Identification of oil palm's consistently upregulated genes during early infections of Ganoderma boninense via RNA-Seq technology and real-time quantitative PCR

ABSTRACT

Basal stem rot (BSR) disease caused by pathogenic fungus Ganoderma boninense is a significant concern in the oil palm industry. G. boninense infection in oil palm induces defense-related genes. To understand oil palm defense mechanisms in response to fungal invasion, we analyzed differentially expressed genes (DEGs) derived from RNA-sequencing (RNA-seq) transcriptomic libraries of oil palm roots infected with G. boninense. A total of 126 DEGs were detected from the transcriptomic libraries of G. boninense-infected root tissues at different infection stages. Functional annotation via pathway enrichment analyses revealed that the DEGs were involved in the defense response against the pathogen. The expression of the selected DEGs was further confirmed using real-time quantitative PCR (qPCR) on independent oil palm seedlings and mature palm samples. Seven putative defense-related DEGs consistently showed upregulation in seedlings and mature plants during G. boninense infection. These seven genes might potentially be developed as biomarkers for the early detection of BSR in oil palm.