A novel expression profile of the Loxosceles intermedia spider venomous gland revealed by transcriptome analysis.

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A novel expression profile of the *Loxosceles intermedia* revealed by transcriptome analysis


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Abstract

Spiders of the *Loxosceles* genus are cosmopolitan, and their venom components possess remarkable biological properties associated with their ability to act upon different molecules and receptors. Accidents with *Loxosceles* are a public health problem in the south of Brazil. To describe the transcriptional profile, a wide cDNA library was produced, and its transcripts were functionally and structurally analyzed. After initial analyses, 1843 tags (ESTs) produced readable sequences that were grouped into 538 clusters, 281 of which were singletons. 985 reads (53% of total ESTs) matched to known proteins. Similarity searches showed that toxin-encoding transcripts account for 43% of the total library and comprise a great number of ESTs. The most frequent toxins were from the LiTx activity. Both phospholipase D and astacin-like metalloproteases toxins account for 9% of total transcripts. Components such as serine proteases, hyaluronidases and venom allergens were also found but with minor representation. Almost 10% of the ESTs encode for proteins involved in cellular processes. These data provide an important overview of the venom gland expression scenario and revealed significant differences from profiles of other spiders from the *Loxosceles* genus. Furthermore, our results also confirm that this venom constitutes an amazing source for agrochemical, industrial and pharmacological applications.
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