Cotton is known for its natural textile fibre, nutrient rich oil and feed. World’s production and consumption of cotton fibre in 2014-15 was 26.18 and 24.24 Million Tons, respectively (ICAC, 2015). Genetic improvement for higher and superior fibre production and modifying cottonseed for better food and feed will ensure effective utilisation of cotton and its by products for betterment of mankind. One of the recent milestone in cotton science is decoding of cultivated cotton genomes and their progenitors, which will further helps in identifying contributing genetic factors for the useful economic traits within Gossypium genus. The genus Gossypium comprises of 46 diploid (2n = 2x = 26) and 6 tetraploid (2n = 4x = 52) species. Diploid species of Gossypium has been categorised in to eight genome groups as A-G and K. Tetraploids cottons (AD genome) have evolved through the process of hybridization followed by polyploidization between cultivated A and D genome diploid species. It is fascinating to note that tetraploid cotton which are known for superior fibre quality and high yield potential have evolved from the inter-specific hybridisation of A genome diploid species (G. arborum) having poor fibre quality traits with D-genome diploid species (G. raimondii) that do not even produce spinnable fiber.

It was estimated that genome size of G. arborum (1,746 Mb/1C) is two times bigger that of G. raimondii (885 Mb/1C) (Hendrix & Stewart, 2005). With the recent advances in scientific and technological processes, diploid progenitor of American cotton, G. Raimondii (DS) genome was successfully sequenced and assembled in 2012 independently by two research groups (Wang et al., 2012 and Paterson et al., 2012). Another putative diploid cultivated donor species, G. arborum (A2) genome was also sequenced and assembled (Li et al., 2014). In this current year, most predominantly cultivated species of cotton, G. hirsutum (AD) genome sequence was assembled and published by two research groups (Li et al., 2015 and Zhang et al., 2015). Major highlights of the published genome sequence information are tabulated here.

### Suggested readings:

<table>
<thead>
<tr>
<th>Cotton Species</th>
<th>Genome Code</th>
<th>Estimated genome size (Hendrix &amp; Stewart 2005)</th>
<th>Sequenced genome size</th>
<th>Materials used in the study</th>
<th>Sequencing platform</th>
<th>N50* Contig Scaffold (kb)</th>
<th>No. of predicted protein coding genes</th>
<th>No. Predicted MicroRNA</th>
<th>Percent repeat sequences</th>
<th>NCBI Accession Code.</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gossypium raimondii</td>
<td>D5</td>
<td>880Mb</td>
<td>775.2Mb</td>
<td>DS-3 (CMD10)</td>
<td>Illumina HiSeq 2000</td>
<td>2,284kb</td>
<td>40,976</td>
<td>348</td>
<td>57.0</td>
<td>PRJNA2769</td>
<td>Wang et al., 2012</td>
</tr>
<tr>
<td>Gossypium raimondii</td>
<td>D5</td>
<td>880Mb</td>
<td>737.8 Mb</td>
<td>G. raimondii</td>
<td>Applied Biosystems 3730xl, Roche 454XLR &amp; Illumina GAIIx</td>
<td>18.8Mb</td>
<td>37,505</td>
<td>364</td>
<td>61.0</td>
<td>PRJNA171262</td>
<td>Paterson et al., 2012</td>
</tr>
<tr>
<td>Gossypium arboreum</td>
<td>A2</td>
<td>1677-1746Mb</td>
<td>1694 Mb</td>
<td>Cv. Shixiya1 (SXY1)</td>
<td>Illumina HiSeq 2000</td>
<td>665.8kb</td>
<td>41,330</td>
<td>431</td>
<td>68.5</td>
<td>SRA150181</td>
<td>Li et al., 2014</td>
</tr>
<tr>
<td>Gossypium hirsutum</td>
<td>AD</td>
<td>2347 – 2489Mb</td>
<td>2,173 Mb</td>
<td>TM-1</td>
<td>Illumina HiSeq 2000</td>
<td>764kb</td>
<td>76,913</td>
<td>301</td>
<td>67.2</td>
<td>PRJNA259930</td>
<td>Li et al., 2015</td>
</tr>
<tr>
<td>Gossypium hirsutum</td>
<td>AD</td>
<td>2347 – 2489Mb</td>
<td>2400Mb</td>
<td>TM-1</td>
<td>Illumina HiSeq 2000 Sanger sequencing</td>
<td>1600kb</td>
<td>70,478</td>
<td>602</td>
<td>64.8</td>
<td>PRJNA248163</td>
<td>Zhang et al., 2015</td>
</tr>
</tbody>
</table>

*Quality indicator of a genome assembly
Pink bollworm incidence noticed in Karnataka

Dr Shivaleela, Asst Prof Raichur and Dr V. Chinna Babu Naik, Scientist, CICR

The incidence of pink bollworm on Bt-cotton hybrids (BG-II) was found for the first time at MARS, Raichur, Karnataka at 100 DAS. Larval recovery and percent infestation in Bt-cotton hybrids (BG-II) 76.00% and 93.00% respectively. However, larval recovery and percent infestation in NBt (DCH-32) at 100 DAS was recorded 112.00% larval recovery and 93.00% infestation in NBt (DCH-32) green bolls were recorded. The incidence of pink bollworm was known in Gujarat but recently it expanded in other cotton growing states like Maharashtra, Telangana, Andhra Pradesh and Karnataka on Bt cotton.

ICAR-CICR celebrated 67th Republic Day

The 67th Republic Day was celebrated in ICAR-CICR with bliss and fervor on 26th January 2016. The National flag was hoisted by Dr. K. R. Kranthi, Director, CICR, Nagpur. In his address, he appreciated and encouraged the scientists and other staff who had contributed for the significant achievements of the institute especially for the efforts put in on, e-Kapas- for sending advisories to farmers through voice SMS, classification of whitefly/CLCuD tolerant and susceptible hybrids in North India for the benefit of farmers, identification of early duration cotton variety bursting in about 110 days, experiment on cropping systems, development and testing of stripper type harvester, survey and resistance monitoring of Pink Bollworm. He also congratulated scientists for best oral and poster presentations in national and international conferences and also for best representation of scientific views in international forums. He asked all the scientists and other staff members to work as a team to address the problems/crisis faced by the Indian cotton farmers. Dr. G. Balasubramani, Secretary, Recreation Club, had arranged various games for all the staff members and the winners were distributed Prizes. All the Staff of ICAR-CICR joined the celebrations.
Visit of training participants of CIPMC to CICR

Forty participants undergoing training at Central Integrated Pest Management Centre, Civil lines Nagpur on "One - month Season Long Training Program on Vegetables" visited CICR, Nagpur on 8th January 2016. Dr Vishlesh Nagrare, Sr Scientist explained the institute activities of CICR.

News Paper Clippings

"Marathwada drought hit cotton yield in Maha"

Nagpur: The severe pest attack in Gujarat and Punjab has led to significant loss of cotton production. Till December end only 10331 lakh bales had arrived in the market from the 10 major cotton growing states. It includes 18331 lakh bales from north zone covering Punjab, Haryana and Rajasthan, 6000 lakh bales from central zone across the states of Gujarat, Maharashtra, Madhya Pradesh, 3855 lakh bales from south zone covering Telangana, Andhra Pradesh, Karnataka and Tamil Nadu.

Keshav Kranthi, director of citrus based Central Institute for Cotton Research, said the unexpected attack of white fly in Punjab and pink boll worm in Gujarat has brought down the yield. Pink boll worm seems to have developed resistance to bell guard H in Gujarat. Also, because of virtually no rain in November and December that extend the total output, this year's production has fallen.

The production has fallen in Maharashtra compared to last year's. The production was 16.80 lakh bales of cotton from Marathwada. Still, Maharashtra and Gujarat continue to be highest producers, he said. As per Cotton Association of India (CAI), this year the estimated production was 61.60 lakh bales and 37.65 lakh bales from south zone covering Telangana, Andhra Pradesh, Karnataka and Tamil Nadu.

Cotton growers, who have suffered losses due to drought, are crying foul over state government not insuring cotton in the compensation list of crops.


Dr. K. R. Kranthi, Director, CICR, Nagpur

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