# ANALISYS OF TARANTULA VENOM FROM GRAMMOSTOLA IHERINGI (MYGALOMORPHAE: THERAPHOSIDAE). PURIFICATION AND BIOCHEMICAL CHARACTERIZATION OF A TOXIN (GI-TX1).

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Spider venoms are complex cocktails of toxins that target a variety of receptors. Most of the initial works on spider venoms have been devoted to the study of medically important species. Venoms of apparent lower toxicity, before neglected, have shown increased interest for scientific studies, because they are sources of important biochemical probes for the pharmacological dissection of molecular processes. Tarantula venoms are rich mixtures of salts, nucleotides, free amino acids, neurotransmitters, polyamines, peptides, proteins and enzymes. In this work we partially characterized the venom of the tarantula *Grammostola iheringi,* by using different approach as: purification (rp-HPLC), sequence (Edman degradation) and molecular mass (ESI-Q-TOF) determinations. Analyses of toxicity in mammals (mice) and insects (house flies) were also performed and showed apparent toxicity for both. We purified and characterized a peptide (Gi-TxI), which was sequenced and compared to that of a Bank data (Swiss Prot), showing similarity with active molecules on ionic channels. Electrophysiological experiments are being conducted to determine the possibly activity of this toxin on ionic channels. The hypothetical structure of this toxin was determined comparing it to the data of Swiss Prot Model. The study of this venom and the characterization of their molecules are of interest to search for biological active components of pharmacological interest.

Keywords: tarantula; spider venom; polypeptide toxins; amino acid sequence; spatial structure; ionic channels.