Newly developed sugarbeet lines with altered postharvest respiration rates differ in transcription factor and glycolytic enzyme expression

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ABSTRACT
Respiration is the principal cause for postharvest sucrose loss in sugarbeet (Beta vulgaris L.) roots. Although reductions in respiration rate could mitigate these losses, developing sugarbeet cultivars and storage procedures that reduce respiration are hindered by a lack of knowledge of the genetic and metabolic factors that control storage respiration rate. Research was conducted to identify genes and gene products that affect storage respiration rate by creating two sugarbeet lines that differ in respiration rate and characterizing gene expression differences between these lines. Sugarbeet lines F1056 and F1057, which differ by up to 42% in respiration rate, were created by divergent selection of a sugarbeet population using root respiration rate after 30 d in storage as the principal selection criterion. RNA sequencing identified 287 differentially expressed genes (DEGs) between these lines on the day of harvest and after 28-d storage. Of these DEGs, nine encoded transcription factors and five encoded enzymes involved in the respiratory pathway. Other DEGs contributed to a variety of biological and molecular functions based on gene ontology classifications. Of respiratory pathway DEGS, genes for NAD+- and NADP+-dependent forms of glyceraldehyde-3-phosphate dehydrogenase were of note due to their high upregulation in the high respiring line and for their established role in glycolysis, a pathway identified as a likely bottleneck in respiratory substrate production. Overall, lines F1056 and F1057 provide new tools for investigating genetic and physiological differences in storage respiration rate, and their DEGs identify candidates for genes affecting sugarbeet root respiration rate.

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