



Genomic Imprinting in South African honey bees

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Colonies of haplodiploid Hymenopteran (ants, bees, and wasps) insects often served as model systems for examining how cooperative behaviour can evolve. More recently, insect colonies have emerged as important systems for understanding within-genome conflict. In eusocial species such as honey bees, queens are polyandrous and mate early in life with an average of 12 males. The queen stores the spermatozoa of each drone in an organ known as the spermatheca, and utilises this stored sperm to fertilize queen- or worker-destined eggs. Honey bee colonies are therefore comprised of subfamilies of workers each of which share the same father. This generates a situation that is ripe with potential for conflict between males to increase the reproductive success of their female offspring. A father that can influence the expression of genes in offspring so that his daughters are more likely to develop as a queen or a reproductive worker has a much greater probability of reproductive success than another male that does not do so. Recently, genes that influence worker reproduction have been found to have paternally-biased expression. That is the allele derived from the father is expressed whereas the maternal allele is switched off. This suggests reproductive conflict between the paternal and maternal genomes of females. The underlying mechanism that influences this maternal and paternal bias remains unknown, but DNA methylation has been proposed as the most likely mechanism. To identify the genes that are modified by mothers and fathers and the mechanisms underlying differentially expressed genes, we generated replicate reciprocal crosses between two African honey bee subspecies, *Apis mellifera capensis* and *A. m. scutellata*. We then sequenced both parents (whole-genome) and offspring (transcriptome and

methylome). The current findings of this work will be discussed.

