

PB-29

## A Genome-wide Identification and the Comprehensive Analysis of the GASA Gene Family in Peanut (*Arachis hypogaea* L.) Under Abiotic Stress

Rizwana B.Syed Nabi<sup>1\*</sup>, Eunyoung Oh<sup>1</sup>, Kwang-Soo Cho<sup>1</sup>, Sungup Kim<sup>1</sup>, Myoung Hee Lee<sup>1</sup>

<sup>1</sup>Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Republic of Korea

### [Introduction]

The Gibberellic acid-stimulated Arabidopsis protein (*GASA*) are family of small cysteine-rich peptides found in plants. This *GASA* gene family is primarily involved in plant development and responses to biotic and abiotic stress. In plants, *Arabidopsis thaliana*, Soybean, Tomato, and Antirrhinum major in the *GASA* gene family is a highly conserved small group of secreted proteins that are involved in a wide range of developmental processes. Despite being present in a wide plant species, their action and functions still remain unclear in many plant species. The *GASA* gene family is not completely characterized in peanuts (*Arachis hypogaea* L.). Peanut is an important oilseed crop belonging to the *leguminosae* family and provide nutrition, food, and feed to human and animals.

### [Materials and Methods]

The experiment was carried out at RDA, Crop Breeding Research Division Miryanag, Gyeongnam South Korea. First, in-silico analysis was conducted to identify the *GASA* genes from the phytozome13 database. After removing redundant genes 41 *GASA* genes were identified in peanuts (*Arachis hypogaea* L.), and a further few genes of *AhGASA* were selected for relative expression and performed the biological experiment under control conditions. Seeds were sterilized with 70% ethanol, washed 4-5 times with dilute water, seeds were soaked in water, and kept in dark condition for 24 hours at 28 °C for uniform germination. Particularly, all the seedlings were grown at 25-28 °C under long-day conditions (16-h-light/8-h-dark). After sowing, watering was done on a regular basis and all plants were treated equally until two weeks. After that, the plant's different parts (leaves, stem, roots) samples have collected for the analyzed relative expression under normal conditions. In further experiments, we will check the expression of these selected *GASA* genes in different plant tissues under drought and salt stress conditions.

### [Results and Discussion]

In this study, we identified 41 *GASA* genes in peanuts through in-silico analysis and further investigated the expression of genes in different plant tissues of peanuts in the seedling stage (leaves, roots, and stem). Based on the phylogenetic analysis 41 *GASA* genes are classified into four major clusters and subclades. Mainly, cluster I and II with 9 and 6 genes, and clusters IV and III comprise the majority of *GASA* genes 15 and 11 respectively. Additionally, based on the in-silico analysis we predicted the post-transcriptional changes of *GASA* proteins under abiotic stress and found its involvement in abiotic stress tolerance. The expression analysis in *Ahgasas* genes 1, 2, 4, 7, 13, 14, 17, and 18 shows high expression in the leaves compared to the stem and roots. And *Ahgasas* genes 3, 8, 9, 15, 16, 20, 21, and 22 show low expression in leaves compared to the stem and roots. We planned to evaluate the expression of these selected *GASA* genes under drought stress. To elucidate the possible functional role of *GASA* genes in peanut plant expression patterns in different plant tissues will help to find the regulatory role of the selected genes. These findings might provide useful information for peanut *GASA* genes and their functional role in abiotic stress tolerance and crop improvement.

### [Acknowledgement]

This work was supported by a grant from the Agenda project (PJ01607603) of the Rural Development Administration Republic of Korea.

\*Corresponding author: E-mail, rizwananabi@korea.kr Tel, +82-55-350-1212