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Analysis of Ozone Exposure Damage of Rice using RNA-Sequencing

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[Introduction]

Recently, the concentration of fine dust causative substances (NO_x, VOC, etc.) in the atmosphere has increased, resulting in high concentrations of Tropospheric ozone (O₃) and increased damage to crops. Tropospheric ozone causes amorphous reddish brown spots on rice leaves, leaf death in severe cases and reduces photosynthesis rate because of chlorophyll destruction. In China and Japan, various studies have been conducted on the damage and yield reduction of rice due to ozone concentration and exposure. This study was conducted to select ozone related mechanisms and related genes using RNA-sequencing.

[Materials and Methods]

The varieties used were ozone-sensitive Wandoaengmi and ozone-insensitive Hwayeong. 150ppb of ozone was sampled at intervals of 3, and 10 days after treatment for 4 days. RNA was extracted and analyzed. By analyzing the RNA-sequencing results, related pathways were analyzed using KEGG.

[Results and Discussion]

The DEG analysis showed that the number of genes whose expression patterns change in ozone-sensitive Wandoaengmi, which is more than Hwayeong, during ozone exposure. Chlorophyll a is decomposed into pheophytin a due to increased expression of magnesium dechelataase gene. The expression of the stress response hormones, ABA and JA biosynthesis genes, was expressed earlier in Wandoaengmi than Hwayeong.

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