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**Proteomic and genomic characterisation  
of venom proteins from  
*Oxyuranus* species.**



**Thesis submitted by  
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In June 2005**

**For the degree of Doctor of Philosophy  
In the School of Pharmacy and Molecular Sciences,  
Discipline of Biochemistry and Molecular Biology  
James Cook University  
Australia**

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Ronelle Welton

June 2005

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## Abstract

The genus *Oxyuranus* includes three of the largest and most feared Australasian snakes, and are listed within the top ten of the world's most venomous snakes. This genus includes *Oxyuranus microlepidotus*<sup>1</sup> (inland taipan), *Oxyuranus scutellatus* (coastal taipan) and the subspecies *Oxyuranus scutellatus canni* (Papuan taipan). Despite comparative differences in the proportions of venom components the *Oxyuranus* species have been reported to be more closely related to each other than to those of any other large Australian elapid snakes. Nevertheless, differences in the clinical presentation of envenomed patients have been described between species. It has also been shown that the antivenom (produced from *O. s. scutellatus*) may not be as effective in bite victims of *O. microlepidotus* or *O. s. canni* compared to *O. s. scutellatus*.

This project was a comparative study designed to substantially build upon previous research into the venom of *Oxyuranus* species. The objectives of this study were: *firstly*, to conduct a comparative study of the composition of venom proteins from the three *Oxyuranus* species; *secondly* to clone and characterise venom specific proteins. This study was primarily conducted utilising fundamental proteomic tools including chromatography, one- and two-dimensional gel electrophoresis (2DE) mass spectrometry and N-terminal sequence determination. The *third* objective was to use a cDNA expression library, constructed using mRNA from a venom gland of *O. s. scutellatus*, to screen with taipan antivenom in order to isolate nucleotide sequences important within the venom.

The venoms from *Oxyuranus* showed remarkable complexity and stability. It was shown that the three *Oxyuranus* venoms share strong similarities in the protein patterning of major proteins. *O. s. scutellatus* and *O. s. canni* venoms exhibited identical protein patterning throughout electrophoretic, fractionation and immunobinding analysis. The venom similarities, together with previous comparative

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<sup>1</sup> (Note for future annotation: *O. s. scutellatus* may be taken to mean the Australian species, the coastal taipan, *Oxyuranus scutellatus scutellatus* (OS in some figures), *O. microlepidotus* to mean the inland taipan or *Oxyuranus microlepidotus* (OM in some figures), and *O. s. canni* to mean the Papuan subspecies *Oxyuranus scutellatus canni* (OSC in some figures))

research using mitochondrial DNA sequencing and morphology studies indicated *O. canni* is not a subspecies but the same species of *O. s. scutellatus*. *O. microlepidotus* on the other hand, though sharing major proteins, revealed patterns distinctly different to *O. s. scutellatus* through electrophoretic and fractionation examinations. Immunobinding studies showed the major banding differences in *O. microlepidotus* were antigenic against taipan antivenom (CSL). These results also indicated that diet, feeding and habitat (captive/wild) do not play a major role in contributing to the venom compositions of the taipan, opposing literature stating the contrary in other species. Variation within the venom composition between the species may be due, instead, to the geographic distances and habitat pressures between the species.

From these comparisons, an antigenic 300 kDa glycoprotein from *O. s. scutellatus* was identified using 15% SDS-PAGE and was isolated using size exclusion and affinity chromatography. This protein was comprised of a homo trimer, three subunits of 100 kDa joined by disulphide bonds. N-terminal sequence shared homology to a previously identified serine protease. This protein cleaved chromogenic substrate S-2288 and Michaelis-Menten kinetics revealed this protein to undergo allosteric interactions. Results of inhibition profiles, pH optimum and kinetic studies confirmed this to be a trypsin-like serine protease. It was highly sensitive to benzamidine and PMSF and was inhibited only by high concentrations of alkylating and reducing agents NEM and iodoacetamide. Metal chelators 1,10-phenanthroline, EGTA and EDTA showed little inhibition; whereas SDS was the only reagent to completely prevent any activity. Based on this evidence it is proposed all three subunits are required for activity. This protease appeared to be present in the venoms of both *O. microlepidotus* and *O. s. canni* and may represent another coagulative enzyme within the venom.

Sequencing studies elucidated the nucleotide sequences of a variety of clones from an *O. s. scutellatus* cDNA library. These clones, translated into full-length protein sequences, included homologous matches to characterised proteins including polymerases, carboxylases, dehydrogenases, Protein disulphide isomerases (PDI's), Heat shock proteins (HSP's) and myosin. Based on the sequences obtained, six PLA<sub>2</sub> toxins, two post-synaptic toxins and the complete factor V component of a prothrombin activator (scutelarlin) were proposed. This study represents the first report of full-length amino acid sequences of taipan venom proteins; previous studies have been conducted

using isolated venom proteins that lack the nucleotide and transit peptide sequences. cDNA and deduced amino acid sequences were compared with those of other snake species. These comparisons conformed to the established primary structures found within the differing peptide classes and, within the putative pre-synaptic neurotoxins, conformed to the evolutionary outline suggested for these sequences.

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## Table of Contents

List of Figures.....	X
List of Tables.....	XII
Abbreviations.....	XIII
<b>Chapter 1 Introduction and literature review</b>	
1.1	<b>Introduction.....</b> 1
1.2	<b>Literature review.....</b> 7
1.2.1	Biology, ecology and distribution of <i>Oxyuranus</i> ..... 7
1.2.2	Clinical presentation after envenomation by <i>Oxyuranus</i> ..... 11
1.2.3	Present state of knowledge of <i>Oxyuranus</i> venoms-summary..... 15
1.2.4	Evolution of Australian snakes and their venoms..... 17
1.2.5	Variance of Venoms..... 20
1.2.5.1	Examples and biochemistry of venom toxins..... 25
1.2.5.1.1	Phospholipases 26
	Neurotoxins 28
	Pre-synaptic neurotoxins 29
1.2.5.1.2	Post-synaptic neurotoxins 34
1.2.6	Proteomic and genomic characterisation of <i>Oxyuranus</i> venom..... 36
1.3	<b>Objectives.....</b> 38
<b>Chapter 2 Materials and methods</b>	
2.1	<b>Materials.....</b> 39
2.1.2	Venom..... 39
2.1.3	Reagents..... 40
2.2	<b>Methods.....</b> 40
2.2.1	Protein protocols..... 40
2.2.1.1	SDS-PAGE 40
2.2.1.2	Venom stability studies 42
2.2.1.3	Liquid chromatography 43
2.2.1.4	Quantification of proteins 45
2.2.1.5	Enzyme activity assays 45
2.2.1.6	Inhibition studies 47
2.2.1.7	Two dimensional gel electrophoresis 47
2.2.1.8	ELISA 48
2.2.1.9	Western blotting 49
2.2.1.10	Immunoscreening 49
2.2.1.11	Glycoprotein detection 50
2.2.1.12	Antibody binding 50
2.2.1.13	Precipitation of proteins 50
2.2.1.14	Determination of amino acid sequence of proteins 51
2.2.2	Molecular biology ..... 52
2.2.2.1	cDNA library; construction and screening 52
2.2.2.2	Agarose gel electrophoresis 54
2.2.2.3	Plasmid DNA 54

2.2.2.4	Restriction enzyme digestions	56
2.2.2.5	Isolation of DNA from agarose gels	56
2.2.2.6	Estimation of DNA	57
2.2.2.7	Ligation of DNA into pGEM-T	57
2.2.2.8	Preparation of competent cells	58
2.2.2.9	Transformation of competent cells	58
2.2.2.10	Precipitation of DNA	58
2.2.2.11	Polymerase chain reaction (PCR)	59
2.2.2.12	Sequencing	62
2.2.2.13	Analysis of sequence data	62

### Chapter 3 Comparison of *Oxyuranus* species venom

<b>3.1</b>	<b>Introduction: Storage of venom</b>	<b>64</b>
<b>3.2</b>	<b>Results</b>	<b>65</b>
3.2.1	Stability studies of whole venom: effect of time, temperature and pH upon the stability of whole venom	66
3.2.2	Electrophoretic analysis	67
3.2.3	Separation and identification of venom components	68
3.2.3.1	Size exclusion chromatography (SEC)	68
3.2.3.2	Ion exchange chromatography	74
3.2.4	Two dimensional gel electrophoresis (2DE)	76
3.2.4.1	Fractionation of whole venom proteins for 2DE	76
3.2.5	Antivenom binding studies	78
3.2.6	Glycosylation of venom proteins	79
<b>3.3</b>	<b>Discussion</b>	<b>81</b>
3.3.1	Details of <i>Oxyuranus</i> snakes venom used within the study	81
3.3.2	Stability study of whole venom	81
3.3.3	Electrophoretic analysis	83
3.3.4	Separation of venom components	86
3.3.4.1	Size exclusion chromatography	86
3.3.4.2	Ion exchange chromatography	88
3.3.5	Two dimensional gel electrophoresis	90
3.3.6	Antivenom binding studies	92

### Chapter 4 Isolation and characterisation of a serine protease from *O. s. scutellatus*

<b>4.1</b>	<b>Introduction</b>	<b>95</b>
4.1.1	Coagulant enzymes	95
<b>4.2</b>	<b>Results</b>	<b>98</b>
4.2.1	N-terminal sequence	98
4.2.2	Serine protease activity	98
4.2.3	Stability of fractionated venom	99
4.2.4	Two dimensional gel electrophoresis	100
4.2.5	Isolation and characterisation of a 300 kDa protein	100
4.2.6	Determination of amino acid sequence	107
4.2.7	PCR	107
4.2.8	Isolation of B2 using specific antibodies	109
<b>4.3</b>	<b>Discussion</b>	<b>110</b>
4.3.1	N-terminal sequence and 2DE	110
4.3.2	Serine protease activity	111
4.3.3	Stability	112
4.3.4	Isolation of the serine protease (B2) from <i>O. s. scutellatus</i>	113
4.3.5	Characterisation of B2	114
4.3.5.1	Sequencing	116
4.3.5.2	PCR	117
4.3.6	Antivenom binding studies to isolate B2	118

## Chapter 5 Nucleotide sequences of venom toxins

<b>5.1</b>	<b>Introduction.....</b>	<b>119</b>
<b>5.2</b>	<b>Results.....</b>	<b>119</b>
5.2.1	Nucleotide sequences isolated from <i>O. s. scutellatus</i> .....	126
5.2.2	Potential peptides isolated from <i>O. s. scutellatus</i> .....	127
5.2.2.1	<i>Oxyuranus</i> sequences sharing homology with PLA <sub>2</sub> s	127
5.2.2.2	<i>Oxyuranus</i> sequences sharing homology to post-synaptic peptides	136
5.2.2.3	<i>Oxyuranus</i> sequence sharing homology to Factor V	139
<b>5.3</b>	<b>Discussion.....</b>	<b>142</b>
5.3.1	Pre-synaptic neurotoxins.....	143
5.3.1.1	Type IA peptides	144
5.3.1.2	Neutral peptide	145
5.3.1.3	Type IB peptides	145
5.3.2	Preliminary alignment of pre-synaptic neurotoxins	148
5.3.3	Post-synaptic neurotoxins.....	150
5.3.4	Factor V.....	152
<b>5.4</b>	<b>Annex for Chapter 5: Details of sequences discussed</b>	<b>154</b>
5.4.1	Details of sequences isolated from <i>O. s. scutellatus</i> cDNA library matching venom PLA <sub>2</sub> neurotoxins.....	154
5.4.2	Details of sequences isolated from <i>O. s. scutellatus</i> cDNA library matching post-synaptic neurotoxins .....	162
5.4.3	Sequence sharing homology to Factor V.....	164

<b>Chapter 6 Conclusions.....</b>	<b>169</b>
Objective 1 .....	169
Objective 2 .....	172
Objective 3 .....	173

<b>References.....</b>	<b>175</b>
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<b>Appendices.....</b>	<b>201</b>
Appendix I Families of snakes the species found within them.....	201
Appendix II Common and scientific names of some Australian snakes....	202
Appendix III Summary of venom toxins found within Australian snakes..	203
Appendix IV Mass spectrometry data.....	207
Appendix V Anion exchange chromatography profiles.....	214
Appendix VI Cation exchange chromatography profiles.....	215
Appendix VII. Phylogram of a neighbour joining distance tree for <i>Oxyuranus</i> putative and peptide sequences. ....	216
Appendix VIII Summary of clones from cDNA library.....	217
Appendix IX Buffers, solutions and primers used for sequencing.....	235
Australian and PNG export and AQIS import permits.....	238

## List of Figures

Figure 1.1	Classification of Genus <i>Oxyuranus</i> .	8
Figure 1.2	Coastal taipan ( <i>O. s. scutellatus</i> )	9
Figure 1.3	Papuan taipan ( <i>O. s. canni</i> ).	9
Figure 1.4	Inland taipan ( <i>O. microlepidotus</i> )	9
Figure 1.5	Brown snake ( <i>Pseudonaja</i> )	9
Figure 1.6	Geographical locations of <i>Oxyuranus</i> species	10
Figure 1.7	Phylogeny of the Family of Elapidae	19
Figure 1.8	Phylogeny of Hydrophiines (sea snake)	19
Figure 1.9	Highly schematic drawing of a nerve fibre and motor end plate.	29
Figure 2.1	Venom milking.	39
Figure 3.1	The effect of pH on the degradation of whole venom (50 µg).	69
Figure 3.2	Effect of pH on the degradation of whole venom (1 µg).	70
Figure 3.3	Successive venom samples obtained over time.	70
Figure 3.4	The effect of protein amounts (µg) on whole venom electrophoretic patterns. (15% SDS-PAGE).	71
Figure 3.5	The effect of protein amounts (µg) on whole venom electrophoretic patterns (7.5% SDS-PAGE).	71
Figure 3.6	Effect of reducing and non-reducing conditions on whole venom electrophoretic patterns (15% SDS-PAGE).	71
Figure 3.7	Effect of reducing and non-reducing conditions on whole venom electrophoretic patterns (15% SDS-PAGE).	71
Figure 3.8	Gel filtration trace of OS venom.	72
Figure 3.9	Comparison of gel filtration profiles of whole venom from OS and OSC.	73
Figure 3.10	Comparison of gel filtration profiles of whole venom from OS and OM.	73
Figure 3.11	Cation exchange chromatography profile of OS whole venom.	74
Figure 3.12	Fractions from cation exchange chromatography separated using SDS-PAGE.	75
Figure 3.13	Two dimensional gel electrophoresis of OS and OM whole venom.	77
Figure 3.14	Two dimensional gel electrophoresis of duplicate samples from OS whole venom.	77
Figure 3.15	The effect of fractionation of OS and OM whole venom at pH 6.0.	78
Figure 3.16	Western blot analysis of <i>Oxyuranus</i> venom proteins.	79
Figure 3.17	Immunobinding study of SEC fractions from OS, OSC and OM whole venom.	80
Figure 4.1	Sites of activity of snake venoms on coagulation (from Tibballs, 1998)	97
Figure 4.2	Protease activity profile from OS and OM whole venom using Chromogenix substrates.	99

Figure 4.3	Specific activity of OS whole venom fractionated by size exclusion chromatography. ....	99
Figure 4.4	Effect of pH 6.0 and 9.0 on OS peak one.....	101
Figure 4.5	Resolution of proteins in peak 1 by two dimensional gel electrophoresis. ....	101
Figure 4.6	Affinity chromatography profile of whole venom. ....	103
Figure 4.7	Whole venom bound and eluted from a benzamidine column. ....	103
Figure 4.8	Peak 1 bound and eluted from a benzamidine column. ....	103
Figure 4.9	The effect of differing buffers on the activity of isolated B2 .....	104
Figure 4.10	Effect of pH upon enzyme activity. ....	104
Figure 4.11	Effect of temperature upon enzyme activity. ....	104
Figure 4.12	Kinetics curve of B2 and comparative catalytic rates. ....	106
Figure 4.13	PCR products from nested PCR. ....	108
Figure 4.14	Primers specific for B2. ....	109
Figure 5.1	Pairwise alignment of putative <i>O. s. scutellatus</i> peptides.....	129
Figure 5.2	Sequence alignment of chosen group IA peptides.....	131
Figure 5.3	Sequence alignment of chosen group IB peptides. ....	132
Figure 5.4	Alignment of the signal peptides from <i>O. scutellatus</i> with other Elapid species..	133
Figure 5.5	Distance alignment of <i>O. s. scutellatus</i> putative and peptide sequences.....	134
Figure 5.6	Distance alignment of <i>O. s. scutellatus</i> pre-synaptic Elapidae sequences.....	135
Figure 5.7	Alignment of R147 and R121 with post-synaptic neurotoxins.....	137
Figure 5.8	Alignment of RW6 with post-synaptic neurotoxins.....	138
Figure 5.9	ClustalW alignment of OS FV and pseutarin.....	141
Figure 5.10	Nucleotide and deduced amino acid sequence of $\beta$ -taipoxin (R24) .....	156
Figure 5.11	Nucleotide and deduced amino acid sequence of $\alpha$ -taipoxin isomer (RW26).....	157
Figure 5.12	Alignment of $\alpha$ -taipoxin isomer (RW26) with $\alpha$ -taipoxin subunit .....	157
Figure 5.13	Nucleotide and deduced amino acid sequence of $\gamma$ -taipoxin isomer (R120).....	158
Figure 5.14	Alignment of clone $\gamma$ -gamma taipoxin isomer (R120) with $\gamma$ -taipoxin.....	158
Figure 5.15	Nucleotide and deduced amino acid sequence of OS1 isomer (R132).....	159
Figure 5.16	Alignment of R132 with <i>O. s. scutellatus</i> OS1. ....	159
Figure 5.17	Nucleotide and deduced amino acid sequence of OS2 isomer (R56).....	160
Figure 5.18	Nucleotide and deduced amino acid sequence of OS2 isomer (R125).....	160
Figure 5.19	Alignment of clones R125 and R56 with OS2. ....	161
Figure 5.20	Nucleotide and deduced amino acid sequence of R147 in two reading frames.....	162
Figure 5.21	Nucleotide and deduced amino acid sequence of R121. ....	162
Figure 5.22	Alignment of R147 and R121. ....	163
Figure 5.23	Nucleotide and deduced amino acid sequence of RW6. ....	164
Figure 5.24	Nucleotide and deduced amino acid sequence of Factor V sequence.....	164

## List of Tables

Table 1.1	Clinical signs and symptoms of OS, OM and OSC.....	14
Table 3.1	Statistics of <i>Oxyuranus</i> species contributing to this study. ....	66
Table 3.2	Summary of the time of elution compared to gel filtration marker (BioRad).....	72
Table 3.3	Fraction number from Figure 3.8 and the % of Buffer B (1M NaCl) the fraction eluted within. ....	75
Table 4.1	N-terminal sequence of four protein bands from OS. ....	98
Table 4.2	Purification Table for B2. ....	105
Table 4.3	Specific activity of OS fractions from ion exchange chromatography.....	105
Table 4.4	Effect of various compounds on the activity of purified B2. ....	106
Table 4.5	Peptides sequenced by mass spectrometry (Sample RW300S). ....	107
Table 5.1	Summary of mRNA sequences from <i>O. s. scutellatus</i> venom gland cDNA library and the sequences they share homology with .....	121
Table 5.2	Summary of clones isolated from the <i>O. s. scutellatus</i> venom gland cDNA library sharing homology with characterised toxins .....	126
Table 5.3	Annotation of suggested toxin residues in pre-synaptic neurotoxins.....	133

## Abbreviations

Ach	acetylcholine
bp	base pairs
BSA	bovine serum albumin
Da	daltons
DAB	diaminobenzidine
DNA	deoxyribonucleic acid
ECL	enhanced chemiluminescence
EDTA	ethylene diamine tetraacetic acid
ELISA	enzyme linked immunosorbant assay
FV	Factor V (coagulation co-factor)
g	gram
HCl	hydrochloric acid
His	histidine
hr	hour
HRP	horse radish peroxidase
hrs	hours
IPTG	isopropyl $\beta$ -D-thiogalactopyranoside
kDa	kilodaltons
LB	Luria Bertani
LD <sub>50</sub>	lethal dose, 50%
M	molarity
$\mu$ g	microgram
$\mu$ l	microlitre
mA	milliamps
ml/min	milliliters per minute
min	minute/s
ng	nanograms
nm	nanometers
Ntx	neurotoxin
OD	optical density (at a given wavelength)
OM	<i>Oxyuranus microlepidotus</i> , <i>O. microlepidotus</i>
ORF	open reading frame
OS	<i>Oxyuranus scutellatus scutellatus</i> , <i>O. s. scutellatus</i>
OSC	<i>Oxyuranus scutellatus canni</i> , <i>O. s. canni</i>
PAGE	polyacrylamide gel electrophoresis
PBS	phosphate buffered saline
PBST	phosphate buffered saline containing 0.05% Tween 20
PCR	polymerase chain reaction
PLA <sub>2</sub>	phospholipase A2
RNA	ribonucleic acid
sec	second/s
SDS	sodium dodecyl sulphate
SDS-PAGE	sodium dodecyl sulphate polyacrylamide gel electrophoresis
TRIS	tris(hydroxymethyl)aminomethane
V	volts
Xgal	5-bromo-4-chloro-3-indoyl- $\beta$ -D-galactopyranoside