Systematics, Phylogeny, Phylogeography and Reproduction of *Neotrigonia* (Bivalvia: Palaeoheterodonta)

Ana Glavinic, BSc (Hon.)

Thesis submitted in fulfilment of the requirements for the Degree of Doctor of Philosophy

School of Biology, Faculty of Science and Engineering Flinders University Adelaide, Australia



June 2010

Table of contents

Declaration	ix
Acknowledgments	x
Preface	_xii
Glossary	_xiii
Abstract	_xiv

Chapter 1: General Introduction	1
Phylogeny	3
Phylogeography	
Doubly Uniparental Inheritance	7
Aspects of Reproduction	8
Aims and Scope of the Thesis	9
References	

Chapter 2: Systematics of <i>Neotrigonia</i>	
Abstract	28
Introduction	29
Methods	30
Results	33
Taxonomy	35
Discussion	43
Acknowledgments	
References	47
Chapter 3: Phylogeny and Phylogeography	67
Abstract	
Introduction	
Methods	
Sample collection	71
Markers and outgroup choice	71

	Extraction and amplification	
	Sequencing	
	Phylogenetic analyses	73
	Mitochondrial population structure	73
Results	5	
	Topology-based species delimitation	
	Genetic distances	75
	Phylogeography and demography	
Discussion Acknowledgments		
Refere	nces	

4: Doubly Unipa	rental Inheritance	97	
Abstract			98
Introduction			99
Methods			101
DN	A extraction, amplification and sequencing		101
	Analyses		103
	Analyses of dataset 1		104
	Analyses of dataset 2		104
	Analyses of dataset 3		104
An	alysis of the origin of DUI		105
Results			105
	Analyses of dataset 1		106
	Analyses of dataset 2		106
	Analyses of dataset 3		107
	Analyses of 16S rDNA data		107
	Analysis of the origin of DUI		107
Discussion			108
Acknowledgme	nts		112
References			113
r 5: Oogenesis			134

135
1

Introduction	136
Methods	138
Results	139
General morphology of gonad tissue and oocytes	139
Protogonia	140
Oogonia	140
Previtellogenic oocytes	140
Vitellogenic oocytes	140
Postvitellogenic oocytes	141
Oocyte size frequency distribution and gonad tissue	141
Discussion	142
Acknowledgments	146
References	147
er 6: General Discussion	163
Extant Species of <i>Neotrigonia</i>	163
Phylogeography	164
Doubly Uniparental Inheritance	166
Oogenesis	167
Conservation implication of the findings	168
Conclusion	170
References	172

<u>Appendix</u>

181
184
187
190
200

List of tables

Chapter 2

2.1. Subset of examined <i>Neotrigonia</i> extant and fossil specimens held at different	
museum collections	52
 2.2. Listing of live collected <i>Neotrigonia</i> specimens and the habitat type they were collected from	5
genus Neotrigonia based on type specimens	56
2.4. Morphological data matrix of characters 1 to 25 used to analyse the subset of	
specimens5	7

Chapter 3

3.1. The location and number of <i>Neotrigonia</i> spp. collected for analyses	86
3.2. Mitochondrial COI diversity of <i>N. margaritacea</i> populations	.87
3.3. Analysis of molecular variance (AMOVA) among all four populations of <i>N</i> .	
margaritacea based on COI data	.88
3.4. Pairwise Φ st among four populations of <i>Neotrigonia margaritacea</i>	89

Chapter 4

4.1. Bivalve ingroup taxa with GenBank (NCBI) accession numbers for COI and 16	S
rDNA sequences used119	
4.2. Outgroup taxa with GenBank (NCBI) accession numbers for COI DNA and 168	\$
rDNA sequences used12	25
4.3. Sequence variability and AMOVA results for mitochondrial COI and 16S rDNA	١
ribosomal genes12	26

Appendix

Appendix I

1.1. Listing of all collected *Neotrigonia* specimens and all locations where collection was attempted either by SCUBA diving, dredging and beach combing......182Appendix IV

4.1. Raw data of diameter measurements for protogonia in each sampling month...2004.2. Raw data of diameter measurements for oogonia in each sampling month.....201

4.3. Raw data of diameter measurements for previtellogenic oocyte	in each sampling
month	202
4.4. Raw data of diameter measurements for vitellogenic oocytes in a	each sampling
month	203
4.5. Raw data of diameter measurements for postvitellogenic oocytes	s in each
sampling month	

List of figures

Chapter 1

1.1. The tree topology of bivalve	22
1.2. Neotrigonia images	23
1.3. Morphology of <i>Neotrigonia margaritacea</i>	24
1.4. Image of a juvenile <i>Neotrigonia margaritacea</i> shell	25
1.5. Image of <i>Neotrigonia margaritacea</i> spermatid	26

Chapter 2

2.1. Morphology of the <i>Neotrigonia margaritacea</i> species complex	61
2.2. Neotrigonia margaritacea is used to depict scored characters used in	
Cladistic analysis	62
2.3. Map of Australia illustrating distributions	63
2.4. Strict consensus tree topology obtained by parsimony analysis of	
morphological characters for type specimens	64
2.5. Adam's consensus tree topology obtained by maximum parsimony	65
2.6. Holotypes or hypotypes for the six confirmed extant species of <i>Neotrigonia</i> .	66

Chapter 3

3.1. Map of Australia showing the locations of <i>Neotrigonia</i> collection9	12
3.2. Strict consensus of four most parsimonious trees (length 351) from COI data9	13
3.3. Strict consensus of seven most parsimonious trees (length 835) from ITS data9)4
3.4. Bayesian consensus tree using combined COI and ITS1 data)5
3.5. Haplotype network of <i>N. margaritacea</i> COI data	6

Chapter 4

4.1. Mitotype network of <i>N. margaritacea</i> COI data	129
4.2. A Bayesian analysis tree based on COI using outgroup taxa as in	
Hoeh et al., (2002)	130
4.3. Bayesian analysis tree based on Cytochrome C oxidase subunit I	
for the Unionoidea and Trigonioidea taxa	131

4.4. A maximum parsimony consensus tree based on 16S rDNA gene	
for Palaeoheterodonta bivalve taxa	
4.5. The origin of DUI	133

Chapter 5

5.1. Diagrammatic representation of oogenesis in <i>Neotrigonia margaritacea</i>	155
5.2. Scanning electron microscopy of gonad tissue	156
5.3. Light microscopy images showing different ovogenesis stages	157
5.4. A portion of the <i>Neotrigonia margaritacea</i> ovary	158
5.5. Transmission electron microscopy images of protogonia and oogonia	159
5.6. Transmission electron microscopy images of previtellogenic, vitellogenic	
and postvitellogenic oocyts	160
5.7. Transmission electron microscopy images of <i>Neotrigonia margaritacea</i>	161
5.8. Temporal variation in <i>N. margaritacea</i> reproductive status over the	
summer months.	162

Chapter 6

6.1. Flow diagram showing a series of decisions and actions involved in	
the conservation assessment process	180
6.2. Flow diagram showing the conservation assessment process for	
Neotrigonia margaritacea in Port Stanvac	181

Appendix 1

1.1. Dredge used for benthic	sampling	
------------------------------	----------	--

Appendix 2

2.1. Compiled results from the Australian connectivity interface	189
---	-----

Appendix 3

3.1. A MP consensus tree based on Cytochrome C Oxidase subunit I using	
outgroup taxa as in Hoeh et al.(2002)	.190
3.2. Bayesian analysis tree based on Cytochrome C Oxidase subunit I	
with outgroup taxa as in Hoeh et al. (2002)	191

3.3. A MP consensus tree based on Cytochrome C oxidase subunit I, RY coded	
and less distant outgroups were used during analysis	192
3.4. A MP consensus tree based on Cytochrome C Oxidase subunit I using	
outgroup taxa as in Hoeh et al., 2002. MP jackknife > 85 values are shown	193
3.5. A MP consensus tree based on Cytochrome C oxidase subunit I for the	
Unionoidae and Trigonioidae taxa, RY coded during analysis	194
3.6. Bayesian analysis tree based on Cytochrome C Oxidase subunit I for the	
Unionoidae and Trigonioidae using less distant outgroup taxa1	195
3.7. A MP consensus tree based on Cytochrome C Oxidase subunit I using	
less distant outgroup taxa. MP jackknife > 85 values are shown	196
3.8. A MP consensus tree based on Cytochrome C Oxidase subunit with less	
distant outgroups and RY coded. MP jackknife > 85 values are shown	197
3.9. Bayesian analysis tree based on 16S RNA	198
3.10. A MP consensus tree based on 16S RNA	199

Appendix 4

Declaration

I certify that this thesis does not incorporate without acknowledgment any material previously submitted for a degree or diploma in any university; and that to the best of my knowledge and belief it does not contain any material previously published or written by another person except where due reference is made in the text.

> ~ Ana Glavinic June, 2010

Acknowledgments

Foremost I would like to thank my supervisors Prof. Greg Rouse, Dr Kirsten Benkendorff, and Prof. Peter Fairweather, for exceptional academic mentoring, guidance and enthusiasm. Thank you Kirsten, for quick turnaround time with drafts, scientific freedom, laboratory space and tremendous amount of support. I am extremely grateful to Greg and Nerida, to sum it up simply, without your support this thesis would have never taken shape. Peter thank you for jumping in at the deep end, your support and encouragement have helped me cross the finish line.

Over the years many people have assisted me either in the field or the laboratory. I would like to formally express my gratitude to Lauren Helgen, Patrick Laffy, Lyndlee Easton, Elena Kupriyanova, Chantell Westly, Joy Frances-Hayes, Peter Costello, and Joseph Bain. I am very thankful to Nerida Wilson and Elena Kupriyanova who unselfishly gave constructive advice for Chapter 3 and 4, and Patrick and Chantell for their feedback for Chapter 5. Thank you Darko Bogdanovic for teaching me tricks of Adobe Illustrator. Thanks to the helpful staff at South Australian Museum, Australian Centre for Evolutionary Biology and Biodiversity and Adelaide Microscopy Centre. Thanks to the Ngerin crew.

I had a lot of emotional support from my friends and without their friendship the PhD duration would have been unbearable; thanks to Aida and Neda for being the best friends one could have. Also thank you to all my friends and family overseas, who repeatedly expressed interest in what I was doing and through that showed support and ensured my sense of belonging. I am indebted to: Melanie Sulda, Melissa Gregory, Patrick Laffy, Chevaun Smith, Alexis Young and all others from 3rd floor for listening to my lunch time moans. Collectively to room 039, thank you for putting up with me through my grumpiest states.

My patient and supportive family deserves a big thank you, especially to my parents Filip and Ljiljana and my grandparents Katica and Damjan who with their combined effort and love have made me in to the person I am today. Thank you to my lovely Jo, encouraging Ivana and Brendan and my little rays of sunshine Mia and Oliver. Jo-thank you for everything that makes our life together the way it is. Ivanamost of all thank you for never backing off and always cheering me on to achieve what I never conceived possible. This research would not have been feasible without generous founding from: Australian Biological Resources Study (ABRS), Mark Mitchell Foundation, Nature SA Foundation, Linnean Society, Waterhouse Club, PADI and Flinders University.

Preface

This is a resubmission of a thesis, which was examined by two anonymous examiners and subsequently read by two advisors chosen by the Faculty. The Faculty permitted limited time for this revision. I have now addressed all of the comments made by examiners, and also acknowledge the helpful advice and suggestions made by advisors. This version of a thesis is a significant improvement upon the original.

This thesis comprises a series of manuscripts dealing with separate parts of the research project. This format is not typical of a traditional thesis, so there are some differences that need to be recognised beforehand. Firstly the tables and figures are not embedded within the text but are found at the end of each manuscript. Secondly, separate reference lists are provided at the end of each chapter. Finally some sections of the thesis can be repetitive at times because each chapter is meant to stand alone and thus can be read independently of the rest of the thesis. I apologise in advance for the repetition.

I wrote all of the chapters, however, other authors have been included for the purpose of publication and to acknowledge here their contribution to each of the separate pieces of work. The following table indicates the contribution of these co-authors to the piece of work:

Chapter	Concept	Method	Data analysis	Manuscript preparation
Ι	AG	AG	AG	AG/KB/PF
II	AG	AG/GR	AG	AG/GR/KB
III	AG	AG/GR	AG/GR	AG/NW/KB
IV	AG	AG/NW/GR	AG/NW/GR	AG/NW/GR
V	AG	AG/GR/ KB	AG/GR/ KB	AG/GR/ KB
VI	AG	AG	AG	AG/KB/PF

Contribution of authors to manuscripts in the thesis:

Where AG=Ana Glavinic, KB= Kirsten Benkendorff*, GR= Greg Rouse*, NW= Nerida Wilson[@] and PF= Peter Fairweather*. * = co-supervisors, @ = a collaborator of Prof. Rouse

Glossary

This glossary contains less common biological terms, but also common terms, which are used throughout the thesis to interpret a particular function or a morphological character.

acinus – singular Acini- a small saclike dilatation in ovaries containing eggs

- **acrosome** A caplike structure at the anterior end of a spermatozoon that produces enzymes aiding in egg penetration.
- **ciliary tracts** the respiratory tract that sweep in unison and help to sweep away fluids and particles.
- ctenidia A gill like structure, a respiratory apparatus of a mollusc.
- **denticulated** Finely toothed or notched, its use in the thesis is to describe the shell margin.

dissoconch – juvenile bivalve shell

- eucheton- a small area on the shell near the umbo in the shape of the shield or a key hole like eucheton.
- **median carinae** Median carinae is a prominent feature on *Trigonia* and *Eotrigonia* specimens and it separates flank with radial ribs away from an area with parallel costae. In case of *Neotrigonia* this line is not as obvious, but it is present separating area from the flank.

metamorphic line- a shell feature delimitating prodissoconch from dissoconch

micropyle - a very small opening in the vitelline layer of an oocyte

- **oogonia** A cell that arises from a primordial germ cell (protogonia) and differentiates into an oocyte in the ovary.
- **palps** an elongated, often segmented appendage usually found near the mouth in invertebrate organisms such as molluscs.

prodissoconch – prejuvenile bivalve shell.

protogonia- a primordial germ cell of an oocyte.

- **spinous** pertaining to or like a spine, in the thesis it is used to describe shell rib ornamentation.
- **synonymisation** the act of identifying two known species to be identical and therefore synonyms.
- vitelogenesis- process of yolk formation in an developing egg.

Abstract

This research investigates the evolution of *Neotrigonia* species (Bivalvia: Palaeoheterodonta), the remaining extant genus of the Trigonioida, a group of bivalves endemic to Australian waters. The intent of this research was to review the current systematics, investigate phylogeny and phylogeography of the genus, and advance scientific knowledge in regard to the presence of doubly uniparental inheritance in *Neotrigonia*, as well as to address some aspects of reproductive strategy and outline the process of oogenesis. The research has resulted in a thesis in manuscript format, where Chapter 1 is a general introduction to the thesis as a whole, Chapters 2-5 inclusive are research manuscripts, and Chapter 6 is a general discussion of the completed research.

In chapter 2, the type material of all of the seven extant, nominal species of Neotrigonia Cossman 1912 are reviewed and illustrated, based on available museum specimens and fresh collections. The type localities and currently-known distributions for each extant species are included. A cladistic analysis was performed using morphological characters of Neotrigonia species living and fossil, using Eotrigonia subundulata and Trigonia miriana as an outgroup. Results from parsimony analysis show that all Neotrigonia form a monophyletic clade, in which living and fossil *Neotrigonia* form reciprocally monophyletic sub-groups. The species status of Neotrigonia bednalli, Verco 1907, is revised based on examination of all available types, museum specimens and a relatively large number of newly-collected specimens from southern Australian waters. This assessment suggests that N. bednalli is a junior synonym of N. margaritacea. Species status is accepted for N. gemma, N. lamarckii, N. uniophora, N. strangei and N. kaiyomaruae. However, reclassification of N. strangei specimens from Western Australia to N. margaritacea would revise the previously disjunct distribution of this species to a narrower range in NSW. This chapter demonstrates the limitations in relying on shell morphology only for species classification in the Neotrigonia.

The contemporary knowledge of ocean currents, temperatures, and geological and climatic history across southern Australian waters represents a useful framework for phylogeographical analyses. There are already a number of studies that show coincident distribution patterns within some marine invertebrate groups across the Maugean, Flindersian and Peronian marine provinces. In Chapter 3, I examine the genetic structure of *Neotrigonia margaritacea* and *Neotrigonia lamarckii*.

Phylogenetic analyses based on COI and ITS gene sequence data reveals a split between southern Australian *Neotrigonia margaritacea* and eastern Queensland *Neotrigonia lamarckii*. The molecular analyses confirmed my synonymisation of *N*. *bednalli* to *N. margaritacea*. Population genetic analyses of the *Neotrigonia margaritacea* COI gene, in four different populations located hundreds of kilometres apart, revealed insight into genealogical pathways amongst haplotypes. These networks showed that there was no shared haplotypes among populations and most populations were significantly far from panmixia. The highest haplotype diversity was recorded from the Port Lincoln (South Australia) population. Haplotype variations across the range are discussed in terms of estimated population sizes and geographical barriers.

Several species of bivalves have been reported to have two mitochondrial DNA types, maternal and paternal. This system of mtDNA inheritance is known as doubly uniparental inheritance (DUI). In Chapter 4, the presence of the DUI phenomenon in *Neotrigonia margaritacea* is investigated within a phylogenetic framework for Paleoheterodonta, using COI and 16S rDNA molecular data. Results indicate the presence of DUI in *Neotrigonia margaritacea* and provide evidence for a masculinization event within this taxon. This phenomenon has so far been identified in six superfamilies of bivalves, so the new record of DUI in *N. margaritacea* was incorporated into a phylogenetic tree addressing the question of a single or multiple origins of DUI in Bivalvia. Parsimony transformations indicate that DUI is likely to be the ancestral state for all Bivalvia.

In Chapter 5, the ultrastructural stages of female gametogenesis are described for *Neotrigonia margaritacea*. The morphology of oocytes and gonad tissue are described for the first time using electron microscopy and histology techniques. Throughout the summer period, the ovary contains oocytes in various developmental stages. Oocytes develop from oogonia derived from protogonia and then undergo three distinct stages of oogenesis: previtellogenesis; vitellogenesis; and postvitellogenesis (or presence of mature oocytes). Based on gonad tissue and oocyte morphology, and as well as laboratory observations, it is inferred that *Neotrigonia margaritacea* is sequentially tachitictic, thus a trickle (continuous) spawner over an extended summer season.

In conclusion the museum collections of *Neotrigonia* and current systematics have provided valuable information on classification and distribution of this relic bivalve genus. Morphological analysis has enabled preliminary synonymisation of species to establish species distributions. The results from molecular data confirmed aspects of phylogeny and revealed phylogeographic structure of *Neotrigonia margaritacea* in Southern Australian waters. The new molecular information regarding the presence of DUI and novel insight into reproductive strategies further our understanding of the evolutionary affinities of *Neotrigonia*. Based on the integration of these multidisciplinary results conservation assessment is suggested for *Neotrigonia margaritacea*.