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Morphological, Transcriptomics and Biochemical Characterization of New Dwarf Mutant of *Brassica napus*

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Highlights

- We obtained a dwarf mutant line in *B. napus* and compared its phenotypes to the wild type.
- Transcriptome analysis of shoot apex samples uncovered DEGs involved in many pathways.
- Auxin-KANADII crosstalk plays a major role in root development.
- Pleiotropic phenotypes of the mutant result from complicated networks.

Abstract

Plant height is a key trait of plant architecture, and is responsible for both yield and lodging resistance in *Brassica napus*. A dwarf mutant line (*bnac.dwf*) was obtained by chemical mutagenesis of an inbred line T6. However, the molecular mechanisms and changed biological processes of the dwarf mutant remain to be determined. In this study, a comparative transcriptome analysis between *bnac.dwf* and T6 plants was performed to identify genome-wide differentially expressed genes (DEGs) and possible biological processes that may explain the phenotype variations in *bnac.dwf*. As a result of this analysis, 60,134,746–60,301,384 clean reads were aligned to 60,074 genes in the *B. napus* genome, and accounted for 60.03% of the annotated genes. In total, 819 differentially expressed genes were used for GO

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