

# Integrative transcriptomics and metabolomics data exploring the effect of chitosan on postharvest grape resistance to *Botrytis cinerea*

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## Abstract

Chitosan has a broad-spectrum antimicrobial activity and has been used to control or delay postharvest decay of fruit. In this study, transcriptomic and metabolomics analyses were used to evaluate the effect of chitosan treatment on the resistance to *Botrytis cinerea* of two grape varieties ('Kyoho' and 'Shine Muscat') that differ in their resistance to this pathogen. Meantime, the effect of chitosan treatment on *B. cinerea* mycelium growth was analyzed by scanning electron microscope. The physiological indicators of disease and antioxidant enzyme activities of grape fruit after chitosan treatment were also measured. The results showed that chitosan treatment inhibited the damage of *B. cinerea* to grape fruit. At same time, chitosan could destroy the mycelium of *B. cinerea* and increase the antioxidant enzyme activities of grape fruit. The differentially expressed genes (DEGs) from treated or non-treated samples with chitosan were mainly enriched in the recognition of fungal diseases, plant hormone biosynthesis and signal transduction, and secondary metabolism. We detected a large number of secondary metabolites using the metabolome that were different in 'Kyoho' and 'Shine Muscat', such as epigallocatechin gallate, catechin, resveratrol etc. In conclusion, chitosan treatment improved disease resistance of grape fruit, and we established a possible model for chitosan regulating disease resistance of 'Kyoho' and 'Shine Muscat'. We found that the expression of DEGs in disease perception, plant hormone biosynthesis and signal transduction, and secondary metabolism differ between 'Kyoho' and 'Shine Muscat' after chitosan treatment, which helps to clarify the possible mechanism of chitosan providing tolerance to *B. cinerea*.