

Genome-wide identification and *in silico* expression profiling of the SOD, APX, and CAT gene families in the Cucurbitaceae species

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[Introduction]

Superoxide dismutase (SOD), ascorbate peroxidase (APX), and catalase (CAT) are representative key enzymatic antioxidants. They play major roles in plants for response and tolerance under most abiotic stresses. Cucurbitaceae species are major crops so research of antioxidant enzyme genes in Cucurbitaceae species is important for breeding of abiotic stress tolerance varieties.

[Materials and Methods]

Sequences and annotation data of five Cucurbitaceae species including cucumber, wild cucumber, melon, watermelon, and bitter melon were collected from cucumber genome database. All phylogenetic trees are made using MEGA7 program.

[Results and Discussions]

In this study, SOD, APX, CAT gene families were identified through genome-wide searches in five Cucurbitaceae species including cucumber, wild cucumber, melon, watermelon, and bitter melon. As a result, in the five species, 67 genes, 59 genes, and 27 genes were identified to encode SOD, APX, CAT, respectively. Through domain search, phylogenetic analysis, and *in silico* subcellular location analysis, features of the genes were characterized. Transcription patterns of SOD, APX, and CAT genes were analyzed by *In silico* expression profiling using RNA-Seq data. Various expression patterns of SOD, APX, and CAT genes in normal cucumber tissues were revealed, and SOD genes were most abundantly expressed in leaf cells. The data of three main antioxidant enzyme genes of five Cucurbitaceae species will be useful for understanding abiotic stress response mechanisms and applying to molecular breeding of Cucurbitaceae crops.

[Acknowledgements]

This work was supported by Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, Forestry and Fisheries (IPET) through Agri-Bio industry Technology Development Program, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) (grant number 116076-03-2-HD0b0).

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