

Title Identification of differentially expressed genes from cherry tomato fruit (*Lycopersicon esculentum*) after application of the biological control yeast *Cryptococcus laurentii*

Author Feng Jiang, Jishuang Chen, Ying Miao, Karin Krupinska and Xiaodong Zheng

Citation Postharvest Biology and Technology Volume 53, Issue 3, September 2009, Pages 131-137

Keywords Postharvest biocontrol; *Cryptococcus laurentii*; Tomato fruit; Induced resistance; Subtractive suppression hybridization (SSH)

Abstract

Postharvest decay of fruit may be controlled by the use of a variety of diverse microorganisms acting as biocontrol agents, but the mechanisms associated with control are not fully understood. In order to gain insight into the action of antagonistic microorganisms on fruit, a forward subtractive suppression hybridization (SSH) cDNA library was constructed. SSH was performed with cDNA from cherry tomato fruit (*Lycopersicon esculentum*) inoculated with water as the “driver” and cDNA from tomato fruit inoculated by *Cryptococcus laurentii* as the “tester”. A total of 150 clones in the SSH library were sequenced and found to represent 50 unigenes. BLASTX results reveal that 35 cDNAs had significant sequence homologies with known sequences in the NCBI database. The identified cDNAs encode proteins involved in cellular processes such as primary metabolism, signal transduction, defense and responses to pathogens, stress-related, cell wall assembly, and photosynthesis and transcription related sequences. Six cDNA clones were selected for temporal expression analysis using RT-PCR. The results show that a number of transcripts encoding proteins/enzymes which are known to be up-regulated under some biotic and abiotic stresses are also up-regulated after the application of biological control yeast to cherry tomato fruit. The expression of these proteins may play a role in increasing fruit resistance to postharvest pathogen infection.