

Comparative Peptidomic Analysis of the Venoms of Three Brown Spider Species: *L. laeta*, *L. intermedia* and *L. gaucho*

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In Brazil, where loxoscelism represent a public health problem, *L.intermedia*, *L. laeta* and *L. gaucho* are the most abundant species at the south and south-east regions. The gravity of the lesions indicates the need of a specific antivenom therapy, and a way to accomplish that is studying the differences of those venoms compositions. In order to establish a peptide profile of the three species, we used an offline peptidomic approach combining RP-HPLC and MALDI-TOF-MS. The components with MW lower than 5 kDa of each venom were separated by Millipore Centricon filters. After lyophilization, the filtrate was separated by RP-HPLC and each fraction was analyzed on a Bruker Autoflex II mass spectrometer. From the 409 peptides detected in mass range 1-5 kDa, 135 are exclusive for *L. laeta*, 137 for *L. intermedia* and 103 for *L. gaucho*. The pairwise comparison of the venoms revealed that 95% of 19 peptides shared by *L. laeta* and *L. intermedia* are overexpressed by *L. laeta*, 75% of the 4 peptides shared by the *laeta* and *gaucho* species are overexpressed in *laeta* and 82% of the 11 peptides shared by the *intermedia* and *gaucho* species are overexpressed in *intermedia*. The three species also share 5 peptides. The results obtained also showed that *L. intermedia* and *L. laeta* peptidomic profile is more similar to each other than the *L. gaucho* one. Future perspectives include the identification of all peptides expressed in each venom, specially the up- and down-regulated ones, and the search for the polyamines in the venoms.

keywords: loxosceles, brown spider, peptidomics