

Genes From the Wild A Bountiful Harvest

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Crops were domesticated for the first time about 10,000 years ago. Humans selected the plants suitable to them, from the huge genetic variation available in the wild. They were completely ignorant about the source of variation in the plant populations. Systematic manipulation of genes for crop improvement is a relatively recent phenomenon, which started only after the rediscovery of Mendel's principles of inheritance in the last century. Phenomenal improvements in the yield of several crop plants such as wheat, corn, rice, cotton etc. have been witnessed. Genetic resources (primarily belonging to the domesticated species) have substantially contributed in these increases. Nevertheless, a few crop plants, for instance sugarcane and tomato have greatly benefited from wild relatives for their improvement. Domestication followed by modern plant breeding have resulted in narrowing down of the genetic base of several crop plants such as wheat and soybean. Plant breeders tend to hybridize genetically related high yielding genotypes in order to breed new cultivars. They believe in: cross best with the best, and hope for the best ! In the process, genetically more diverse, but poor yielding wild relatives do not find a place in the breeder's crossing block. Limited genetic diversity in crop plants makes them genetically incapable to resist major losses due to insect and disease epidemics. For example, whitefly epidemic devastated cotton crop on approximately 1.5 million ha in north Indian states of Punjab, Haryana, and Rajasthan during 2015, resulting in reduction of cotton productivity in Punjab from five year (2010-2014) average of 573 kg lint ha⁻¹ to 197 kg lint ha⁻¹ (Kumar et al. 2020). It would not be out of place to mention the Southern corn leaf blight epidemics of 1970, which led to huge drop in maize yields in the United States. In this case, susceptibility to the disease was associated with wide spread use of a single cytoplasmic male sterility source. This prelude underscores the risks of genetic uniformity/similarity of crop cultivars and the urgent need for widening the genetic base by introducing novel alleles from the related wild species, unadapted germplasm and landraces etc.

Crop productivity is not exempted from the consequences of climate change. It has been suggested that higher temperatures may result in reduced water use efficiency, considerable fruit drop in cotton, thereby lowering the yield and altering the fibre quality (Bange and Broughton 2023). Among the various biotic stresses, cotton leaf curl disease (CLCuD) is a serious threat to Upland cotton cultivation in North-Western India and Pakistan. Huge economic losses (US\$ 5 billion) from 1992-1997 in Pakistan (Bridson and Markham 2000) and about 40% drop in cotton

yield in India (Bhattacharyya et al. 2017) have been documented. The disease has spread to China as well. These three Asian countries produce nearly 49 per cent of the global cotton and account for 84.5 per cent of the world's cotton farmers (Kranthi 2022). Therefore, management of this malady is crucial for sustainable global cotton production. Unfortunately, resistance to this viral disease is no more available in Upland cotton as the previously resistant Upland cotton cultivars/stocks have been compromised due to the emergence of new resistance-breaking viral strains. Several related cotton species such as *Gossypium thurberi*, *G. anomalum*, *G. arboreum* (Akhtar et al. 2010); *G. herbaceum*, *G. gossypoides* (Azhar et al. 2013); *G. armurianum* (Pathak et al. 2016); *G. robinsonii* (Azhar et al. 2011); *G. stocksii* (Nazeer et al. 2014) etc. are known to possess resistance to CLCuD. It is difficult to transfer genes/traits from related species to Upland cotton due to one or the other barriers/bottlenecks. Though working with related/wild species is pretty challenging and frustrating, yet it is very much a rewarding exercise. For instance, we had to pollinate 15,898 flowers of the interspecific hybrid (*G. hirsutum*/*G. armurianum*) with Upland cotton, only to obtain four backcross plants ! After several backcrosses followed by numerous rounds of self-fertilization, we were able to develop cotton advance lines possessing resistance to CLCuD. A single major gene introgressed from *G. armurianum* conferring resistance to CLCuD has been mapped. Another potent source of CLCuD resistance is Mac 7, an introgression line of Upland cotton (Zaidi et al. 2020). Several QTL associated with CLCuD resistance were identified on chromosomes 3, 5, and 16 in Mac 7 (Schoonmaker et al. 2023).

Bollworms used to inflict heavy losses to cotton crop in India. Development and commercialization of transgenic Bt cotton provided a big relief from the bollworm infestation. However, Bt cotton hybrids grown in the country are highly susceptible to sap-feeding insect pests (Kranthi and Stone 2020), resulting in the shift in pest profile from bollworms to sap suckers. Climate changes too have an important role to play in the insect pest dynamics. Studies on population dynamics of key pests in the Indian Punjab show that thrip incidence is increasing and their population remains high throughout the cotton season. Similarly, leafhopper scenario has changed in the last decade with higher population throughout the crop season. Whitefly still remains a key challenge as evidenced by the occurrence of whitefly epidemics in 2015, which destroyed cotton crop on 1.5 million ha in North India. Resistance/tolerance to these sucking insect pests is available in the related species. For instance, *G. arboreum*, one of the two cultivated diploid cotton species possesses strong resistance to leafhopper (Sidhu and Dhawan 1980; Nibouche et al. 2008). Using bulked segregant analysis in the interspecific population derived from Upland cotton × *desi* cotton crosses, we tagged two SSR markers (NAU 922 and BNL 1705) located on chromosomes A5 and A11 respectively, with leafhopper tolerance (Jindal et al. 2022). Mac 7, an introgression line developed by the United States Department of Agriculture possesses tolerance to whitefly as well . We have identified two genomic regions associated with white tolerance in Mac 7. In another study, we found that *G. arboreum* genotype was more tolerant to thrips as compared to Upland cotton.

It is said that seeing is believing. However, appearances may be misleading sometimes. For example, fruits of *L. hirsutum*, a wild tomato species do not change colour even after ripening and remain green. However, genes for enhanced red pigment (lycopene) have been introgressed from this species into cultivated tomato ! (c.f. Tanksley and McCouch 1997). Similarly, genes for increased fruit weight have been introduced into cultivated tomato from *L. pimpinellifolium*, which possesses very small sized fruits ! (Tanksley et al. 1996). Upland cotton and Pima cotton are the products of a hybridization event that happened about 1 - 2 million years ago and involved progenitor species resembling today's *G. herbaceum* (AA) and *G. raimondii* (DD). Several molecular genetic studies have demonstrated that many genes conferring better fibre properties reside onto the D-genome. It is interesting to note that the D-genome donor itself is lintless !

Literature is full of reports where related species/wild relatives of crop plants have been used to incorporate genes of economic importance . Of the 52 species recognized so far in the genus *Gossypium*, only four are being cultivated for their fibre, suggesting an untapped ocean is available to the cotton scientists for exploration and utilization. The availability of cotton genomics resources and advance biotechnological tools would facilitate this endeavour . I take this opportunity to suggest that a "Centre of Excellence on Pre-Breeding of Cotton" may be established. Let us join hands for improving cotton as it is always better to become collaborators rather than competitors.

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