주제-05

Characterization of enzymes for the elucidation of defense mechanisms to response stresses

Nam-Jin Chung¹ and <u>Seung Jae Lee²*</u>

¹Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 54896, Republic of Korea ²Department of Chemistry and Institute for Molecular Biology and Genetics, Chonbuk National University, Jeonju 54896, Republic of Korea

[Introduction]

High salinity is a major abiotic stress that effects the growth and development of plants. These stresses can influence flowering, production of crops, defense mechanisms and other physiological processes. Previous studies have attempted to elucidate salt-tolerance mechanisms in order to improve plant growth and productivity in the presence of sodium chloride. One such plant that has been studied in detail is *Salicornia*, a well-known halophyte, which has adapted to grow in the presence of high salt.

[Materials and Methods]

To further the understanding of how *Salicornia* grows and develops in high saline conditions, *Salicornia herbacea* (*S. herbacea*) was grown under varying saline concentrations (0, 50, 100, 200, 300, 400 mM) and the resulting phenotype, ion levels, and metabolites were investigated. 100 mM NaCl was determined to be the optimal condition for the growth of *S. herbacea* and increased concentration of salts directly diminished the internal concentration of other inorganic ions including Ca^{2+} , K⁺, and Mg²⁺ ions. Metabolomics were performed on the roots of the plant as a systematic metabolomics study has not yet reported from the roots of *Salicornia*. Using ethyl acetate and methanol extraction followed by high resolution ultra-performance liquid chromatography coupled with mass spectrometry (UPLC-MS), 1,793 metabolites were identified at different levels of NaCl.

[Results and Discussions]

Structural and functional analysis demonstrated that the concentration of 53 metabolites was increased as the concentration of NaCl increase. These metabolites have been linked to stress responses, primarily oxidative stress responses, which increases under saline stress. Most metabolites can be classified as polyols, alkaloids, and steroids. Functional studies of these metabolites show that shikimic acid, vitamin K1, and indole-3-carboxylic acid are generated from defense mechanisms including the shikimate pathway to protect against reactive oxygen species (ROS) generated by salt stress. This metabolite profiling provides valuable information of the salt-tolerance mechanisms of S. herbacea and may be applied for bioengineering plants to improve salt-tolerance.

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*Corresponding author: Tel. +82-63-270-3412, E-mail. Slee026@jbnu.ac.kr