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SUGAR BEET RESPONSE TO COLD: A qPCR BASED GENE EXPRESSION PROFILING

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The exposure to low temperatures of young sugar beet plantlets may lead to serious losses of sucrose productivity and quality. Technological advances in high-throughput molecular analysis lead to a better knowledge of the complex regulation of gene expression underlying the cold response in *Arabidopsis thaliana*, a model for many other important crop species like sugar beet (*Beta vulgaris*). For sugar beet, specific extensive genomic data are relatively limited. Integrated "dry/wet" approaches, and advanced high-throughput techniques, based on real-time PCR, are able to reveal gene expression fluctuations induced by abiotic stresses treatments, allowing overcome such limits.

Our goal was the gene expression profiling of several sugar beet genes involved in sucrose quality and yield by real-time PCR, in order to investigate how and if cold stress modulates their transcription levels in different organs of the plant. A previous selection of the most suitable reference gene for the species, organ, developmental stage and treatments was necessary to validate the data obtained. After this preliminary selection, seven putative housekeeping genes were characterised, their Ct analyzed by "comparative Ct method" and the index of stability (M) calculated by GeNorm software. Tubulin, rRNA and elongation factor1α were found to be the most suitable reference genes in our conditions and materials, and were therefore employed to normalize the data relative to the target genes analyzed. The expression of twelve target genes was quantified in leaf and roots of young sugar beet plantlets exposed to low temperature treatments; the results indicate organ-specific variability and stress-modulated transcription in some conditions, especially for the genes directly involved in the sucrose biosynthetic pathway (SBSS1, SBSS2, SPS1 and SPS2).