

Characterization of Transcription Factors Involved in Early Defense Response during Interaction of Oil Palm *Elaeis guineensis* Jacq. with *Ganoderma boninense*

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Abstract : Oil palm production generates high export earnings to many countries especially in Southeast Asian region. Infection by necrotrophic fungus, *Ganoderma boninense* on oil palm results in basal stem rot which compromises oil palm production leading to significant economic loss. There are no reliable disease treatments nor promising resistant oil palm variety has been cultivated to eradicate the disease up to date. Thus, understanding molecular mechanisms underlying early interactions of oil palm with *Ganoderma boninense* may be vital to promote preventive or control measure of the disease. In the present study, four months old oil palm seedlings were infected via artificial inoculation of *Ganoderma boninense* on rubber wood blocks. Roots of six biological replicates of treated and untreated oil palm seedlings were harvested at 0, 3, 7 and 11 days post inoculation. Next-generation sequencing was performed to generate high-throughput RNA-Seq data and identify differentially expressed genes (DEGs) during early oil palm-*Ganoderma boninense* interaction. Based on de novo transcriptome assembly, a total of 427,122,605 paired-end clean reads were assembled into 30,654 unigenes. DEGs analysis revealed upregulation of 173 transcription factors on *Ganoderma boninense*-treated oil palm seedlings. Sixty-one transcription factors were categorized as DEGs according to stringent cut-off values of genes with log2 ratio [Number of treated oil palm seedlings/ Number of untreated oil palm seedlings] $\geq |1.0|$ (corresponding to 2-fold or more upregulation) and P-value ≤ 0.01 . Transcription factors in response to biotic stress will be screened out from abiotic stress using reverse transcriptase polymerase chain reaction. Transcription factors unique to biotic stress will be verified using real-time polymerase chain reaction. The findings will help researchers to pinpoint defense response mechanism specific against *Ganoderma boninense*.

Keywords : *Ganoderma boninense*, necrotrophic, next-generation sequencing, transcription factors

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