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Introductory Chapter: Cotton Research Highlights

Ibrokhim Y. Abdurakhmonov

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1. Introduction

Cotton, derived from the Arabic word 'quotr' [1], belongs to *Gossypium* genus, which was also derived from the Arabic word 'goz', meaning a soft substance [2]. Cotton is a unique natural fiber producing most common fiber crop of the world, which provides humanity with cloth and vegetable oil, medicinal compounds, meal and hull for livestock feed, energy sources, organic matter to enrich soil, and industrial lubricants [3]. The genus *Gossypium* includes five 52-chromosome species ($2n=4x=52$) that arose some 1–2 million years ago [4–6] through allotetraploidization between the extinct representatives of A and D cotton genomes. Current representatives of putative ancestor-like A-genome species ($2n=2x=26$) are *G. herbaceum* (A_1) and *G. arboretum* (A_2), referred as the Old World cottons, whereas a putative ancestor like 'D-genome' species is *G. raimondii* (D_5) Ulbrich ($2n=2x=26$), referred as the New World cottons. There are five allotetraploids and 45 extant diploid cotton species that are classified into eight genomic groups (A to G, and K) [4]. The two allotetraploid cultivated species include the *G. hirsutum* [AD]₁ and *G. barbadense* [AD]₂. The remaining three wild tetraploids, *G. tomentosum* [AD]₃, *G. mustelinum* [AD]₄, and *G. darwinii* [AD]₅, are endemic to the Hawaii, Brazil, and Galapagos Islands, respectively.

Based on archeological evidence, humans utilized cotton fiber from at least more than four to seven thousand years ago, and cotton started to be grown as a fiber crop around three thousand years ago [1, 7]. Demands for natural fiber and cotton products had historically developed that advanced cotton research for the past century. Progressive scientific advances on cotton biotechnology and decoding of cotton genomes have resulted in the development of novel cotton cultivars with high yield, early maturity, improved resistance to pests, and superior fiber quality; however, a negative correlation between fiber traits and yield components/maturity as well as genetic "bottlenecks" in cultivar germplasm still hinders to overcome

conventionally longstanding problems of simultaneous yield and quality improvements in cotton [3, 8].

Cotton is grown on around 32–36 million-hectares area of tropical and northernmost agricultural latitudes in over 80 countries of the world [8, 9] to fulfill the current global needs of humanity for the natural fiber. For the past decade, however, global cotton production, demand, and market significantly fluctuated that caused a pressure on farmers, consumers, and traders. Area for cotton farming decreased by 9% to 31.1 million hectares leading to a total annual production of 21.74 million metric tons (MMTs) in 2015/16 [10]. The world average yield was 699 kg per hectare in 2015/16 and also decreased by 9% compared to previous season although the average yield is expected to increase to 735 kg/ha that would lead to increase a total world production by ~5% to 22.7 million tons in 2016/17 [10]. Similarly, world cotton consumption saw its 'ups' and 'downs' from 2007 and has been on decline since 2011 (~23 MMT) [11]; it has been 23.7 million tons in 2015/16 [12] with a similar expected consumption of 23.7 million tons in 2016/17 [10]. In other words, for the past two years world cotton production did not match world consumption of cotton, making the deficit to be covered from cotton stocks [13].

The significant fluctuations in world cotton production and consumption and decreasing yields require world cotton science to pursue new research directions and develop innovations to substantially increase and stabilize cotton production worldwide [14, 15]. In that, innovations on increasing yield with the improvements of fiber quality without affecting the maturity and other key agronomic traits are the key challenges faced by the cotton research community. In parallel, due to global climate change, increased heat and drought stress and biosecurity issues, it is demanded to improve drought, salt and heat tolerance traits as well as to increase the resistance characteristics of cotton cultivars to better respond to existing and emerging bacterial, fungal, and insect pest infestations [15, 16]. At the same time, increasing human population highlights an urgent need for investigations on cottonseed feed and food product qualities as well as cottonseed marketing, which moved cotton research and its increased financing in this direction for the past decade period [17]. Moreover, a continuous lower price of synthetic fibers compared to cotton prompts researchers to make cotton competitive with manmade fibers through improvements in quality, while being friendly to the environment [3, 15, 16].

2. Cotton research updates and advances

Cotton research has witnessed many progressive developments over the past half a century to address the above-mentioned challenges and limitations, and cotton researchers worldwide have initiated and performed largely coordinated research projects in every aspects of cotton sciences. These efforts have greatly accelerated cotton research worldwide and helped to address the key issues of cotton production and farming [7, 14].

Some of the best examples of these progressive developments of cotton research can be the worldwide collection, maintenance, and inventory efforts of 53,000 [18] to 63,946 [14, 19] world cotton germplasm resources preserved in major cotton-growing countries. Cotton research community has extensively developed cotton genetic mapping population re-

sources, and characterized large sets of DNA-based molecular markers such as simple sequence repeats (SSRs) and other restriction site-derived polymorphisms [20]. Researchers have widely and successfully applied molecular marker technology [21] to create densely covered genetic linkage maps of cotton genome(s) using various mapping populations. Scientists also succeeded to characterize cotton germplasm resources using both traditional quantitative trait loci (QTL) and modern linkage disequilibrium (LD)-based association mapping strategies [20–23]. Furthermore, cotton researchers have successfully developed a SNP marker system, and with the emergence and application of high-throughput next generation sequencing (NGS) technologies, a large number of SNPs were developed and made available for cotton research and breeding [24–27]. These advances provided an opportunity of shifting molecular marker applications from restriction enzyme or SSR-based characterizations toward SNP-based analyses and high-throughput genotyping by sequencing (GBS)-based mapping methods [14, 24].

As a result of advances on molecular markers and genetic mapping of important cotton traits, cotton breeding research has enriched with molecular breeding techniques and “breeding by design” approaches such as modern marker assisted-selection and genomic selection. This has not only accelerated the development of superior cotton cultivars with reduced cost and time, but it also helped in widening the “conventionally-narrow” genetic base of novel cultivars via introducing ‘yet-unexploited’ genetic diversities from cotton germplasm resources [8, 14, 20–23, 28]. Further, molecular marker technology has helped to establish and genetically differentiate 13 homeologous chromosome pairs accelerating cotton cytogenetics and genetics studies [29]. Detailed cytogenetic studies and the characterization of aneuploidy and translocation lines identified almost all 26 chromosomes of allotetraploid cottons and provided an innovative way of replacing the *G. hirsutum* (referred to as Upland cotton [8]) chromosome pairs with corresponding chromosome pairs of other cultivated and wild allotetraploids such as *G. barbadense*, *G. mustelinum*, and *G. tomentosum*. This effort created unique sets of chromosome substitution backcross (CS-B) cotton germplasm resources of Upland cottons that are widely used as a novel direction in cotton improvement, supplementing and enhancing conventional cotton breeding programs worldwide [30, 31].

Development of cotton genetic engineering (GE) and somatic embryogenesis research have further revolutionized cotton science and production for the past 30-year period, resulting in the development and commercialization of “biotech” cotton varieties of insect-pest and herbicide tolerance traits [7]. GE research with transgenic, cisgenic, and intergenic approaches and its integration with traditional and modern breeding methods such as backcross, gene stacking, and forward breeding [32] have helped and carry a great promise to boost the yield and quality of cotton, which undoubtedly opened a new era for cotton production worldwide [3, 7].

Most revolutionizing efforts and achievements of cotton research for the past 10 years, however, were the successful completion and assembly of whole genomes of the two diploids (D_5 and A_2 genomes) [33–35] and two widely cultivated Upland (*G. hirsutum*) [36, 37] and Sea Island allotetraploid cotton genomes (*G. barbadense*) [38]. These achievements have greatly accelerated current cotton research programs and undoubtedly will foster the exploitation of genetic signatures behind the key cotton traits, helping to overcome the above-mentioned negative

correlation and narrow diversity obstacles through a 'skilled' utilization and introduction of the complex effect genetic signatures. For example, due to understanding cotton genomes and genetic signatures, cotton researchers have discovered the key genes conditioning major fiber quality traits of cotton, where the improvement of key characteristics of fiber quality is the most priority task of cotton biotechnology worldwide [15, 20]. As an example, these findings include but not limited to the characterization and biotechnological utilization of (1) *GhMYB2A* and *GhMYB2D* genes and its trans-acting regulatory miR828 and miR858 signatures in trichome and fiber development [39]; (2) cotton phytochrome gene family and its RNA interference (RNAi) in simultaneous improvement of major fiber characteristics and several important agronomic traits of Upland cotton [40]; and (3) phytochrome signaling genes, affecting cotton fiber development through the regulation of the respiratory electron-transport chain and reactive oxygen species [41]. These advances, with many other seminal discoveries [7] that could not be covered in this short introduction chapter, provided novel biotechnological strategies to improve complex cotton fiber quality traits and paved the ways and opportunities to compete with man-made fibers.

The characterization of small RNA and microRNA world of cotton, including long noncoding natural antisense transcript (lncNAT) and long noncoding RNA (lncRNA) loci in *Gossypium* spp [15] and their functional associations with the genetic and epigenetic regulation of many complex traits of cotton were the other seminal achievements of cotton research in the past decade. "All of these natural miRNAs, lncRNA, and lncNAT are the key candidate loci to elucidate many challenging functional questions in cotton that will serve as a base for designing novel RNAi approaches and studies in the near future" [15]. These innovative developments in cotton research have provided "golden" opportunities for improving fiber quality parameters, oil and seed quality traits, cotton fertility and embryogenesis, pests, viral, bacterial, and fungal disease, and abiotic stresses through application of novel transgenomics (e.g., antisense and RNAi) [9, 15, 42] and genome editing tools (e.g., CRISPR/Cas) for cotton [43].

Cotton research advances for the past decade period include also the development of cotton bioinformatics research and resources to analyze and utilize a large volume of "gossypomics" data [44, 45] in the plant genomics and postgenomics era. This opened a new paradigm for the development of fine-tuned innovations for cotton breeding and farming with the integration of knowledge gained from "omics" sciences, system biology, and chemical genomics as well as from the translation of the concept of "personalized agriculture" [28], which should increase cotton production worldwide [14].

Similarly, progressive advances were made to understand cotton crop physiology in a complex view from seed germination to maturation stages under different temperatures, water, light, and nutrient applications, as well as in the event of global climate change scenarios [46, 47], which affects cotton yield and quality [16]. Cotton farming and management practices, the utilization of new generation of chemical and biological fertilizers and their assessment tools, including modern conservation tillage, winter cover cropping, site-specific nutrient applications [48], and remote sensing technologies [49], as well as integrated pest and disease management programs [50] have greatly accelerated and improved cotton production worldwide.

Cotton research community has also witnessed the advancements of cotton harvesting mechanizations and machinery [51], modifications in cotton ginning equipment and approaches [52], improvements in cotton fiber quality testing methodology and instrumentation such as high volume instrumentations (HVIs) and advanced fiber information system (AFIS) and cotton classification. All these along with developments in cotton combing, spinning, fabric manufacturing as well as fiber and yarn finishing technologies [53] have not only helped to grow the cotton industry, and increase the satisfaction and demand of consumers for natural fiber but also equipped cotton genetics/breeding programs with in-depth-trait-analysis tools to breed superior quality varieties of cotton and consumers demand.

At the same time, the above-highlighted past-decade scientific and technological advances; current challenges and demand of cotton production, market fluctuations; global climate change and increased biosecurity issues due to adapted and emerging pests and diseases; and global food security policies, as mentioned above, emphasize an urgent need to determine future new research directions, priority tasks and updated approaches and view for cotton research, which recently is well highlighted by world cotton research community under the leadership of International Cotton Advisory Committee (ICAC) [54]. This document highlights many new cotton research directions and grand tasks ahead requiring global collaborations, preparation of new generation of cotton scientists, large investments, and funding. In this context, to timely update, enhance, coordinate, and initiate largely integrated collaborative research and educational programs, discussions, and conferences on global cotton science, cotton researchers have recently established a new international organization, International Cotton Researchers Association (ICRA) [55], that together with ICAC and its member governments, International Cotton Genome Initiative (ICGI), universities and research institutions, is trusted to be a key player for the development and address new directions of cotton research in future.

3. Highlights of chapters

The book aimed to collect the latest research results of to cover some of the past decade achievements and updates on cotton research. Topics are generally divided in five sections including (1) cotton research structure and institutions, cotton agronomy, physiology and crop management, (2) cotton genetics, breeding and biotechnology, and (3) cotton-based products and textile research.

In particular, among many other proposed chapters from Iran and Uzbekistan, the first section incorporated a chapter from Venugopalan and his colleagues of the Central Institute for Cotton Research, India on cotton research structure and institutions in India, the largest cotton growing country in the world with about 12 million-hectares production area in 2016/17 [10]. Venugopalan and his colleagues successfully traced historical evolution of cotton research of the country with current research directions, developments, achievements, and “institutional mechanism responsible for varietal release, seed production and transfer of technology”. The chapter has also discussed future challenges and solutions of the cotton sector in the country and beyond.

In the cotton agronomy, physiology and crop management topic, Yali Zhang and his colleagues from the Shihezi University of China and Australian National University of Australia reviewed the mechanisms of cotton photoprotection during the leaf movement and drought conditions in nonfoliar organs, its impact on photosynthetic capacity and enzymes influencing the cotton yield. A multi-institutional joint chapter authored by Ademar Pereira Serra and his colleagues from Brazil and Tunisia presented a methodology chapter on the use of compositional nutrient diagnosis (CND) to better and efficiently assess the status, dynamics, interactions, and demand of nutrients in cotton that have advantages over the traditional methods of fertilizer management. Cotton research advances in farming and cultivation of cotton are well discussed by Jianlong Dai and Hezhong Dong from Shandong Academy of Agricultural Science, China. In a Chinese example, authors reviewed “the achievements, challenges, countermeasures and prospects for intensive cotton cultivation” highlighting a need to apply the light and simplified farming and cultural system for future sustainable cotton production in China. Further, Price and his colleagues from USDA-ARS, USA have presented a research study on the use of winter cover crops in a corn and cotton plantings. Results have shown an importance of early cover plant planting and its late termination that led to increased biomass accumulation, helping to suppress early-season weeds in cotton and corn plantations. Researchers have suggested optimal schemes for winter cover crops using crimson clover or rye crops.

The cotton genetics, breeding and biotechnology section has included four chapters. The first chapter of Yuksel Bolek and his colleagues from Kahramanmaraş Sutcu Imam University and Agriculture University Faisalabad of Pakistan has been devoted to review the achievements and perspectives of molecular breeding of cotton. The chapter has described the development and types of DNA markers, genetic mapping approaches and mapping population resources, breeding challenges for polygenic traits and schemes for molecular breeding, including marker-assisted backcrossing, pedigree selection, gene pyramiding, and marker-assisted recurrent selection as well as database resources in cotton. Authors also reviewed the efforts on some advanced approaches and technologies such as NGS, GBS, association mapping, and ‘targeting induced local lesions in genomes (TILLING)’. The review demonstrated significant advances made on molecular breeding and genomics of cotton for the past decade and highlighted future perspectives. Multi-institutional collaborative chapter of Marina Sanamyan and her colleagues from Uzbekistan and the USA has described advances made on the molecular and cytogenetic characterization of “yet-unexplored” cotton cytogenetic collection of Uzbekistan. Using microsatellite markers and a well-defined tester set of translocation lines, authors succeeded to detect the chromosome identity of “unknown” monosomic lines from the collection, which will be useful for cotton genetics and improvement programs. In a continuation of highlighting the cotton genetics and breeding advances of cotton research community, Selome Nyaku and his colleagues from research institutes of Ghana and the USA reviewed the achievements of world laboratories on the identification of tolerance and resistance mechanisms, and evaluation, introgression and functional analysis of reniform nematode resistance genes in cotton. It is noteworthy to mention that reniform nematode is one of the most devastating diseases causing approximately \$130 million loss every year in the U.S. cotton belt [56]. Authors provided a positive conclusion on great perspectives of current omics-derived results to solve reniform resistance problems in cotton.

A book chapter on cotton biotechnology has incorporated the chapter by Abdul Qayyum Rao and his colleagues from the University of the Punjab and the University of Central Punjab, which reviewed the advances made on plant transformation techniques, and its application and suitability for tissue culture of cotton. Authors have described plant regeneration, embryo formation, and genetic vector constructions used in cotton transformation, largely concentrating on all major transformation techniques and methods used in plant transformation, their advantages and disadvantages, and suitability for cotton transformation.

The last section of the book consists of three chapters on cotton-based products and textile research efforts. Multi-institutional group of H.-B. Yue and his colleagues presented their research results on the utilization of glandless cotton seed flour to produce environmentally nonhazardous bioplastic films. Authors have investigated optimum synthesis conditions and various chemical modifications with the analysis and characterization of structure, stability, and biodegradability of obtained bioplastics in different thermal and water treatment conditions. This chapter concluded the usefulness of these cottonseed-derived bioplastics, and among other important points in this direction, highlighted that the cotton seed-derived bioplastics can be significantly improved through the genetic modifications of amino acid compositions of specific cotton seed proteins. The two other chapters are related to modern approaches for textile finishing of cotton fibers. In particular, Franco Ferro and his colleagues from Italy have presented a chapter on UV-assisted differential cotton fiber dyeing using direct and reactive dyes that yields various chromatic effects. This chapter highlighted UV-aided surface modifications of cotton fabrics to improve oil and water repellency, and the use of UV grafting based chitosan finishing to obtain washing resistant antimicrobial cotton fabrics. Similarly, Issa M. El Nahal and his colleagues from Al-Azhar and Islamic Universities of Gaza, Palestine, investigated different methods of synthesis of metal oxide nanoparticles and their deposition onto cotton fibers that resulted in enhancement of antimicrobial activity of cotton fabrics. Authors' contributions exemplified the advances made on application of modern nanotechnologies for cotton textile research.

4. Conclusions

The cotton research has significantly progressed in the last 30 years that resulted in many seminal and historic discoveries in many aspects of cotton science. Cotton research community decoded whole genome of important cotton species, and thus opened a new era for more "targeted" research than ever. Highlighting some updates, all 12 chapters compiled in this book cover a wide range of cotton research topics and describe the latest developments in cotton science and research from both developed and developing country perspectives. The editor of this book is sure that the chapter materials will enrich data, results, and opinions on the progress of worldwide cotton research that should be useful for readers interested with this unique and the most important fiber crop of our planet.

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Author details

Ibrokhim Y. Abdurakhmonov

*Address all correspondence to: ibrokhim.abdurakhmonov@genomics.uz;
genomics@uzsci.net

Center of Genomics and Bioinformatics, Academy of Science of the Republic of Uzbekistan,
Tashkent, Uzbekistan

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