HOW TO BE THE RIGHT SIZE - GENE EXPRESSION ANALYSIS AND GENE REGULATORY NETWORK APPROACHES IN HONEY BEE DEVELOPMENT

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The development of female larvae of the honey bee, *Apis mellifera,* into the morphologically distinct queen and worker castes is initially triggered by differential feeding regimes. This subsequently results in caste-specific endocrine states, where a high level of juvenile hormone in the hemolymph protects the larval ovaries of queen larvae from degeneration via an apoptotic program. With a fully sequenced genome it is now possible to investigate how differential feeding can drive differential gene expression. In non-hypothesis-driven approaches we search for putative regulatory motifs shared between genes revealed by suppression subtractive hybridization as differentially expressed in queen and worker larvae. Mapping such shared motifs back to the honey bee genome allowed the construction of networks which exhibited strong topological differences between the two castes. In order to get hands on questions such as, why are queens bigger than workers, we elected the insulin signaling pathway for a candidate gene approach. We analyzed the expression profiles of the two predicted insulin receptors genes and of the two insulin-like peptides. Surprisingly, these genes were not overexpressed in queen larvae, indicating a crosstalk between the insulin signaling pathway and juvenile hormone.

key words: *Apis mellifera* / differential gene expression / insulin signaling