High-throughput immuno-profiling of mamba (Dendroaspis) venom toxin epitopes using high-density peptide microarrays

Snakebite envenoming is a serious condition requiring medical attention and administration of antivenom. Current antivenoms are antibody preparations obtained from the plasma of animals immunised with whole venom(s) and contain antibodies against snake venom toxins, but also against other antigens. In order to better understand the molecular interactions between antivenom antibodies and epitopes on snake venom toxins, a high-throughput immuno-profiling study on all manually curated toxins from Dendroaspis species and selected African Naja species was performed based on custom-made high-density peptide microarrays displaying linear toxin fragments. By detection of binding for three different antivenoms and performing an alanine scan, linear elements of epitopes and the positions important for binding were identified. A strong tendency of antivenom antibodies recognizing and binding to epitopes at the functional sites of toxins was observed. With these results, high-density peptide microarray technology is for the first time introduced in the field of toxinology and molecular details of the evolution of antibody-toxin interactions based on molecular recognition of distinctive toxic motifs are elucidated.

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