

## TRANSCRIPTOMIC ANALYSIS OF cDNA LIBRARY FROM VENOM GLANDS OF *Loxosceles laeta* SPIDER

Almeida, D.D.<sup>3</sup>; Junqueira-de-Azevedo, I.L.M.<sup>2</sup>; Kobashi, L.S.<sup>2</sup>; Gonçalves-de-Andrade, R. M.<sup>1</sup>; Ho, P.L.<sup>2</sup>; Tambourgi D.V.<sup>1</sup>; Fernandes-Pedrosa, M.F.<sup>1,3</sup>

<sup>1</sup> Laboratório de Imunoquímica, Instituto Butantan, SP, Brazil; <sup>2</sup> Centro de Biotecnologia, Instituto Butantan, SP, Brazil; <sup>3</sup> Departamento de Farmácia, CCS, Universidade Federal do Rio Grande do Norte, RN, Brazil.

The bite of spiders belonging to the genus *Loxosceles* can induce a variety of clinical symptoms, including dermonecrosis, thrombosis, vascular leakage, haemolysis, and persistent inflammation. The causative factor is a sphingomyelinase D (SMaseD) that cleaves sphingomyelin into choline and ceramide 1-phosphate and has intrinsic lysophospholipase D activity toward LPC. In order to generate a global panorama of the transcriptional activity of spider venom glands we have constructed a plasmid cDNA library from *Loxosceles laeta* venom glands mRNA to generate an *Expressed Sequence Tags* (ESTs) database. Sequences from 3008 independent clones were assembled in 1357 clusters (326 contigs and 1031 singlets), represented the transcripts profile of this tissue. The first 1200 clusters were analyzed and the repertoire of putative toxins corresponded to 159 sequences (13%) of all the transcripts. Sphingomyelinases represented the most abundant transcripts with 76 clusters (48%). We also found others transcripts corresponding to metalloproteinases, serinoproteinases, C-lectins, cystein-rich and inhibitors of toxins. Among the 545 clusters matching cellular proteins, the major part represents molecules involved in gene and protein expression, reflecting the specialization of this tissue for toxin synthesis.

**Supported by:** FAPESP, CNPq.

**Key words:** *Loxosceles laeta*, *expressed sequence tags* (ESTs), transcriptome.