Tityus serrulatus venom gland: new sodium channel toxins through RNA-Seq

Ana Paula Vimieiro Martins¹, Flávia de Faria Siqueira², Evanguedes Kalapothakis¹

¹ Federal University of Minas Gerais, ² Federal Institute of Minas Gerais

According to Brazilian Ministry of Health, Tityus serrulatus (Brazilian yellow scorpion) is the species responsible for most of severe accidents in Brazil, which can lead to death. For more than one decade, the number of scorpion accidents in Brazil is increasing and for the moderate and most severe cases, the antivenom is the only effective treatment available. However, its production is very expensive and most of its antibodies are produced against venom compounds that are not toxic to mammals. There are many researches trying to solve or reduce these problems, and all of them request deep scorpion venom knowledge. High throughput transcriptomic sequencing technologies (RNA-Seq) have enabled great progress toward this. Although T. serrulatus venom has been extensively studied, many of its elements have not been described or characterized. RNA-Seq technology have already been performed for others scorpion species, but this is the first time it is applied for the transcriptome of Brazilian yellow scorpion. It is evident the necessity of deeper studies about T. serrulatus venom toxins, especially due to its medical relevance and as an important source of biotechnological tools. At this work, it was done a partial transcriptome of T. serrulatus telson. A unique MiSeq run was performed for cDNA sequencing and downstream analysis proved that variable assembly parameters affect the diversity of identified transcripts. The transcriptome herein described was efficient to identify 13 possible new NaTx with primary structure highly different from those of neurotoxins previously described for the species. Sodium channel toxins (NaTx) are known by their important role in lethality due to scorpionism. These molecules are potential target for immunization studies. This result agrees with the diversity of NaTx reported by recent proteomic researches. Based on this transcriptome, many other venom molecules are going to be annotated and added to previous biochemical information to extend the knowledge about *T. serrulatus* venom.

Funding support: FAPEMIG, CNPq, CAPES