

# Metalloproteinases diversity in the venom gland of Peruvian spider *Loxosceles laeta* revealed by transcriptome analysis

Raissa Medina Santos<sup>1</sup>, Clara Guerra Duarte<sup>2</sup>, Priscilla Alves de Aquino<sup>1</sup>, Anderson Oliveira do Carmo<sup>1</sup>, César Bonilla<sup>3</sup>, Evanguedes Kalapothakis<sup>1</sup>, Carlos Chavez-Olortegui<sup>1</sup>,

*1 Universidade Federal de Minas Gerais*

*2 Fundação Ezequiel Dias*

*3 Instituto Nacional de Salud*

## Abstract

Envenomation caused by spiders from *Loxosceles* genus (brown spiders) is a worldwide public health problem. *Loxosceles* their venom is composed of several toxins responsible for dermonecrotic, hemorrhagic and edema effects. In Peru, *L. laeta* is considered the most medical relevant species. A family of metalloproteases, also named astacin-like proteins, was described in *Loxosceles* venom with great importance for hemostatic disorders in natural or experimental envenomations. A new generation sequencing library of venom extracted from the Peruvian spider, *L. laeta*, was constructed for the first time using the TruSeq<sup>TM</sup> RNA Sample Prep Kit v3 Set A (Illumina) kit and the sequencing was performed on the MiSeq by the paired-end technique for identification of molecular diversity of metalloproteases toxins. In this work, we describe some of the identified metalloproteases enzymes with a high degree of identity (over 50%) with molecules from other *Loxosceles* spp spiders. Results obtained in this work represent the first landscape of components of a Peruvian spider venom gland, revealing the complexity of molecules expressed in this tissue, with great potential for future uses in medical and evolutionary studies.

Funding: FAPEMIG, CNPq, CAPES