



Plant biochemistry and its relative analysis with soil diversity of cotton species

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ABOUT THE STUDY

Cotton (*Gossypium* spp.) is a significant natural fibre crop that supplies oil and feed to society in addition to providing fibre to the textile industry. In *Gossypium*, there are 7 tetraploids ($2n=52$ chromosomes) with the genome designation AD and 43 diploids ($2n=26$ chromosomes), which have been divided into 7 genomes from A to G. Out of the 50 *Gossypium* species, only two diploids (*G. arboreum* and *G. herbaceum*) and two tetraploids (*G. hirsutum* and *G. barbadense*) are grown for their spinnable fibre globally; the other 46 species are wild. India stands out among cotton-growing nations because it raises all four Cultivated Cotton Species (CSS)—*G. hirsutum*, *G. barbadense*, *G. arboreum*, and *G. herbaceum* under a diverse agro-ecological system.

The breeding of better cotton to reduce biotic and abiotic stressors for ongoing production and quality enhancement is a major objective of the cotton research community globally. Cotton is farmed in 75 different nations across the world. Wild Cotton Species (WCS), one of the *Gossypium* species, operate as a genetic reservoir for a number of distinctive features (wider adaptation, pest and disease resistance, and yield contributing variables), which cotton growers can use for prebreeding and genetic improvement in Cultivated Cotton Species (CCS). Introgressive hybridization has been crucial in improving cotton by introducing features from several wild and domesticated species that are resistant to disease (black arm, rust, wilt), insects (jassids, boll weevil), drought, and male sterility (cytoplasmic male sterility).

Plant research has placed a lot of emphasis on figuring out the relationships between crop plants and their wild relatives since doing so will aid in domesticating and improving crops. The superiority of wild species in withstanding biotic and abiotic stresses when compared to their cultivated counterparts has been demonstrated by

numerous germplasm studies and breeding programmes, despite the fact that conventional wisdom has it that tolerance gene are negatively correlated with yield. The use of wild species for crop improvement is hindered by a lack of data on phenotypic and genotypic differences, as well as other genetic variants (ploidy, hybridization barrier, linkage, etc.), and a significant amount of the natural variation in the wild species of cotton remains untapped.

Despite the fact that cotton breeding programmes generally use phenotypic and genotypic data to select parents for prebreeding and introgression research, they ignore the inherent qualities of the plant and the soil since there is a lack of data. Therefore, gathering data on fundamental soil biological traits and biochemical characteristics of plants aids breeders in selecting qualities that are significant from an agronomic standpoint. The variety in soil and plant biology of cultivated and wild cotton species, however, has not yet been the subject of any studies. In order to comprehend the variations in soil biological and plant antioxidant/defense enzyme activity among the grown and chosen wild cotton species, a comparative investigation was carried out.

In order to serve as a source for introgression studies for ongoing and future crop improvement efforts, various *Gossypium* germplasm collections, including wild species and land races, are currently conserved through national gene banks around the world. The variety in soil and plant biology of cultivated and wild cotton species, however, has not yet been the subject of any studies. We wanted to know how WCS and CCS differed from one other in terms of biological characteristics of the soil and plant antioxidant and defence activities.

Among the *Gossypium*, WCS act as a genetic storehouse for a variety of unusual features that are helpful for CCS's genetic development. Although phenotypic and genotypic

data are mostly used in cotton breeding strategy for parent selection and prebreeding, due to a lack of data, plant biochemistry and soil biology attributes were

disregarded. Additionally, there were no attempts made to compare the variety of soil and plant biology between WCS and CCS.