



Resequencing unveiled the genetic basis of important traits in Cotton

- Dr Santosh HB and Dr A Manivannan, Scientists, ICAR-CICR

Cotton is one of the most important cash crops grown worldwide. It is known that the modern cultivated allotetraploid cotton (*Gossypium hirsutum* and *Gossypium barbadense*) have evolved from their 'A' genome diploid progenitors (*Gossypium herbaceum* var *africanum*) and 'D' genome diploid progenitor (*Gossypium raimondii*). The recent issue of the journal '*Nature Genetics*' published two research papers having a great potential impact on future of cotton improvement through cutting edge resequencing technology. In one of the study by Xiongming Du and co-workers, the high-quality *G. arboreum* genome assembly (Li, *et al.*, 2014) was upgraded through integration of different technologies achieving lower number of incongruities and substantially longer syntenic blocks in the corresponding chromosomes of the 'At' subgenome. They resequenced 230 *G. arboreum* (A_2) and 13 *G. herbaceum* (A_1) accessions representing most of the phenotypic and geographical diversity known for diploid cottons in China to generate a map of genome variations, on 'Illumina HiSeq 2500' platform, with an average coverage depth of ~6.0x for each accession. They have identified 17,883,108 high-quality SNPs and 2,470,515 indels, with an average of 10.5 SNPs and 1.4 indels per kilobase. A total of 242,449 SNPs (1.36%) and 16,816 (0.68%) indels were located in coding regions of 36,205 *G. arboreum* genes. Using the sequence information thus generated, they analyzed the population structure and genomic divergence trends to identify the genetic basis of important traits. They have identified 98 significant peak associations for 11 agronomically important traits in *G. arboreum* through genome wide association study (GWAS). This study is expected to provide the needed vital information in understanding the evolution of the 'A' genome of cotton and the identified candidate loci may also facilitate the genetic improvement of cotton lint production.

In another study, Zhiying Ma and co-workers have resequenced a core collection of upland cotton comprising 419 accessions with 6.55-fold coverage depth and identified approximately 3.66 million SNPs for evaluating the genomic variation. They have identified a total of 3,665,030 population SNPs of which 224,201 were located within 17,446 protein-coding genes, 70,959 were located in upstream or downstream regions, and the remaining 3,369,870 SNPs were located in intergenic regions. They evaluated these accessions across six agroecologically diverse locations sprawling three cotton-growing regions in China for two years (total 12 environments) and conducted GWAS to identify the genomic regions influencing 13 fiber-related traits. They found more SNPs for fiber quality than fiber yield, and more fiber genes were detected in the 'Dt' than the 'At' subgenome. They reported 7,383 unique SNPs located within or near 4,820 genes of upland cotton which are significantly associated with the fiber-related traits. They found that fibre length had the highest number of associated SNPs, followed by maturity and spinning consistency index. They further found that 4,754 and 2,587 loci associated with fiber-related traits were located in the 'Dt' and 'At' subgenome, respectively. This study collected the largest cotton sequence dataset reported till date to identify several previously undescribed causal genes for days to flowering, fiber length, and fiber strength. It also highlights the profound effect of domestication and breeding in increasing the frequency of elite alleles through phenotypic selection. Both the studies emphasize the potential application of resequencing technology in future of cotton breeding and improvement through molecular-marker selection and genetic manipulation.

Suggested Reading

1. Li, F. et al. (2014). Genome sequence of the cultivated cotton *Gossypium arboreum*. *Nature Genetics*, 46: 567–572.
2. Du X. et al., (2018). Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits, *Nature Genetics*, 50: 796–802.
3. Ma Z. et al. (2018). Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield, *Nature Genetics*, 50: 803–813.

Sh Alok Kumar Gupta, ICAR Governing Body Member Visits ICAR-CICR, Nagpur

Shri Alok Kumar Gupta, Hon'ble member of the ICAR-Governing Body along with Shri Naresh Sirohi, National Vice President, Kisan Morcha visited ICAR-CICR, Nagpur in the forenoon of 9th April, 2018. Dr. D. Blaise, Head, Crop Production Division and Director (In-charge), ICAR-CICR welcomed the dignitaries and provided a brief introduction about the institute and the activities of ICAR-CICR. The dignitaries visited the Biotechnology, Bt Referral, Molecular Biology and Crop Improvement laboratories and interacted with scientists who explained the research work being done. Later, an interactive meeting under the Chairmanship of Shri Alok Kumar Gupta was held in the Director's Committee room. Dr. M. V. Venugopalan, Principal Scientist (Agronomy) & In-charge PME Cell made an elaborate presentation on cotton highlighting the history of cotton, the glorious period of *desi* cotton and the turning points in the history of cotton in India with which cultivation of *desi* cotton was replaced by American (*G. hirsutum*) cotton and intra-*hirsutum* hybrids including BT cotton. He also presented the research achievements of ICAR-CICR and the efforts envisioned by ICAR-CICR to reintroduce *desi* cotton in 15-20% area and American Cotton varieties to 35-40% area and restricting the cultivation of hybrids to fertile soils in the irrigated regions. All the scientists actively participated in the deliberations. Summing up the discussions, Shri A.K. Gupta, Hon'ble member of the ICAR-Governing Body, appreciated the efforts of the scientists of ICAR-CICR and thanked the participants for providing an insight of the current cotton scenario and the way forward. The meeting ended with a formal vote of thanks proposed by Dr. D. Blaise, Head, Crop Production Division and Director In-charge.



Produced and Published by:

Chief Editor :

Associate Editor, design & Media Support :

Editors:

Dr Vijay N. Waghmare, Director, CICR

Dr. S. M. Wasnik

Dr. M. Sabesh

Dr Dipak Nagrale, Dr H. B. Santosh,

Dr D. Kanjana , Dr. Sain, Dr Rakesh Kumar

& Dr Pooja Verma,

Publication Note: This Newsletter presented online at http://www.cicr.org.in/cotton_innovate.html

Cotton Innovate is the Open Access CICR Newsletter

The Cotton Innovate – is published weekly by

ICAR-Central Institute for Cotton Research

Post Bag No. 2, Shankar Nagar PO, Nagpur 440010

Phone : 07103-275536; Fax : 07103-275529;

email: cicrnagpur@gmail.com, director.cicr@icar.gov.in

Citation : Cotton Innovate, Issue-1 Volume-6, 2018,
ICAR-Central Institute for Cotton Research, Nagpur.