High-throughput epitope profiling of snake venom toxins
unveiling the complexity of antigen-antibody interactions of antivenoms

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High-throughput epitope profiling of snake venom toxins – unveiling the complexity of antigen-antibody interactions of antivenoms

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Introduction
Insight into the molecular details of polyclonal antivenom antibody specificity is a prerequisite for accurate prediction of cross-reactivity and can provide a basis for design of novel antivenoms. In this work, a high-throughput approach was applied to characterize linear epitopes in venom proteins from 82 venoms of four African mammals and three neurotoxic cobra snakes obtained from public databases.

Studying linear epitopes using peptide microarrays
The venom library was generated by combinatorial synthesis and expanded by using synthetic peptides. Light-directed solid-phase synthesis was performed to synthesize custom peptide microarrays. The epitopes were tested for binding to venom protein libraries. A Venn diagram was used to visualize the epitopes identified for each venom type.

High number of epitopes recognized by SAIMR antivenom
The Venn diagrams illustrate the overlap of epitopes recognized by the antivenom. Only peptides identified in both experiments with each antivenom, corresponding to the overlap in Venn diagram part A-C, are included.

Key residues for antivenom toxin recognition
The key residues for antivenom toxin recognition are shown in the table. Type 1 α-neurotoxins and Type 2 α-neurotoxins are classified based on their binding to the antivenom.

Antivenoms antibodies bind to functional sites of toxins
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Conclusions
Custom-designed high density peptide microarray technology enables parallel automated identification of linear epitopes of snake neurotoxins.

Trend: antivenom antibodies recognize and bind to epitopes at the functional sites of toxins.

Perspectives
Determination of linear epitopes in snake venom toxin epitopes may provide the basis for:
- Explaining the molecular basis of antivenoms para-specificity
- Guiding next-generation antivenoms based on DNA immunization and immunization with synthetic epitope strings

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