

Detoxification related genes in gut of *Coptotermes curvignathus*

ABSTRACT

Coptotermes curvignathus (*C. curvignathus*) are subterranean termites that feed on living-tree as their sole diet, which consist mainly of cellulose, hemicelluloses, lignin, plant allele chemical and other environmental residues such as insecticide. The xenobiotic compounds, plant allele chemical and insecticide are hazardous to termites health and need to be transported out of their body via xenobiotic and detoxification metabolism. This paper highlighted the potential enzymes that play vital role in the xenobiotic and detoxification metabolism. Transcriptomic data were generated from 200 termite's digestive system using Illumina HiSeq 2000. Raw data was trimmed and assembled by SOLEXAQA and Bowtie before loaded into Gene Ontology based data mining software, Blast2GO (B2G). The result showed that, *C. curvignathus* contain enzymes that involved in all three biotransformation phases of xenobiotic and detoxification metabolism, which included cytochrome P450s monooxygenases, glutathione S-transferase, carboxylesterase, UDPglucuronyltransferases and N-acetyltransferase. The result of this study is the first insight into Cc xenobiotic pathway.

Keyword: *Coptotermes curvignathus*; Xenobiotic; Detoxification; Cytochrome P450; Glutathione S-transferase