

## Differences in Soil Biological, Plant Biochemistry, and Defense Enzyme Activities

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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 50 Gossypium species, only two diploids (G. *arboreum* and G. *herbaceum*) and two tetraploids (G. *hirsutum* and G. *barbadense*), as well as 46 wild species, are cultivated globally for their spinnable fibre. India stands out among cotton-growing nations because it raises all four Cultivated Cotton Species (CCS) 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. Among the *Gossypium* species, Wild Cotton Species (WCS) act as a genetic reservoir of a number of distinctive features that cotton growers can employ to improve the genetics of CCS by prebreeding. The transfer of fibre quality, disease resistance, insect resistance, drought resistance, and male sterility features from several wild and domesticated species to cotton has been greatly aided through introgressive hybridization. Additionally, the mating of domesticated plant species with wild species can also convey advantageous features that can change the make-up of plant and microbial communities, potentially resulting in the health of the plants and soil.

Plant research has placed a lot of emphasis on figuring out the relationships between crop plants and their wild cousins 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 genes are negatively correlated with yield. The use of wild species for crop improvement is hindered by a lack of information on phenotypic and genotypic differences, as well as other genetic variants. As a result, a sizable 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.

Breeders are further assisted in speeding up the selection of features of agronomic value by information generation relating to fundamental plant biochemical and soil biological traits. 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. Our research will increase knowledge of the biochemical and biological characteristics of soil that differ between farmed and wild cotton species, finally complete the cotton database, and assist cotton breeders in choosing distinctive qualities for their crop improvement initiatives.

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.

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