

Discovery of pathogenesis related and effector genes of *Erwinia mallotivora* in *Carica papaya* (Eksotika I) seedlings via transcriptomic analysis

ABSTRACT

A comparative transcriptome of *Erwinia mallotivora* library across early infection time points (6, 24 and 48 h) on papaya seedling *Carica papaya* (Eksotika I) was performed. A total of 5,680 genes were identified as differentially expressed genes (DEGs). The highest numbers of DEGs in all three *E. mallotivora* infection time points were accounted in the biosynthesis of secondary metabolites, microbial metabolism in diverse environments and ATP binding cassette transporters based on KEGG-based analysis. The functional annotation of the DEGs via Gene Ontology analysis has revealed a highly complex (more than 2,000 functional terms) yet a specific virulence strategy adapted by *E. mallotivora* across the infection time points. Our findings have uncovered the key factors and pathogenicity mechanism adopted by *E. mallotivora* as the infection progresses.

Keyword: Papayas; Phytopathogenic bacteria; Plant-pathogenic bacteria; Bacterium; Phytopathogens; DNA sequences