## W683 Mining genes for cold tolerance in sugarcane toward development of functional markers

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Sugarcane (Saccharum hybrids), being a (sub)tropical crop, is sensitive to sub-freezing temperatures. Cold temperatures limit the length of its growing season and affect the growth and development, thereby causing significant crop losses before and after harvest. Lack of freeze tolerance among the available sugarcane germplasm in Louisiana is attributed to rigorous selection pressure for sucrose genes. But, existence of genetic variability in cold stress response of interspecific hybrids, especially those with germplasm of S. spontaneum, can be exploited to produce sugarcane plants that can tolerate freezing temperatures and hence allow expansion of sugarcane acreage into diverse geographic regions such as northern Louisiana and additional states. To accomplish the goal of finding new alleles for cold tolerance, we made a comparative transcriptome profiling of a cold tolerant clone Ho02-144 vis-à-vis a susceptible clone L79-1002 by using an anneal control primer (ACP)-based mRNA differential display technique. Forty differentially expressing genes (DEGs) were isolated of which 29 were upregulated and 11 were downregulated under cold stress. Expression analysis through (semi)quantitative RT-PCR of the DEGs revealed a putative cold stress response network in the tolerant clone Ho02-144. Mining of the cold-responsive genes identified 11 DEGs with simple sequence repeats. Genotyping of a set of Louisiana sugarcane cultivars and their ancestors with these 11 EST-derived SSRs produced 170 polymorphic alleles that generated a definitive population structure. These informative allele-specific functional markers will be useful for marker-assisted breeding of sugarcane where improved cold tolerance is an important trait for industry success.

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