

OR375*The function of DNA methylation in social insects*Brendan Hunt, Karl Glastad, Soojin Yi, **Michael Goodisman**

Phenotypic plasticity is a fundamentally important process that allows organisms to develop phenotypes well suited to the environment. The production of alternate phenotypes in insects relies on epigenetic inheritance, which plays a key role in regulating gene expression. DNA methylation is one of the most widely conserved forms of epigenetic information. However, the function of DNA methylation in insects remains poorly understood. The goal of our research program is to gain a greater understanding of the importance of DNA methylation and its role in the epigenetic landscape of social insects. We use computational and empirical methods to determine the function and evolution of DNA methylation. We have found that DNA methylation is targeted to genes in insect genomes. In addition, methylated genes tend to be uniformly and highly expressed. Thus, methylation is strongly associated with patterns of gene expression. We have also found that DNA methylation is associated with ploidy variation. Phenotypically-dissimilar diploid males, queens, and workers are more similar to one another in terms of DNA methylation than are phenotypically-similar haploid and diploid males in fire ants. These results indicate that DNA methylation may be involved in ploidy compensation. Evolutionary analysis indicates that targets of DNA methylation are largely conserved in fire ants and honeybees. Thus patterns of DNA methylation do not differ dramatically among social insect species. Finally, we have discovered that DNA methylation is associated with several active histone modifications in social insect taxa. Thus, overall, our research indicates that DNA methylation is a single part of a larger, conserved, integrated epigenetic landscape in social insect genomes.