

Transcriptome Analysis of unfed *Triatoma infestans* midgut

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Triatoma infestans is one of the main vectors of *Trypanosoma cruzi*, a protozoan etiological agent of Chagas' disease in Latin America. In order to obtain knowledge regarding the molecules present in *T. infestans* midgut, we analyzed Expressed Sequence Tags (ESTs) from a cDNA library of unfed *T. infestans* midgut. 453 cDNAs were sequenced and 244 high quality sequences were assembled in 137 Contigs. These sequences were blasted against several databases: NR, CDD, Pfam, GO, Kog, Mit-pla, Rrna and Smart. After Cluster analysis, the Contigs were classified according their predicted functions. Remarkably, 9 Contigs (6.56%) revealed sequences related to antimicrobial functions, such as defensins and lysozyme. We also found 9 Contigs (6.56%) presenting sequences encoding to proteins with possible role in oxidative stress, among them catalase, an antioxidant enzyme involved in detoxification of reactive oxygen species (ROS), which are bound to be produced in high levels upon blood digestion. Two Contigs (1.45%) coded for infestin and brasiliensin, serine protease inhibitors which interfere in the host blood coagulation inhibiting thrombin. Regarding digestive aspects, four aspartyl proteases, which are enzymes involved in digestion in Triatomines, were identified. One Contig was found to be a putative cysteine protease inhibitor from cystatin 2 family. This molecule will be expressed, purified and characterized. Our perspectives are to produce several of these recombinant proteins to confirm their structure-function relationships.

Supported by: FAPESP and CNPq.

Keywords: Contig; midgut; transcriptome; *Triatoma infestans*.