# Transcriptomic and metabolomic changes in postharvest sugarbeet roots reveal widespread metabolic changes in storage and identify genes potentially responsible for respiratory sucrose loss

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## Abstract

Endogenous metabolism is primarily responsible for losses in sucrose content and processing quality in postharvest sugarbeet roots. The genes responsible for this metabolism and the transcriptional changes that regulate it, however, are largely unknown. To identify genes and metabolic pathways that participate in postharvest sugarbeet root metabolism and the transcriptional changes that contribute to their regulation, transcriptomic and metabolomic profiles were generated for sugarbeet roots at harvest and after 12, 40 and 120 d storage at 5 and 12°C and gene expression and metabolite concentration changes related to storage duration or temperature were identified. During storage, 8656 genes, or 34% of all expressed genes, and 225 metabolites, equivalent to 59% of detected metabolites, were altered in expression or concentration, indicating extensive transcriptional and metabolic changes in stored roots. These genes and metabolites contributed to a wide range of cellular and molecular functions, with carbohydrate metabolism being the function to which the greatest number of genes and metabolites classified. Because respiration has a central role in postharvest metabolism and is largely responsible for sucrose loss in sugarbeet roots, genes and metabolites involved in and correlated to respiration were identified. Seventy-five genes participating in respiration were differentially expressed during storage, including two bidirectional sugar transporter SWEET17 genes that highly correlated with respiration rate. Weighted gene co-expression network analysis identified 1896 additional genes that positively correlated with respiration rate and predicted a pyruvate kinase gene to be a central regulator or biomarker for respiration rate. Overall, these results reveal the extensive and diverse physiological and metabolic changes that occur in stored sugarbeet roots and identify genes with potential roles as regulators or biomarkers for respiratory sucrose loss.

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