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Spatio-temporal Profiling of Primary Metabolite in Plant

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[Introduction]

Plants are extremely depending on photosynthesis to synthesize carbon compounds during their growth stage. Therefore, proper balance of carbon compounds for each organ in the plant is very important for plant growth and development, and yield improvement. In botanical research, a research method through metabolite profiling analysis is used to identify important factors related to crop yield. In general, metabolites in plants are closely related to plant growth and primary metabolism, and are very diverse, such as sugars, organic acids, nucleic acids, amines, fats, and amino acids. Plants require the synthesis and transformation of carbon compounds to maintain appropriate levels of metabolites under the changing light and temperature during the growing season. The synthesis and transport of metabolites are determined by how effectively crops use limited resources in response to environmental changes, and this is the process by which plants optimize metabolism for continuous growth. Understanding the metabolic response of these crops can provide insight into biological response mechanisms. Accordingly, the objective of this study was conducted to obtain basic and applied data on the improvement of stable crop productivity under changing environmental conditions. to achieve our goal, we employed the high throughput technology (metabolomics) by GC-TOFMS.

[Materials and Methods]

To conduct research, the seeds of *Oryza sativa* L. cv. Ungwangbyeon was germinated and the selected seedlings were planted in a pot (115 x 115 x 160 mm). Overall management of rice cultivation follows the Rural Development Administration standard manual (RDA, Korea). Metabolomic analysis of leaf blades, leaf sheaths, roots, and grains harvested at 12-hour intervals (noon and midnight) at the tillering and heading stages, respectively, to understand the metabolomic changes according to the organ, time, and growth stage of rice. Analysis of hydrophilic compounds (e.g., amino acids, sugars, organic acids, and sugar alcohols) Samples were analyzed on an Agilent 7890A GC (Agilent Technologies, Santa Clara, CA, USA) equipped with a Pegasus TOF-MS ((Leco, St. Joseph), Michigan, USA)

[Results and Discussion]

During the night at tillering stage, most of the sugars, amino acids, shikimic acid, and quinic acid in the roots increased compared to the daytime. During the night at heading stage, sugars metabolism tended to decrease in roots but mostly increase in grains. Most of the amino acid content in the leaf sheath increased at night. In particular, lysine content increased significantly. Alanine tended to decrease relatively at night. In leaf blades and leaf sheaths, organic acids, intermediate products of the TCA cycle, were mostly decreased, but citric acids were increased in both the tillering and heading stages. The fact that specific changes appeared in the comparison of metabolites during the vegetative and reproductive stages and day/night suggests the need for further research in accordance with environmental changes in the future.

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