

Venomics: conceptual model to decipher encrypted codes in scarce proteins

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During the last years, the field of proteomics has evolved considerably, becoming an invaluable tool to study scarce and rare venoms. Benefitting from recent developments on mass spectrometry, such as MS/MS and peptide sequencing capabilities, and in the fields of liquid chromatography and 2D electrophoresis, several reports present the analysis of arthropod and snake venom using proteomic strategies. In this work, focus will be given on peptidomics and venomics approaches used to unveil the hidden secrets of some scarce venoms or neglected material, showing that a new dimension was given to toxinology field by such technical improvements. For example, *Micrurus* spp venoms are rare raw material and their proteic compositions are poorly studied. The use of venomics approach can lead us to discover novel protein families and to understand which of those families' representatives are involved in clinical aspects of *Micrurus* envenoming and anti-serum cross-reactions. Likewise, many other venoms from marine animals and other invertebrates can be used as a source of new peptides and proteins scaffolds whose can be used as new leads to drugs developments. In this sense, examples will be given on *de novo* peptide sequencing and post-translational modifications studies by mass spectrometry, which is a crucial technique used to discover new structures in scarce and neglected materials.