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Modular approaches to the genetic basis of division of labor

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Honeybee workers pass through four distinct developmental stages as they age. These temporal castes are specialized for particular task sets such as nursing, food processing and nest building, and foraging. Some of these castes work together requiring tight coordination of activity. The genetic (and general mechanistic) basis of this social system has received much attention, with the regulatory basis of the transition to foraging receiving the most attention. Thousands of genes have been identified that differ between nurses and foragers, for example, many of them transcription factors or other regulatory genes. This work has focused primarily on brains and has used microarrays. This talk will present work using RNA-Seq that expands on this work to consider the genetic basis of the nurse bee to forager transition across ten separate honeybee tissues. In particular, we focus on how expression of genes associated with juvenile hormone and insulin/insulin-like signaling differ across the tissues, implying modular regulation of tissue specific social functions with caste transitions. This work expands greatly our already impressive understanding of the regulatory genetic basis of complex social behavior in bees.