

Epigenetics regulation of gene expression by DNA methylation in insect models

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Female honeybees have two distinctly separate castes that either work (workers) or reproduce (queens). Physically the two castes are highly different in both appearance and biology, yet they can both originate from a single fertilised egg. Queen-destined larvae are fed royal jelly and this nutritional stimulus initiates developmental divergence toward the queen caste. DNA methylation, that is chemical changes to DNA bases by the addition of a methyl group, can influence the activation or repression of genes. DNA methylation has been suggested by previous research as a means of controlling caste determination during early larval development. Our aim was to identify the initial molecular response to royal jelly in larvae that are yet to commit to their developmental fate, in order to unravel the very first and most critical genetic and epigenomic changes that underlie caste determination in honeybees.

We have identified significant changes in both gene expression and DNA methylation as early as 2hrs after feeding on royal jelly. These data which are being prepared for peer-review and publication, represent the most comprehensive dataset ever produced to profile this process in honeybees, and offer significant insight into the molecular mechanisms underlying caste determination.