

P193*Stamping the royal seal with DNA methylation***Mat Welch**, O Edwards, H Millar, R Lister, B Baer

Background: Female honeybees have two distinctly separate castes that either work (workers) or reproduce (queens). Phenotypically the two castes are highly divergent and exhibit caste-specific morphological traits, yet they both originate from fertilised eggs. Queen-destined individuals are fed royal jelly and this nutritional stimulus initiates queen development. Epigenomic modifications allow phenotypically plastic shifts in response to external stimuli such as dietary cues, by tethering the genome to the environment. Epigenome dynamics are facilitated in-part by DNA methylation, which is known to be critical for caste determination during early larval development. Our aim is 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.

Study Design: We collected young larvae prior to the caste determination and provided them with royal jelly to artificially initiate queen development. To determine the initial trigger(s), we placed age-matched (+/-1 hr) 1 day old larvae in either worker comb (control) or artificial queen cells with fresh royal jelly. Pooled larvae (n=6) were then collected 0, 2, 4, 6 and 8 hrs after placement and for a total of 4 biological replicates. Each of these replicates were used to make independent transcriptome and methylome libraries and sequenced on an Illumina HiSeq 2000. Results about the initial molecular responses to royal jelly feeding will be presented and discussed in a broader context of caste determination in social insects.