

XIII Argentine Congress of Bioinformatics and Computational Biology

XIII International Conference of the Iberoamerican Society of Bioinformatics

III Annual Meeting of the Ibero-American Artificial Intelligence Network for Big BioData







Transcriptomic meta-analysis to elucidate the presence and expression of neuropeptides in insect embryos

Lavatti, Nicolás¹; Baricalla, Agustin^{1,2}; del Valle, Daiana^{1,2}; Rivera-Pomar, Rolando^{1,2} (nlavatti@comunidad.unnoba.edu.ar)

1 – UNNOBA, 2 – CONICET

INTRODUCTION

- Neuropeptides (NPs) are small peptides that result of the enzymatic processing of larger proteins precursors. They act as neurotransmitters, neuromodulators and growth factors, and participate in feeding, courtship, urination and circadian cycle, among others.
- Examples of NPs in early development are Trunk (Drosophila melanogaster) and PTTH (Bombyx mori), with their receptor Torso.
- Little is known about the expression and function of NP genes during the embryonic development.
- The present work aims to elucidate the presence of NP precursor genes through embryonic development across different species of class Insecta.

METHODS

- Literature review to align the embryo stages with datasets and allow interspecies comparison.
- Identification of existing NPs in each species.
- **RNA-Seq embryo data search** in public databases.
- **DGE assays** to compare NP expression.
- **RT-qPCR** to experimentally detect NPs in *O. fasciatus*.







Fig. 1. Alignment of embryo stages of development. The relative position (0-100%) of each RNA-Seq dataset is visualized. The colored regions mark the three main comparable stages across species, early (yellow), middle (light-blue) and late (red) embryo. These stages were stablished given the blastoderm formation, beginning of gastrulation, and subsequent events, respectively. Unfertilized embryo data in certain species is also showed. To the right, total time of embryo development is indicated in hours/days after egg laying (hAEL/dAEL).



Fig. 2. Heatmap of RNA-Seq analysis for 52 selected NP precursor genes. Expression values were measured in transcript per million (TPM) normalized by species (columns), and then scaled by NPs (rows). Colors indicate low (blue), mid (light-yellow) and high (orange-red) expression values, while absent NPs are showed in grey.



Fig. 3. NP expression in Oncopeltus fasciatus embryo. A) gel electrophoresis analysis of RT-qPCR products. 1: 0-24; 2: 0-6; 3: 6-24; 4: 24-48; 5: 48-72; 6: 72-96; 7: 96-120; 8: 120-144 hAEL. B) barplot indicating the relative expression levels of NPs at 0-6 hAEL. The horizontal line stands for the transformed cutoff value (Ct=35 or [(1/Ct) * 100] = 2.8557).

ACKNOWLEDGMENTS

CONCLUSIONS AND FUTURE PERSPECTIVES

- We observed neuropeptide expression *in silico* through all the compared embryo stages of development.
- We have experimentally proved the presence of several NPs in early embryo stages of *O. fasciatus*.
- We look forward to search for expression patters that could infer the existence of totally or partially shared NPs within Orders or presented in all Insecta Class.
- To the A. v. Humboldt Foundation and the Gauss Chair of the Goettingen Academy of Sciences for financial support and to the Max planck Institute for multidisciplinary sciences (Goettingen).
- To Ariel Chipman for kindly sharing the Oncopeltus fasciatus transcriptome data.
- To the CCAD for the public availability of the computational clusters used to process all the data.







