

MOLECULAR BASIS OF MOISTURE STRESS TOLERANCE IN COTTON GOSSYPIUM HIRSUTUM

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India is the largest cotton producing country in the world. Moisture stress is one of the major cause for low productivity in rainfed cotton. Understanding molecular basis for moisture stress tolerance expedite breeding for drought resistance, current study aimed evaluation and validation of moisture stress effect on expression pattern of candidate genes in cotton (*G. hirsutum* L.). The effect of physio-biochemical traits in response to moisture stress was observed and data was analyzed through SPSS software, which showed significant difference between conditions of all traits irrespective of genotypes. The molecular study of differential quantitative gene expression was studied by real-time PCR and data was analyzed through rotor gene 6000 software with significant value ($r=0.1$). Twenty eight known up regulating genes under moisture stress did not up regulate equally in all drought tolerant genotypes. The differential up regulation of different genes in response to moisture stress among diverse genotypes was recorded. For example in leaf tissue, up regulated CAB1 was in leaf tissue of genotypes RAJ-2, Bikaneri nerma, PH1009, CCH1831, 5433A2A03N83 and RHC0811 recorded higher photosynthetic rate and up regulated CER1 in leaf tissue of Khandwa-2, F-2226, RAJ-2 and Bikaneri nerma helps to reduce transpiration rate. Similarly, for regulation of biochemical metabolic process, expression of WRKY70 in RS-810, F-2226, JK-4 AK-23 and CCH1831 genotypes accumulate proline for osmotic adjustment. Genes, pod10 and pod7 leads to increase higher peroxidase enzyme activity in CCH1831, PH1009, AK-23, Bikaneri nerma, 5433A2A03N83, F-2226 and it act as defensive mechanism against toxic ROS molecules. However these genes viz., CAB1, CER1, WRKY70, pod10 and pod7 were not found or their expression was less than two fold in susceptible MCU-5. Therefore, in susceptible cotton (*G. hirsutum*) genotypes, above considered parameters showed higher reduction of physio-biochemical attributes.

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