STRUCTURAL STUDIES OF THE CHITIN-BINDING DOMAIN OF AEDES AEGYPTI PERITROPHIC PROTEIN BY NMR

<u>da Silva, F.C.</u>¹; de Paula, V.S.¹; Alvarenga, P.H.²; Oliveira, P.L.²; Jacobs-Lorena, M.³; Lery, L.M.S.⁴; Valente, A.P.¹; Almeida, F.C.L.¹

¹Centro Nacional de Ressonancia Magnetica Nuclear Jiri Jonas, IBqM, UFRJ, Rio de Janeiro, Brasil; ²IBqM, UFRJ, Rio de Janeiro, Brasil; ³Case Western Reserve University, Departmente of Genetics, USA; 4 IBCCF, UFRJ, Rio de Janeiro, Brasil.

In response to the feeding, hematophagous mosquitoes secrete the peritrophic matrix (PM) that covers the alimentary bolus and separates it from the epithelium. The *Aedes aegypti* peritrophic matrix protein (AeIMUC1) is formed by: a signal peptide, three chitin-binding domains and a mucin-like domain. Previous studies suggested that recombinant AeIMUC1 play important role in heme detoxification during blood digestion. The objective of this work is to study the chitin-binding domain (rQBD1) of the AeIMUC1 by NMR. rQBD1 was expressed, purified and characterized by mass spectrometry, circular dichroism (CD) and nuclear magnetic resonance (NMR). By mass spectrometry we confirmed a compatible molecular weight, although this protein presents anomalous migration in SDS-PAGE, corresponding to a dimer. The CD spectrum showed a negative peak in 205 nm and its NMR spectrum showed good chemical shift dispersion and sharp lines compatible with a folded protein. The current data are promising and show the feasibility to determine the structure of rQBD1 for NMR. We are now labeling the protein with ¹⁵N for further NMR experiments.

Support: Instituto Milênio de Biologia Estrutural em Biomedicina e Biotecnologia, CNPq, FAPERJ, ICGEB-Trieste.