

Accepted Manuscript

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

Jin-Qi Ma, Hong-Ju Jian, Bo Yang, Kun Lu, Ao-Xiang Zhang, Pu Liu, Jia-Na Li



PII: S0378-1119(17)30208-1
DOI: doi: [10.1016/j.gene.2017.03.030](https://doi.org/10.1016/j.gene.2017.03.030)
Reference: GENE 41836

To appear in: *Gene*

Received date: 3 December 2016
Revised date: 24 January 2017
Accepted date: 23 March 2017

Please cite this article as: Jin-Qi Ma, Hong-Ju Jian, Bo Yang, Kun Lu, Ao-Xiang Zhang, Pu Liu, Jia-Na Li , Genome-wide analysis and expression profiling of the GRF gene family in oilseed rape (*Brassica napus* L.). The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. *Gene*(2017), doi: [10.1016/j.gene.2017.03.030](https://doi.org/10.1016/j.gene.2017.03.030)

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

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

Jin-Qi Ma¹, Hong-Ju Jian¹, Bo Yang, Kun Lu, Ao-Xiang Zhang, Pu Liu, Jia-Na Li^{*}

College of Agronomy and Biotechnology, Southwest University, Chongqing, China

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

^{*} Corresponding author at: Chongqing Engineering Research Center for Rapeseed, College of Agronomy and Biotechnology, Southwest University, Tiansheng Rd 2#, Beibei, Chongqing, 400715, China

Email address: ljn1950@swu.edu.cn (J.-N. Li).

¹ These authors contributed equally to this work.

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

Download English Version:

<https://daneshyari.com/en/article/5589527>

Download Persian Version:

<https://daneshyari.com/article/5589527>

[Daneshyari.com](https://daneshyari.com)