ABSTRACT

The human-abetted introduction of commensal species (i.e. those that opportunistically exploit the anthropogenic environment for food and shelter, e.g. rats, cockroaches etc.) to new areas has occurred throughout history. This has resulted in detrimental ecological changes worldwide but, from a viewpoint of human knowledge, a beneficial corollary of these translocations is that the species in question can be used as proxies to study the movement of the humans who transported them. I reconstruct colonisation histories of three widespread commensal mammalian species in the Western Indian Ocean, the black rat *Rattus rattus*, house mouse *Mus musculus* and Asian house shrew *Suncus murinus*, through phylogeographic studies (the geographic distribution of genetic lineages) of maternally-inherited mitochondrial markers, and zooarchaeological data. The DNA analyses are conducted on samples largely derived from museum specimens collected up to 110 years ago, and from archaeological bones (in the case of rats). I show considerable cryptic diversity in all three species, particularly in mice for which we find a potential major new lineage. Certain lineages within each species predominantly reveal long-distance translocations within the Indian Ocean, but high resolution geographic and genetic clustering is also evident, particularly in Asian house shrews. Phylogeographic structuring of the three species in East Africa and the southern Indian Ocean region (e.g. Madagascar, Reunion, etc.) indicate connections with Arabia, the Middle East, and India in the Islamic period from the first millennium AD, and later European connections during the Age of Exploration. Closer to the origins of the three species (the Indian subcontinent in all cases), range expansions in Eurasia and nearby islands relate to early to mid Holocene human populations, but also with signals of later secondary colonisations. Through ancient DNA studies I found genetic continuity between temporally separated populations of black rats suggesting population persistence, and high levels of diversity in Songo Mnara, a Swahili stonetown in

Tanzania. Knowledge of the colonisation history and genetic diversity of an introduced species is essential to understand their resilience in novel landscapes, and to identify pathways of invasion and, by proxy, human trade and exchange networks that facilitated their dispersal. My research contributes significantly to that end for three socially, economically and ecologically important species that are well-established in the Indian Ocean region and beyond.

PREFACE

My research forms a part of a larger multidisciplinary project spearheaded by Dr. Nicole Boivin (University of Oxford) called the Sealinks Project (www.sealinksproject.com). The project investigates early maritime connections in the Indian Ocean and seeks to understand the socio-cultural, economic and environmental impacts of these connections through the synthesis of archaeological, genetic, linguistic and palaeoecological studies. My research focuses on biological proxy lines of evidence and was guided by Dr. Jeremy Searle (Cornell University), through his interest in evolutionary biology of small mammals and their application in tracing human histories (www.sites.google.com/site/thesearlelaboratory). It quickly became a collaboration involving many archaeologists, biologists, morphometricians, historians and field researchers, and was especially influenced by members of Crossing the Green Sea project and the D.E.A.D Lab based in Durham and Aberdeen Universities. My research benefitted immensely from the ancient DNA expertise of Dr. Greger Larson (Durham University). The value of such a deeply collaborative project, involving such a diverse range of specialists is made clear by the influence it has had on the genuinely interdisciplinary nature of my research, particularly within the fields of genetics and zooarchaeology.

ACKNOWLEDGEMENTS

For my dad, in loving memory: with alacrity, equanimity, and occasionally puerility.

Acknowledging all the deserving people who have helped progress my DPhil, both academically and personally, would be a tome in itself, so instead I am inclined to keep it brief. My mum and sister deserve great recognition for always offering love, help and encouragement, especially over the last few years. My deepest thanks go to my supervisors, Nicky and Jeremy, who offered me a great opportunity and let me follow my interests in a supportive, unconstrained manner. It is only through the academic, technical and personal support from fellow PhD students, group members, researchers, field biologists, archaeologists, to name but a few, that I have been able to complete my thesis, and I would like to thank the Searle Lab, Sealinks crew, Steve Goodman and Martin Walsh in particular for their help. I am very grateful to the Cornell University community, who welcomed me from across the pond, and to Greger Larson and the DEAD Lab, who welcomed me up North. I appreciate that I could not have undertaken my research if it were not for the museums, archaeologists and biologists who provided me with samples. To my friends - thank you for keeping me sane.

DECLARATION OF OWN WORK

This research has been a collaboration involving many researchers and institutions, in particular two other research students, Alex Trinks (Durham University) and Ardern Hulme-Beaman (AHB) (University of Aberdeen). AHB contributed to molecular work for the Asian house shrew (Chapter 3) by co-designing Primer Set 1, co-extracting museum specimens, and by extracting and amplifying the bulk of modern specimens. In each chapter, I have acknowledged the work that is included in my thesis that is done by other parties (except as outlined here). All analysis and all written work are my own.

TABLE OF CONTENTS

LIST OF FIGURES AND TABLES

Figures