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Signaling pathway integration in honeybee, Apis mellifera*, caste development*

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Caste polyphenism is the morphological manifestation of the highly efficient and evolutionarily successful division of labor in social insects, but understanding how a single genotype can give rise to two very distinct phenotypes in response to environmental signals is a challenging task for developmental biologists. In the honeybee , queen larvae receive copious amounts of royal jelly throughout larval development, while workers are fed less frequently and initially receive a diet less rich in sugar. This triggers differential responses in several signaling pathways, including juvenile hormone (JH), EGF receptor, insulin/insulin-like signaling and the TOR pathway. All of these are major developmental regulators in insects and conserved response systems to nutritional status. The JH titer is much elevated in queen larvae and plays a key role in inhibiting programmed cell death in the larval ovary. Similarly, TOR signaling is also an important factor for queen development. Unexpectedly, insulin signaling has now been shown to be of only minor importance for queen development, even though the sugar concentrations in royal jelly is higher in worker jelly. This has led us to investigate the role of the role of the respiratory metabolism in caste development, revealing overexpression of hypoxia core genes in worker larvae, thus indicating an endogenous hypoxia condition in these. With all these signaling pathway data in mind, and seeing that their gene expression patterns in bee larvae diverge from current views on their function in Drosophila and other model organisms, we are now mapping the integration of these pathways to reveal molecular mechanisms underlying caste morphology. Financial support: FAPESP (Brazil)