

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

Raissa Medina Santos¹, Clara Guerra Duarte², Priscilla Alves de Aquino¹, Anderson Oliveira do Carmo¹, César Bonilla³, Evanguedes Kalapothakis¹, Carlos Chavez-Olortegui¹,

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™ 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