

SPP 2349 (GEvol): Genomic basis of evolutionary innovations.

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Title:

Comparative and experimental approaches to the transcriptomics and genomic regulation of eusociality in the sweat bees

Abstract

Eusociality is a major evolutionary innovation that has independently evolved several times across the insects. Using one lineage of sweat bee (Hymenoptera: Halictini) in which eusociality has arisen once, been elaborated upon and subsequently lost repeatedly, we propose to investigate variation in gene expression and its regulation associated with the gain and subsequent loss of eusociality. Through a cross-species comparison of the expression profiles and genome-wide chromatin accessibility of ancestrally solitary, eusocial and derived solitary species, we aim to reveal those genetic and regulatory changes that are associated with the gain, elaboration and loss of sociality using RNA-seq and ATAC-seq approaches. These analyses will be strengthened by investigation of a facultative social species in a common-garden experiment to test proposed regulatory mechanisms underpinning the expression of sociality. Previous analysis of the sweat bees has suggested pivotal roles for juvenile hormone and pheromone production, which provide candidates for in-depth analysis of gene expression and its regulation in response to social environment. Through a comprehensive analysis spanning changes in gene expression and its regulation through to phenotype, we aim to highlight functional transcriptomic and genomic changes that may have driven sociality in this plastic lineage of bees. Through sequence analyses of differentially expressed genes, we will also investigate how caste-conditional gene expression influences expected patterns of protein evolutionary rates, thereby contributing to the understanding of the influence of eusociality on genome evolution.