

Characterisation of Ant Venom

Peptides and Proteins

Samira Ryma Aili

BMedSc (Hons)

Submitted in fulfilment of the requirements for the degree of Doctor of Philosophy from:

School of Life Sciences, University of Technology Sydney

2018



Certificate of Authorship and Originality

I, Samira Ryma Aili, certify that the work in this thesis has not previously been submitted for a degree nor has it been submitted as part of requirements for a degree except as fully acknowledged within the text.

I also certify that the thesis has been written by me. Any help that I have received in my research work and the preparation of the thesis itself has been acknowledged. In addition, I certify that all information sources and literature used are indicated in the thesis.

This research is supported by an Australian Government Research Training Program Scholarship.

Signature of Student

Production Note: Signature removed prior to publication.

Date: 16th April 2018

Table of Contents

Certificate of Authorship and Originalityii		
Acknowledgementsvi		
List of Publications		
Conference Proceedingsix		
List of Figuresxi		
List of Tablesxii		
Abbreviationsxiii		
Abstract 1		
Chapter One: Overview of the Thesis		
1.1. Introduction		
1.2. Aims of the thesis		
1.3. Dissertation organisation		
Chapter Two: Diversity of Peptide Toxins in Stinging Ant Venoms		
Compound Abstract		
Compound Abstract		
•		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms 25 Compound Abstract 25 Chapter Four: Ant Venom Insecticidal and Antibacterial Activity 56 Compound Abstract 56 4.1. Introduction 57		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms 25 Compound Abstract 25 Chapter Four: Ant Venom Insecticidal and Antibacterial Activity 56 Compound Abstract 56 4.1. Introduction 57 4.2. Methods 60		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms 25 Compound Abstract 25 Chapter Four: Ant Venom Insecticidal and Antibacterial Activity 56 Compound Abstract 56 Compound Abstract 56 A.1. Introduction 57 4.2. Methods 60 4.2.1. Supply of ant venoms 60		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms25Compound Abstract25Chapter Four: Ant Venom Insecticidal and Antibacterial Activity56Compound Abstract564.1. Introduction574.2. Methods604.2.1. Supply of ant venoms604.2.2. Bicinchoninic acid (BCA) assay.60		
Chapter Three: The Biochemical Toxin Arsenal from Ant Venoms25Compound Abstract25Chapter Four: Ant Venom Insecticidal and Antibacterial Activity56Compound Abstract564.1. Introduction574.2. Methods604.2.1. Supply of ant venoms604.2.2. Bicinchoninic acid (BCA) assay604.2.3. Insect toxicity testing61		

4.3.1. Ant venom insecticidal activity	
4.3.2. Minimum Inhibitory Concentration Assay	′s71
4.3.3. Whole venom MALDI-TOF MS	
4.4. Discussion	
4.5. Conclusion	
Chapter Five: Peptidomic and Proteomic Analysis	s of Electrically Stimulated and Manually
Dissected Paraponera clavata Venom	
Compound Abstract	
Chapter Six: Comparisons of Protein and Peptide	Complexity in Poneroid and Formicoid Ant
Venoms	
Compound Abstract	
Chapter Seven: A Holistic Investigation of Parapone	ra clavata Venom Gland Transcriptome and
Venom Proteome	
Compound Abstract	
7.1. Introduction	
7.2. Methods	
7.2.1. RNA isolation and Illumina sequencin	g 157
7.2.2. Quality control and de-novo assembl	y 158
7.2.3. Contig functional annotation	
7.2.4. Venom collection for proteomics	
7.3. Results	
7.3.1. Paraponera clavata venom gland trar	nscriptome profile164
7.3.2. Paraponera clavata venom proteome	
7.3.3. Paraponera clavata toxins	
7.3.4. Novel P. clavata toxins	
7.4. Discussion	
7.4.1. Paraponera clavata transcriptome	
7.4.2. Holistic proteomic/ transcriptomic in	vestigation 200

7.5.	Conclusion and future directions	203
Chapter I	Eight: Concluding Remarks and Future Directions	205
Supplem	entary Material	208
Referenc	es	209

Acknowledgements

First and foremost I would like to thank my supervisor Graham Nicholson. I couldn't have chosen a better supervisor to do my PhD with. I am forever grateful for all you've done for me and your patience with my constant emails/ questions and visits to your office. I appreciate all the extra weekend/ plane time/ after-hours work you've dedicated to helping me. I chose you as a supervisor because you came across as the most organised of my lecturers – a fact that proved to be very true and has inspired me to follow in your footsteps. I have learnt so much in our 4/5 years together about travelling, organising my diary, my mac, communicating, fixing figures and of course science-ing. I hope more students will benefit from your wisdom and you continue being the greatest supervisor one could hope for. Your constant support when stuff goes wrong and attitude of "if it was easy everyone would be doing it" and reassurance definitely helped ease my PhD journey.

To Matt, my other supervisor who is also always there for me and is always willing to answer my questions after initially saying no. Your knowledge about everything is a constant inspiration. Despite being initially terrified of you, it wasn't long till I realised I was very wrong. Your help in the first couple of years the lab was invaluable, especially when Graham is away. I'm glad I was a member of the proteomics family whose support is part of the reason I stayed on for a PhD. You have taught me so much about science but also a lot about other random things such as metal bands, bikes and cars.

I would like to thank Dr Axel Touchard, as without him this project would not have taken place. The number of ants you've collected and glands you've dissected for me is innumerable. Thank you to Dr Pierre Escoubas as well, for his contribution in collections and feedback throughout the project. A big thanks also goes to Hadrien L., Frederic P., Alain D., and Jerome., who've all played a role in the various ant collections.

Thank you Regan Hayward! A life saver with all your help in analysing the transcriptomics and excel tricks. I would also like to thank A/ Prof Garry Myers for your guidance with the transcriptomics work.

I'd like to thank Prof Kini for giving me the opportunity to go over to Singapore and funding the part of the transcriptomics project. Special thanks to Mrinalini for introducing me to the land of transcriptomes as well and her feedback and guidance.

vi

Another big thank you goes to Sandy P. Gonzalez who has been supporting me in many aspects of the last stages of my PhD thesis stress and helping me with my transcriptomics data analysis and interpretation as well.

I would like to thank Dr. Jaye Liu and Prof. Liz Harry from the iThree institute, UTS for their help in the antibacterial activity assays and for providing me with the bacteria.

To the proteomics crew (Jacqueline, Ben, Iain, Marcelo, Krish, Kate, Michael, Ronnie, and Jerran) your support and friendship is invaluable. You adopted me as a part of your group, seeing as I was the only person in my lab group. Our Lorne adventures will be forever remembered and cherished. A special thank you to Mike, my metabolic buddy and computer shortcut wiz, for all your help and friendship particularly in the last week with teaching approaching. As well as to Jacqueline, aka my breakfast and gym partner, Thursday traditions need to be me maintained forever! Your blonde moments never cease to entertain me; it's been great sharing your crochet and knitting hobbies.

I'd also like to thank all my other UTS friends Brendan, Isa, Megan, Chris, Louis, Emma, Dan and Louis. In particular, thank you to Emma my sprout buddy for always being there for me and helping me format this thesis the day after you got back from your holidays. Your strength and commitment is always an inspiration and I'm glad I've had the privilege of knowing and befriending you.

I'd also like to thank the markers for taking the time to review this thesis and the Australian Government Postgraduate Award Scholarship I received throughout my PhD candidature.

Finally, I would like to thank my Family. My mum Ghania, dad Arezki, and sisters (Sadia, Hanna, Massilia, Zahia and Rama). Your support and understanding of my long hours spent away from home is truly appreciated. Without you I wouldn't be here and I hope to one day be able to explain what I actually do "all day at uni". Particular thanks to my parents for sacrificing a lot to give us a good education. I hope I made you proud.

List of Publications

- Aili, S. R., Touchard, A., Escoubas, P., Padula, M. P., Orivel, J., Dejean, A., & Nicholson, G. M. (2014). Diversity of peptide toxins from stinging ant venoms. *Toxicon*, 92, 166-178.
- 2) Touchard, A., Aili, S. R., Fox, E. G. P., Escoubas, P., Orivel, J., Nicholson, G. M., & Dejean, A. (2016). The biochemical toxin arsenal from ant venoms. *Toxins*, 8(1), 30.
- 3) Touchard, A., Koh, J., Aili, S. R., Dejean, A., Nicholson, G. M., Orivel, J., & Escoubas, P. (2015). The complexity and structural diversity of ant venom peptidomes is revealed by mass spectrometry profiling. *Rapid Communications in Mass Spectrometry*, 29(5), 385-396.
- Aili, S. R., Touchard, A., Koh, J. M., Dejean, A., Orivel, J., Padula, M. P., & Nicholson, G. M. (2016). Comparisons of protein and peptide complexity in poneroid and formicoid ant venoms. *Journal of proteome research*, *15*(9), 3039-3054.
- 5) Aili, S. R., Touchard, A., Petitclerc, F., Dejean, A., Orivel, J., Padula, M. P., & Nicholson, G. M. (2017). Combined peptidomic and proteomic analysis of electrically stimulated and manually dissected venom from the South American bullet ant *Paraponera clavata*. *Journal of proteome research*, *16*(3), 1339-1351.

Conference Proceedings

Venoms to Drugs Conference, Noosa, QLD, Australia Oral Presentation "An integrated proteomic and transcriptomic analysis of venom gland toxins from the bullet ant <i>Paraponera clavata</i> "	2017
TEDx Youth Sydney Oral Presentation, fast ideas session Ant venom to the rescue	2017
AMP Amplify Ignite PhD pitch competition Oral presentation "Ants: the solution to world hunger"	2017
XII Congress of the Pan American Section of the International Society on Toxinology, Miami, USA Oral Presentation "Ant venom as a novel source of bioinsecticide leads"	2016
Sydney Protein Group Thompson Prize finalist, Sydney Oral Presentation "Ant venom as a source of bioinsecticides"	2016
The 21 st Lorne Proteomics Symposium, Lorne, Victoria Poster presentation "Peptidomic and proteomic comparison of electrically stimulated and manually dissected venom of the bullet ant <i>Paraponera clavata</i> "	2016
University of Technology Sydney 3-minute thesis competition Oral presentation "Ant venom derived insecticides"	2015
The 18 th world congress of the International Society on Toxinology, Oxford, United Kingdom Oral presentation	2015
"Ant venom as a source of bioinsecticide and antimicrobial drug leads" The 20th Lorne Proteomics Symposium, Lorne, Victoria Lightning talk and oral presentation: awarded best poster prize "Characterisation of the peptide and protein content of ant venoms for use as bioinsecticide and antimicrobial leads"	2015
New horizons 31 st Combined Health Science Conference, Kolling Institute RNSH Poster presentation "Characterisation of the Antimicrobial and Insecticidal Peptides From Ant Venoms"	2014
APAF 2 nd Proteomics and Beyond Symposium, Sydney Oral presentation "Characterisation of Poneroid and Formicoid ant venoms"	2014

The 19th Lorne Proteomics Symposium, Lorne, Victoria2014Lightning talk and oral presentation: awarded best poster prize"Characterising the peptide and protein diversity of Neotropical and Australian ant
venoms and the identification of novel peptide toxins for bioinsecticide discovery"

New horizons 30th Combined Health Science Conference, Kolling Institute RNSH 2013 Oral presentation

"Characterising the diversity of Neotropical and Australian ant venoms: Novel peptide libraries for bioinsecticide discovery"

List of Figures

Figure 4.1: Lateroventral cricket injections of toxin solution
Figure 4.2: Apparatus used for insect toxicity testing
Figure 4.3: Acute toxicity of <i>E. tuberculatum</i> whole venom in crickets
Figure 4.4: House crickets after an acute toxicity assay
Figure 4.5: Acute toxicity profile of <i>E. tuberculatum</i> whole venom in crickets
Figure 4.6: Acute toxicity of <i>E. brunneum</i> whole venom in crickets
Figure 4.7: Acute toxicity of <i>O. hastatus</i> whole venom in crickets
Figure 4.8: Acute toxicity of <i>N. commutata</i> whole venom in crickets
Figure 4.9: MIC results of O. hastatus venom against S. aureus
Figure 4.10: MIC results of <i>N. commutata</i> venom against the bacteria <i>S. aureus</i> and <i>E. coli</i> 73
Figure 4.11: <i>N. commutata</i> MIC assay dose-response curve
Figure 4.12: MALDI-TOF mass spectra of four crude ant venoms75
Figure 7.1: Summary of the P. clavata combined proteome/ transcriptome methodology 158
Figure 7.2: Peptide toxin nomenclature system using a spider venom peptide example 161
Figure 7.3: Proposed protein toxin nomenclature
Figure 7.4: Distribution of protein hits to different hymenopteran species
Figure 7.5: Gene Ontology classification of contigs with BLASTx hits
Figure 7.6: Abundance and expression levels of <i>P. clavata</i> toxins
Figure 7.7: Protein categories in <i>P. clavata</i> venom
Figure 7.8: Amino acid sequence alignment of δ -paraponeritoxin-Pc1e isoforms 178
Figure 7.9: δ-Paraponeritoxin-Pc1e LC-MS/MS coverage
Figure 7.10: Amino acid sequence alignment of omega-conotoxin-like contigs 180
Figure 7.11: Amino acid alignment of <i>P. clavata</i> phospholipase A2 isoforms
Figure 7.12: Alignment of hyaluronidase-like proteins from P. clavata and other ants 183
Figure 7.13: Alignment of icarapin-like proteins
Figure 7.14: Amino acid alignment of arginine kinase transcripts
Figure 7.15: Alignment of serine proteases from <i>P. clavata</i> and other insect species
Figure 7.16: Distribution of novel <i>P. clavata</i> toxin-like peptides with four or more cysteines. 188
Figure 7.17: Novel P. clavata toxins with a predicted inhibitor cysteine knot (ICK) structural
framework
Figure 7.18: Novel P. clavata toxins with predicted conotoxin framework I cysteine structural
framework 190
*Discourse whether Clause lists data are included at a circle structure data data are included at a second are the

*Please note that the Figures listed above include those in chapters 4 and 7 only.

List of Tables

Table 4.1: Composition of insect saline solution for insect toxicity testing of venom. 61
Table 4.2: Categories of neurotoxicity signs in crickets 63
Table 7.1: Toxin keyword search list. 159
Table 7.2: Assembly statistics and downstream metrics from the P. clavata venom gland
transcriptome analysis
Table 7.3: Top 20 most expressed toxins (based on TPM) from P. clavata venom gland
transcriptome BLASTx and Tox Note searches
Table 7.4: Paraponera clavata toxin transcripts identified by proteomics analysis and their
BLASTx hit

*Please note that the Tables listed above include those in chapters 4 and 7 only.

Abbreviations

1,5-DAN	1,5-Diaminonaphtalene
1D-SDS-PAGE	One dimensional - sodium dodecyl sulphate - polyacrylamide gel electrophoresis
2D-SDS-PAGE	Two dimensional - sodium dodecyl sulphate - polyacrylamide gel electrophoresis
AA	Amino acid
AChE	Acetylcholinesterase
ACN	Acetonitrile
BCA	Bicinchoninic assay
BSA	Bovine serum albumin
Bt	Bacillus thuringiensis
BLAST	Basic local alignment search tool
СНСА	α-Cyano-4-hydroxycinnamic acid
CID	Collision induced dissociation
cDNA	Complementary deoxyribonucleic acid
Cys	Cysteine
DDT	Dichlorodiphenyltrichloroethane
DTT	Dithiothreitol
DNA	Deoxyribonucleic acid
EPA	Environmental Protection Agency
ESI-MS	Electrospray ionisation mass spectrometry
FA	Ferulic acid
FAO	Food and Agriculture Organisation
GABA	γ-Aminobutyric acid
GM	Genetically modified
Gln	Glutamine
Glu	Glutamic Acid

IEF	Isoelectric focussing
IPG	Immobilised pH gradient
ІСК	Inhibitor cysteine knot
KD ₅₀	Median knockdown dose
kDa	Kilodaltons
LD ₅₀	Median lethal dose
LC-MS/MS	Liquid chromatography tandem mass spectrometry
m/z	Mass-to-charge ratio
NanoESI-QTOF MS	Nano electrospray ionisation quadrupole time-of-flight mass spectrometry
Lys	Lysine
MALDI-TOF MS	Matrix-assisted laser-desorption ionization/time-of-flight mass spectrometry
mRNA	Messenger ribonucleic acid
MS	Mass spectrometry
NIS	Normal insect saline
PAGE	Polyacrylamide gel electrophoresis
PI	Isoelectric point
PLA ₂	Phospholipase A ₂
RP-HPLC	Reversed-phase high-performance liquid chromatography
RPM	Revolutions per minute
SCX	Strong cation exchange
Ser	Serine
SDS	Sodium dodecyl sulphate
TFA	Trifluoroacetic acid
WHO	World Health Organisation

Abstract

Venom peptides are currently being developed as novel therapeutics and bioinsecticides. Given that ants use their venoms for predation and defence against insects, and other organisms, they are a potential source of these peptides. Although ants represent one of the largest groups of venomous animals, little is known about their venom composition. The present study therefore investigated the peptidome, proteome and transcriptome of a range of poneroid and formicoid ant venoms.

Initial experiments sought to confirm the insecticidal and antibacterial activity of whole ant venom using house crickets and minimum inhibitory concentration assays, respectively. Several ant venoms showed significant paralytic and insecticidal activity and others showed antibacterial activity peptides confirming the utility in studying ant venoms.

Subsequent experiments investigated the difference in venom composition obtained using differing venom collection methods: manual venom gland dissection or electrical stimulation. The peptide and protein components of the bullet ant (*Paraponera clavata*) were compared and revealed numerous proteins of which 96 could be assigned a biological function, and 70% of which were common to both collection methods. However, the peptidomic analysis revealed over 300 peptides of which only 30% were common to both collection methods. Therefore, each method reveals a unique set of peptides and proteins.

The peptide components of six different ant species were also characterised. The venoms were found to contain between 132–1032 peptides, but the large number of undescribed proteins and peptides highlighted the need for a transcriptomic investigation. Accordingly, an integrated approach using a combination of shotgun proteomics in parallel with Illumina sequencing of the venom gland transcriptome was used to identify toxins in the venom of *P. clavata*. A BLASTx search of the assembled contigs revealed 354 proteins with homology to existing toxins. Alignments of some of these toxins revealed novel insights into their role in ant venom.

A Tox|Note analysis revealed several predicted novel peptide toxins, with some conforming to the conotoxin cysteine frameworks VI/VII and framework I, both of which have yielded therapeutic drug and bioinsecticide leads. The translated transcriptome was then used as a database to query the MS/MS data obtained from the shotgun experiment which identified 44 toxins. Several of these were not identified in the transcriptome BLASTx search, such as δ -

1

paraponeritoxin-Pc1e (formerly poneratoxin). These results reveal the advantages of combining proteomic and transcriptomic methods, and further demonstrates the richness and diversity of ant venoms as potential sources of bioactive compounds.