Gene set enrichment analysis of neuroendocrine system of the silkworm Bombyx mori

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Silkworm Bombyx mori represents a model organism for studying the neuroendocrine system in invertebrates. This system of nervous organs and endocrine glands regulates large number of life functions including movement, ecdisis, courting and mating. We have analysed strand-specific Illumina RNA-seq data from B. mori samples originated from different endocrine glands of both sexes and several developmental stages. Reads were mapped to the B. mori transcriptome using the Bowtie 2 aligner. Since the silkworm genome is abundant in repetitive sequences (Mita et al., 2004), the mapping allowing unlimited multimappings (required by eXpress) was extremely computing demanding. Transcript level RNA-seq quantification was performed using the eXpress tool based on an online expectation–maximization algorithm. Obtained data were consequently analysed in several gene set enrichment packages, including topGO and goplots (both R packages), where highly expressed genes were clustered and visualised, according to the functional GO enrichment analysis, and clustered by gene expression level.

Acknowledgements
The study is supported by the APVV-0827-11, VEGA 2/0164/15, IMTS 2623012002 and IMTS 2621012002 grants.

References