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

Engmark, Mikael; Andersen, Mikael Rørdam; Laustsen, Andreas Hougaard; Patel, Jigar; Sullivan, Eric; De Masi, Federico; Hansen, Christian Skjødt; Kringelum, Jens Vindahl; Lomonte, Bruno; Gutiérrez, José María; Lund, Ole

Publication date:
2016

Document Version
Publisher's PDF, also known as Version of record

Citation (APA):
High-throughput epitope profiling of snake venom toxins – unveiling the complexity of antigen-antibody interactions of antivenoms

Mikael Engmark1,2, Mikael R. Andersen2, Andreas H. Laustsen2,3, Jigar Patel4, Eric Sullivan4, Federico de Masi1, Christian S. Hansen1, Jens V. Kringleum1, Bruno Lomonte5, José Maria Gutiérrez5, and Ole Lund1

Introduction

Insight into the molecular details of polyvalent antivenom antibody specificity is a prerequisite for accurate prediction of cross-reactivity and can provide a basis for design of novel antivenoms1. In this work, a high-throughput approach was applied to characterize linear elements in epitopes in 82 toxins from four African mamba and three neurotoxic cobra snakes obtained from public databases.

Studying linear epitopes using peptide microarrays

Key residues for antivenom toxin recognition

Antivenoms antibodies bind to functional sites of toxins

Conclusions

Custom-designed high density peptide microarray technology enables parallel automated identification of linear elements of epitopes in snake neurotoxins.

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

Perspectives

Determination of linear elements 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

Affiliations

1. Technical University of Denmark, Department of Bio and Health Informatics, Aagaard Bygd, Lyngby
2. Technical University of Denmark, Department of Biotechnology and Biomedicine, Aagaard Bygd, Lyngby
3. University of Copenhagen, Department of Drug Design and Pharmacology, Faculty of Health and Medical Sciences, Denmark
4. Rockwell Automation, Madison, Wisconsin, USA
5. Instituto Clodomiro Picado, Facultad de Microbiología, Universidad de Costa Rica, San José

References


Acknowledgement

We would like to thank Morten Nielsen for scientific discussion and the Novo Nordisk Foundation for financial support (grant number NNF13OC0005613)