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Genome-wide analysis and expression profiling of the *GRF* gene family in oilseed rape (*Brassica napus* L.)

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Abbreviations: GRF, Growth regulating-factor; BI, Bayesian Inference method; NJ, Neighbor Joining method; GA, gibberellic acid; QLQ, glutamine leucine glutamine; WRC, tryptophan arginine cysteine; KNOX, KNOTTED1-LIKE HOMEOBOX; miR396, microRNA396; GIF, GRF-INTERACTING FACTOR; NLS, localization signal; AN3, ANGUSTIFOLIA 3; DREB2A, DEHYDRATION-RESPONSIVE ELEMENT BINDING PROTEIN2A; HI, harvest index; BLAST, Basic Local Alignment Search Tool; PCR, polymerase chain reaction

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Abstract: Growth regulating-factors (GRFs) are plant-specific transcription factors that help regulate plant growth and development. Genome-wide identification and evolutionary analyses of *GRF* gene families have been performed in *Arabidopsis thaliana*, *Zea mays*, *Oryza sativa*, and *Brassica rapa*, but a comprehensive analysis of the *GRF* gene family in oilseed rape (*Brassica napus*) has not yet been reported. In the current study, we identified 35 members of the *BnGRF* family in *B. napus*. We analyzed the chromosomal distribution, phylogenetic relationships (Bayesian Inference and Neighbor Joining method), gene structures, and motifs of the *BnGRF* family members, as well as the *cis*-acting regulatory elements in their promoters. We also analyzed the expression patterns of 15 randomly selected *BnGRF* genes in various tissues and in plant varieties with different harvest indices and gibberellic acid (GA) responses. The expression levels of *BnGRFs* under GA treatment suggested the presence of possible negative feedback regulation. The evolutionary patterns and expression profiles of *BnGRFs* uncovered in this study increase our understanding of the important roles played by these genes in oilseed rape.

Keywords: *Brassica napus*; *GRF*; Expression analysis; GA response