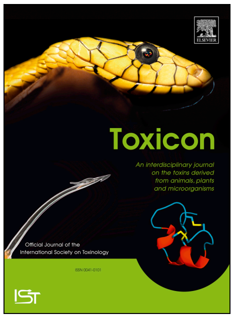

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The diversity of venom components of the scorpion species *Paravaejovis schwenkmeyeri* (Scorpiones: Vaejovidae) revealed by transcriptome and proteome analyses

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Abstract

The recent publication of high-throughput transcriptomic and proteomic analyses of scorpion venom glands has increased our knowledge on the biodiversity of venom components. In this contribution, we report the transcriptome of the venom gland and the proteome of the venom for the scorpion species *Paravaejovis schwenkmeyeri*, a member of the family Vaejovidae. We report 138 annotated transcripts encoding putative peptides/proteins with sequence identity to known venom components available from different databases. A fingerprint analysis containing the molecular masses of 212 components of the whole soluble venom revealed molecular weights of approximately 700 to 13,800 Da, with most detected proteins ranging from 1,500 to 3,000 Da. Amino acid sequencing of venom components by LC-MS/MS allowed the identification of fragments from 27 peptides encoded by transcripts found in the transcriptome analysis. Enzymatic