

Abstract

Transcriptomic analysis of foraging decision making patterns in Honey bee (*Apis mellifera*)

Honey bees are an important model for studies of neural and behavioral plasticity (especially of social behavior), learning, and memory. Honey bees have also been used extensively to study the genetic components of behavior and how regulation of genes due to environmental stimuli produce variation of phenotypes. This allows us to look at expression patterns at specific moments of behavior, and how these can change as a consequence of environmental factors or behavioral shift. For example, foragers can decide which flowers to visit and which flower patches it will inform to the colony based on nectar concentration and accessibility. These behavioral patterns have been studied through the Octopamine, Dopamine (and their respective repressors) signaling pathways. However, the molecular mechanisms underlying these behaviors have not. For this work, we plan on constructing foraging fields using the flower patch model as described in Cakmak et al., 2009 and conduct behavioral assays described in Giray et al., 2015 to collect and classify foragers into specific categories, assess the underlying molecular expression mechanisms of behavior of each forager category through the use of Next Generation RNA sequencing techniques and study genetic expressional trends and create a generic baseline that can be incorporated into other organisms to better describe the process of decision making. The results of this research can help us to understand human diseases associated with memory, learning, and decision making.