

Loxoscin: First Antimicrobial Peptide Isolated from the Venom of the Brown Spider *Loxosceles gaucho*

Segura, P.J.^{1,2}; Silva Jr, P.I.¹

¹ Special Laboratory of Applied Toxicology, Butantan Institute, SP, Brazil

² Laboratory of Natural Products Chemistry, University of Tolima, Tolima, Colombia

Introduction: Despite the great advances made on the field of antibiotic therapy in recent years, infectious diseases remain major causes of death in human population due to the great ability of microorganisms to develop resistance to conventional antibiotics, compromising their effectiveness. Because of this, it has become urgent to find novel sources of non-traditional antibiotics in order to develop new drugs effective against pathogenic microorganisms. In this regard, brown spiders (*Loxosceles* genus) venom emerges as a promising candidate for the discovery of novel antimicrobial molecules. These organisms are part of *one of the most successful* orders in the animal kingdom and live in environments with high proliferation of pathogenic microorganisms, so it is clear that brown spiders count with a highly effective defense mechanism that may involve the direct action of antimicrobial molecules against infectious agents. **Objective:** Isolate and characterize antimicrobial molecules present in the venom of *Loxosceles gaucho* spider. **Materials and Methods:** The venom was extracted by electrostimulation of the poison glands of the *spiders*, purified by RP-HPLC and the antimicrobial activity of the isolated molecules was determined by liquid growth inhibition assay of different microorganism. Finally, the molecule of interest was characterized by mass spectrometry and its possible structure was predicted using the I-TASSER server. **Discussion and Results:** We isolated an anionic peptide with molecular weight of 1.69577 kDa, active against the Gram-negative bacteria *Escherichia coli* and *Pseudomonas aeruginosa*, and was named Loxoscin. Its structure contains 16 amino acid residues: VGTDFSGNDDISDVQK and presents a remarkable similarity with a specific fragment of the phospholipase-D LgRec1, suggesting that the peptide may be the result of an enzymatic fragmentation process, which may be constitutive or inducible. **Conclusion:** The particular characteristics presented by the Loxoscin make it a promising model for the design of structurally novel drugs to help combat infectious diseases.

Keywords: Antimicrobial peptides, *Loxosceles*, venom,

Financial Support: FAPESP and CNPq