

## THE ANALYSIS OF *MICRURUS CORALLINUS* (CORAL-SNAKE) TRANSCRIPTOME

Leão, L.I.<sup>1,2</sup>, Ho, P.L.<sup>1,2</sup>, Junqueira-de-Azevedo, I.L.M.<sup>1,2</sup>

<sup>1</sup> Centro de Biotecnologia, Instituto Butantan, São Paulo, SP, Brazil

<sup>2</sup> Departamento de Biologia e Genética Evolutiva, Universidade de São Paulo, SP, Brazil. [Lucianaleao@butantan.gov.br](mailto:Lucianaleao@butantan.gov.br)

The transcriptomic characterization of snake venom glands has proved to be a fast and efficient way to describe the general composition of toxins. Several species from the Viperidae family were analyzed so far, but none from the Elapidae family. Here we generated Expressed Sequence Tags (ESTs) from the venom glands of *Micrurus corallinus* (coral snake), an Elapidae snake commonly found in tropical forest areas. The 1438 ESTs were grouped in 611 clusters through a software pipeline and annotated. We were able to identify 7 putative types of toxins, representing 46% of ESTs that had their sequences partially or totally described for the first time. These include mainly three-finger proteins (24%) of several types and phospholipases A2 (PLA2s) (16%) that may represent post- and pre-synaptic neurotoxins, respectively. Besides, type C lectins, metalloproteases and other toxins were also found showing a high diversity of components in the venom. Likewise, the transcripts related to cellular proteins represent also 46% of this databank, mostly involved in gene expression, reflecting its high specialization in toxin synthesis. In conclusion, the transcriptomic databank helped to identify putative Elapidae toxins and also allowed the identification of candidates to antigens in a future antielapidic serum based on recombinant proteins. Support: FAPESP.