

Comparative transcriptome profiling of seed germination process in two contrasting sodium chloride tolerance of Brassica napus L. cultivars

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SIN874165614656

January 2, 2021

Abstract

Seedlings survival rate under salinity stress, vegetative growth, production yield and quality are highly related to seed germination and early growth performance. Germination of rapeseed cultivars is differing under NaCl stress, but the molecular mechanism of salinity in rapeseed poorly understood. In current study, we carried out integrative transcriptome analyses of four seed germination phases from two rapeseed cultivars under normal and NaCl stress conditions. The different pairwise comparisons of this study provides a comprehensive view of the dynamic biochemical processes that underpin salt tolerance and seed germination under salt and normal conditions. Our analysis identified DEGs for salt tolerance between the two cultivars were 5,325, 6,941, 5,835, and 9,114 down-regulated and 4,463, 4,710, 5,431 and 10,997 up-regulated in YSS/ZSS at 0h, 12h, 24h, and 48h, respectively. Furthermore, we identified the expression profiles and main pathways in each growth phase. For seed germination process, a considerable DEGs number, including those involved in "Pentose phosphate pathway", "Pyruvate metabolism", "Protein processing in endoplasmic reticulum", and "Glycolysis / Gluconeogenesis" pathways were specifically and transiently induced at the first 12 hours. "Photosynthesis", "Carbon fixation in photosynthetic organisms", "Amino sugar and nucleotide sugar metabolism", "Glyoxylate and dicarboxylate metabolism", "Plant hormone signal transduction", and "Glutathione metabolism" were enriched at the 48 hours. In the comparison of salt tolerance between the two cultivars, the "plant hormone signal transduction", "MAPK signaling pathway-plant", and "starch and sucrose metabolism pathways were significantly enriched. More specifically, in the plant hormone signal transduction pathway, the genes regulated to Auxin signal transduction i.e. AUX1, TIR1, CH3 and SAUR exhibited significant upregulation that regulate cell enlargement and growth. Genes related to Cytokinin (AHP, and A-APR), Gibberellin (DELLA and TF), Brassinosteroid (BSK, BZR1/2, TCH4 and CYCD3), and Jasmonic acid (JAZ and MYC2) signal transduction were upregulated (Figure1). Our results provide new insights about transcript dynamics controlling plant hormone signal transduction pathway involved in the salt tolerance during the seed germination of rapeseed plants.