Isolation of cDNA Clones Differentially Expressed from the Dung Beetle *Copris tripartitus* Stimulated with Lipopolysaccharide

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Insects have to defend themselves from infection by a side variety of potential bacteria, fungi and parasites in natural habits, and have therefore evolved efficient host-defense mechanisms for successful survival. The Copris tripartitus lives in an environment with abundant pathogens. Therefore, it can be supposed that Copris tripartitus living in the pathogen-abundant environment must have peptides against bacteria. In this study, to find some antibacterial peptides responsible for bacteria resistance, the suppression subtractive hybridization and GeneFishing DEG system were employed to identify differentially expressed genes in the dung bettle, Copris tripartitus, immunized with lipopolysaccaride. Results showed that one cDNA clone from 11 subtracted clones were selected through dot blot analysis. The differential expression patterns of the selected cDNA clone was confirmed by Northern blot analysis. Full-length nucleotide sequence of selected cDNA clone was determined by 5' and 3' rapid amplication of cDNA ends(RACE). The nucleotide sequence deduced from selected full-length cDNA showed no significant homologies to those of reported nucleotides. Although expression of a novel gene was detected and remained marginally increased by saline, results of Northern blotting showed that a novel gene was stimulated with E.coli and laminarin. Antibacterial peptide, Coleoptericin, was also inducible by lipopolysaccharide in Copris tripartitus immunized with lipopolysaccaride. RT-PCR and Northern blot analysis were performed to confirm that Coleoptericin are differentially expressed in Copris tripartitus. Full-length nucleotide sequence of Coleoptericin were determined by 5' and 3' rapid amplication of cDNA ends.