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The History and Relationships of Northern Platypus
(*Ornithorhynchus anatinus*) Populations
A Molecular Approach

by

Stephen H Kolomyjec

B.A., Olivet College, 2005

Grad. Dip. Research Methods, James Cook University, 2006

A Thesis submitted to
James Cook University
School of Marine and Tropical Biology
in fulfilment of the degree of
Doctor of Philosophy
in the discipline of Zoology and Tropical Ecology

October 2010

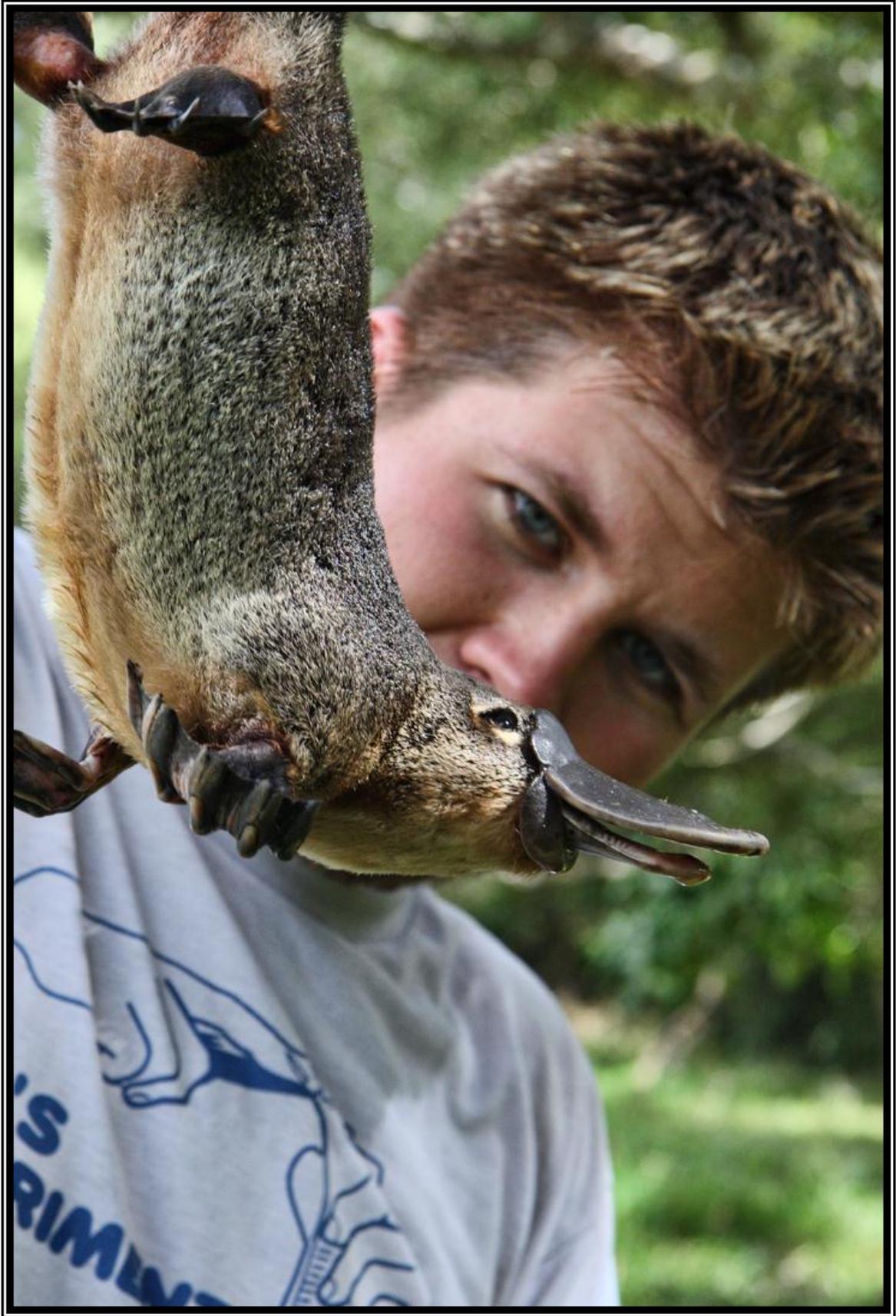


Photo: J Davis

Frontispiece: *Ornithorhynchus anatinus*

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**STATEMENT OF SOURCES
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DECLARATION OF ETHICS**

I declare that this thesis is my own work and has not been submitted in any form for another degree or diploma at any university or other institution of tertiary education. Information derived from the published or unpublished work of others has been acknowledged in the text and a list of references is given.

I also declare that all research procedures reported in the thesis complied with the guidelines of and was approved by the Animal Ethics Committee of James Cook University under Ethics Approval No. A1222. A copy of the original ethics approval and other regulatory permits can be found in appendix 1.

Stephen H Kolomyjec

6/16/2010
Date

STATEMENT OF CO-AUTHORSHIP

The research that went in to the production of this thesis has resulted in several publications and as such has collaboratively involved other individuals in various capacities. While the bulk of the work is the author's, it is important to recognise the input of the co-authors. The publications produced as part of this thesis are as follows:

Kolomyjec SH, Parsons JG, VanDerWal J, and Johnson CN. (in prep) Climate and the platypus (*Ornithorhynchus anatinus*). *Journal of Mammalogy*.

Kolomyjec SH, Grant TR, and Blair, D. 2008. Ten polymorphic microsatellite DNA markers for the platypus, *Ornithorhynchus anatinus*. *Molecular Ecology Resources*, **8**, 1133 – 1135.

Kolomyjec SH, Chong JYT, Blair D, Gongora J, Grant TR, Johnson CN, and Moran C. 2009. Population genetics of the platypus (*Ornithorhynchus anatinus*): a fine scale look at adjacent river systems. *Australian Journal of Zoology*, **57**, 225-334.

Kolomyjec SH, Grant TR, Johnson CN, and Blair D. (in review). Restriction of gene flow in the platypus (*Ornithorhynchus anatinus*) due to a large dam. *Australian Mammalogy*.

Kolomyjec SH, Grant TR, Johnson CN, and Blair D. (In prep) Regional population structuring and conservation units in the platypus (*Ornithorhynchus anatinus*). *Journal of Mammalogy*.

The people and institutions listed below have contributed to the research and publication that have lead to this thesis:

David Blair (James Cook University) and **Christopher N Johnson** (James Cook University) as the author's PhD supervisors have assisted with all aspects of the PhD. This includes: initial project planning, field design, grant writing and funding, and the preparation of publishable manuscripts.

Tom R Grant (University of New South Wales) provided invaluable training on the capture and handling of platypuses in the wild, personally collected samples for analysis and assistance in the preparation of publishable manuscripts.

Jennifer G Parson (James Cook University) and **Jeremy VanDerWal** (James Cook University) have provided conceptual and technical support with climate and distribution modelling.

Josephine Y T Chong (University of Sydney) in a collaborative effort and a part of her Honours degree extracted and genotyped some of Tom R Grant's samples for inclusion in the author's analyses. **Jaime Gongora** (University of Sydney) and **Christopher Moran** (University of Sydney) provided Josephine with supervisory support and provided the author with editorial assistance in the preparation of a publishable manuscript.

We, the undersigned, agree with the above statement of contribution and co-authorship for each of the above published (or submitted) peer-reviewed manuscripts contained within this thesis:

David Blair
(Candidate's Primary supervisor)

Mike Kingsford
(Head of School)

Acknowledgements

There are many people that I would like to thank for their help and support along the journey that has been my PhD.

Supervision

My project supervisors Christopher Johnson and David Blair have provided invaluable support on so many levels. From project planning to funding to publication, as well as advice both professional and personal, my degree would not have been possible without them.

Funding

Support from the following external funding bodies has made this project a success: the National Geographic Society (USA), the Winifred Violet Scott Foundation (Australia), and the Skyrail Foundation (Australia). Internal funding from James Cook University in the form of the Graduate Research Scheme grant and Internal Research Allocation (IRA) funds have also helped greatly along the way.

Fieldwork

Without the help of so many eager volunteers and generous land owners the intensive field component of my research would have been impossible. In particular, I would like to thank Bree Clouten, Jenifer Davis, Duncan Jardine, and Kate Stookey for the repeated field trips that they helped me with. John McKenna, Brian Furber, Barry Grogan and Mike Sheehy as land owners, always made me feel welcome during my research. Also of huge help in finding study sites were Alastair Freeman, Alan Gillanders, and Ross McLennan. Their keen interest in my project and extensive local knowledge proved invaluable.

Vital interstate samples were provided from New South Wales by Dr. Tom R Grant (University of New South Wales), from Victoria by Dr. Kath Handasyde (University of Melbourne) and from Tasmania by Rachelle Olsson Herrin (University of Tasmania).

I should also thank the Queensland Government (the Environmental Protection Agency and the Department of Primary Industry and Fishing) for granting the permits needed for the project.

Institutional

James Cook University also provided valuable institutional support by providing office space (Mammal Ecology Lab), lab space (MEEL; Molecular Ecology and Evolution Lab), analytical services (Ainsley Calladine and the GAF; Genetic Analysis Facility) and vehicles (Julie Fedorniak). I would also like to thank James Cook University and the Graduate Research School for awarding me with the JCU Co-Funded Research Scholarship which has made life a heck of a lot simpler it was before hand.

In addition, I would like to thank Stewart Nichol and the University of Tasmania for providing me with the office space and resources I have needed while writing this thesis.

Special Thanks

I would like to offer a particularly special thank you to Tom R Grant, who trained me in the capture and handling of platypuses, has answered my endless and often random questions, and has provided insight that only someone that has dedicated their life to the study of the platypus could do.

Abstract

The Aim of this study was to understand the distribution and genetic structure of platypus populations in Australia, and in particular to investigate the interactions of distribution and genetic structure. The research considered the entire distributional range of the platypus, but with a special focus on the scientifically neglected platypus populations of northern Queensland. Platypuses in north Queensland are smaller than their southern counterparts and have a more reddish colouration. There appears also to be a break in the distribution of the platypus between about Mackay and Townsville, which corresponds to the catchment of the Burdekin River and which geographically separates northern platypuses from southern populations. The relationship of northern and southern platypus populations of mainland Australia, together with the biogeographic significance to the platypus of the Burdekin break, was a binding thread throughout the study. However, before that relationship could be inferred there were several smaller gaps in the knowledge regarding the distribution of platypus that had to be filled. These gaps were represented by several intriguing questions: Where do platypuses occur and why is their distribution limited to those areas? And, how are local populations of platypuses structured and how do they relate to each other? With these key pieces of information it was possible to expand the scope of the study to a distribution-wide level.

Using distribution modelling software (MaxEnt), climate data and 4,315 occurrence records, I produced a climate-based distribution model to describe the current distribution of the platypus. The two most important climate factors determining environmental suitability for the platypus were precipitation during the driest quarter (which was positively associated with platypus occurrence) and maximum temperature (negatively associated), to the near exclusion of all other variables (53.8% and 41.2% contributions respectively). This distribution map supported the existence of a significant distribution break occurring in northern Queensland. Separate modelling of the northern and southern distributions revealed differences in the limiting factors in each part of the range. To the south, precipitation during the driest quarter and maximum temperature remained the two most important factors (76.2% and 18.9%

contribution respectively). However, in the north additional environmental factors were important. These were temperature seasonality, precipitation during wettest quarter, minimum temperature, and precipitation seasonality, with respective contributions to habitat suitability of 34.7%, 22.6%, 19.2%, 16.7% and 3.5%.

The initial species distribution model was projected onto palaeo-climate data representing the last glacial maximum (c. 22,000 years before present). This palaeo-model indicated that overall conditions were less favourable for the platypus at that time, and that the gap between the northern and southern portions of the distribution would have been even more pronounced, although there may have been connectivity between Tasmania and the mainland via the Bass land bridge. The platypus distribution was also projected forward to predict the effects of anthropogenic climate change. An aggregated mean across the complex models involved in this suggested a likely decline in range of approximately 15% by the year 2070 with best/worst case scenarios depicting an increase of 3.5% or a decrease of 65% respectively. The areas affected by these distributional changes were the marginal fringes surrounding the main areas of distribution.

After developing a reliable set of 12 microsatellite DNA markers for the study it was possible to investigate population structure and dynamics from a molecular perspective. At the finer scale of investigation (comparisons within and between adjacent river systems), I showed that despite individual sample sites within a river systems having some genetic differentiation, they generally exhibited a strong isolation-by-distance pattern within the system (e.g. Hawkesbury-Nepean system: $r = 0.7315$, $p = 0.02$). Moreover, significant differentiation between systems as suggested by pairwise F_{st} , AMOVA and Bayesian population clustering techniques indicates that the physical separation of river basins does limit gene flow and is responsible for local population structuring. The detection of several first generation migrants (13 of 120 samples) also provided a genetic indication that platypuses must move between river basins, which would require overland movement to occur more often than previously thought. I also showed that a large dam inhibited within-river gene flow and could lead to increased differentiation between populations: the construction of the Nepean Dam has lead to higher

differentiation occurring within a single river (above vs. below dam pairwise $F_{st} = 0.07681$) then occurring between two rivers at three times the distance and requiring an overland crossing (Wingecarribee River vs. Nepean River pairwise $F_{st} = 0.05978$).

Genetic analysis across the entire platypus distribution revealed three evolutionarily significant units within the platypus distribution that are in strong consensus with the observations gathered from the distribution modelling. These represent the isolated Northern Region, the Southern Mainland Region, and Tasmania. Within these evolutionarily significant units six discrete population clusters were identified, which formed the basis of five proposed management units for the platypus (two clusters were combined due to the presence of active gene flow). Attempts to investigate population sub-clusters within these clusters were futile as genetic admixture between local river systems rendered their level of distinctiveness below that of discrete conservation units. Future conservation and management planners will have to keep in mind that not all platypuses are created equal; there are distinct groups that must be considered independently in order to maintain the genotypic and phenotypic features that currently exist across the species.

Table of Contents

STATEMENT OF ACCESS.....	III
STATEMENT OF SOURCES AND DECLARATION OF ETHICS.....	IV
STATEMENT OF CO-AUTHORSHIP	V
ACKNOWLEDGEMENTS	VII
ABSTRACT	IX
TABLE OF CONTENTS	XII
LIST OF TABLES.....	XIV
LIST OF FIGURES.....	XV
LIST OF PLATES.....	XVI
SECTION 1 – BACKGROUND.....	1
CHAPTER 1 – GENERAL INTRODUCTION	2
<i>The platypus</i>	2
Distribution.....	2
Home ranges and dispersal	4
Taxonomic history of the platypus	5
Evolutionarily Significant Units and Management Units	6
Threats and challenges.....	7
<i>Beyond the platypus</i>	8
<i>Aims of the study</i>	8
<i>Scientific questions</i>	9
<i>Thesis presentation</i>	9
<i>References</i>	10
SECTION 2 – HISTORY.....	13
CHAPTER 2 – CLIMATE AND THE PLATYPUS	14
<i>Abstract</i>	15
<i>Introduction</i>	16
<i>Materials and Methods</i>	18
Location data	18
Bioclimatic Modelling.....	19
Present.....	19
Past distribution.....	20
Future	20
<i>Results</i>	21
Present.....	21
Last Glacial Maximum	23
Effects of future climate change	24
<i>Discussion</i>	25
<i>Acknowledgements</i>	29
<i>References</i>	29
SECTION 3 – RELATIONSHIPS	35
CHAPTER 3 – MICROSATELLITE DNA MARKER DEVELOPMENT	36
<i>Abstract</i>	37
<i>Primer Note</i>	38
<i>Acknowledgements</i>	41
<i>References</i>	41
CHAPTER 4 – POPULATIONS AND RIVER SYSTEMS	43
<i>Abstract</i>	44
<i>Introduction</i>	45
<i>Methods</i>	47
Study Area.....	47
Sampling and Genotyping	48

Genetic diversity and data quality	49
Population structure and gene flow	49
<i>Results</i>	51
Genetic diversity and data quality	51
Population structure and gene flow	54
<i>Discussion</i>	57
<i>Conclusion</i>	60
<i>Acknowledgements</i>	61
<i>References</i>	61
CHAPTER 5 – ANTHROPOGENIC BARRIERS	68
<i>Abstract</i>	69
<i>Methods</i>	71
Sampling and genotyping	71
Population differentiation	73
<i>Results</i>	73
Patterns of allelic diversity	73
Population differentiation	73
<i>Discussion</i>	74
<i>Acknowledgements</i>	77
<i>References</i>	77
CHAPTER 6 – RELATIONSHIP OF POPULATIONS AT THE DISTRIBUTION SCALE.....	81
<i>Methods</i>	85
Sampling and genotyping	85
Population clustering and differentiation.....	86
<i>Results</i>	88
Population Clusters.....	88
Population differentiation	90
<i>Discussion</i>	91
Regions as evolutionarily significant units	91
Clusters and management units	92
<i>Acknowledgements</i>	95
<i>References</i>	96
SECTION 4 – CONCLUSIONS.....	101
CHAPTER 7 – CONCLUSION.....	102
<i>Overview</i>	102
<i>History</i>	102
<i>Relationships</i>	103
<i>Future studies and applicability to other species</i>	104
<i>References</i>	105
COMPLETE BIBLIOGRAPHY	107
APPENDIX	119
APPENDIX 1 – PERMITS	120
APPENDIX 2 – DATA SHEETS	130
APPENDIX 3 – RAW DATA	131

List of Tables

Table 2.1	Climatic constraints on platypus habitat across Australia.	22
Table 2.2	Climatic constraints on platypus habitat based on region.	23
Table 2.3	Predicted distributional changes due to climate change.	24
Table 3.1	Microsatellite loci from <i>Ornithorhynchus anatinus</i> .	40
Table 3.2	Details of reagent mixtures A-E concentrations for 15 µl PCR reactions.	41
Table 4.1	Additional microsatellite loci from <i>Ornithorhynchus anatinus</i> .	49
Table 4.2	Detailed population genetics data.	51
Table 4.3	Genotypic Linkage disequilibrium p-values.	53
Table 4.4	Pairwise F_{st} values at microsatellite loci among sample sites.	53
Table 4.5	Private and shared alleles.	54
Table 4.6	Analysis of Molecular Variance.	55
Table 5.1	Population differentiation.	74
Table 6.1	Pairwise F_{st} values.	91
Table 6.2	Proposed management units for the platypus.	94

List of Figures

Figure 2.1	Sightings based occurrence records of the platypus across Australia.	18
Figure 2.2	Present day distribution of the platypus.	21
Figure 2.3	North and South regions modelled separately.	23
Figure 2.4	Distribution of the platypus during the Last Glacial Maximum .	24
Figure 4.1	Location of sample sites used in this study.	48
Figure 4.2	Assignment plot.	56
Figure 4.3	Structure results.	57
Figure 5.1.	Location and detailed view of the Nepean Dam and sample sites.	72
Figure 6.1	Species distribution model for <i>O. anatinus</i> .	84
Figure 6.2	Sampled river basins and localities.	86
Figure 6.3	The relationships of detected Regions and population clusters.	89
Figure 6.4	Map of relative gene flow.	90

List of Plates

Plate 1 Close-up of platypus	1
Plate 2 Release of platypus	13
Plate 3 Demonstration of regional size difference	35
Plate 4 Platypus returning to water	101
Plate 5 Collecting morphometric data	119