

**Title** Identification of genes involved in the response of banana to crown rot disease  
**Authors** Ludivine Lassois, Patrick Frettinger, Luc de Lapeyre de Bellaire, Philippe Lepoivre and Haissam Jjakli  
**Citation** Molecular Plant-Microbe Interactions 24 (1): 143-153. 2011.  
**Keywords** crown rot disease; banana

### **Abstract**

Variations in banana susceptibility to crown rot disease have been observed but the molecular mechanisms underlying these quantitative host–pathogen relationships are still unknown. This study was designed to compare gene expression between crowns of banana fruit showing a high susceptibility ( $S^+$ ) and crowns showing a low susceptibility ( $S^-$ ) to the disease. Comparisons were performed at two situation times: i) between crowns ( $S^+$  and  $S^-$ ) collected 1 h before inoculation and ii) between crowns ( $S^+$  and  $S^-$ ) collected 13 days after inoculation. Gene expression comparisons were performed with cDNA-amplified fragment length polymorphism (AFLP) and results were confirmed by real-time reverse-transcription polymerase chain reaction. Among genes identified as differentially expressed between  $S^+$  and  $S^-$  crowns, two were involved in signal transduction, three in proteolytic machinery, two had similarity to pathogenesis-related protein 14, one to a CCR4-associated factor protein, and one to a cellulose synthase. Paradoxically, the overexpression of the cellulose synthase gene was associated with banana showing a high susceptibility in both pre- and post-inoculation situations. Finally, the cDNA-AFLP identified a gene that seems to be associated with the quantitative banana responses to crown rot disease; this gene encodes a dopamine- $\beta$ -monooxygenase, which is involved in the catecholamine pathway. To our knowledge, this work is the first to address both pre- and post-infection gene expression with the same host–pathogen combination and distinct susceptibility levels.