

OR301*Transcriptomics on social interactions in termites: effects of soldier presence*

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The organization of social-insect colonies requires sophisticated mechanisms to regulate caste composition according to colony demands. In termites, although it has been known that soldier is responsible for inhibiting workers to differentiate into soldiers, the mechanism underlying the regulation of soldier differentiation is still unclear. Since genome-wide approaches for the identification of genes involved in social interactions are expected to clarify this issue, we performed transcriptome analyses by Next Generation Sequencer to identify genes expressed in workers that are up-regulated by the soldier existence in the subterranean termite *Reticulitermes speratus*. In our analyses, we applied the artificial induction of soldier differentiation by juvenile hormone (JH), where the inhibitory effects of soldier differentiation by the soldier presence were evaluated. By comparing transcriptomes prepared from workers that were kept with or without soldiers under the JH induction, the 181,244 contigs (i.e. potential transcripts) that covered 70% of the protein-coding genes in *Drosophila melanogaster*, were obtained by transcriptome sequencing and de novo assembly. Using the contigs, expression analyses were performed to identify genes differentially expressed in each experimental treatment, showing that only a small number of genes were up-regulated by soldier presence. Gene Ontology (GO) analysis showed that some of those are responsible for the negative regulation of cell cycle and transportation of xenobiotic substances, suggesting that they could be involved in the developmental arrest and pheromonal regulations in workers. It was also found that many genes were up-regulated by JH application and actually included factors for JH regulations and insulin signaling pathways. By identifying the candidate genes underlying the regulatory mechanisms of social interactions, it is suggested that the suppression of soldier differentiation by the soldier presence could be accomplished by the expressions of a small number of genes that repress the majority of genes required for soldier differentiation.