Identification and biological implications of *Apis mellifera* pupal phase overexpressed genes

NUNES FMF[1], COSTA MCR[1], BONETTI AM[2], SOARES SC[1], BARBUZANO F[1], FERREIRA CA[1], SANTOS ARD[1], MARQUES AA[1], MENEZES CCBO[1], PEREIRA GSP[1], VALENTE V[1], MAIA RM[1], SOUSA JF[1], FOCOSI JR R[1], UNGARO AO[1], PINHEIRO DG[1], ESPINDOLA FS[2], SOARES AEE[1], ESPREAFICO EM[1], BITONDI MMG[3], HARTFELDER K[3], SIMÕES ZLP[3], PAÇÓ-LARSON ML[1], SILVA JR WA[1]

1 – Faculdade de Medicina de Ribeirão Preto, Universidade de São Paulo

Av Bandeirantes, 3900 - 14049-900, Ribeirão Preto – Brazil – francis@rge.fmrp.usp.br

2 – Instituto de Genética e Bioquímica, Universidade Federal de Uberlândia

3 – Faculdade de Filosofia, Ciências e Letras de Ribeirão Preto, Universidade de São Paulo

ABSTRACT

Apis mellifera presents particular characteristics that motivate the investigation of its biology, especially its genetics[1, 2, 3]. Although *A. mellifera* is one of the most extensively studied organisms in the world, very little is known about its genome[4]. The present study shows *A. mellifera* gene expression profiles including ontogenetic development stages, and validates the expression of genes associated to pupal phase. A total of 11,296 ORESTES[5] sequences were generated, from which 4,870 were validated *in silico*, according to stringent bioinformatic analyses parameters. From these sequences, 1,327 were classified as *Apis*ESTs, 1,007 as Orthologs and 2,536 as No matches. Despite the No matches data represent 22.45% of total sequences, it is estimated that 80% from the presented data are unknown sequences, once *A. mellifera* sequences found in public databases are not well annotated. Seven genes showed high expression during all pupal development: sparc, IDGF-like protein, chickadee, eukaryotic initiation factor 4E binding, SgAbd-1, replication licensing factor MCM5, heat shock protein hsp20.8A; genes that can be related to larval tissue remodeling events, maintenance of differentiated tissues, apoptosis, cell division control and immunity. These data try to elucidate complex biological matters and molecular events that occur during *A. mellifera* development and can also serve as a basis to Hymenoptera studies.

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