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Genotype-dependent Regulation of Drought-Responsive Genes in Tolerant and Sensitive Sugarcane Cultivars

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Abstract: Drought is the most damaging among the major abiotic stresses. Transcriptomic studies allow a global overview of expressed genes, providing the basis for molecular markers development. Here, the HT-SuperSAGE technique allowed the evaluation of four drought-tolerant cultivars and four -sensitive cultivars, after 24 h of irrigation suppression. We identified 9,831 induced unitags from roots of the tolerant cultivars with different regulations by the -sensitive cultivars after the applied stress. These unitags allowed a proposal of 15 genes, whose expressed profiles were validated by RT-qPCR, evaluating each cultivar independently. These genes covered broad metabolic processes: ethylene stress attenuation (*ACCD*); root growth (β -*EXP8*); protein degradation [ubiquitination pathway (*E2*, *20SP β 4*); plant proteases (*AP*, *C13*)]; oxidative detoxification (*TRX*); fatty acid synthesis (*ACC*); amino acid transport (*AAT*), and carbohydrate metabolism

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