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BnaC01.BIN2 and BnaC03.BIN2 modulate plant height and yield potential in *Brassica napus*

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Background:

Reducing plant height is an important strategy for enhancing resistance to lodging, improving the harvest index, and increasing the yield stability of rapeseed. Although several genes that regulate rapeseed plant height have been identified, the genetics mechanisms underlying rapeseed plant height regulation remain poorly understood, and desirable genetic resources for rapeseed ideotype breeding are scarce.

Objective:

The objective of this study was to identify, clone, and investigate the functional genes responsible for regulating rapeseed plant height and evaluate their potential for rapeseed breeding, with the aim of providing valuable germplasm resources and theoretical guidance for improving rapeseed yield through ideotype breeding programs.

Methods:

The semi-dwarf rapeseed mutant *Df4* and *Df5* was developed through ethyl methane sulfonate mutagenesis. Combined BSA and Brassica 50K SNP BeadChip Array analysis, Next-generation sequencing, map-based cloning, and transgenic transformation were performed to determine the functional genes responsible for *Df4* and *Df5*. The loci responsible for the functional divergence of these genes were identified through genetic transformation experiments. The mechanism of how these genes regulate plant height in rapeseed was investigated using transcriptome data. Near-isogenic lines were used to clarify the genetic effects of the mutations on agronomic traits and to evaluate the effects of different degrees of dwarfism on rapeseed yield.

Results:

Our results demonstrated that *BnDF4* and *BnDF5* is the crucial gene for regulating rapeseed plant height. The semi-dominant alleles of *BnDF4* and *BnDF5* significantly reduce plant height by inhibiting cell elongation in the lower internodes. We identified brassinosteroid-insensitive 2, *BnaC01.BIN2* and *BnaC03.BIN2*, as the functional genes responsible for *Df4* and *Df5*, respectively, which are functionally similar but exhibit some differentiation. Transcriptome analysis showed that several cell expansion-related genes were downregulated in the semi-dwarf mutants. Heterozygosity in the *BnDF4* and *BnDF5* alleles resulted in small stature with no marked changes in other agronomic traits. Hybridization using *BnDF4* and *BnDF5* in the heterozygous condition resulted in strong yield heterosis through optimum intermediate plant height. Compared to *Df4*, the weak mutant *Df5* does not exhibit significant growth defects during the seedling stage and is more valuable for breeding purposes. Our findings suggest that *Df4* and *Df5* are valuable germplasm resources for improving rapeseed yield in breeding programs.

Conclusions:

In conclusion, our study identified and characterized the critical genes *BnaC01.BIN2* and *BnaC03.BIN2* responsible for rapeseed plant height regulation. Our findings provide valuable germplasm resources and theoretical guidance for improving rapeseed yield through ideotype breeding programs. The identified genes offer potential targets for future molecular breeding efforts aimed at developing semi-dwarf rapeseed varieties with improved agronomic performance.