

Elevated ozone levels affect metabolites and related biosynthetic genes in tartary buckwheat

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Abstract

Global climate change and the industrial revolution have increased the concentration of tropospheric ozone, a photochemical air pollutant that can negatively affect plant growth and crop production. In the present study, we investigated the effects of O₃ on the metabolites and transcriptome of tartary buckwheat. A total of 37 metabolites were identified by gas chromatography coupled with time-of-flight mass spectrometry, and principal component analysis was performed to verify the metabolic differences between non-treated and O₃-treated Tartary buckwheat. The levels of most metabolites (threonic acid, tryptophan, sucrose, and raffinose) decreased significantly after the O₃ treatment. On the contrary, the levels of two anthocyanins, cyanidin 3-O-glucoside and cyanidin 3-O-rutinoside, increased more than 11.36- and 11.43-fold, respectively after the O₃ treatment. To assess the effect of O₃ on the genomic level, we analyzed the expression of anthocyanin biosynthesis pathway genes in O₃-treated and non-treated buckwheat using quantitative real-time reverse transcription PCR. We found that the expression of all anthocyanin pathway genes increased significantly in the O₃-treated buckwheat compared to that in the non-treated buckwheat. Altogether, our results suggested that O₃ affected the transcripts and metabolites of tartary buckwheat, which would eventually cause phenotypic changes in plants.

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