Investigating Antivenom Function and Cross-Reactivity – a Study of Antibodies and Their Targets

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Snake Antivenom: an Essential Medicine – and a Black Box
Venomous snakebites are regarded as one of the World’s most neglected tropical diseases/conditions with up to 2.5 million victims every year. The best-practice treatment for envenoming derived from the blood of large mammals (typically horses or sheep) immunized with venom of one or more snake species. The active toxin-neutralizing components in antivenom are complex mixtures of antibodies (or fragments thereof). The individual antibodies are adapted by the immune system of the production animal to bind specific to parts of each tox in the immunization procedure. In many cases antivenom is also able to neutralize some – or even all – toxic effects of snakebites from related snake species.

Proteomics-based studies aiming at quantifying the extent of such cross-protection of antibodies against venom from related snake species are referred to as antivenomics. The current state-of-the-art antivenomics protocol involves affinity chromatography of venoms with immobilized antibodies. Although proven effective in clinical applications antivenomics fail to explain how this cross-reactivity is working at the molecular level and must be performed for one snake venom-antivenom pair at a time.

Knowledge of interactions between the immunoreactive parts (referred to as epitopes) of a toxin or macromolecule in general and the corresponding antibodies is a prerequisite to understand and predict neutralization potential of a given antivenom against any fully characterized snake venom. Although antivenom to snakebites is a prerequisite to understand and predict neutralization potential of a given antivenom to snakebites from related snake species many cases antivenom is also able to neutralize some – or even all – toxic effects of snakebites from related snake species.

Ideas and Perspectives
- Identify linear peptides from snake toxins that can bind antibodies in antivenom using custom designed high-density peptide microarray technology. See figure 1
- The microarrays in this study have to contain five technical replicates of 93 261 15-mer peptides derived from pit viper snake species (sub-family Viperidae).
- Localize epitopes in pep tide hits
- Characterizing important antibody-toxin interactions based on allowed variation of epitope
- Predict cross-reactivity of antivenoms on a protein family level and thereby expand the clinical applications of existing antivenoms to other snake species or suggest changes in immunization mixture to improve the medicine
- Learning from nature’s preferences for specific epitopes, it will be possible to estimate the number of antibodies needed to neutralize the critical toxins for any given snake
- In the long run this may result in recombinant immunization mixtures and even lead to the first fully recombinant antivenom

Amino acid sequence of snake toxin

Addition of antibody mixture from immunized animal + secondary fluorescent antibody

leukocyte peptide synthesized on high density microarray

Data for analysis

Figure 1 – Schematic overview of principle in peptide microarray experiments

References

Contact information

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