



Unveiling the expression dynamics of genes involved in bee sociality

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Bees are a great model to study the evolution of social behaviour since in several taxa within this group sociality seems to have evolved independently. Which originated a great diversity of social life styles. The tribes Apini and Meliponini are comprised only by highly eusocial bee species, whereas various levels of sociality can be detected in other tribes, being the vast majority of bees indeed solitary. Although the molecular evolution of eusociality has been the subject of many studies, specific genetic changes involved in this behaviour have not been completely understood. Fundamental questions about shared and derivate gene pathways involved in the different social systems are still open. Recently new sequencing technologies have allowed gene expression studies of non-model and model organisms in a deep and non-directional way, which is promising for evolutionary studies of complex behavioural traits. Herein, some of these new molecular tools were used to investigate the gene expression profile of different bee species with distinct behaviours. Using an innovative experimental approach, designed to avoid biological and technical confounding factors, we report 787 genes possibly involved in bee sociality. Many of these genes were successfully found in the transcriptome of other bee species in a moderate expression level. Therefore, future comparative studies with these “life style genes”, in different lineages, are straightforward. Additionally, DNA methylation analyses corroborate recent results that the overall amount of methylation is not directly correlated to bee behaviour, instead the DNA methylation context is more likely related to differential methylation involved in social dynamics.