FURTHER ANALYSIS OF A CDNA LIBRARY FROM *RHODNIUS PROLIXUS* OVARIAN FOLLICLES

Medeiros MN[1], Paiva-Silva GO[2], Mesquita RD[3], Braz GRC[4], Oliveira PL[2], Capurro ML[5], Masuda H[2], Machado EA[1]

1-Programa de Biologia Celular e Parasitologia, IBCCF, UFRJ, Rio de Janeiro, Brasil.
2- Programa de Biologia Molecular e Biotecnologia, IBqM, UFRJ, Rio de Janeiro, Brasil.
3- Coordenação de Biotecnologia, CEFETEQ Nilópolis, Rio de Janeiro, Brasil.
4- Departamento de Bioquímica, IQ, UFRJ, Rio de Janeiro, Brasil.
5- Departamento de Parasitologia, ICBII, USP, São Paulo, Brasil.

Rhodnius prolixus is an important vector of Chagas' Disease and a classical model of insect reproduction due to its dependence of feeding as a signal for oogenesis. Despite that, little is known about its physiology at the gene level. The ongoing *Rhodnius prolixus* Genome Project promises to shed light to this field. As part of this project, we constructed a cDNA library of isolated ovarian follicles to analyze relevant transcripts in developing oocytes. Follicles in different developmental stages were submitted to dissection of epithelium, mRNA extraction, being its mRNA used to the construction of a cDNA library using a commercial kit. The transcriptome was made by random sequencing this resulting library, and the obtained sequences were submitted to different databases. *Rhodnius* follicle transcriptome showed many sequences related to oogenesis and embryogenesis in other species and important matches related to the mosquito *Anopheles gambiae*. Interestingly, we have also found many matches for regulatory proteins and transcription factors. Functional analysis of selected sequences is under progress. Support: CNPq, FAPERJ and PRONEX.