PSF.AGR.8

EXPRESSION PROFILE OF DIFFERENTIALLY-REGULATED GENES DUE TO INFECTION OF *Colletotrichum musae* IN BANANA (*Musa* spp. VAR. SEENIKESEL)

N. C. Y. Jayasundara, U. M. Aruna Kumara, D. M. De Costa

Department of Agricultural Biology, Faculty of Agriculture, University of Peradeniya

Anthracnose caused by *Colletotrichum musae* causes significant qualitative and quantitative yield losses of dessert banana at the postharvest stage. However, the varieties of banana grown in Sri Lanka show a wide variation in terms of the severity of anthracnose development. Determination of the genetic basis of the variation of development of anthracnose in the different varieties of banana would be useful to design effective management measures of the disease. Therefore, the present study was conducted to identify genes responsive to *C. musae* infection in a dessert banana variety, *Seenikesel* which is relatively resistant to postharvest anthracnose development.

A cDNA library already constructed from fruit peel tissue of banana (var. *Seenikesel*) inoculated with *C. musae* was subjected to differential hybridization. Two types of total RNA probes, one prepared from *C. musae* infected peel tissue and another prepared from non-infected peel tissue of var. *Seenikesel* were used for hybridization. Total RNA isolated from the peel tissues infected with and without *C. musae* were initially subjected to cDNA synthesis and the synthesized cDNA were labelled by Digoxygenin for total RNA probe preparation. Up- and down-regulated cDNA clones due to differential hybridization were selected by comparing the chemiluminesent signals developed on a Nylon membrane having cDNA clones arrayed onto it. The genes expressed or suppressed due to *C. musae* infection were identified by amplifying the cDNA fragments harboured by up-and down-regulated clones, respectively. The PCR products were subjected to DNA sequencing and homology search was done to determine the putative genes due to *C. musae* infection.

The present study identified 20 up-regulated clones by differential screening of the cDNA library of banana (var. *Seenikesel*) infected with *C. musae*. DNA sequencing and subsequent homology search identified 10 putative genes/protein products which are up-regulated due to *C. musae* infection. The expression profile of differentially regulated genes was categorized based on the NCBI database. Results revealed several functional classes of Banana Expressed Sequence Tags (ESTs) with up-regulated genes in response to infection by *C. musae*. The identified ESTs belonged to defence-related, stress-induced, protein synthesis and stabilization functional categories.

Funding: National Research Council (Grant no. 07-42).