Monoclonal human IgGs capable of neutralizing elapid neurotoxins in vivo

Pus, Urska; Laustsen, Andreas Hougaard; Karatt-Vellatt, Aneesh; Griffiths, Daniel T.; Oscoz, Saioa; Andersen, Mikael Rørdam; Harrison, Robert; Casewell, Nicholas; Lomonte, Bruno; McCafferty, John

Total number of authors: 11

Published in: Toxicon

Link to article, DOI: 10.1016/j.toxicon.2018.10.154

Publication date: 2019

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

Link back to DTU Orbit

S44
neutralize medically relevant toxins from the aforementioned snakes. Fully human IgGs were discovered and assessed for their ability to affect primarily poor agricultural workers. The severity of a snakebite is a serious public health issue in many tropical countries associated with severe envenomings that occur in Queensland health alone being over 15 million dollars annually. In some species, the venom is known to be cardiac specific. We determined the venom effects using a live animal model with real time cardiac monitoring. Two species of box jellyfish were used, namely Chironex fleckeri and Carukia barnesi. Cardiac output was measured (including aortic and mitral outflows) through a doppler monitoring system. We discuss the implications of these results in terms of first aid management.
Keywords: jellyfish venom, Chironex fleckeri, Carukia barnesi, cardiophysiology, first aid.

145 MONOCLONAL HUMAN IgGs CAPABLE OF NEUTRALIZING ELAPID NEUROTOXINS IN VIVO


Abstract

Cobratoxin (CFTX-1) is a cardiotoxic and hemolytic protein that is potentially responsible for the rapid cardiovascular collapse in human envenomation victims. Based on secondary structure analysis of CFTX-1, previous studies have predicted several helical regions and concluded that this toxicity is a pore-forming toxin. We synthesized two putative helical regions (CFTX-142-67 and CFTX93-120) from CFTX-1 and conducted a structural analysis with nuclear magnetic resonance (NMR) spectroscopy. CFTX-142-67 does not form a structure in aqueous solution, but does form a helical structure in the presence of SDS. CFTX93-120 is relatively hydrophobic and aggregates in aqueous solution, but forms a helical structure in the presence of SDS, consistent with the structure of this region in the CFTX-1 model predicted using I-TASSER. Our results are also consistent with residues 93–120 in CFTX-1 being involved in membrane-spanning. This study confirms the presence of helical regions in CFTX-1 derived peptides, providing the first experimental structure information relating to this protein, and insight into its function.
Keywords: Chironex fleckeri venom, CFTX-1, Cubozoan toxins, Pore forming toxins, NMR

147 GUIDING ANTIVENOM DEVELOPMENT THROUGH LINEAR VISUALIZATION OF VENOMICS DATA


Abstract

Snakebite is a serious public health issue in many tropical countries affecting primarily poor agricultural workers. The severity of a snakebite is related to the amount of venom injected and its composition of toxins. To help guide clinicians in predicting development of envenomation, we have developed a linear visualization tool, which will be freely available at tropicalpharmacology.com, for better display of venomics data. The tool can also provide venom and antivenom researchers with an intuitive overview of venom compositions and the amount of toxins likely to be injected by various venoms snakes. The advantage of this illustration method, compared to the standard pie chart, is that it allows for easy, quantitative comparisons between snake venom proteomes. Another benefit is the facility of fast identification of the toxins with the highest medical relevance for a given envenoming in correlation with their absolute abundance.

Here, some of the functionalities and areas of application will be presented, including inter-/intraspecies venom comparisons and quick elucidation of which toxin families may be critical in a given envenoming case. Finally, future possibilities and features will be discussed.
Keywords: Visualization tool, Antivenom development, Venomics, Toxicoenomics

148 A DEMONSTRATION OF VARIATION IN VENOM COMPOSITION OF DABOIA RUSSELLI (RUSSELL’S VIPER), A SIGNIFICANTLY IMPORTANT SNAKE OF MYANMAR, BY TANDEM MASS SPECTROMETRY

Abstracts / Toxicon 158 (2019) S1–S88

S45

Silvia L. Saggiomo*, Jamie Seymour. Australian Institute of Tropical Health and Medicine, James Cook University, McGregor Road, Cairns, QLD 4878, Australia

* Corresponding author.
E-mail address: silvia.saggiomo@my.jcu.edu.au (S.L. Saggiomo).

Abstract

Cubozoans include jellyfish that range from the most venomous animal on the planet, through small jellyfish that cause Irukandji Syndrome to others that have no effects on humans. These animals have a massive negative impact on the planet, through small jellyfish ranging from the most venomous animal on the planet, through small jellyfish that cause Irukandji Syndrome to others that have no effects on humans. These animals have a massive negative impact on the planet, through small jellyfish ranging from the most venomous animal on the planet, through small jellyfish that cause Irukandji Syndrome to others that have no effects on humans. These animals have a massive negative impact on the planet, through small jellyfish ranging from the most venomous animal on the planet, through small jellyfish that cause Irukandji Syndrome to others that have no effects on humans. These animals have a massive negative impact on the planet, through small jellyfish ranging from the most venomous animal on the planet, through small jellyfish that cause Irukandji Syndrome to others that have no effects on humans. These animals have a massive negative impact on the planet, through small jellyfish ranging from the most venomous animal on the planet, through small jellyfish that cause Irukandji Syndrome to others that have no effects on humans. These animals have a massive negative impact on the planet, through small jellyfish ranging from the

146 CHARACTERISATION OF PREDICTED HELICAL REGIONS IN THE CHIRONEX FLECKERI CFTX-1 TOXIN

Athena Andreossos, Paramjit S. Bansal, Michael J. Smout, David Wilson, Jamie E. Seymour, Norelle L. Daly. Centre for Biodiversity and Molecular Development of Therapeutics, AITHM, James Cook University, Cairns, QLD, Australia

* Corresponding author.
E-mail address: norelle.daly@jcu.edu.au (N.L. Daly).

Abstract

The Australian big box jellyfish, Chironex fleckeri, belongs to a family of cubozoan jellyfish that are known for their potent venoms. C. fleckeri toxin 1 (CFTX-1) is a cardiotoxic and hemolytic protein that is potentially responsible for the rapid cardiovascular collapse in human envenomation victims. Based on secondary structure analysis of CFTX-1, previous studies have predicted several helical regions and concluded that this toxin is a pore-forming toxin. We synthesized two putative helical regions (CFTX-142-67 and CFTX93-120) from CFTX-1 and conducted a structural analysis with nuclear magnetic resonance (NMR) spectroscopy. CFTX-142-67 does not form a structure in aqueous solution, but does form a helical structure in the presence of SDS. CFTX93-120 is relatively hydrophobic and aggregates in aqueous solution, but forms a helical structure in the presence of SDS, consistent with the structure of this region in the CFTX-1 model predicted using I-TASSER. Our results are also consistent with residues 93–120 in CFTX-1 being involved in membrane-spanning. This study confirms the presence of helical regions in CFTX-1 derived peptides, providing the first experimental structure information relating to this protein, and insight into its function.
Keywords: Chironex fleckeri venom, CFTX-1, Cubozoan toxins, Pore forming toxins, NMR