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Transcriptomic analysis of a *Sorghum bicolor* landrace identifies a role for beta-alanine betaine biosynthesis in drought tolerance

Van der Westhuyzen, Christiaan W
Council for Scientific and Industrial Research
Pretoria, 0001, South Africa
Email: CvdWesthuizen@csir.co.za

Abstract

Sorghum is indigenous to Africa and a remarkably drought tolerant cereal crop. In this study, the genetic response mechanisms involved in sorghum's tolerance to progressive water deficit and re-watering were investigated in a South African landrace (designated LR6), using cDNA microarrays comprising 35,899 transcript probes. Significant differential expression of 902 transcripts, including 128 transcripts with currently unknown functions, was altered in response to progressive water stress and re-watering. The modulated sorghum genes had homology to proteins involved in growth, regulation, and protection. Gene Ontology (GO) analysis identified significant enrichment of 26 genes involved in the 'response to abiotic stimulus' GO category during severe stress. The expression of two genes associated with beta(b)-alanine betaine biosynthesis was validated with quantitative RT-PCR. Importantly, the detection of b-alanine betaine in sorghum leaf extracts using NMR spectroscopy, and the significant increase in relative abundance during severe stress supports the microarray and qRT-PCR findings, thereby highlighting a role for b-alanine betaine biosynthesis in drought tolerance of sorghum. In future, crop improvement initiatives that consider metabolic engineering of the b-alanine betaine biosynthesis pathway should be explored.