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DIFFERENTIAL GENE EXPRESSION IN FOXTAIL MILLET (*Setaria italica)* UNDER WATER STRESS

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ABSTRACT

Foxtail millet (*Setaria italica* L.) is an important food and fodder grain crop in arid and semi-arid regions of Asia and Africa. Being an elite drought-tolerant crop, foxtail millet is thought to be an excellent experimental model in studying abiotic stress tolerance system. In recent years, semi-quantitative RT-PCR has emerged as a versatile technique in transcriptomics, as it can generate rapid measurement of mRNA levels in minimal tissue samples. The present study deals with semi-quantitative RT-PCR of gene specific markers for drought stress viz. DREB1 and DREB2 in two contrasting foxtail millet accessions IC97109 and IC97189. Based on the IDV values, the relative upregulation of DREB2 due to dehydration stress in tolerant accession was found to be 7.86 % whereas, DREB1 showed the relative upregulation of about 18.67% respectively. DREB1 and DREB2 showed higher expression in both unstressed and stressed condition in tolerant accession, IC97189. Analysis on the expression profiling of these genes revealed that the expression of genes was upregulated by water stress treatment, suggesting their role in drought tolerance of *Setaria italica* L.

KEYWORDS: Differential Expression Profiling, Semi-Quantitative RT-PCR, *Setaria italica*, Abiotic Stress