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Epitopic Profiling of Antibody Response against Neurotoxins from the Black Mamba (Dendroaspis polylepis)

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1. Introduction

black mamba (*Dendroaspis* Polylepis) is among the most dangerous snakes in the world, with a venom dominated by three-finger toxins and dendrotoxins¹. Among the three-finger toxins, the α -neurotoxins (α -NT) are the most important², and these are conserved between snake species.

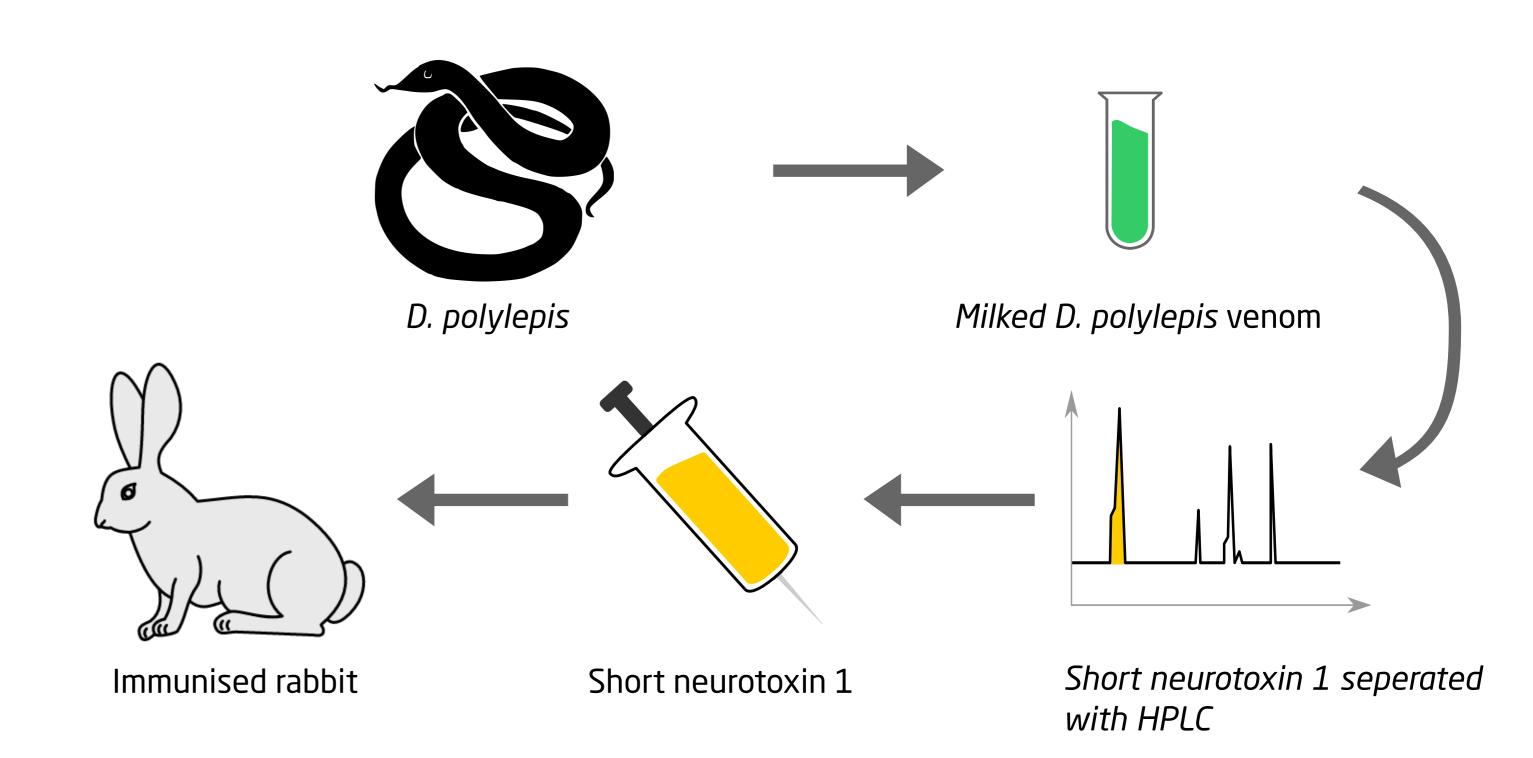
Cross-reactivity between threefinger toxins is known to occur, and understanding this phenomenon in depth may help guide future design of antivenoms to obtain optimal specificity against medically important toxins from different snake species.

Using a bioinformatic approach, we investigated the cross-reactivity between three-finger toxins for a rabbit antiserum raised against short neurotoxin 1 from *D. polylepis* (SN1-DP).



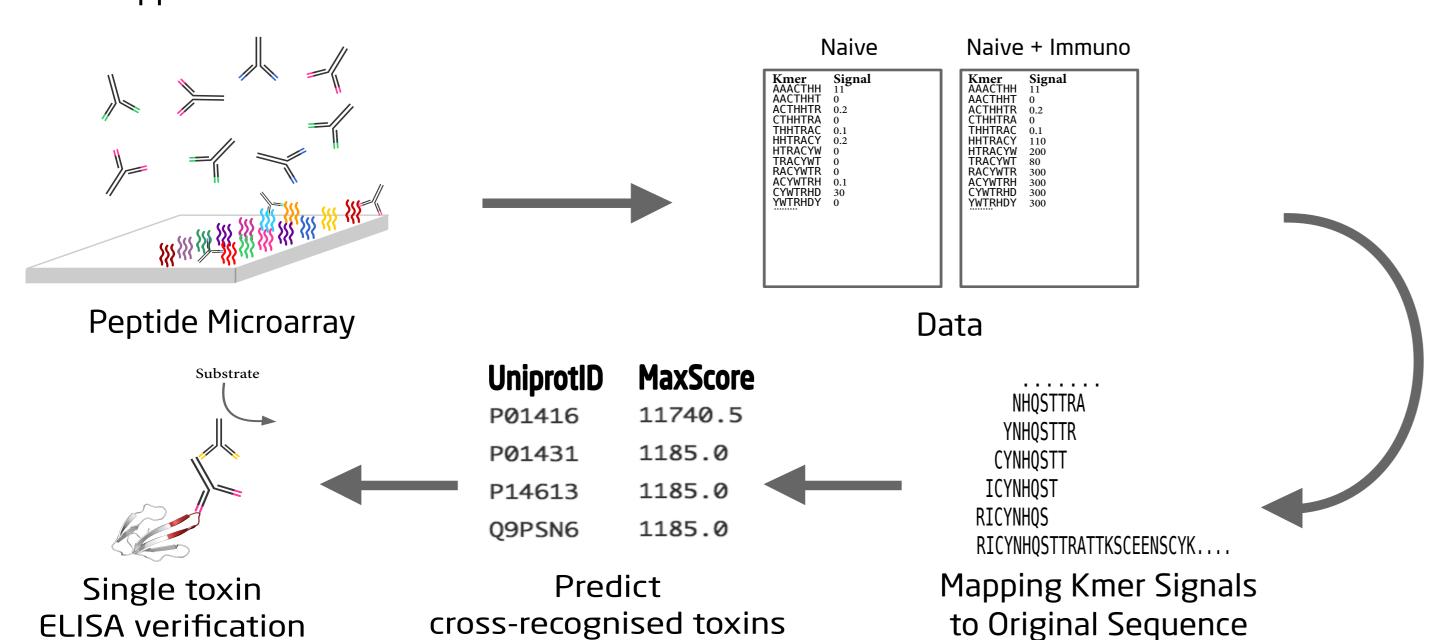
2. Immunisation

The venom of *D. polylepis* was obtained, SN1-DP was isolated and used for immunisation of a rabbit.



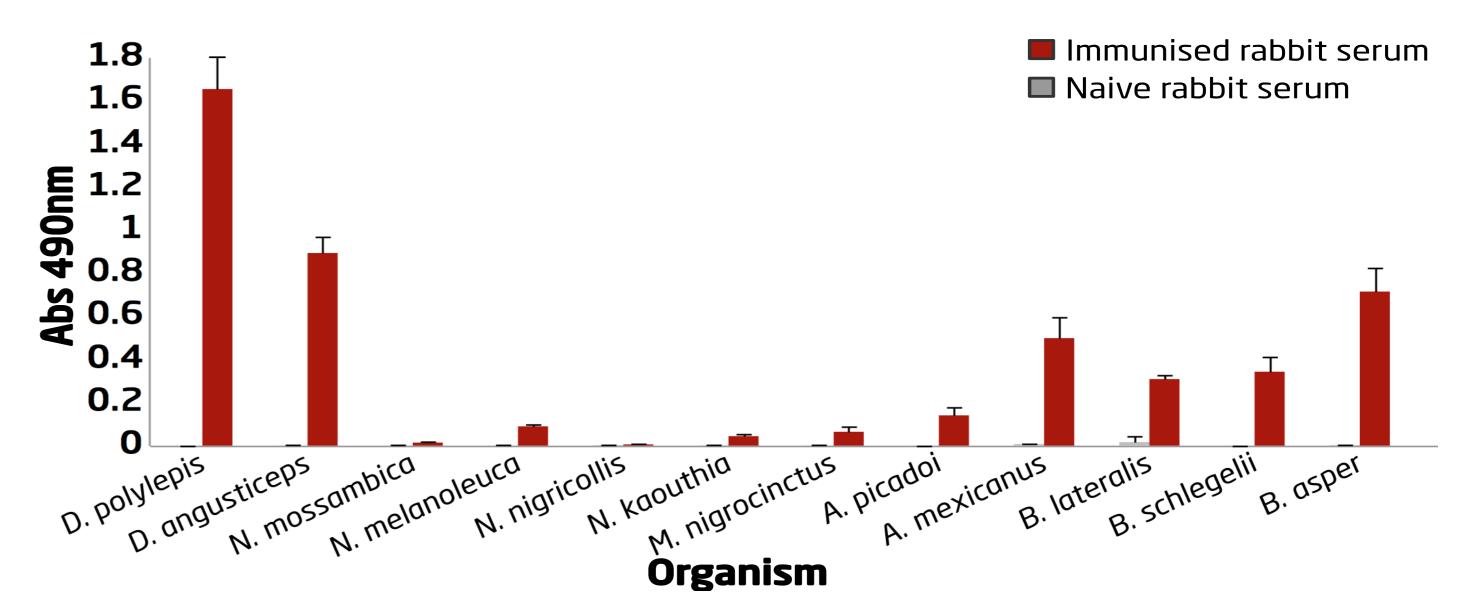
3. Project Flow

A peptide microarray covering all possible epitopes of all known three-finger toxins was synthesised, and binding of antibodies from the rabbit serum to individual toxin epitopes was detected and mapped back to toxin structures.



4. ELISA

An ELISA experiment containing various snake venoms was performed using the rabbit antisera immunised with SN1-DP. This shows reactivity with D. polylepis whole venom, strong crossreactivity with the related *D. angusticeps* venom, and some cross-reactivity with very unrelated venoms.



5. Mapped Signals

A sequence markup plot was constructed for all toxins within the same sub-subfamily of positive control SN1-DP (UniprotID: P01416).

Comparing the high antibody binding regions of SN1-DP and the second highest scoring toxin it shows the that Y28R possibly has a high impact, which also confirms that Tyrosine (Y) is more common in epitopes than Arginine (R)³. But it does look like it maintains its signal downstream even with the mutations *TII35:37YRT*. Due to the normalisation of each sequence, it should be noted that all marked positions in P01416 have a larger signal than any signals in the other toxins.

$$AAsignal = \sum_{k \in \{8,12,15\}} AA \in k_{mer}$$
 $MaxScore = max(AAsignals)$

UniprotID	Organism	MaxScore	Sequence
P01416	D. polylepis	11740.5	RICYNHQSTTRATTKSCEENSCYKKYWRDHRGTIIERGCGCPKVKPGVGIHCCQSDKCNY
P01431	N. mossambica	1185.0	LECHNQQSSEPPTTTRCSGGETNC <mark>YKKRWRDHRGYRTERG</mark> CGCPTVKKGIELNCCTTDRCNN
P14613	N. kaouthia	1185.0	LECHNQQSIQTPTTTGCSGGETNC <mark>YKKRWRDHRGYRTERG</mark> CGCPSVKNGIEINCCTTDRCNN
Q9PSN6	N. sputatrix	1185.0	LECHDQQSSQTPTTTGCSGGETNC <mark>YKKRWRDHRGYRTERG</mark> CGCPSVKNGIEINCCTTDRCNN
P60770	N. atra	1185.0	LECHNQQSSQTPTTTGCSGGETNC <mark>YKKRWRDHRGYRTERG</mark> CGCPSVKNGIEINCCTTDRCNN
P60771	N. kaouthia	1185.0	LECHNQQSSQTPTTTGCSGGETNC <mark>YKKRWRDHRGYRTERG</mark> CGCPSVKNGIEINCCTTDRCNN
Q9PTTØ	N. naja	1185.0	LECHNQQSSQTPTTTGCSGGETNC <mark>YKKRWRDHRGYRTERG</mark> CGCPSVKNGIEINCCTTDRCNN
Q9YGJ6	N. sputatrix	1110.0	LECHNQQSSETPTTTGCSGGETN <mark>CYKKSWRDHRGYRIE</mark> RGCGCPSVKKGIEINCCTTDRCNN
Q9YGJ5	N. sputatrix	1110.0	LECHNQQSSQAPTTTGCSGGETN <mark>CYKKSWRDHRGYRIE</mark> RGCGCPSVKKGIEINCCTTDRCNN
			15060-

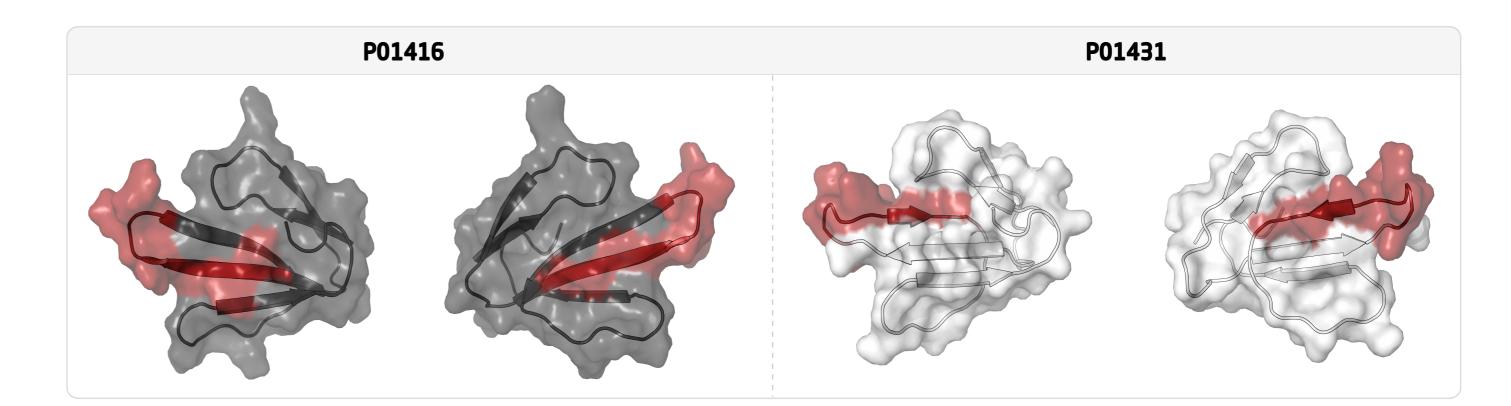
6. Structural Comparison

Due to the observed elimination of the start region on the sequence markup plot, the top toxin (P01431) was modelled due to the lack of a PDB structure using SWISS-MODEL⁴.

The structure for SN1-DP (PDB: 1NTX) and the modelled P01431 structure were compared in PyMOL⁵, and their amino acid sequences showing a high degree of antibody binding were marked in red.

Red regions:

P01416: RICYNHQSTTRATTKSC--EENSCYKKYWRDHRGTIIERGCGCPKVKPGVGIHCCQSDKCNY P01431: LECHNQQSSEPPTTTRCSGGETNCYKKRWRDHRGYRTERGCGCPTVKKGIELNCCTTDRCNN



Conclusion & Future

A high chance of antivenom cross-reactivity between short neurotoxins from different snake species exists due to conservation of important epitopes in these toxins. Future ELISA experiments containing SN1-DP and some of the toxins with high signal will be conducted to further support the results observed in this bioinformatic analysis.

References

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- 3: Kringelum et al. Molecular immunology 53.1 (2013): 24-34.
- 4: Biasini et al. Nucleic acids research (2014): gku340.

2: Laustsen et al. Toxicon 104 (2015): 43-45.

5: PyMOL Version 1.7.4 Schrödinger, LLC 6: Black Mamba image, Herman Pijpers - www.flickr.com (Adapted)

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