

RNA-seq analysis revealed key genes associated with salt tolerance in rapeseed germination through carbohydrate metabolism, hormone, and MAPK signaling pathways

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ABSTRACT

Seedling survival, growth, and yield are highly associated with seed germination performance. Germination of rapeseed differs under NaCl stress among cultivars, but the molecular mechanism of salinity tolerance in rapeseed is poorly understood. In the current study, in contrast to the trend of the hydrogen peroxide level, the activities of superoxide dismutase, catalase, and ascorbate peroxidase were increased in the salt-tolerant (Yangyou9; YY9) cultivar as compared with the salt-sensitive one (Zhongshuang11; ZS11). Integrative transcriptome analysis of four seed germination phases was carried out on the two rapeseed cultivars, which showed a substantial transcriptional change at 24 and 48 h. Different pairwise comparisons were performed to provide a comprehensive view of the biochemical processes that underpin salt tolerance and seed germination. Plant hormone signal transduction, MAPK signaling, glycolysis/gluconeogenesis, fermentation, and tricarboxylic cycle pathways were significantly enriched. Genes related to auxin (Aux) signaling, i.e., *BnaAUX1*, *BnaTIR1*, *BnaGH3.5/17*, and *BnaSAUR* were associated with salt tolerance through activating the germination process. Genes related to cytokinin (Ck; *BnaAHP1/3/4* and *BnaA-ARR3/4/8/9*), gibberellin (GA; *BnaPIF3/4/5*), brassinosteroids (BRs; *BnaBAK1*, *BnaBSK*, *BnaBZR1/2*, *BnaTCH4*, and *BnaCYCD3*), and salicylic acid (SA; *BnaNPR1/3/5*, *BnaPR1*, and *BnaTGA2/4*) signaling transductions were linked to salt tolerance at the germination stage. While genes related to abscisic acid (ABA; *BnaPP2C* and *BnaABF*) and ethylene (Eth; *BnaEIN3* and *BnaERF1/2*) were relatively upregulated in the dry seeds and salt-stressed sensitive cultivar, therefore, these genes may participate in salt sensitivity and seed dormancy. Moreover, the enzymatic activities (fructose-bisphosphate aldolase and isocitrate dehydrogenase) and content of phytohormones (indole-3-acetic acid (IAA), Ck, and GA) were significantly ($p < 0.05$) higher in YY9 than in ZS11, while ABA content showed a reverse trend, indicating the reliability of the RNA-seq data. Overall, this is the first study that provides new insights about transcripts involved in the salt tolerance during seed germination of rapeseed.

Keywords:

Brassica napus

Salinity

Transcriptome

Seed germination

MAPK

Hormone signaling