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Combining physio-biochemical characterization and transcriptome analysis reveal the responses to varying degrees of drought stress in *Brassica napus*

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Background:

Brassica napus is one of the most important oil crops around the world. Along with global warming, the frequency of drought stress is increasing, and fresh water supplies for irrigation are decreasing. The frequent occurrence of seasonal drought and persistent drought seriously affected the growth and development of B. napus and its agricultural production.

Objective:

Our aim was to analyse the physio-biochemical traits changes of B. napus in response to different degrees of drought stress, identified the differentially expressed genes controlling these physio-biochemical traits changes and verify the functions of the key differentially expressed gene.

Methods:

the experimental approach and methodology used in this study:

Pot culture experiment and weighing method to control soil relative water content; High-performance liquid chromatography-tandem mass spectrum for determination of ABA content; RNA-Seq alignment and differential expression analysis; Gas chromatography and mass spectrometry for determination of Wax/Cutin; Quantitative Real-Time PCR analysis; Scanning Electron Microscopy; Li-Cor 6800 for photosynthetic parameter measurements; Vector construction and genetic transformation; Western blot analysis.

Results:

By combining physio-biochemical characterization and transcriptome analysis, we studied the response of B. napus plants to different degrees of drought stress. Some physio-biochemical traits, such as fresh weight, dry weight, abscisic acid content, net photosynthetic rate, stomatal conductance, and transpiration rate, were measured, and the total content of the epidermal wax/cutin, as well as their compositions, was determined. The results suggest that both stomatal transpiration and cuticular transpiration are affected when B. napus plants are subjected to drought stress. A total of 795 up-regulated genes and 1050 down-regulated genes were identified under severe drought stress by transcriptome analysis. Gene ontology enrichment analysis of differentially expressed genes revealed that the up-regulated genes were mainly enriched in the stress response processes while the down-regulated genes were mainly enriched in the chloroplast-related parts affecting photosynthesis. Moreover, overexpression of BnaA01.CIPK6, an up-regulated DEG, was found to confer drought tolerance in *B. napus.*

Conclusions:

The characterization of multiple physio-biochemical traits and comparative transcriptome analysis proved to be powerful strategies for analysing the response of B. napus to varying degrees of drought stress. The changes in fresh weight, dry weight, ABA content, photosynthesis-related parameters, epidermal wax crystal morphology, the content and composition of wax/cutin were detected under different degrees of drought stress. Furthermore, a total of 1845 differentially expressed genes were identified under severe drought stress. A large number of differentially expressed genes were involved in various biological processes such as photosynthesis and stress responses. Among them, Overexpression of BnaA01.CIPK6 confers drought tolerance in B. napus. The discovery of these drought-responsive genes lays a foundation for future studies. And our results provide the understanding of the molecular mechanisms underlying the regulatory network of B. napus drought stress resistance.