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Pathways related to ROS production, clearance and signal transduction during cold response in *Brassica napus* L. with strong cold resistance

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Background:

Brassica napus L. has been considered an important cash crop and oil crop. However, it is difficult to popularise and apply B. napus in north China because of its weak cold resistance.

Objective:

To clarify the mechanism of cold stress on gene regulation and signal transduction in B. napus.

Methods:

We performed the transcriptome sequencing and gene expression, Go and KEGG pathways profiling was analysed under the natural (25°C) and cold (4°C) conditions of cold tolerant 16VHNTS309 and cold sensitive Tianyou 2238 of B. napus seedlings. Subsequently, more complete genomic annotation was obtained by sequencing.

Results:

A total of 6127 and 8531 differentially expressed genes (DEG) were identified in B. napus of 16VHNTS309 and Tianyou 2238, respectively. Analysis of the expression patterns of 23 differentially expressed genes (DEGs) by quantitative real-time PCR (qRT-PCR) confirmed the accuracy of the RNA-Seq results. Under cold stress, 58 pathways in strong cold-resistant B. napus 16VHNTS309 showed significant changes (qValue <0.05), while 9 pathways in weak cold-resistant B. napus Tianyou 2238 showed significant changes (qValue <0.05). This indicated that B. napus has a complex and ingenious network regulation system, which could coordinate various problems encountered in the process of plant growth and development to a certain extent. After 48h of cold stress treatment, several genes related to reactive oxygen species (ROS) clearance, such as antioxidant VB6, sulphur metabolism, peroxisome, and phagosome, were significantly up-regulated in B. napus 16VHNTS309, suggesting that B. napus 16VHNTS309 has a strong ROS clearance ability.

Conclusions:

There were significant expressions of several genes in the signal pathway of Ca2+, MAPK and transcription factors related to ROS, which further suggested that the varieties with strong cold resistance had complex signal regulation mechanism. A comprehensive analysis of stomatal cell results, physiological parameters of ROS, ABA and H2S, and transcriptomic data showed that appropriate ROS interacted with ABA and H2S to regulate stomatal closure in B. napus 16VHNTS309 under the scavenging action of antioxidant enzymes.