Molecular interactions between the biocontrol agent *Metschnikowia fructicola* and citrus fruit tissue and *Penicillium digitatum*

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Abstract

To gain better understanding of the molecular interactions between the yeast biocontrol agent *Metschnikowia fructicola* and citrus fruit and *Penicillium digitatum*, microarray analysis was performed on grapefruit surface wounds using an Affymetrix Citrus GeneChip in concert with transcriptomic analysis, using RNA-Seq technology. The data indicated that yeast application induced, among others, the expression of the genes encoding respiratory burst oxidase (*Rbo*), phenylalanine ammonia-lyase (*PAL*), chalcone synthase (*CHS*) and 4-coumarate-CoA ligase (4CL). In contrast, three genes, *peroxidase* (*POD*), *superoxide dismutase* (*SOD*) and *catalase* (*CAT*), were down-regulated in grapefruit peel tissue treated with yeast cells. Moreover, suppression was correlated with significantly higher levels of hydrogen peroxide, superoxide anion and hydroxyl radical production in yeast-treated surface wounds. Interestingly, large amounts of hydrogen peroxide were detected inside yeast cells recovered from wounded fruit tissue, indicating the ability of the yeast to activate reactive oxygen species when it is in contact with plant tissue. In the antagonist-pathogen interaction, genes related to transmembrane, multidrug transport and to amino acid metabolism were induced. In the antagonist-fruit interaction, expression of genes involved in oxidative stress, iron homeostasis, zinc homeostasis, and lipid metabolism were induced. This study provides the first global picture of gene expression changes in grapefruit in response to the yeast antagonist *M. fructicola*.