Abstract

To gain insight into the antagonistic molecular mechanisms displayed by the biocontrol epiphytic-yeast *Pichia guilliermodii* (isolate LCBG-03), its patterns of gene expression were evaluated during direct and indirect induction with *Penicillium digitatum* EfiA, a well-known fungal phytopathogen during the postharvest processing of citrus. Assays of *in vitro* antagonistic activity indicated a strong inhibitory effect on fungal growth and spore germination by the yeast, even when yeast–fungus interaction was performed on a rich medium. Antagonist gene expression was evaluated in induced condition as well as in direct interaction using differential expressed sequence tags (ESTs) obtained by two methodologies; suppression subtractive hybridization (SSH) and differential display (DD). We obtained the genetic response of the yeast under three different specific metabolic conditions: starvation by carbon source competence, sensing of extracellular metabolites produced by active mycelium of *P. digitatum* (membrane system) and induction by fungal cell walls. As a result, we observed just one EST, associated as expected to energy metabolism in starvation conditions; for the membrane system, seven ESTs were obtained by the SSH methodology, all related with some of the following metabolic networks: energy, nitrogen, cell cycle, ABCtransporters, response to stress and one unknown sequence. The induced (fungal cell walls) system produced the highest number of ESTs, with a total of 22, including all the metabolic networks mentioned above for the membrane system plus ESTs associated with signal transduction.