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*Reference transcriptome for a facultatively eusocial bee, Megalopta genalis*

**Beryl M. Jones**, William T. Wcislo, Gene E. Robinson

One remarkable feature of the eusocial insects is their extreme phenotypic plasticity, with reproductive division of labor between morphologically distinct queen and worker castes. This plasticity occurs as a result of environmental influences during development, with the same genotype leading to multiple phenotypes. While much is known regarding the developmental influences underlying queen-worker differentiation in highly eusocial insects, we know little about how reproductive division of labor evolved across the multiple independent origins of eusociality. Here we report a new reference transcriptome for *Megalopta genalis*, a facultatively eusocial neotropical sweat bee (Halictidae) which displays a wide range of social behaviors within a single population. Phylogenetic studies of bees point to a solitary ancestral lifestyle, suggesting that mechanisms underpinning social behavior in *M. genalis* may represent some of the ones important in the evolutionary transitions from solitary to social reproduction that occurred in bee lineages. We present life stage- and sex-specific gene expression across 20 adults and 20 pre-adult individuals of *M. genalis*, using Illumina HiSeq sequencing technology and Trinity for assembly. We describe great variation in gene expression across individuals, and evidence for caste-specific gene expression in the brains and abdomens of adult females despite their behavioral flexibility. The phylogenetic position and facultative sociality of *M. genalis* makes them ideal for studies of eusocial evolution at the molecular level, and the availability of this reference transcriptome allows for further comparative questions regarding social evolution in bees.