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Allele-specific methylation in the honeybee, Apis mellifera

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Nearly a third of all genes in *A. mellifera* have been found to be methylated, with the occurrence of differentially methylated genes associated with the establishment of distinct developmental and behavioural phenotypes of queens and workers. It is unclear whether DNA methylation drives changes in key regulatory pathways leading to these alternate phenotypes, or if these changes are driven by other mechanisms. The functional characterisation of methylated genes involved in directing development and behavioural maturation will help define the exact role that DNA methylation plays in modulating phenotypic outcomes in *A. mellifera*. One gene in which this is presently being carried out is the gene encoding lysosomal-alpha-mannosidase (alpha-LAM), a conserved enzyme involved in carbohydrate metabolism. alpha-LAM displays a high level of polymorphism, with sequence variation being linked to dramatic changes in DNA methylation. Significantly, this is an indication that the underlying DNA sequence itself may direct changes in methylation. Utilising single drone-inseminated queens we have genotyped individuals, and bisulfite sequencing and gene expression analyses are being performed. Analysis of this allele-specific methylation will help elucidate the mechanisms driving context-dependent expression of alpha-LAM, and will provide a framework from which broader conclusions about the role of DNA methylation in *A. mellifera* can be drawn.