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Metabolomics Analysis of Lettuce by Treatment by Sulfur ConcentrationHyeong-Cheol Kim¹, Su-Min Yun², Ji-Hyun Kim², Hyun-Jin Kim³, Jung-Sung Chung^{2*}¹Division of Applied Life Science, Graduate School, Gyeongsang National University²Department of Agronomy, Gyeongsang National University³Department of Food Science and Technology, Gyeongsang National University**[Introduction]**

Recently, in order to better understand the relationship of nutritional quality of food, various O-mix technologies such as genomics, proteomics, and metabolomics have been applied. Among these techniques, metabolomics is a useful tool for determining the chemical changes caused by differences in fertilizer components when growing crops. Therefore, in this study, the profile of metabolites according to low and high sulfur concentrations during lettuce cultivation was performed to obtain detailed information on the changes of metabolites using LC-MS and GC-MS.

[Materials and Methods]

Under the blue and red light of LEDs, lettuce leaves treated with low and high sulfur concentrations were lyophilized and pulverized with liquid nitrogen. For LC-MS analysis, the residues were separated with 20% methanol using terfenadine as an internal standard. After centrifuging, the supernatants were analyzed by ultra-performance liquid chromatography quadrupole time of flight MS (UPLC-Q-TOF MS, Waters Corp., Milford, MA, USA). For GC-MS analysis, all dried samples were dissolved in 70 μ L of methoxyamine hydrochloride in pyridine (20 mg/mL) containing dicyclohexyl phthalate as an internal standard and incubated at 37°C for 90 min. The methoxylated samples were then derivatized using 70 μ L N,O-bis(trimethylsilyl) trifluoroacetamide with 1% trimethylchlorosilane at 70°C for 30 min. The derivatized samples were analyzed by GC-MS (Shimadzu Corp., Kyoto, Japan).

[Results and Discussion]

The p-values of all normalized chromatogram intensities of lettuce metabolites obtained via GC-MS and LC-MS analysis were analyzed to identify metabolites that contribute to the observed difference between the low and high sulfur groups. Fifty two metabolites including acidic compounds, amino acids, sugars, lipid metabolites, and volatile compounds were identified as the major contributors to the differences in the groups on the PLS-DA score plot for GC-MS data. Based on the identified metabolites, a metabolomic pathway was proposed, and it was confirmed that carbohydrate metabolism, TCA cycle, and lipid metabolism are the main processes that change at low and high sulfur concentrations. These results provide useful insights into the effect of concentration-specific treatment of sulfur on physiological and chemical changes in lettuce.

[Acknowledgement]

This work was supported by the Gyeongsang National University Fund for Professors on Sabbatical Leave, 2020.

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