

1.2 Elucidation of genetic basis of water use efficiency in sorghum and pearl millet through genome-wide association studies and transcriptome profiling.

*TIGR2ESS research partnerships shed new light on genetic basis of **Water Use Efficiency (WUE)** in sorghum and pearl millet which links phenotypes to drought resilience and yield enhancement. Detecting the principal genes responsible for increasing a plant's tolerance to extreme conditions requires advanced biotechnological tools to ensure that we understand the basis to drought resilience and can breed crops for the future*

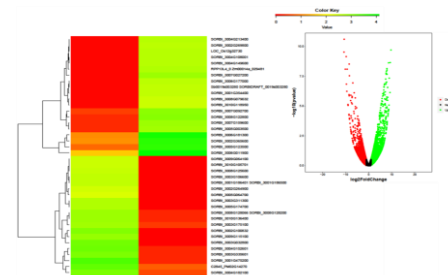
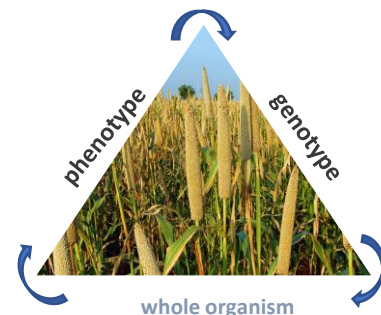
Collaborating phenotyping and molecular breeding teams at ICRISAT investigated genetic variation in sorghum and pearl millet with the aim of identifying tolerance traits which will keep pace with predicted climate change. Integrated genomic approaches which include Genome Wide Association Studies (GWAS) and transcriptome analyses across contrasting lines or individuals were used to pin-point alleles, candidate genes and gene networks that couple with improved WUE.

Global diversity panels, analysed over two seasons by ICRISAT's phenotyping team, included all basic and intermediate races of Sorghum and represented the genetic diversity of pearl millet across 27 countries. Once phenotyped, marker trait associations (MTAs) were established using GWAS for data generated under well-watered and water-stressed conditions. These MTAs were annotated to identify putative candidate genes involved in drought adaptation and WUE in sorghum and pearl millet.

Sorghum and pearl millet lines with natural resilience to drought were selected based on phenotypic data. Genome-wide transcriptome analysis by deep sequencing was done for contrasting lines in order to identify differentially expressed genes (DEGs) and gene networks associated with WUE and physiological and developmental traits.

The research identified promising sorghum and pearl millet lines for WUE associated traits. The promising lines will be exploited to serve as valuable QTL donors for improving trait using MABC/FB. GWAS and transcriptome profiling facilitated the identification of candidate genes and QTLs related to drought adaptation and water use efficiency in sorghum and pearl millet.

This study was directly linked with the analysis of stomatal and other molecular physiology studies at the University of Essex, allowing a fully integrated investigation of promising lines for future breeding programmes.



Transcriptome analysis for root samples of contrasting sorghum genotypes under water stressed conditions

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