

Biodiversity of Indian Germplasm of Cotton and Its Use for Genetic Enhancement

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Cotton production in India was stagnant at 12.3 to 17.7 million bales over the decade 1992–2003. The introduction of new technologies during the early part of the decade, notably Bt-cotton technology, hybrids, and insecticides with novel modes of action resulted in doubling of production and productivity from 2001–2007. It is generally believed that amongst the new technologies, Bt-cotton has contributed the greatest in enhancing productivity levels in all the major cotton producing countries of the world. However, Bt-cotton incorporated Cry1Ac, which is the most toxic Bt-protein to bollworms, known to be the best amongst all known Bt-toxins characterized until date. The recent spurt in the transgene deployment of new genes represents an additional array of toxins to broaden the target pest spectrum, to enhance the efficacy of Cry1Ac and also to increase gene diversity as one of the resistance management strategies. It is likely that the gains obtained due to the Bt-technology may not be sustainable infinitely, therefore, apart from the search for new xenobiotic genes, it is important to utilize the gene pools available within the existing cotton germplasm to develop better cultivars that can have a long lasting effect in reducing pest populations and enhance productivity across the globe. The two diploid species, *Gossypium arboreum* and *G. herbaceum*, which have their origins in Asia, are categorized under the "primary germplasm" pool of diploid species. Primary germplasm pool represents a group of biologically compatible species, with a high recombination potential. Thus far the gene pool of the cultivated *Gossypium* diploid species appear to have been the least exploited, despite having greater genetic diversity as compared to the gene pool of the cultivated *Gossypium* allotetraploid species. The *G. arboreum* germplasm of India with about 1800 accessions can be an extremely valuable resource for the genetic improvement of tetraploid cotton, especially for several favorable traits including fiber qualities, color and resistance to biotic and abiotic stresses. The secondary and tertiary gene pools are yet to be exploited, due to poor biological compatibility with the cultivated genotypes. The recent advances in the development of fiber specific ESTs and large insert cotton BAC resources provide a great scope for genetic improvement. Several DNA marker linkage maps have been published. DNA microsatellites (Simple sequence repeats, SSRs) have been identified in the cotton genome and are being placed on linkage maps. However, if the ambiguities due to gene duplication and homeologies in the tetraploid genome have to be resolved, it would be necessary to develop physical maps and integrate them with the genetic maps. Genetic and physical maps with diploid species would have the advantage of circumventing the problems associated with gene duplication and homeologies associated with the tetraploid genome. Markers for the useful traits can be used for introgression of the useful traits for improvement of the "primary germplasm" pool so that the current imbroglio with a relative saturated productivity status is broken, so as to ensure that the enhanced production and productivity levels continue to grow unabated.