# What (molecular) time is it?

## Using ancient DNA to date evolutionary events

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

April 2012

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#### **Abstract**

This work aims to explore the use of genetic sequences sampled serially through time (heterochronous data), to infer the timescale of past evolutionary events. Such data can be generated from preserved sub-fossil or fossil organismal remains (like mummified tissues, fossilized bones or coprolites), and then used to observe genetic modifications in real-time. Most importantly, the dates of the samples provide firm temporal tie points for their genetic sequences, and can be used to calibrate phylogenetic reconstructions.

This thesis presents several case studies where ancient DNA was used to re-calibrate evolutionary timescales. In every situation, the use of heterochronous data led to elevated molecular rate estimates, resulting in the reconstruction of younger timescales, as compared to estimates based on fossil calibrations. These observations are in agreement with the recent demonstration that molecular rates vary according to the time period over which they are calculated.

This work shows that, ancient DNA offers crucial temporal information to reliably estimate the timescale of recent population evolution, and is generally the only source of direct calibration available for this specific timeframe.

Along with the results specific to each organism studied (hyena, bison and human), an emphasis was placed on the methodological aspects of the use of ancient DNA to generate timed phylogenetic inferences. Additionally, simulated data and mathematical modelling were used to extend the understanding of specific aspects of the temporal dependence of molecular rates.

The results discussed in the present study help to further elucidate the evolutionary mechanisms behind the molecular clock concept, and have implications for the development and application of statistical models to obtain accurate time estimates from genetic data.

Thesis declaration

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Ho, SYW, R Lanfear, L Bromham, MJ Phillips, J Soubrier, AG Rodrigo, A Cooper.

2011. Time-dependent rates of molecular evolution. Molecular ecology 20:3087

3101.

Soubrier, J, M Steel, MSY Lee, C Der Sarkissian, S Guindon, SYW Ho, A Cooper. 2012.

The influence of rate heterogeneity among sites on the time dependence of molecular rates.

Molecular Biology and Evolution 10.1093

Julien Soubrier

20<sup>th</sup> April 2012

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### Acknowledgements

I would like to thank my principal supervisor Alan Cooper for giving me the opportunity to work at the Australian Centre for Ancient DNA, his constant challenging scientific discussions, and his kind support throughout the three years of my PhD candidature in Australia. I am very grateful to my co-supervisors, Simon Ho, Wolfgang Haak and Mike Lee, for their enthusiastic guidance and encouragements.

I would like to recognize all fellow members at the ACAD for providing such a friendly working environment, where passion for science and a sharing of knowledge go along with after-hour events. In particular, all the thesis writing group fellows were a great support.

I would like to show my gratitude to Vicki Thomson for her unceasing technical, intellectual and friendly support during the long hours we spent at work trying to simultaneously finish our theses (but also trying to get the best coffee in the lab); Bastien Llamas for his endless enthusiasm and inspiration at sorting illustrations, presentations, paragraphs and shell scripts, but mostly for his friendship; and Maria Lekis for her invaluable support throughout my PhD.

This work would not have been possible without the financial and intellectual support of The Genographic Project, in collaboration with the National Geographic, IBM and the Waitt Family Foundation.

I would like to thank all co-authors of the manuscripts presented in this thesis, for their support and helpful comments.

I would also like to acknowledge the people who spent time in discussions, and explanations during conferences, workshops or visits, notably Mike Steel, Alexei Drummond, Stephane Guindon, David Bryant, David Penny, Jerry Taylor, Mark Pagel, Rob Lanfear, Matt Philipps, Lindell Bromham and Chris Simon.

I am extremely grateful to Christophe Douady and Manolo Gouy for teaching me a lot about scientific research during my Masters in Lyon; Sandrine Hughes for training me in ancient DNA techniques; and Ludovic Orlando for introducing me to this fascinating field of paleogenetics, and for his helpful advice on studies and career choices.

I would also like to thank Profs. Pierre Joly and Michel Aigle for the passion they put in their lectures, which were decisive moments for my choosing to continue in research.

Finally, on a more personal note, I would like to thank the people, in and out of the lab, that made me feel welcome in this foreign environment, and helped transform this time in Australia into an amazing experience. Among them,

Bastien, Emmanuelle, Clio, Camille, Damien, Virginie, Rethish, Hugh, Patricia, Sarah, Doreen, Kimi and Jess. I am heartily grateful to Emma, Yves, Chris, Sacha, Bea, Quentin and all the Apoptose group from the master, for being such great friends regardless of the distance, with a special thanks to Adrien. I can't find the words to express the gratitude I feel for my wife for following me in this adventure, for her support and patience, and for making the past two years the most joyful moment of my life by giving birth to an amazing little boy, Noah, who always manages to make me smile at the end of the day. I owe my deepest gratitude to my family for inestimable support, their encouragement and their visits to Australia, my parents Marc and Françoise, but also Evelyne, Pierre, Jean-Pierre, Clara, André, Mimi, Françoise, Marilou, Clément, Paulette, Bernard and Evelyne, with a immense thank you to Laurence.