environmental conditions for fibre and major agronomic traits to conduct QTL-mapping using set of chromosome specific DNA markers.

Association mapping.

To apply modern genetic mapping methodology, for the first time, Uzbek cotton germplasm resources including a global set of ~1000 *Gossypium hirsutum* L. (so called Upland cotton - one of the widely grown allotetraploid cotton species) accessions from 37 cotton growing countries and 8 breeding ecotypes as well as wild landrace stocks, were characterized at molecular level and the extent of linkage disequilibrium (LD) for the cotton genome were identified [10, 16, 17, 18, 24]. The feasibility of LD-mapping in tagging of useful genes from germplasm resources was shown.

Further, the important fibre quality (fibre length and strength, micronaire, uniformity, reflectance, elongation and ect.) traits were measured in two distinct environments of Uzbekistan and Mexico. This study allowed researchers to design an "association mapping" (AM) study to find biologically meaningful marker-trait associations for important fibre quality traits that accounts for population confounding effects [17]. Several SSR markers associated with main fibre quality traits along with donor accessions were identified and selected for MAS programs [16, 18].

To enhance power of AM in cotton, based on above-mentioned association mapping studies on a global set of *G. hirsutum* germplasm resources, 17 most diverse *G. hirsutum* accessions were selected and used in genetic crosses with Uzbek cultivar Namangan-77, a genetic standard for *G. hirsutum* [10, 48, 63]. This effort led to create a nested association mapping (NAM) populations for cotton. A panel of 3400 $F_{2,3}$ generation NAM population individuals was developed and is being phenotyped for important agronomic and fibre traits in multiple environmental conditions of Uzbekistan. These NAM population individuals are also