In silico Genome-wide Study of NAC Gene Family in Brassica juncea (L.) for the Prediction of Abiotic-stress Responsive Genes

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Brassica juncea, an allotetraploid species, is an important germplasm resource for canola improvement, due to its many beneficial agronomic traits, such as heat and drought tolerance. Moreover, abiotic stress on account of drought, heat, salinity, etc, negatively affects growth and productivity in Brassica species. NAC transcription factors form a large plant-specific gene family that is involved in the regulation of tissue development and stress response. However, this gene family was not studied in B. juncea, an important multipurpose crop worldwide. The purpose of this study was to use a genome-wide method to identify, characterize and predict gene function of the NAC gene family in B. juncea. In total, 136 NAC genes were identified in the genome of B. juncea, in this study using Blastp. The NAC genes were named from BjuNAC1 to BjuNAC136 based on chromosomal distribution, which also indicated their wide distribution in the genome. On the basis of domain composition, the NACs were phylogenetically classified into sub-groups which was also substantiated by the gene structure and motifs of NAC proteins. Based on FPKM analysis of data available for drought, heat, and salt stress, 86 NAC genes were found differentially expressed during at least one of the three aforementioned stresses. 3 Novel genes were found to be differentially expressed during all three stresses. This is the first report that describes the genome-wide analysis of the NAC gene family in B. juncea which will help scientists in the production of a more robust Brassica crop. Future application of this work can help increase worldwide crop yields to feed a growing population, estimated to reach 9.7 billion people by 2050.

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