MITOCHONDRIAL DNA ANALYSIS
OF THE
EVOLUTION AND GENETIC DIVERSITY OF
ANCIENT AND EXTINCT BEARS

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THESIS DECLARATION

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Mitochondrial phylogeographic analyses of modern populations can be used to make inferences about the impacts of the last glacial maximum (LGM) and anthropogenic disruption on late Pleistocene and Holocene ancestral populations. However, it is becoming more and more evident that ancient DNA studies greatly augment traditional mtDNA studies based only on extant lineages, and can reveal more complex scenarios than those hypothesised from modern data alone.

Ancient DNA studies allow us to trace historic and ancient gene flow through time, giving a dynamic temporal and geographic understanding of genetic diversity. This is particularly informative when molecular data can be coupled with environmental or chronological information (such as radiocarbon dated specimens) allowing links to be made between climatic or anthropogenic disruptions and the genetic response of populations or species.

This PhD research used ancient DNA techniques to investigate a number of biogeographic scenarios in relation to the phylogeography of brown bears (*Ursus arctos*) in Europe (Chapter 2-4) and across the Eurasian continent (Chapter 5) throughout the Late Pleistocene and Holocene periods. Similarly, a study of the genetic diversity and phylogeography of the extinct giant short-faced bear (*Arctodus simus*) in North America was undertaken (Chapter 6) to provide a comparison with the dynamic phylogeographic history of contemporaneous Beringian brown bears (Barnes *et al.*, 2002). Additionally, the deeper evolutionary history of the extinct Tremarctine bears was investigated using a molecular approach (Chapter 7) in an attempt to clarify the phylogenetic relationships of this lineage which have remained unresolved by morphological analyses.

The research presented in this PhD thesis reinforces the important role that ancient DNA can play in understanding the mtDNA population dynamics and movements of taxa in response to environmental or anthropogenic changes through time. It stresses once again that the use of modern data alone is likely to lead to over-simplified or inaccurate views of past evolutionary history. Ancient DNA studies such as those presented here allow us to develop a more complex understanding of Quaternary phylogeographic patterns in a small number of taxa for which a sufficient number of samples can be obtained, and may guide future research to determine if similar patterns exist for other less-well studied species.

Figure 1.1: A map showing the geographical distribution of the ancient DNA samples used in the study. The map highlights areas where the samples were collected, including coastal regions and inland locations. The data was obtained from multiple sources, including archaeological sites, ancient caves, and ancient environments.
out, and for putting up with my endless New Zealand jokes! Trevor Worthy and Jenny Jones – thanks for everything - it was lovely getting to know you both and I hope you’ll be back in Adelaide before too long. Thanks also to some of the ex-ACADers who didn’t stay for long but did make my PhD more enjoyable while they were around – Dean Male and Laura Watson. There were also many wonderful visitors to ACAD over the years: Sanne Boessenkool – I remember celebrating Sinterklaas in Adelaide, and the picnic lunches watching the black swans by the river. Renae Pratt – all the fun times at the Evolution conference in Christchurch with you and the Massey group, and for helping co-ordinate those monthly teleconferences!

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# TABLE OF CONTENTS

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Thesis declaration</td>
<td>i</td>
</tr>
<tr>
<td>Thesis abstract</td>
<td>ii</td>
</tr>
<tr>
<td>Acknowledgements</td>
<td>iii</td>
</tr>
<tr>
<td>Table of contents</td>
<td>v</td>
</tr>
<tr>
<td>List of figures</td>
<td>xiii</td>
</tr>
<tr>
<td>List of tables</td>
<td>xv</td>
</tr>
</tbody>
</table>

## CHAPTER 1. INTRODUCTION

1.1 THE ROLE OF QUATERNARY CLIMATE FLUCTUATIONS & HUMANS ON GLOBAL BIODIVERSITY

1.2 USING GENETICS TO STUDY THE EFFECTS OF CLIMATE CHANGE & HUMAN IMPACTS IN THE QUATERNARY

1.3 OVERVIEW OF ANCIENT DNA
   1.3.1 Problems and challenges with working on ancient DNA
   1.3.2 Ancient phylogeographic studies

1.4 BEARS
   1.4.1 Genetic diversity and phylogeography of brown bears
   1.4.2 Unresolved issues within the Tremarctine bear lineage

1.5 SCOPE OF THIS THESIS
   1.5.1 Ancient DNA analysis of post-glacial Scandinavian brown bears
   1.5.2 From Iberia to Alaska: ancient DNA links late Pleistocene brown bears across the Holarctic
   1.5.3 Post-glacial phylogeography of European brown bears
   1.5.4 Ancient Eurasian brown bear phylogeography
   1.5.5 Ancient DNA reveals different phylogeographic histories for the extinct New World giant short-faced bear (Arctodus simus) and the brown bear (Ursus arctos)
   1.5.6 Evolutionary relationships of the Tremarctine bears
   1.5.7 Conclusions

1.6 REFERENCES
Statement of authorship for Chapter 2 .................................................................24

CHAPTER 2. ANCIENT DNA ANALYSIS OF POST-GLACIAL SCANDINAVIAN
BROWN BEARS 27

2.1 ABSTRACT 27

2.2 INTRODUCTION 27

2.3 MATERIALS & METHODS 28

2.3.1 Samples 28

2.3.2 Ancient DNA Extractions 28

2.3.3 PCR Amplifications 29

2.3.4 Verification/Validation of aDNA results 29

2.3.5 Phylogenetic Analysis 30

2.4 RESULTS 30

2.5 DISCUSSION 34

2.6 ACKNOWLEDGEMENTS 36

2.7 REFERENCES 36

Statement of authorship for Chapter 3 40

CHAPTER 3. FROM IBERIA TO ALASKA: ANCIENT DNA LINKS LATE
PLEISTOCENE BROWN BEARS ACROSS THE Holarctic 44

3.1 SUMMARY 44

3.2 RESULTS AND DISCUSSION 44

3.3 EXPERIMENTAL PROCEDURES 47

3.4 ACKNOWLEDGEMENTS 47

3.5 REFERENCES 48
5.3.1 Mitochondrial DNA diversity in Eurasia 76
5.3.2 Temporal and geographic distribution of mtDNA diversity 76
5.3.3 Independent DNA replications 87
5.3.4 Radiocarbon dating results 87
5.3.5 Sequence alignment & phylogenetic analysis 87

5.4 DISCUSSION 89
5.4.1 Spatial and temporal distribution of Clade 3a 89
5.4.2 Spatial and temporal distribution of Clade 3b 91
5.4.3 Detection of Clade 4 in Continental Eurasia 93
5.4.4 Addressing the predictions based on the conclusions of Korsten et al. (2009) 95

5.5 CONCLUSIONS 95
5.5.1 Future directions 97

5.6 ACKNOWLEDGEMENTS 97

5.7 REFERENCES 98

CHAPTER 6. ANCIENT DNA REVEALS DIFFERENT PHYLOGEOGRAPHIC HISTORIES FOR THE EXTINCT NEW WORLD GIANT SHORT-FACED BEAR (Arctodus simus) AND THE BROWN BEAR (Ursus arctos) 100

6.1 INTRODUCTION 100

6.2 MATERIALS & METHODS 101
6.2.1 Samples 101
6.2.2 Ancient DNA extractions 101
6.2.3 PCR amplifications 102
6.2.4 Validation of aDNA results 102
6.2.5 Phylogenetic analyses 103
6.2.6 Statistical genetic measures 103

6.3 RESULTS 104

6.4 DISCUSSION 111
CHAPTER 7. EVOLUTIONARY RELATIONSHIPS OF THE TREMARCTINE BEARS

7.1 INTRODUCTION

7.2 MATERIALS & METHODS

7.2.1 Samples

7.2.2 Ancient DNA extractions

7.2.3 Modern DNA extractions

7.2.4 PCR amplifications

7.2.5 Validation of ancient DNA results

7.2.6 Phylogenetic analysis of the evolutionary relationships of the Tremarctine bears

7.2.7 Estimation of divergence dates of the Tremarctine bears

7.2.8 Variation within South American bear species

7.3 RESULTS

7.3.1 Evolutionary relationships of the Tremarctine bears

7.3.2 Divergence estimates

7.4 DISCUSSION

7.4.1 Evolutionary relationships within the Tremarctine bears

7.4.2 Tremarctine bear divergence date estimates

7.4.3 Palaeobiology of Arctotherium tarijense

7.4.4 Genetic variation among A. tarijense individuals

7.4.5 Genetic variation among T. ornatus individuals
CHAPTER 8. GENERAL DISCUSSION

8.1 THESIS SUMMARY

8.1.1 Post-glacial phylogeography of Scandinavian brown bears

8.1.2 From Iberia to Alaska: ancient DNA links late Pleistocene brown bears across the Holarctic

8.1.3 Post-glacial phylogeography of European brown bears

8.1.4 Genetic diversity of ancient Eurasian brown bears

8.1.5 Genetic diversity and phylogeography of the extinct giant short-faced bears

8.1.6 Evolutionary relationships of the extinct Tremarctine bears

8.2 FUTURE DIRECTIONS

8.2.1 Brown bear mitogenomics

8.2.2 Genetic diversity of modern Clade 1 brown bears in Scandinavia

8.2.3 Extending the Eurasian brown bear study

8.2.4 Future directions for the Tremarctine bears

8.3 REFERENCES

CHAPTER 9. BIBLIOGRAPHY

APPENDIX 1. Supporting information for Chapter 2

Appendix Table 1.1. Comprehensive list of all samples analysed in Chapter 2

Appendix Table 1.2. List of previously published samples obtained from GenBank and included in these analyses

Verification/Validation of aDNA results

Appendix Figure 1.1. Maximum Parsimony analysis
Appendix Table 5.4 List of 27 previously published homologous Pleistocene Beringian brown bear control region sequences (135bp) used for genetic diversity calculations displayed in Chapter 6 Table 6.2

Cloning results

Appendix Figure 5.1 Maximum parsimony analysis of 137 bp ATP8 sequences from *Arctodus simus*

APPENDIX 6. Supporting information for Chapter 7

Independent replication results

Appendix Figure 6.1. Maximum Parsimony Analysis

REFERENCES

APPENDIX 7. Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary

LIST OF FIGURES

**Figure 1.1** Post-glacial recolonisation routes postulated for three paradigm taxa based on modern mtDNA phylogeographic structure. 4

**Figure 1.2** Schematic comparison of a modern and a temporal (e.g. ancient DNA) dataset. 6

**Figure 1.3** Distribution of major brown bear mtDNA clades and subclades. 12

**Figure 1.4** Phylogeny of bears based on Bayesian analysis of whole mitochondrial genomes. Figure adapted from Krause et al., 2008 (Appendix 7). 13

**Figure 2.1** Map of Europe showing the location of samples that yielded genetic data. 31

**Figure 2.2** Neighbor-joining phylogeny showing the placement of Holocene Scandinavian sequences in relation to key European brown bear haplogroups. 33

**Figure 2.3** Haplotype network of western European bears (clade 1) based on 193-bp control region mtDNA. 34

**Figure 3.1** Median-joining network of global brown bear mtDNA control region haplotypes 45

**Figure 3.2** Map showing the location of the Asieko 3c individual. 45

**Figure 4.1** Hewitt’s proposed post-glacial recolonisation routes of European brown bear clades based on genetic and fossil evidence. 51

**Figure 4.2** Haplotype network of Western European (Clade 1) brown bears. 60

**Figure 4.3** Frequency distribution of dated Clade 1 brown bear mtDNA sequences. 63

**Figure 4.4** Map of Europe showing the approximate distribution of post-glacial brown bear mtDNA clades. 65

**Figure 4.5** Models for post-glacial brown bear recolonisation of Europe. 66

**Figure 5.1** Approximate current distribution of brown bear haplogroups (extant without circles, extinct with circles) as presented in Korsten et al., (2009). 70

**Figure 5.2** Approximate distribution of ancient and historic Eurasian brown bear samples from which DNA was obtained in this study. 86

**Figure 5.3** Minimum spanning mtDNA Haplotype network for n=61 Eurasian brown bear sequences generated in this study (Panel A) and this study combined with the homologous 135-bp sequences from n=205 additional modern Eurasian sequences reported by Korsten et al. (Panel B). 88
Figure 5.4 Approximate distribution of Haplogroup/Clade 3a samples in this study. 90
Figure 5.5 Approximate distribution of Haplogroup/Clade 3b samples from this study. 92
Figure 5.6 Approximate distribution of Haplogroup/Clade 4 samples in this study. 94
Figure 6.1 Location of *Arctodus simus* samples used in this study. 102
Figure 6.2 Maximum parsimony analysis of *Arctodus simus*. 108
Figure 6.3 Minimum spanning mtDNA haplotype network of *Arctodus simus*. 109
Figure 7.1 Hypothesised phylogeny of the Tremarctine bears based on morphological characteristics. 118
Figure 7.2 Maximum clade probability tree displayed as a chronogram from the BEAST analysis of the unpartitioned 694 bp mtDNA alignment. 126
Figure 7.3 Topology comparison of the bear phylogeny based on whole mitochondrial genome studies (A) Krause *et al.*, 2008 and (B) Yu *et al.*, 2007 and fourteen nuclear genes (C) Pages *et al.*, 2008. 127
Figure 7.4 Five alternative hypotheses for the evolutionary relationships of the Tremarctine bears. 129
Figure 7.5 Map showing approximate distributions of *Tremarctos floridanus, Arctodus simus, Arctotherium sp.* and *Tremarctos ornatus*. 131
# LIST OF TABLES

**Table 1.1** Summary list of authenticity criteria & guidelines applied to the ancient DNA studies presented in this thesis. 8

**Table 1.2** Summary of published brown bear publications (1994-2009) highlighting the number of different studies and variable size and position of mtDNA sequences analyses in each publication. 14

**Table 2.1** Samples analysed. 31

**Table 3.1** Divergence dates of brown bear clades. 46

**Table 4.1** List of new and previously published post-glacial (<18,000 ybp) Clade 1 (Western European lineage) bear sequences included in the analysis. 55

**Table 4.2** Genetic diversity measures for 108 post-glacial western European (Clade 1) brown bears based on 131-bp control region mtDNA sequences. 60

**Table 5.1** Radiocarbon dates and associated isotope data for the bear samples dated as part of this study. 75

**Table 5.2** Haplotype list of Eurasian brown bear sequences generated in this study (haplotypes 1-19) with equivalent haplotypes from Korsten et al. (2009) indicated. 78

**Table 6.1** List of ancient bone samples used in this study from which a minimum of 135-bp Control Region sequence was obtained. 105

**Table 6.2** Genetic diversity measures of late Pleistocene giant short-faced bears and contemporaneous Beringian brown bears. 112

**Table 7.1** South American bear samples extracted for this study. 120

**Table 7.2** Primer sequences, primer combinations, annealing temperatures (Ta) and approximate size of product. 121

**Table 7.3** List of previously published bear mtDNA genome sequences used in this study. 123