Comparative Proteomics of Snake and Lizard Venoms: Unveiling the Molecular Basis of Venom Diversity and Adaptation

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Abstract: Venom protein profiling is a method used to analyze the composition and structure of proteins in venom. Venom contains a variety of neurotoxins and enzymatic proteins, which have toxic effects on human and animal organisms. By identifying the proteins in the venom, we can better understand the toxic mechanism of the venom, and provide important references for biomedical research and clinical treatment. The basic steps of venom protein profiling include sample preparation, mass spectrometry and data analysis. Based on this, the protein component analysis was carried out and the results were summarized.The diversity of snake venom and lizard venom can be explained by their protein composition and structure.Their differences at the protein level determine their different functions and pathways of action in toxicology, while also providing important resources for biodiversity and drug development.

Keywords: Snake Venom; Lizard; Protein Components

1. Venom identification

1.1 Identification process

First, a protein sample needs to be extracted from the venom and put through the proper handling and purification steps to remove impurities and increase the purity of the protein. Next, the sample is analyzed using a mass spectrometer. A mass spectrometer is a tool that separates, detects and identifies protein molecules. Common methods of mass spectrometry include mass spectrometry (MS) and mass spectrometry Data interpretation (MS/MS). Mass spectrometry can provide information about the molecular mass of a protein, while mass spectrometry data interpretation can provide more detailed information about the protein sequence and structure. Finally, through the analysis of the mass spectrometry data, the different protein components present in the venom can be identified and their structure and function can be further analyzed. This information is of great significance for understanding the mechanism of venom toxicity as well as for developing new anti-venom drugs. The identification of venom protein profiles has broad application prospects in the research field and drug development. Through in-depth understanding of the protein components in venom, it can provide an important reference for biomedical research, such as the development of novel drugs or antitoxins by simulating and modifying the structure of venom proteins. In addition, the identification of venom protein profiles can also provide strong support for the taxonomic study of poison pests and the molecular identification of venom.

1.2 Identification results

1.2.1 Venom protein components

The venom of the green ringed sea snake is a complex mixture of proteins containing a variety of biologically active toxin components. By using reversed-phase high performance liquid chromatography (HPLC), the researchers successfully isolated 20 liquid component peaks from the crude venom of the green ringed sea snake. These peaks were separated by further SDS-PAGE, resulting in 26 protein bands that were identified by mass spectrometry. According to the mass spectrometry identification, the

researchers found that Cysteine venom was mainly composed of three toxin families, namely phospholipase A2, three-finger toxin and cysteine-rich secreted protein. Among them, phospholipase A2 accounted for 40.1% of the total venom protein, three-finger toxin accounted for 58.1%, and cysteine-rich secreted protein accounted for only 1.8%. Further analysis showed that alkaline phospholipase A2 and long-chain neurotoxins were the main components of the phospholipase A2 and three-finger toxin families, accounting for 22.6% and 38.9% of the total, respectively. In general, liquid peak 1-9 mainly contained three-finger toxins, accounting for 54.9% of the total protein of snake venom; Liquid peak 10-19 mainly contained phospholipase A2, accounting for 40.1% of the total protein. At the same time, liquid peak 10, 12-14 also contained a small amount of three-finger toxins, accounting for 3.2%. But liquid peak 20 only contained cysteine-rich secreted protein. These findings are not only of great significance for the in-depth understanding of the composition and toxic mechanism of the venom, but also provide an important basis for further research and development of effective anti-toxic drugs.

1.2.2 Protein components of lizard venom

The protein obtained from the lizard venom was separated and purified by DEAE-Sepharose CL-6B anion exchange chromatography, Spehadex G-50 gel chromatography and Macro-prep High S cation exchange chromatography, and the results of identification. After purification and identification, the obtained two proteins were named CTX-1 and CTX-2 respectively, and their molecular weights were about 9.499 KDa and 9.548 KDa. The yields were 1.76% and 3.73%, respectively. The inhibitory effects of different concentrations of cytotoxins on the proliferation of HSC-LX2 and HL7702 cells were evaluated by CCK-8 assay. The results showed that the inhibition rate of cell proliferation increased with the increase of CCK-8 concentration, showing a dose-effect relationship. The minimum effective concentration of CTX-1 on HSC-LX2 cells was 0.5μg/ml and IC50 was 2.50μg/ml. The minimum effective concentration of CTX-1 against HL7702 cells was 8μg/ml and IC50 was 18.97μg/ml. In summary, CTX-1 and CTX-2, two proteins isolated and purified from lizard venom, and their proliferative inhibitory effects on HSC-LX2 and HL7702 cells were discussed. These results contribute to further research on the active substances contained in lizard venom and its therapeutic potential against cancer cells.

2. Results and Discussion

There are some distinct proteomic differences between lizard venoms and snake venoms. Proteomics is the scientific field that studies the protein composition and function of living organisms, and it can provide important information when analyzing the differences between lizard venoms and snake venoms.

The venom of a venomous snake consists mainly of protein toxins, such as neurotoxins, blood toxins, and digestive toxins. In contrast, lizard venom has a smaller variety of toxins, but contains some unique protein toxins, such as antithrombin and bactericidal peptides. Second, lizard venom and snake venom also have different protein compositions.

Through proteomics techniques, it is possible to analyze the type, amount and structure of proteins in lizard venom and snake venom. It has been found that the protein in lizard venom is mainly distributed in the thrombin family, protease family and antimicrobial peptide family. In contrast, the proteins in snake venom are mainly distributed in the neurotoxin family, the blood toxin family and the digestive toxin family. In addition, the protein structure of lizard venom and snake venom is also different.

The proteins in lizard venoms are mostly linear, while the proteins in snake venoms have more complex three-dimensional structures. This difference in structure may be related to their different functions and mechanisms of action. Overall, there are clear proteomic differences between lizard venoms and snake venoms. Their toxicity, mechanism of action and potential medicinal value can be better understood through analysis of their protein composition, quantity and structure. The study of proteomics will provide an important scientific basis for our understanding of lizard venom and snake venom.

3. Conclusion

Snake venom and lizard venom are two common animal venoms that differ at the protein level and exhibit diversity.

First, the protein composition of snake venom and lizard venom is quite different. The study found that the proteins in snake

venom mainly consist of toxins and enzymes, while the proteins in lizard venom are mainly toxins. Poisonous snakes can be divided into neurotoxins, vasoactive toxins, thrombin, hemolysin and other types of toxins, and lizard venom is neurotoxins as the main component. These different protein compositions determine their different functions and pathways of action in venomology.

Second, there are differences in protein structure between snake venom and lizard venom. The toxins in snake venom usually have a complex three-dimensional structure, which allows them to act on intracellular receptors and channels and cause reactions with a variety of physiological effects. In contrast, lizard toxins are relatively simple in structure, but still have powerful neurotoxicity.

In addition, the proteins in snake venom and lizard venom show remarkable species diversity. Different species of snake venom and lizard venom differ in their protein composition, and this diversity has played a key role in evolution, allowing them to adapt to different predation and defense strategies. At the same time, this diversity also provides a rich resource for the pharmaceutical industry, and many snake venoms and lizard toxins have been developed into drugs or used in scientific research.

In conclusion, the diversity of snake venom and lizard venom can be explained by their protein composition and structure. Their differences at the protein level determine their different functions and pathways of action in venomology, while also providing an important resource for biodiversity and drug development.

References

[1] Zeng XD, Cheng B, Mei T, Liu W, Zhang XC. Effects of snake venom hemagglutinin injection combined with omeprazole on hemoglobin level and coagulation index in patients with upper gastrointestinal bleeding [J]. Chinese Medical Innovation, 2023, 20(14):1-5.

[2] Shao QH, Liu XM, Huang L, Feng YF. Mesh meta-analysis of efficacy and safety of four snake venom hemagglutinases combined with proton pump inhibitors for non-varicose upper gastrointestinal bleeding [J]. Chinese Pharmacy, 2019, 34(05): 600-606.

[3] Ye SF, Jiang LF. Clinical effect of snake venom thrombin combined with omeprazole for injection in the treatment of acute gastrointestinal bleeding [J]. Clinical Rational Use of drugs, 2019, 16(01): 73-75.

[4] Li RJ, Lei JW, Lin AQ. Application of Esomeprazole combined with hemagglutinase in upper digestive tract hemorrhage and its effect on plasma NO, COR and GAS [J]. Modern Practical Medicine,202,34(11):1434-1436.

[5] Hou XW, Zhuang XJ, Yu YY, Zhao X, Liu GH. Clinical application value of snake venom hemagglutinin combined with autologous venous blood injection in pulmonary puncture biopsy [J]. Journal of Interventional Radiology, 2002,31(10):1000-1003.

[6] Yin F, Wang ZH. Effect of endoscope injection of snake venom hemagglutinase combined with intravenous infusion of omeprazole in the treatment of ulcerative upper gastrointestinal bleeding [J]. Journal of Molecular Imaging, 2019, 45(05): 678- 682.

[7] Zhu F, Liu JL. Clinical effect of somatostatin combined with endoscopic metal titanium clip for hemostasis and spraying and injection of snake venom hemagglutinin in the treatment of upper gastrointestinal bleeding [J]. Journal of Clinical Medicine Research and Practice, 2002,7(26):53-56+65.

[8] Zeng XY, Lin YL, Liu YJ, Huang YT, Gong LM, Liu T. Effect of snake venom on lipopolysaccharids-induced inflammation of RAW264.7 macrophages [J]. Central South Journal of Pharmacology,2022,20(08):1820-1824.

[9] Miao HQ, Su DL, Chen XX. Practice and literature analysis of pharmaceutical care for a case of hemagglutination-induced coagulation disorder caused by snake venom for injection [J]. Chinese Pharmaceutical Industry, 2019,31(14):119-122.

[10] Li YT, Sun Y, Zhao LH, Liu XY, Chen L. Inhibition of tumor metastasis by platelets from Agkistrodon Agkistrodon venom [J]. Journal of Wannan Medical College, 2012, 41(03): 217-220.

[11] GoncalvesMachado L, et al. Extracellular Vesicles from Bothrops jararaca Venom Are Diverse in Structure and Protein Composition and Interact with Mammalian Cells[J]. Toxins,2022,14(11).

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