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Promoter analysis of the mushroom body-preferential genes of the honeybee

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Mushroom bodies (MBs) are a higher center of the insect brain, and comprise interneurons called the Kenyon cells (KCs). There are four KC subtypes (class I large-, middle-, small-, and class II KCs) in the honeybee (*Apis mellifera* L.) MBs. Recent study indicated that parasitism, but not sociality, is associated with the evolution of the elaborate MBs in Hymenopteran insect brains. How each KC subtype contributes to the honeybee social behaviors, however, remains largely unknown. We have so far identified many genes expressed in a KC subtype-preferential manner in the honeybee brain. We expect that analyses of the function and regulatory mechanisms of genes expressed in a KC subtype-preferential manner may contribute to our better understanding of the molecular and neural bases underlying the honeybee social behaviors. In the present study, we aimed to clarify regulatory mechanism(s) of the KC subtype-preferential gene expression in the honeybee brain. We previously used cDNA microarray to comprehensively search for candidate genes expressed preferentially in the honeybee MBs. In the present study, we focused on three genes, phospholipase C epsilon (PLCe), Synaptotgmin 14 (Syt14), and discs large 5 (dlg5), whose expression seemed highly enriched in the honeybee MBs, among the candidate genes identified. Quantitative RT-PCR and in situ hybridization revealed that PLCe is expressed almost selectively in all KC subtypes, while Syt14 and dlg5 are expressed almost selectively in the lKCs in the honeybee brain, suggesting that these three genes are most appropriate for the analysis of KC subtype-selective promoters. We used electroporation to introduce and express reporter genes, in which gfp is ligated downstream of the upstream regions of the above three genes, in the honeybee brain. So far, basic but not MB-selective promoter activities were detected in the genomic regions around the transcription start site of each gene.