

A Model for Modulation of Hebbian Plasticity and Its Potential Role in Regulating Attention in the Honey Bee (*Apis mellifera*)

Brian H Smith, School of Life Sciences, Arizona State University

A honey bee colony contains a mixture of many different genotypes because of multiple mating by the queen, which is important for integration of colony function. With respect to learning performance, my lab and others have shown that foragers differ in how they perform on basic learning tasks, and that this variation arises from their genotypes. For example, repeated exposure to an odor without reinforcement produces Latent Inhibition, which is revealed by slower learning about the now 'familiar' odor relative to a 'novel' one. We have shown that we can establish high and low lines with respect to how workers perform on this task. Field colonies treated with foragers of one genotype or the other, or to a mixture, show that this genotype reflects attention to known resources versus exploration for new ones. QTL mapping of high and low lines has shown that the biogenic amine receptor *Amtyr1* is associated with different behavioral performance. We have disrupted functioning of this gene to show how it affects Latent Inhibition, which combined with computational modeling and mapping its distribution in the brain suggests a model of how it is integrated as a kind of gain control into neural circuitry. *Amtyr1* has now been implicated in several disparate behaviors in honey bees. From a mechanistic standpoint, why, and how, can one gene have such broad phenotypic effects? The answer may lie in how *Amtyr1* works with a broader set of genes, potentially different sets in different areas, that may be engaged in gene networks.