OR381

Investigating genomic imprinting: an epigenetic cycle in the honeybee methylome

Robert Drewell, Eliot Bush, Emily Remnant, Garrett Wong, Suzannah Beeler, **Benjamin Oldroyd**

In honeybees (*Apis mellifera*) the epigenetic mark of DNA methylation is central to the developmental regulation of caste differentiation, but may also be involved in additional biological functions. In this study, we examine the whole genome methylation profiles of three stages of the haploid honeybee genome: unfertilised eggs, the adult drones that develop from these eggs, and the sperm produced by these drones. These methylomes reveal distinct patterns of methylation. Eggs and sperm show 381 genes with significantly different CpG methylation patterns, with the vast majority being more methylated in egg. Adult drones show greatly reduced levels of methylation across the genome when compared to both gamete samples, suggesting a dynamic cycle of methylation loss and gain through the development of the drone and during spermatogenesis. The distinct methylation patterns at these genes suggest parent-specific epigenetic marking in the gametes. The potential developmental and evolutionary implications of methylation in eggs and sperm and how this may relate to predictions of genomic imprinting in this eusocial insect will be discussed.