

OR341*Caste specific pheromone-related gene expression in honeybee mandibular glands***Abraham Hefetz**, Osnat Malka, Elina Lastro-Nino, Christina Grozinger

Social context is often a primary regulator of social behavior, but genes that affect or are affected by it have rarely been investigated. In the honeybee the queen mandibular gland (MG) pheromone mediates reproductive dominance, its absence prompting ovary activation and queen pheromone production in workers. It was therefore interesting to investigate the effect of caste and social environment on genome-wide expression patterns in the MG. We used microarrays to examine virgin and mated queens, queenright (QR) and queenless (QL) workers, with and without activated ovaries. Approximately 2554 transcripts were significantly differentially expressed among these groups, with caste and social context being the main regulators of gene expression patterns. Among these, 27 genes involved in production of the fatty-acid derived MG pheromone were differentially expressed in a caste selective manner, revealing 4 regulatory gene-expression steps that distinguish the queen from worker pheromone biosynthesis pathways. The first step involves stearic acid that although is a common precursor for these pheromones in queens and workers, its production and activation seems nonetheless to be controlled by different, caste specific genes. The second step involved the ω -1 fatty acid hydroxylation via caste selective Cyp 450 genes. The next regulatory step is the expression of caste specific genes that are responsible for chain shortening via β -oxidation. The final regulatory step, the oxidation of 9-hydroxy-2-decenoic acid to 9-oxo-2-decenoic acid is entirely queen specific. These differential gene expressions emphasize the occurrence of disparate pheromone biosynthetic pathways for queens and workers, adding another dimension regarding the regulation of these important pheromones. Gene ontology analysis also revealed genes of different functional categories whose expression was impacted by caste (oxidation-reduction activity, immune response, and several metabolic and biosynthetic processes) or by the social environment (protein catabolism), suggesting that the MG serve more than being a pheromone source in honeybee biology.