



## **Differential expression of developmental genes in response to the morphogenetic hormones in *Apis mellifera***

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The development in honeybees is mainly controlled by the action of two major hormones, juvenile hormone (HJ) and 20-hidroxycdysone (20E). These hormones triggers gene cascades, which results in phenotypic, physiological and behavioral changes. However, the responses triggered by the hormones varies depending on the developmental stage in which the organism is. Besides hormones, a class of non-coding RNAs, the microRNAs, regulates gene expression at a post-transcriptional level during insect development. In this study, we analyzed the relationship between genes and hormones, at the final stages of the development of *Apis mellifera*. The expression profile of the genes, ultraspiracle (Usp), fushi tarazu transcription factor 1 (ftz-f1), ecdysone receptor (EcR), calponin (chd64), insulin- receptor 2 (inr2) Krüppel homolog 1 (Kr-h1), germ-cell expressed (gce), early trypsin (et), and their regulators miRNA-34, miRNA-281, miRNA-252a and miRNA-252b were assessed from 5<sup>th</sup> instar larvae to newly emerged adult by qPCR. We also tested if the expression of genes and miRNAs was affected by hormonal treatment (20E and JH). Most of the genes seems to respond to hormonal variation in pupal stages as they do in larval stages. However, gce and chd64 seem to have a different role during final stages of development, once gce showed a quick response to 20E treatment and no response to HJ in pupal. This was not expected since gce is a nuclear receptor of HJ in insects. In addition, we concluded that Usp is an Immediate Early Gene, as it responded rapidly to hormonal treatments (60 min) and quickly restored its level (30 min later). This study describes new components to the regulatory network that regulates bee development. Financial support: FAPESP Proc. Nr. 2016/06657-0, 2016/13854-6.