



## **The genome of the eusocial *Frieseomelitta varia* stingless bee: a model species for reproductive dominance studies**

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*Frieseomelitta varia* is a stingless bee species characterized by a remarkable reproductive behavior. The queen holds the monopoly of reproduction, and there is no register of egg-laying workers, even in the absence of the queen. The complete queen dominance makes *F. varia* a key species in the field of comparative genomics to understand caste systems evolution, division of reproductive labor, and eusociality. We sequenced the genomic DNA of a single *F. varia* pharate-adult male using the Illumina protocol in a HiSeq2500 platform. Genome assembly scaffolding, gene prediction and manual curation were performed and validated by comparison with an *F. varia* RNA-seq library and with protein data available for several bee species. The genome of *F. varia* comprises ~275 Mb and 10,526 genes. A large portion of these genes (8,200) is orthologous to *A. mellifera* genes. Based on the chromosome position of *A. mellifera* orthologs, the *F. varia* scaffolds were joined in tentative linkage groups. Special attention was given to the genes related to reproduction and ovary activation, which were characterized in relation to other insect species. Predicted immune genes were validated by RT-qPCR. We identified gene sets for non-coding RNA, including tRNAs, snRNAs, rRNAs, sno/scaRNAs, and microRNAs. The mitochondrial genome of *F. varia* was assembled by mapping the 9,518,616 reads against known Apoidea mitochondrial genomes. The mitochondrial genome is 15,144 bp in length, and encompasses 13 protein-encoding genes, 22 tRNAs and 2 rRNAs. Phylogenetic analysis using *F. varia* mitochondrial genes showed the closest relationship to *Melipona* species. This data contributes to post-genomic research on bee systematics and evolution, as well as has the potential to elucidate queen dominance mechanisms leading to a complete or partial inhibition of ovary activation in the workers.