

Proteome analysis of honeybee brain from worker subcastes with distinct social roles

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Honeybee (*Apis mellifera*) is a social insect showing complex and integrated behaviors. Its ability to read several well-defined sets of social signals is fundamental for the modulation of its activities and its social system. In this work, the proteomes of nurse and forager worker subcaste honeybee brains were compared by using two-dimensional gel electrophoresis analysis within pI range of 4–7 and mass range of 15–120 kDa. More than 20 possible candidate proteins with differentially expressed concentrations (up- or down-regulated) were detected by computational gel image analysis. Most of them were identified by Peptide Mass Fingerprinting through a MALDI-TOF high resolution mass spectrometer. Nurse brain showed increased expression of MRJP1 and MRJP2, which are major royal jelly proteins related to determination of castes and social functions during the honeybee larvae differentiation. Other proteins implicated in protein synthesis were also up-regulated in the nurse brain. Experienced foragers overexpressed alpha-glucosidase and proteins related to energetic metabolism. Such comparative neuroproteomics results may contribute to understanding the behavior and ontogenetic differentiation of two subcastes with distinct social roles of the honeybee *A. mellifera*.

KEY WORDS: *Apis mellifera*, Brain, Proteome, Peptide mass fingerprint, MALDI-TOF.

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