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Dynamics of DNA methylation in honeybees: development and environment

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Numerous species of social insects are able to produce castes that are phenotypically distinct but that do not present any systematic difference at the genome level. In the Western honeybee (*Apis mellifera*), DNA methylation has been identified as a central epigenetic mechanism responsible for the developmental plasticity of females. In this species, different nutritional environments trigger specific epigenetic programs that will ultimately give rise to distinct castes (queens and workers). In order to understand the dynamics of epigenetic landscapes and how these changes influence development and behaviour, it is important to disentangle the various causes that can alter the epigenetic state. The factors that shape epigenetic signatures include various interplays between genetic background, development and environment. The honeybee haplo-diploid sex-determination system and its nutritionally-driven caste-determination system provide an attractive system to start disentangling the forces govern DNA methylation profiles. In this talk, three determinants of the honeybee DNA methylation landscapes will be contrasted: 1) the different ploidy of males and females, 2) the nutritional environment of queens and workers, and 3) short term differences through a conditioning experiment. Some of the challenges pertaining to the analysis and interpretation of DNA methylation data from complex heterogeneous samples containing a mixture of tissues and cell types will also be discussed.