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Non-coding RNAs in honeybee caste determination

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In honeybees (*Apis mellifera*), three contrasting adult castes (phenotypes) are produced from the same genome; two diploid females (a sterile worker and the highly reproductive queen) and the haploid male (drone). While sex determination is genetically controlled, phenotypic differentiation between the two female castes has recently been shown to be associated with changes in the epigenome, specifically changes in DNA methylation patterns, in response to dietary composition (royal jelly). In more recent times, the role of another class of epigenetic modifiers, that of small non-coding RNAs, has become an area of major interest in regards to the regulation of phenotypic and developmental plasticity. This talk will discuss recent findings from our laboratory concerning the expression profile of microRNAs between the three major castes using next-generation high throughput sequencing, and how differences in these profiles may relate to phenotypic output. Mature miRNAs are 20-24 nucleotide long molecules which form part of a larger RNA-induced silencing complex (RISC), providing sequence-specific targeting of mRNA molecules. Most commonly, the binding of a RISC-complex to a target mRNA sequence induces translational repression or mRNA degradation. Increasing evidence suggests that small RNAs help confer genetic robustness by reinforcing transcriptional programs.