DIFFERENTIAL GENE EXPRESSION IN THE LARVAL HONEY BEE (APIS MELLIFERA) OVARY

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The development of the female castes of Apis mellifera is based on a single genotype, that can alternatively give rise to a queen or worker phenotype depending on the diet received during the larval stages. Such differential feeding triggers endogenous responses in signaling pathways and the endocrine system which, in turn, promotes differential gene expression related to the development of the two phenotypes. The major difference between queens and workers is related to the reproductive system, viz., the number of ovarioles in adult individuals. This occurs as a result of extensive programmed cell death during the larval stage. This project aimed to analyze the differences in gene expression patterns in the ovaries of larval workers and queens. From a series of microarray assays we selected a set of 12 differently expressed genes for validation by qPCR. These analyses were performed on ovaries dissected from workers of four larval stages representing critical phases of ovary development. Two predicted genes (GB46223 and GB54419) were expressed significantly at high levels in the L4 stage and decreased in the posterior stages. The genes (GB18737, GB10869, GB18969, GB40976, GB50902 and GB13966) were expressed at higher levels in the initial phases (L4 and L5F1) whereas other transcripts (GB19297, GB12860, GB13214, GB17328) were more expressed in the laters phases (L5F2 and L5F3). Taken together these results lead to infer that these genes are relevant during ovary differentiation, once their expression is strongly modulated during stages when programmed cell death takes place.