



Studying the genetics of colony-level traits using GWAS in honey bees (*Apis mellifera*)

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Eusociality evolved multiple times in Animals and involves division of labour between individuals that cooperate to benefit the group. In solitary species, genetic mutations can influence an individual's trait and these mutations can spread or decline within a population as a function of the individual's fitness. In contrast, eusocial animals have collective traits (i.e. colony-level traits) that are emergent properties of a complex system composed of many genetically distinct individuals interacting together. The complex genetics and evolution of colony-level traits is not well understood, in part because the typical tools for studying genetics in solitary organisms are not immediately applicable to studying traits performed by groups of individuals interacting in complex ways. Here I will present an overview of BeeOmics – a large-scale effort to study the genetics of colony-level traits in honey bees using genome wide association mapping. The BeeOmics consortium quantified several colony level traits in approximately 1000 Canadian honey bee colonies, including several measures of social immunity, colony defence, foraging, and overwintering. We sequenced the composite genome of each colony at approximately 150X coverage. Unlike typical genome wide association mapping where individual phenotypes are correlated with individual genotypes, our study will correlate colony phenotypes with colony allele frequencies at over 7 million mutations in the honey bee genome. This work will link genetic diversity at specific mutations with colony-level trait differences in Canadian honey bees. Additionally, a pool of workers from each colony will be subjected to proteomic analyses of tissues involved in sensory perception and behaviour. The proteomic analyses will provide us with expression data on thousands of proteins, allowing us to link genetic diversity with changes in protein expression and changes in colony behaviour.