Molecular diversity of the venom gland from Peruvian scorpion *Hadruroides lunatus* revelead by transcriptome analysis.

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The venom of Peruvian scorpion Hadruroides lunatus, which is the most medically relevant species in Peru have been poorly characterized. These venoms can hold diverse undiscovered bioactive peptides, enzymes and toxins. The identification of new toxins and peptides have pharmacological, biotechnological and medical implications. In this work, we describe the analysis of the transcriptome from venom glands extracted from the Peruvian scorpion Hadruroides lunatus, performed with the Illumina MiSeq platform. Using a high-throughput methodology, we describe the universe of transcripts and putative peptides that are expressed in this venom glands. The library was prepared using the TruSeq RNA Library Kit, with enrichment for polyadenylated transcripts and selection for fragments with mean size of of 200 bp. Sequencing was performed using the Illumina MiSeq V3 Kit, generating paired-end reads of 301 bp. Twenty eight millions of reads were produced and collapsed using PEAR v0.9.8, forming single reads, and transcripts assembly was carried out using rnaSPADES v3.9.1. In total, 231,685 transcripts were assembled and translated into 29.699 putative peptides using TransDecoder. The search for sequence similarity using Blastp against a database composed by 6534 toxins and venoms deposited at Uniprot revealed 668 peptides with similarity with at least one protein from database. We identified 400 possible proteases and more than 300 molecules, including toxins and peptides with high biotechnological and medical values. Non buthidae scorpions are known to contain a large amount of bioactive peptides. In this work, we describe some of the identified enzymes, antimicrobial peptides, toxins for potassium, sodium and calcium channels with a high degree of identity (over 50%) with molecules from other scorpions and arthropods. The results obtained in this work represent the first landscape of components of a scorpion venom belonging to the Iuridae family, revealing the complexity of molecules expressed in this tissue, with great potential for future uses in medical and evolutionary studies.