Transcriptomic and proteomic analysis of the mechanisms involved in enhanced disease resistance of strawberries induced by *Rhodotorula mucilaginosa* cultured with chitosan

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Abstract

Rhodotorula mucilaginosa cultured in a medium amended with chitosan significantly enhances biological control efficacy against postharvest fungal diseases of strawberries. The molecular mechanisms underlying the enhanced disease resistance of strawberries, however, have not been explored. In this study, a transcriptomic and proteomic approach was used to analyze the induced resistance response in strawberry. Results revealed that several genes involved in JA/ET, ABA and GA signal transduction pathways, as well as downstream genes and protein, were up-regulated by *R. mucilaginosa* cultured in a medium amended with 0.5% (w/v) chitosan. Several genes and proteins related to the synthesis of resistance-related compounds and processes were also up-regulated, including genes related to ROS regulation, and genes involved in cell wall reinforcement. Collectively, results indicated that disease resistance in strawberry can be induced by *R. mucilaginosa* cultured with chitosan. A global view of gene expression and protein abundance in hosts treated with an antagonist provides a theoretical reference for understanding the enhancement of disease resistance of fruits by antagonistic yeast incubated with elicitors, information that will also help in obtaining regulatory approval for the commercial use of yeast as biocontrol agents.