

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



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A thesis submitted for the degree of Doctor of Philosophy at the University of Adelaide

September 2010

## THESIS DECLARATION

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# THESIS ABSTRACT

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.

Barnes I, Matheus P, Shapiro B, Jensen D, Cooper A (2002) Dynamics of Pleistocene Population Extinctions in Beringian Brown Bears. *Science* **295**, 2267-2270.

## ACKNOWLEDGMENTS

Firstly I would like to thank my supervisors Dr. Jeremy Austin and Prof. Alan Cooper for giving me the opportunity to undertake my PhD research under their guidance at the Australian Centre for Ancient DNA. It had been a dream of mine to work on an ancient DNA project, and they helped me to make this a reality. Jeremy in particular has been a great supervisor, not only did he provide excellent guidance and support in the lab and in-depth discussions and feedback on my thesis writing, but he also introduced me to the joy of making homebrew beers!

A big thank you also must go to Sue Cathew and Bob Hill, Heads of the School of Earth & Environmental Sciences at the University of Adelaide. If they had not listened to me and been so understanding and encouraging in the first year of my PhD I would not have persevered.

I would like to thank all my research collaborators who sent their precious bear samples to me for analysis, and those who provided samples to Alan's collection over the years. There are so many people who contributed to the sample collection prior to and during my PhD, many of whom I may not be aware of, but without their samples I could not have undertaken this project. These people include but are not limited to: Kjartan & Eivind Østbye, Stein-Erik Lauritzen, Kim Aaris-Sorensen, Ian Barnes, Beth Shapiro, Jacobo Weinstock, Martina Pacher, Doris Nagel, Doris Doeppes, Leopoldo Soibelzon, Fabiana Martin, Flavia Morello, Alfredo Prieto, Pat Wrin, B. Hockett, Pavel Kosintsev, Gregor Larson, Gert Skipper, Rachel Norris, Anthony Wilkes, Brandy Jacobsen, Link Olson, and Gordon Jarrell. I would also like to thank Ludovic Orlando, Catherine Hanni, Cristina Valdiosera, Ian Barnes, Beth Shapiro and Jacobo Weinstock for performing independent validations of ancient DNA extractions, PCR amplifications and/or cloning of samples analysed as part of my research project.

I would like to acknowledge the travel funding I received from the Russell Baudinette PhD Travel Scholarship which helped to allow me to travel to and present my preliminary PhD research results at the international Evolution conference in Christchurch in 2007. I will never forget the experience of presenting my PhD research for the first time at such a prestigious scientific meeting, or the many friendships that arose from attending that conference.

I would also like to thank all my friends and colleagues in the Darling Building from the Australian Centre for Ancient DNA, the School of Earth & Environmental Sciences and EBU lab at the South Australian Museum. I can't mention everyone by name, but there are a few people who stand out and I would specifically like to acknowledge. Aaron Camens – I couldn't have asked for a better desk buddy in our crowded PhD office – I have so many great memories – the CAVEPS conference trip via the Great Ocean Road, all the good times at the Central Markets on Friday nights, the crazy toy critter collection on your desk and the jelly-bean polar bear just to name a few. Thanks also for lugging the cases of bear/beer from the supermarket to our weekly journal club for me, and for trying to teach me to develop a better taste in beers (sorry Aaron I'm still drinking Cascade lights – got to love a beer with an extinct animal on the label). Nic Rawlence, thanks for being there and always willing to help

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!

I'd like to thank my colleagues and supervisors in my current lab group at the Basil Hetzel Institute – especially Richard D'Andrea and Carolyn Butcher, for all their flexibility and understanding while I've been finishing writing up my thesis.

I would like to thank my family in Sydney: my parents Andrew & Vicky and my brother Chris, for all their support and encouragement throughout the ups and downs of my PhD. It was a pretty big step moving to Adelaide away from you, and I really appreciate all the love and support you have given me from so far away.

Last but not least – I'd like to thank Jason Pengilly for all his love and support over the last two years. I wouldn't have met you if I hadn't come to Adelaide to start my PhD and I don't think I could have finished it without your support. Thanks for being there, making me happy and keeping me (in)sane.

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