Interrogating the venom of the viperid snake Sistrurus catenatus edwardsii by a combined approach of electrospray and MALDI mass spectrometry

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The complete sequence characterization of snake venom proteins by mass spectrometry is rather challenging due to the presence of multiple isoforms of different protein families. In the present study, we have investigated the tryptic digest of the venom of the viperid snake Sistrurus catenatus edwardsii by a combined approach of liquid chromatography coupled to either electrospray (online) or MALDI (offline) mass spectrometry. These different ionization techniques proved to be complementary and we were able to identify a great variety of isoforms of diverse snake venom protein families, as evidenced by the detection of unique peptides of the corresponding proteins. For example, all predicted eleven isoforms of serine proteinases and six isoforms of metalloproteinases (out of six predicted) of the venom of Sistrurus edwardsii were distinguished using this approach. We also identified additional snake venom proteins not encountered in a previous transcriptome study of the venom gland of this snake. In essence, our results support the notion that complementary ionization techniques of mass spectrometry allow for the detection of even subtle sequence differences of snake venom proteins, which is fundamental for future structure-function relationship and possible drug design studies.

Keywords: snake venom, proteome, protein isoforms, mass spectrometry

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