The epigenetic basis of nutrition-mediated caste identity in the honey bee

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The capacity of the honey bee to produce three phenotypically distinct organisms or castes (queen, sterile female worker and a haploid male drone) from one genotype represents one of the most remarkable examples of developmental plasticity in any phylum. The queen-worker morphological and reproductive divide is environmentally controlled during post-embryonic development by differential feeding. Previous studies have implicated metabolic flux acting via epigenetic regulation, in particular DNA methylation and microRNAs, in establishing distinct patterns of gene expression underlying caste-specific developmental trajectories. We produce the first genome-wide maps of chromatin structure in the honey bee at a key larval stage where developmental canalization into queen or worker is virtually irreversible. We find extensive genome-wide differences in H3K4me3, H3K27ac and H3K36me3, many of which correlate with caste-specific transcription. Furthermore, we identify H3K27ac as a key chromatin modification, with caste-specific regions of intronic H3K27ac directing the worker caste. We suggest that these regions harbour the first examples of caste-specific enhancer elements in the honey bee. Our results demonstrate a key role for chromatin modifications in the establishment and maintenance of caste-specific transcriptional programmes in the honey bee. We show that at 96hrs of larval growth the queen-specific chromatin pattern is already established, whereas the worker determination is not, thus providing experimental support for the perceived timing of this critical point in developmental heterochrony in two types of honey bee females. In a broader context, our study provides novel data on environmentally-regulated organismal plasticity and the molecular foundation of the evolutionary origins of eusociality.