

SNAKE VENOMICS

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Venoms of *Viperidae* and *Crotalidae* snakes contain proteins that interfere with the coagulation cascade, the normal haemostatic system and tissue repair. Envenomations by these snakes result in persistent bleeding and is still a serious threat in developed and underdeveloped countries, causing 50.000 deads annually. The only effective treatment for systemic envenomation is administration of an antivenom. However, polyclonal antisera include numerous antibodies with specificities not confined to the toxic targets. Hence, knowledge of the toxin composition of venoms could be devised to design immunization protocols with toxin-specific antibodies with greater specificity and effectiveness than conventional systems. Despite its potential value, little is known about the composition of most venoms. The protein composition of the venoms of species of genera *Viperinae* (*Macrovipera*, *Cerastes*, *Echis*, *Bitis*) and *Crotalinae* (*Sistrurus*, *Crotalus*, *Agkistrodon*, *Bothrops*, *Bothriechis*, *Lachesis*, *Atropoides*, *Cerrophidion*, *Porthidium*) were analyzed by RP-HPLC, N-terminal sequencing, MALDI-TOF MS, and in-gel tryptic digestion, peptide mass fingerprinting and CID-MS/MS. As expected from the rapid amino acid sequence divergence of venom proteins by accelerated evolution, with a few exceptions, the product ion spectra did not match to any known protein using the MASCOT. The CID-MS/MS spectra were manually interpreted and the deduced peptide ion sequences submitted to BLAST search. This approach allowed us to assign unambiguously all of the isolated venom fractions to known protein families. Our proteomic approach complement transcriptomic studies by showing the relative abundance of the proteins that are secreted into the venoms. Venom proteomes are composed of proteins belonging to only a few protein families, each venom showing distinct degree of complexity. Geographical, individual and ontogenic venom variations are also observed. The applications of venomomics to phylogeny and antivenom characterization will be discussed.