



Is worker reproduction influenced by sperm-specific DNA methylation in the honey bee?

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Kin-selected conflicts are an inherent feature of social evolution. Queen honey bees are extremely polyandrous so each colony is comprised of up to 30 worker subfamilies, each sired by a different father and possessing different reproductive traits. This increases the genetic diversity within the colony, but also paves the way for genomic conflicts. Genes favouring worker reproduction are indeed predicted to be over-expressed when paternally inherited, while under-expressed when derived from the queen. Epigenetic modifications of the genome such as DNA methylation have the potential to regulate gene expression in a parent-of-origin manner. The existence of sperm-specific methylation profiles could lead to subfamily-dependent reproductive traits. However, this has never been investigated in social insects. In this study, we first compared the genome-wide methylation profiles of the semen of individual males. A large number of methylated sites were common between all samples, yet we found vast differences between each individual semen methylome, both at the site and gene level. Differentially methylated genes were often found in association with allele polymorphisms, indicating a strong link between epigenetic specificity and genotype. To investigate the functional outcome of sperm-specific methylation, we then performed artificial inseminations of queens with different males, retaining half of their semen for sequencing. We assessed the reproductive traits of each subfamily in the worker progeny together with the methylation profile of their ovaries in presence and absence of the queen, and compared them with their fathers' methylomes. We discuss the evolutionary implications of this double layer of genetic and epigenetic variability for the expression of kin-selected conflicts in insect societies.