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Genomic analysis, evolution, and functional profiling of GASA family genes revealed their conserved role in enhancing growth and development in cabbage

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Abstract

Gibberellic acid stimulated arabidopsis (GASA) gene family play an important role in plant growth and development. However, little information is available on these cysteine-rich short proteins in different plant species. This is the first comprehensive strategy to use available genomic data to explore the GASA gene family in *B.oleracea*. GASA proteins regulate several developmental processes, including organ growth, cell division, fruit ripening, bud dormancy, stem development, blooming time, and seed generation. The gene structure, promoter region, expression and phylogenetics of all BoGASAs were analyzed. This study reported fifteen different members of the BoGASA gene family, which were mapped onto five chromosomes. The phylogenetic and sequence composition analysis incorporating GASA members from Arabidopsis, sunflower, peanut, soybean and cabbage distributed the fifteen identified BoGASA genes into five well-conserved subgroups. A conserved GASA domain was found in all identified BoGASA genes and exhibited similar characteristics. The cis-acting element analysis implied that cabbage GASA genes contained many cis-elements associated with hormone, Light and growth response. To check the expression of BoGASA genes towards cuticular wax biosynthesis, the two types of *B.olearacea*: the wild type and the glossy mutant (nwg1) were comparatively analysed. Expression profile analysis derived from transcriptome data showed that the genes BoGASA1, BoGASA2, BoGASA12 were upregulated from the wild-type to mutant type, while the expression of other genes showed downregulation. The BoGASA2 showed maximum upregulation while BoGASA5 showed maximum downregulation from wild to mutant variety.

Keywords: GIBBERELIC-ACID STIMULATED ARABIDOPSIS (GASA); gene expression; genome wide; chromosomal mapping

