

Comparative Transcriptome Analysis of Sucrose Biosynthesis-Associated Gene Expression Using RNA-Seq at Various Growth Periods in Sugar Beet (*Beta vulgaris* L.)

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Sugar beet (*Beta vulgaris* L.) is one of the most important sugar crops and provides up to 30% of the world's sugar production. In this study, we mainly performed RNA-sequencing to obtain identify putative genes involved in biosynthesis pathway of sucrose in sugar beet and comparative transcriptomic analyses in the four developmental stages (50, 90, 160 and 330 days after seedling). As a result of the sugar content analysis, it was increased significantly from 50 to 160 days after seedling (DAS), and then decreased at 330 DAS. On the other hand, the taproot weight, length, and width were increased during all the growth periods. Out of 21,451 genes with expressed value, 21,402 (99.77%) genes had functional descriptions. Among the three comparisons, S1 (50 DAS) vs. S2 (90 DAS), S1 vs. S3 (160 DAS), and S1 vs. S4 (330 DAS), expression profiling of the transcripts was identified 4,991 with differentially expressed genes (DEGs). By comparing the top 20 enriched gene ontology (GO) terms as three comparisons, the top GO terms were commonly confirmed with external encapsulating structure, cell wall, and extracellular regions. In addition, the 38 enriched candidate genes related to sucrose biosynthetic pathway were screened from the entire DEG pool, and the candidate genes might be providing a basic data for further sugar metabolism studies in development of sugar beet taproot.

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