Megafauna and Methods
New Approaches to the Study of Megafaunal Extinctions

Organized by Jillian Swift and Patrick Roberts
Max Planck Institute for the Science of Human History
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The extinction of large-bodied animals (often termed ‘megafauna’) during the Late Pleistocene and Holocene has been described as one of the most significant events in recent Earth history. While climate change, disease, and even extraterrestrial impacts have been postulated as significant contributors, the potential role of our species in this process has proved of significant interest, particularly in addressing the impacts of *Homo sapiens* on the world’s ecosystems following its expansion beyond Africa. Teasing apart natural and human impacts on large fauna has proven highly challenging, and requires both regional and global approaches, as well as a broad suite of scientific methods. In this workshop we seek to examine how megafaunal extinctions are studied, and explore how new methods in such fields as ancient DNA research, proteomics, ZooMS, palaeoecology and computational modeling might be combined with large-scale interdisciplinary efforts that bring together researchers from different projects, regions and/or disciplines. The aim is develop a novel, multi-proxy, collaborative research project aimed at improving the narratives and scope of megafaunal studies. Our hope is that this will help to test ideas regarding the timing and nature of lasting human impacts on the world’s ecosystems.

Format: *Speakers are asked to focus on how new methods and approaches and how these might be leveraged to generate a novel approach to the topic of megafaunal extinctions. Our goal is to have as much discussion and interaction as possible. Please keep talks to a maximum of 15 minutes, allowing at least 5 minutes for questions after each presentation.*

DAY 1
Monday, 20 February

8:00-8:30 Arrival and coffee at Max Planck Institute for the Science of Human History

SESSION 1: New Approaches to Megafaunal Extinctions and the Max Planck Institute for the Science of Human History

8:30-8:40 **Nicole Boivin (Max Planck Institute for the Science of Human History)**
Welcome

8:40-8:55 **Jillian Swift (Max Planck Institute for the Science of Human History)**
Megafauna and Methods: Laying the groundwork for innovative approaches to megafaunal extinctions

8:55-9:10 **Michael Petraglia (Max Planck Institute for the Science of Human History)**
Did humans shape environments in the Pleistocene?

9:10-9:30 Initial thoughts from workshop participants

SESSION 2: New Molecular Techniques for Taxonomic Identifications

Chair: Christopher Johnson (University of Tasmania)

9:30-9:45 **Frido Welker (Max Planck Institute for Evolutionary Anthropology)**
The potential of ancient protein research to rhinoceros extinction events

9:50-10:05 **Viviane Slon (Max Planck Institute for Evolutionary Anthropology)**
Recovering mammalian mitochondrial DNA from Late and Middle Pleistocene sediments by hybridization capture

10:10-10:25 **Michael Bunce (Curtin University)**
Scrapheap Challenge: Insights gained from analyzing ancient DNA preserved in bulk bone

10:30-11:00 Discussion

What is the potential for these analyses to bring new light to preexisting sites/assemblages? Which collections are the best candidates? How are these methods best applied? What are some pitfalls to be aware of, and how to deal with these?

11:00-11:30 Coffee Break

SESSION 3 – Megafauna from Molecules

Chair: Christina Warinner (Max Planck Institute for the Science of Human History)

11:30-11:45	**Patrick Roberts (Max Planck Institute for the Science of Human History)** Mass spectrometry approaches to megafaunal extinctions in South Asia
11:50-12:05	**Gifford Miller (University of Colorado Boulder)** The potential for stable isotopes of C, O, and N in avian eggshell to constrain the factors contributing to megafaunal extinction
12:10-12:25	**James Fellows Yates (Eberhard-Karls-Universität Tübingen, Max Planck Institute for the Science of Human History)** Central European Late Pleistocene woolly mammoths: Insights from ZooMS, stable isotopes and aDNA
12:30-1:00	Discussion

How to make molecular techniques more accessible, useful to megafaunal studies? How to bridge communication gaps between methodological specialists and megafaunal experts, and across disciplinary boundaries?

1:00-2:00 Catered Lunch at the Institute

SESSION 4: Refining Chronologies for Megafaunal Extinctions

Chair: Julien Louys (Australian National University)

2:00-2:15	**Rachel Wood (Australian National University)** Radiocarbon dating skeletal remains
2:20-2:35	**Eileen Jacob (University of Oxford)** Radiocarbon dating the response of Late Pleistocene carnivores to human and climate change
2:40-2:55	**Michael Waters (Texas A&M University)** A new view of the peopling of the Americas and temporal overlap of humans with late Pleistocene megafauna in North America
3:00-3:30	Discussion

Where is the chronological record for megafaunal extinctions sparse & how do we improve this? Is there a "chronometric hygiene"/best practice for establishing chronologies specifically relevant to megafaunal extinction causes/consequences?

3:30-4:00 Coffee Break

SESSION 5 – Climate, Paleoenvironment, and Human-Animal Interactions

Chair: Michael Waters (Texas A&M University)

4:00-4:15 **Simon Haberle (Australian National University)**
Dung fungi as a proxy for megafaunal population dynamics in the Indo-Pacific

4:20-4:35 **Kristina Douglass (Smithsonian Institution)**
New methodological and theoretical approaches to understanding human-ratite interactions and ratite extinctions

4:40-4:55 **Christopher Johnson (University of Tasmania)**
Using paleoecology and modelling to understand past interactions of megaherbivores and vegetation

5:00-5:30 Discussion

What are new areas of opportunity for paleoenvironmental studies to contribute to discussions around megafauna? What are advantages and potential quandaries for employing proxy data and modeling to address extinctions? Are some records more robust than others?

6:30 pm Dinner at Noll Restaurant, City Centre, Jena

DAY 2
Tuesday, 21 February

8:30-9:00 Arrival and coffee at the Max Planck Institute for the Science of Human History

SESSION 6 – Integrating Evidence for Megafaunal Extinctions at Multiple Scales of Analysis

Chair: Rachel Wood (Australian National University)

9:00-9:15 **Judith Field (University of New South Wales)**
Thinking about the foundations of studying megafauna and the extinction process: Moving the data forward

9:20-9:35 **Joe Dortch (University of Western Australia)**
Megafauna mass deaths at Lancefield Swamp, south-eastern Australia: A case study in extinction processes

9:40-9:55 **Natalia Villavicencio Figueroa (University of California, Berkeley)**
Late Quaternary extinctions in South America: Chronology, environmental changes, and human impacts at regional scales

10:00-10:30 Discussion

What are the most effective approaches for modeling megafaunal extinctions? What are the biggest challenges to synthesizing data at different scales of analysis (geographic, taxonomic, etc.)? What can be done to improve or refine current models?

10:30-11:00 Coffee Break

SESSION 7 – Insights on Megafaunal Extinctions from Less-Studied Regions and Taxa

Chair: Kristina Douglass (Smithsonian Institution)

11:00-11:15 **Eline Lorenzen (Natural History Museum of Denmark, University of Copenhagen)**
Paleogenomic insights into the demographic history of Arctic whales

11:20-11:35 **Tyler Faith (University of Queensland)**
Ecological context of late Quaternary large mammal extinctions in southern Africa's Cape Floral Region

11:40-11:55 **Alexis Mychajliw (Stanford University)**
Mammals, humans, and climate: Contrasting patterns of continental and Caribbean extinctions

12:00-12:15 **Julien Louys (Australian National University)**
The other Quaternary extinctions: Forgotten taxa, ignored regions, and their bearing on megafauna extinctions

12:20-1:00 Discussion

How do we figure less-studied regions and taxa more prominently into these discussions?

1:00-2:00 Catered Lunch at the Institute

SESSION 8 – Looking Towards the Future

2:00-3:30 **Breakout Group Discussion**

Group 1 In the Field: New excavations, sites, underexplored regions (*Michael Petraglia)*

Group 2: In the Lab: Innovative applications of new methodologies (*Patrick Roberts, Jillian Swift*)

Group 3: Consortium: Organizing steps for the future (*Nicole Boivin*)

Questions of Interest:

- *What shape should a new collaborative project/projects take?*
- *What are the next steps for pursuing these aims (new excavation, new analyses, additional collaborators, etc.)*?
- *What resources are available for generating new data and analyses?*

3:30-5:00 Reassemble for joint discussion

5:00-5:30 Wrap-up discussion, outline of future plans

6:30 pm – Dinner at Saigon Restaurant, City Centre, Jena

Michael Petraglia
Max Planck Institute for the Science of Human History

Did Humans Shape Environments in the Pleistocene?

Archaeologists continue to convincingly demonstrate that humans have dramatically transformed global ecosystems since the adoption of agriculture in the Holocene. However, we know very little about the way in which Pleistocene hominins potentially transformed and shaped their ecosystems. While this is the case, we know that multiple human species, some with significant niche constructing behaviours, repeatedly expanded their geographic ranges in the Pleistocene. The majority of debates about the effects of humans on their environments centre on their contributions to megafaunal extinctions. Yet, little attention has been paid to how our earlier hominin ancestors may have modified ecosystems as a consequence of subsistence-related activities and other behavioural activities. Here we briefly review evidence to demonstrate that the subsistence activities of hominins had an effect on local and regional environments as humans expanded their niches and territorial ranges in the Pleistocene. We argue that hominins probably shaped their habitats through the use of fire and, more convincingly, through the procurement and quarrying of raw materials for stone tool manufacture. Anthropogenic transformation of the natural world would appear to have begun in the Pleistocene, albeit on a different scale than in the Holocene. Such broader evidence is weighed up against the question of how humans potentially contributed to the extirpation and extinction of megafauna.

Petraglia, M. 2017. Hominins on the Move: An Assessment of Anthropogenic Shaping of Environments in the Palaeolithic. In: Human Dispersal and Species Movement: From Prehistory to the Present. Edited by N. Boivin, R. Crassard and M. Petraglia, Cambridge University Press, Cambridge, UK, in press.

Frido Welker
Max Planck Institute for Evolutionary Anthropology

The potential of ancient protein research to rhinoceros extinction events

Rhinoceroses form a significant clade of Pleistocene megafauna that experienced at least two extinction events in the last 200,000 years. The five surviving rhinoceros species continue to experience increasing human pressure due to rhinoceros horn poaching and intensification of agricultural practices, putting three out of five extant species on the brink of extinction (Critically Endangered; IUCN Red List), with at least one sub-species reproductively extinct (the northern white rhinoceros). For Pleistocene time periods, a detailed spatiotemporal overview of woolly rhinoceros (Coelodonta antiquitatis) extinction across Eurasia has previously been provided, highlighting some important areas and time periods requiring further research. Interestingly, very little is known about the extinction chronology of the genus Stephanorhinus (or its phylogenetic position) which has at least temporarily coexisted with the woolly rhinoceros in Europe. In part, this shortage of data might be explained by the typically minor contribution of rhinoceros remains to archaeological and anthropological bone assemblages.

Here, some recent contributions from the field of palaeoproteomics regarding this megafauna family will be presented (ZooMS, COL1 phylogenetics). They include de novo/error tolerant protein sequences from both extinct genera and five extant rhinoceros species. Although ZooMS taxonomic resolution for this family is low, additional ZooMS screening of Late Pleistocene sites in Eurasia is already identifying additional Rhinocerotidae remains. These would be suitable to specifically investigate the extinction chronologies of various rhinoceros species through future ancient DNA, radiocarbon dating and palaeoproteomic research.

Viviane Slon
Max Planck Institute for Evolutionary Anthropology

Recovering mammalian DNA from Late and Middle Pleistocene sediments by hybridization capture

Sediment abundantly features in archaeological sites, making it a readily available source of information. Previous studies have shown that DNA of animals and plants can be retrieved from ancient sediments by targeting short regions in their genomes by PCR [e.g., 1, 2]. We present a more general approach, allowing the recovery of mitochondrial (mt) DNA fragments from a large array of mammalian species. In this procedure, DNA is extracted from 50-100mg of sediment. Aliquots of the DNA extracts are converted into DNA libraries, which are then subjected to hybridization capture using probes covering the full mitochondrial genomes of over 200 mammals [3]. Following sequencing, the isolated DNA fragments are assigned to a taxon of origin; and their authenticity is verified based on the presence of damage patterns typical of ancient DNA [4].

We applied this methodology to 84 sediment samples excavated in Late and Middle Pleistocene layers of six Eurasian archaeological sites. We recovered ancient mammalian mtDNA in 60 samples from five of the sites, from layers as old as ~240 thousand years ago. A variety of ancient taxa were detected, including extinct megafauna such as the woolly mammoth and woolly rhinoceros. Although issues pertaining to data interpretation in the context of extinction events need to be addressed, we show the feasibility of using mammalian mtDNA recovered by hybridization capture from ancient sediments to study past biodiversity.

References

1. Willerslev, E., et al., Diverse plant and animal genetic records from Holocene and Pleistocene sediments. Science, 2003. 300(5620): p. 791-5.
2. Haile, J., et al., Ancient DNA reveals late survival of mammoth and horse in interior Alaska. Proc Natl Acad Sci U S A, 2009. 106(52): p. 22352-7.
3. Slon, V., et al., Mammalian mitochondrial capture, a tool for rapid screening of DNA preservation in faunal and undiagnostic remains, and its application to Middle Pleistocene specimens from Qesem Cave (Israel). Quaternary International, 2016. 398: p. 210-218.
4. Briggs, A.W., et al., Patterns of damage in genomic DNA sequences from a Neandertal. Proc Natl Acad Sci U S A, 2007. 104(37): p. 14616-21.

Michael Bunce
Curtin University

Scrapheap Challenge: Insights gained from analyzing ancient DNA preserved in bulk-bone

Michael Bunce, Dáithí C. Murray, Alicia Grealy, Frederik Seersholm, Kealoha Kinney & Daniel Werndly

Trace and Environmental DNA (TrEnD) laboratory, Curtin University , Perth, WA.
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Fossil bones provide a unique window into the past but they are often difficult to interpret. Only a small proportion of animals are preserved as fossils – an even smaller fraction are then recovered and able to be identified morphologically. We have developed a globally applicable next generation DNA sequencing method that offers a genetic perspective on fossil assemblages with the aim of rapidly overlaying genotype data over more traditional methods of study. Our approach is called bulk-bone metabarcoding (BBM). BBM involves the conversion of largely non-diagnostic bone fragments into powder which is then genetically indexed, amplified and sequenced on NGS platforms.

This presentation will showcase some BBM data from a variety of sites across Australia, New Zealand, Hawaii, USA, Asia, Madagascar and Armenia. The data generated using BBM provides some key insights into past biodiversity and faunal turnover. Moreover the approach is an efficient way to assess DNA preservation both within and between fossil sites. Taken together, bulk-bone metabarcoding provides a powerful and cost-effective way to study past biodiversity. The method is particularly well suited to analysing zooarcheological assemblages and thus investigate anthropogenic impacts on biota including megafauna.

Patrick Roberts
Max Planck Institute for the Science of Human History

Mass spectrometry approaches to megafaunal extinctions in South Asia

It is becoming increasingly apparent that in order to discern the causation of megafaunal extinctions it is essential to take regionally- and taxonomically-specific approaches, rather than relying on broad generalisations. Research in South Asia is a prime example of this. In southern India the extinction of *Theropithecus* sp. is an exception amongst a picture of general continuity from 200,000 years ago to present. By contrast, in Sri Lanka, a number of extinctions of large mammals, including *Panthera pardus* and *Panthera leo*, occur during the Pleistocene. Diverse methodologies, including those utilizing mass spectrometry, provide an important means of producing datasets detailed enough for contextual studies of megafaunal decline. Stable isotope analysis has a long history of documenting the local environments, dietary trends, and mobility patterns of fauna, from the Miocene to the present, while ZooMS has shown great promise in identifying Pleistocene taxa from fragmented remains.

However, these approaches have been relatively under-utilised in contextual approaches to megafaunal extinctions during the Pleistocene. Here, I review three major ways in which mass spectrometry studies of extinct fauna can be used to assess causation behind their decline, with reference to South Asia and beyond: i) large-scale identification of large and often fragmented faunal assemblages, ii) assessing changes in diet and mobility for the taxa of interest through time, and iii) reconstructing the local palaeeoenvironmental context of the taxa of interest through time by analyzing associated remains. I conclude by arguing that these methods can provide high-resolution information regarding the ecological changes faced by a given taxa in a given locale. Moreover, the growing use of these methods will facilitate inter-taxon and inter-region comparison of changing megafaunal diets, mobility, and environments – enabling more powerful, specific discussions of extinction causation.

Gifford Miller
University of Colorado Boulder

Stable isotopes of C, O, and N in avian eggshell to reconstruct climate, environments, and human-megafauna impacts

The calcite composition of eggshell provides a medium more likely to be preserved than skeletal remains in many environmental settings. And the isolation of organic molecules within the crystalline stucture of the eggshell results in long preservation with minimal opportunities for contamination or diffusional loss. The eggshell matrix is ideal for radiocarbon and amino acid racemization dating and in some instances U-series dating, as well as OSL dating of surrounding sand grains, providing reasonable chronological control for the past ~200 ka in many environments. In optimal settings it is possible to obtain long time-series of monospecific eggshell for paleoenviromental reconstructions. Carbon isotopes are set by the food consumed by the female bird, with C-isotopes in eggshell calcite reflecting food consumed in the weeks before egg calcification whereas C-isotopes in organic molecules has a longer time averaging of several months. Oxygen isotopes are set by the isotopic composition of ingested water in the weeks before calcification, and nitrogen isotopes are determined by the food source and hydroclimate, with strong differences depending on the trophic level of consumed foods. We have used the carbon isotopes in both carbon sources and oxygen in eggshell of the extant Australian emu spanning 100 ka+ collected in several regions to evaluate changes in diet and hydroclimate for >50 ka prior to human colonization and subsequently, and use comparisons of nitrogen isotopes to evaluate whether the extinct giant bird Genyornis was a carnivore or herbivore. Collectively our data suggest and abrupt reduction in dietary variability and restructuring of the ecosystem-moisture balance relation coincident with human colonization and Genyornis extinction 50 to 45 ka.

James Fellows Yates
Eberhard-Karls-Universität Tübingen
Max Planck Institute for the Science of Human History

Central European Late Pleistocene Woolly Mammoths: Insights from Zooarchaeology, ZooMS, Stable Isotope and aDNA data

Dorothée G. Drucker; Ella Reiter; Simon Heumos; Frido Welker; Susanne C. Münzel; Piotr Wojtal; Martina LázniĊková-Galetová; Nicholas J. Conard; Alexander Herbig; Hervé Bocherens; Johannes Krause

Ancient DNA from late Pleistocene woolly mammoths has uncovered previously unknown migrations and mitochondrial clade replacements prior to the extinction of the species. Despite recent discoveries of additional maternal clade replacements in Europe, previous work has led to uneven sampling across Eurasia by focusing on North East Eurasia and North America. Furthermore, most studies have focused on large scale population dynamics only, thus overlooking possible site-level changes.

In this study we have successfully utilised a multi-method species identification screening (Zooarchaeology, ZooMS, Stable Isotopes, aDNA) of fragmentary remains of megafauna from late Pleistocene Central Europe. This cross-validation of species level identification of morphologically unspecific bone fragments identified as ‘mammoth/rhino sized’ was performed using a laboratory workflow requiring minimal sampling. We generated twenty woolly mammoth mitochondrial genomes and a subset of complementary stable isotopic data from four sites that have previously shown unusual palaeoecological or skeletal characteristics of the local woolly mammoth populations. Comparing mitochondrial clades to radiocarbon dates shows continuity in maternal lineages at each site located in Germany or Poland, indicating that maternal clades are not related to the unusual characteristics of two sites. Previously, the two clades that occupied Europe were considered to have been geographically and temporally separate. Our data suggests that it was more likely that the two clades overlapped and possibly coexisted, but why one clade ‘survived’ over the other remains unclear. This highlights the need for greater understanding of intra-species population loss and replacement prior to the woolly mammoth extinction.

Rachel Wood
Australian National University

Radiocarbon dating skeletal remains

Radiocarbon dating is the method most commonly used to build chronologies spanning the last 50,000 years. It is particularly important when examining megafaunal extinctions and human occupations because it is one of the most precise methods during this period, and it can be used to directly date skeletal remains. In high latitudes the cold or temperate climates allow proteins to survive well beyond 50,000 years, and it is often possible to extract and purify these for radiocarbon dating. Extensive research over the past 50 years has resulted in a number of 'pretreatment' protocols which can effectively remove carbon containing contaminants from these proteins, and enable accurate dates to be obtained. Large numbers of bones can often be dated from a stratigraphic sequence, allowing precision to be increased and hypotheses tested using Bayesian modelling.

However in warmer regions, typically stretching from Mediterranean latitudes to southern Australia, protein rapidly degrades and it is rarely possible to extract enough for radiocarbon dating in Pleistocene deposits. There is a pressing need to develop methods to directly date skeletal remains from these regions. One potential avenue is the development of a method to accurately radiocarbon date the mineral phase in tooth enamel. Currently radiocarbon dates on enamel tend to be 10,000s of years too young in the Pleistocene due to contamination from carbonate in the groundwater. However, recent work has demonstrated that most contaminants are located at the crystallite boundaries, raising the possibility that they can be removed. Accurate dates have not yet been obtained on Pleistocene enamel, but significant improvements have been made.

A final topic which will be briefly addressed in this presentation is the treatment of minimum ages in chronologies. Radiocarbon dating of enamel currently provides a minimum age, as does the increasingly applied method of U-series dating of bone or dentine. This minimum age information can be crucial, particularly where dating is so challenging. However, it does raise problems in interpretation and statistical modelling.

Eileen Jacob
University of Oxford

Radiocarbon dating Late Pleistocene megafauna responses to humans and climate change

During the previous Ice Age and early Holocene, over twenty genera of large mammals went extinct from Europe. Abrupt climate change and the dispersal of modern humans into Europe have both been blamed for these extinctions. To further this debate, fossils must be precisely dated to establish correlation with climatic events and/or human activity. Radiocarbon dating presents a potential solution, as it directly dates faunal bone and can produce dates up to 50,000 BP. Current radiocarbon data, however, are problematic for several species. Datasets are often small and of incomplete geographical coverage. This is partly due to the challenges of dating degraded bone collagen, as is often found in southern Europe. Furthermore, up to 70% of Pleistocene radiocarbon dates may underestimate true age (Higham et al. 2009), and dates often come with errors too large to match to high-resolution climatic events with confidence.

I aim to address these weaknesses by using robust pretreatment methods to date bone from regions and species with few direct dates. I have focused on carnivores in southern Europe, as these species have few direct dates and the region is problematic for sample preservation. In addition to using ultrafiltration, routine in ORAU since 2000, we are also using compound-specific dating to improve accuracy and expand our ability to date poorly-preserved samples. When combined into a GIS model with climate records and archaeological evidence, these new results will improve understanding of how megafauna responded to humans and climate change.

References

Higham, T., Brock, F., Peresani, M., Broglio, A., Wood, R., Douka, K., 2009. Problems with radiocarbon dating the Middle to Upper Palaeolithic transition in Italy. Quaternary Science Reviews 28, 1257–1267.

Michael Waters
Texas A&M University

A New View of the Peopling of the Americas and the Temporal Overlap of Humans with Late Pleistocene Megafauna in North America

Clovis has long been considered the oldest archaeological evidence for humans in the Americas. Rigorous dating of Clovis archaeological sites shows that they date between 12,600 and 13,000 cal yr B.P. and possibly as early as 13,300 cal yr B.P. Over the last few decades, several credible archaeological sites have demonstrated that humans occupied the Americas by 15,000 cal yr B.P. Many of the archaeological sites dating to the late Pleistocene have Megafauna remains. These sites show that humans hunted and interacted with megafauna in North America for over 2000 years before their extinction around 12,600 to 12,700 years ago. New research is underway in the American Southeast using Sporormiella and aDNA to track the late Pleistocene extinction process.

Simon Haberle
Australian National University

Dung fungi as a proxy for megafauna population dynamics in the Indo-Pacific

Dung fungi preserved in sedimentary archives are being used as proxies for megafauna population dynamics (extinctions and population abundance change) through time. A range of new studies in the Indo-Pacific region have linked megafauna decline to the arrival of people on island environments (most notably in Australia). I will present data from new research that examines the nature of the dung fungi record across a range of sedimentary contexts (lakes, swamps, marine and rockshelter sediments) and from a range of timescales

(10's to 1000's of years) associated with island environments across the Indo-Pacific region (Madagascar, Australia and New Guinea). The prospects and pitfalls of this research will be discussed.

Kristina Douglass
Smithsonian Institution

New methodological and theoretical approaches to understanding human-ratite interactions and ratite extinctions

The disappearance of Madagascar’s megafauna and its relation to the island’s human settlement has long raised more questions than satisfactory answers. Among the extinct Malagasy fauna are the giant elephant birds (Aepyornithidae), whose bones are rarely recovered in sub-fossil and archaeological contexts, but whose eggshell is abundant in surface scatters, dunes and archaeological deposits in the southern and southwestern Madagascar. Elephant bird eggshell, however, has, until recently, been disregarded as an important source of data in understanding the birds’ extinction and people’s interaction with them. New approaches to the analysis of elephant bird eggshell will be discussed with the aim of encouraging interdisciplinary work on eggshell. Furthermore, research into the extinction of Madagascar’s largest endemics has not systematically and holistically considered how diverse communities engaged with their environment, beyond the hunting of larger terrestrial fauna. In coastal areas, for example, much work must be done to more fully reconstruct human-environment interactions that include both the terrestrial and marine environments, in order to contextualize evidence of human-megafauna interaction and exploitation.

Christopher Johnson
University of Tasmania

Using paleoecology and modelling to understand past interactions of megaherbivores and vegetation

Judith Field
University of New South Wales

Thinking about the foundations of studying megafauna and the extinction process – moving the data forward

Our current approaches to the study of megafauna extinctions globally is defined by a number of limiting factors including research agendas of different individuals/groups, availability of sites/fossils for study, access to specific methods (isotopes, aDNA etc) and time since sites were discovered. In the area I have been most interested in, that of Sahul (Pleistocene Australia-New Guinea) extinctions, the focus in recent years has been on obtaining dates for the known fossil assemblages and a reliance on the dating methods of ESR /Ur series and OSL methods. Where fossil assemblages have been absent, proxy data has been used to infer their presence, or that of humans.

The issue isn’t the terminal ages of the known fossils preserved but understanding the processes leading to their disappearance (see Wroe and Field, 2006). For this reason we need to turn our attention more fully to understanding the population biology and distributions of now extinct Pleistocene fauna (and flora).

As with all of these studies new discovery projects are important. With so few well provenanced sites known from Sahul (Australia/New Guinea), recent focus has been more on re-dating sites excavated previously or revisiting data collected by others. The efficacy of proxy data is yet to be demonstrated, especially with reference to studies of microfossils such as Sporormiella. We must strive to bring together diverse studies and approaches to be able to move forward in this discussion.

Some of the important features of megafauna species still to be understood include:

- the preferred habitats of megafauna species – distribution across environmental zones and latitudes (Isotope studies, landscape comparisons) (e.g. Horton, 1984, Brookman and Ambrose 2013);
- diet breadth in megafauna communities, environmental constraints (palaeoenvironmental data, isotopes, DNA, microwear, structural) (eg Prideaux et al, 2009; de Santis et al, 2016);
- interconnectedness between different species – niche overlap and environmental heterogeneity.

Aspects of the fossil record which need to be integrated with the study of megafauna species include:

- unravelling time averaging in fossil deposits (REE analyses, stratigraphic analyses);
- better communication of taphonomic aspects of fossils assemblages (geomorphological studies);
- understanding that different depositional contexts will require different approaches (e.g. cave sites versus open sites);
- establishing the connections between depositional context and dates produced – what are we actually dating?

Some case studies will be discussed as examples of how we can further our understanding of these issues. Furthermore, we need to take some lessons from those studying modern extinction events and recognise that these are synergistic processes and require consideration of all possible factors (e.g. Brook et al., 2008)

References

Brook, B.W., Sodhi, N.S., Bradshaw, C.J.A 2008. Synergies among extinction drivers under global change. Trends in Ecology & Evolution, 23(8), 453-60.

Brookman, T.H., Ambrose, S.H. 2013 .Kangaroo tooth enamel oxygen and carbon isotope variation on a latitudinal transect in southern Australia: implications for palaeoenvironmental reconstruction. Oecologica 171(2), 403-416Wroe, S. & Field, J. 2006. A review of the evidence for a human role in the extinction of Australian Megafauna and an alternative explanation. Quaternary Science Reviews 25, 2692-2703.

de Santis, L., Field, J., Wroe, S., Dodson, J. 2016. Dietary responses of Sahul (Pleistocene Australia-New Guinea) megafauna to climate and environmental change. Paleobiology PAB-LE-2015-0006.R1

Horton, D.R., 1984. Red kangaroos: last of the Australian megafauna. In: Martin, P.S., Klein, R.G. (Eds.), Quaternary Extinctions: A Prehistoric Revolution. The University of Arizona Press, Tucson, Arizona, pp. 639–680.

Prideaux, G. J., L. K. Ayliffe, L.R.G. DeSantis, B. W. Schubert, P. F. Murray, M. K. Gagan, and T. E. Cerling. 2009. Extinction implications of a chenopod browse diet for a giant Pleistocene kangaroo. Proceedings of the National Academy of the Sciences, USA 106:11646-11650.

Wroe, S. & Field, J. 2006. A review of the evidence for a human role in the extinction of Australian Megafauna and an alternative explanation. Quaternary Science Reviews 25, 2692-2703.

Joe Dortch
University of Western Australia

Megafauna mass deaths at Lancefield Swamp, south-eastern Australia: A case study in extinction processes

The remains of thousands of giant kangaroos (*Macropus giganteus titan*) in one location make for an impressive paleontological site. The macropod bone beds at Lancefield Swamp, Victoria (south-eastern Australia), span the period of human arrival in

Australia, yet the site provides limited evidence of human activity. Exploration of the factors causing mass deaths has focused on the timing of site formation events and local and regional context environmental changes. Recently published results from OSL and ESR analyses, combined with taphonomic and sedimentological studies, indicate that *in situ* macropod remains date from c. 80,000 to c. 45,000 years ago. The faunal assemblage, dominated by megafaunal adult *Macropus*, is consistent with mass die-offs due to severe drought. Such droughts may have recurred during the climatic variability of Marine Isotope Stages 4 and 3. Only the very youngest fossil deposits at Lancefield are coeval with the earliest human arrivals, so anthropogenic causes cannot be implicated in most macropod deaths at the site. It also appears that megafauna recovered between putative drought periods, and either disappeared or were dwarfed some millennia after humans appeared in the record. A human role in these processes is not ruled out, but its influence appears to be complex and prolonged. Comparable palaeo-records are needed to address this question. Nevertheless the Lancefield case study illustrates the benefits of multi-disciplinary approaches at both site-specific and regional scales.

Natalia Villavicencio Figueroa
University of California, Berkeley

Late Quaternary extinction in South America: Chronology, environmental changes and human impacts at regional scales

During the Late Quaternary Extinction event South America was one of the most severely impacted continents losing around 82% (53 genera) of its entire large mammal species. As for many other places on earth, human impacts and climate changes proper of the Pleistocene-Holocene transition have been proposed as possible drivers of this extinction event in South America.

In this continent human arrival and late glacial climate changes occurred within a relatively short span of time, although marked regional differences are present in the timing and direction of climate change as well as in the timing of human arrival. This last stamen highlights the importance of performing regional scale analyses in order to understand how the possible drivers of extinction operated. In this talk I will discuss two main aspects with regards to the magfauanal extinctions in South America: 1) radiocarbon dating of megafauna specimens in order to improve the chronology of extinction for the continent and, 2) regional scale analysis of the extinction chronology of megafauna and its relation to human arrival and environmental changes for Southern Patagonia, the high Andes of Peru and the Lake district of Chile.

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Eline Lorenzen
Natural History Museum of Denmark
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Palaeogenomic insights into the demographic history of Arctic whales

Despite multiple studies on the impact of climate change on terrestrial mammals in the Arctic there have been no equivalent studies of marine mammals. This remarkable gap in our knowledge is due to the difficulty of assembling long-term data sets because most marine mammals die at sea. The narwhal, one of only two toothed whale species endemic to the Arctic, has a remarkable tusk, which has been collected and coveted by prehistoric humans through millennia. Using a unique collection of ~100 narwhal remains spanning the Holocene and Late Pleistocene, we will gain insight into how climate impacted the ecological and demographic history of marine megafauna species. The data set may provide a baseline for climate-induced change that can be used in a terrestrial context, as any demographic shifts predating industrial whaling cannot be attributed to humans. The samples are in the process of being screened for endogenous DNA content.

Tyler Faith
University of Queensland

Ecological context of late Quaternary large mammal extinctions in southern Africa's Cape Floral Region

The demise of earth’s megafauna over the last ~100,000 years has captured the attention of Quaternary scientists since the 19th century, in part because it is possible that human played a decisive role. In the global context, the losses in Africa have received relatively little attention and are considered to be poorly understood. The extinction record from southern Africa’s Cape Floristic Region (CFR), however, is more detailed than in many parts of the world. This presentation reviews the ecological context of CFR extinctions that occurred since the Last Glacial Maximum. Zooarchaeological assemblages from the CFR document the extinction of five ungulate grazers near the Pleistocene-Holocene transition, including the Cape zebra (Equus capensis), the long-horn buffalo (Syncerus antiquus), the giant wildebeest (Megalotragus priscus), the southern springbok (Antidorcas australis), and an unnamed caprine antelope. Paleoenvironmental archives provide abundant evidence that climate-driven environmental change played a decisive role in these extinctions. These losses represent the most recent example of a long-term extinction process characterized by the extinction of grassland species over the last ~1 million years.

Alexis Mychajliw
Stanford University

Mammals, humans, and climate: Contrasting patterns of continental and Caribbean extinctions

The Caribbean mammal fauna provides a significant opportunity to evaluate species responses to global change across the recent past. Multiple waves of culturally distinct humans (Europeans and indigenous peoples) and the non-native species that accompanied them have radically transformed the Caribbean's ecosystems. Today, the islands of the Greater and Lesser Antilles harbor ~53 native mammal species, many of which are threatened by human activities. Explorations of the recent paleontological record (~20,000 years ago), however, have revealed a past mammalian fauna of 100+ species, including extinct endemic families and genera of sloths, rodents, monkeys, and shrew-like insectivores. While the Caribbean was home to only two true megafaunal genera of sloths, their biogeography, unique mammal fauna, and distinct timing of human arrival provide an illuminating counterpart to the narrative of continental extinctions, with the potential to isolate extinction mechanisms. We use an interdisciplinary approach to describe the dynamics of extinction and survival of Caribbean mammals in response to anthropogenic and environmental stressors. We model the true last occurrence dates of mammal lineages using the Gaussian-resampled, inverse-weighted McInerny (GRIWM) method and compare extinction timing with reconstructed body sizes. Using radiocarbon dates of archaeological sites, we describe patterns of past human population densities through time with summed calibrated probability distributions. Bayesian change point analyses provide a quantitative method for pinpointing periods of vegetation change from pollen records. By quantitatively reconstructing the dynamics of species and the challenges they faced, we provide lessons on species survival from the past that can be applied towards planning for conservation in the future.

Julien Louys
Australian National University

Quaternary island extinctions: forgotten taxa, ignored regions, and their bearing on Martin's megafauna extinction hypothesis

The megafauna extinction hypothesis has engendered considerable discussion in the more than 50 years since Paul Martin first proposed his global Pleistocene extinction model. While Martin's original hypothesis has undergone some reframing and refinement since it was first proposed, nevertheless it remains the catalyst and backbone for a debate that continues to be highly vociferous and unresolved. Absent from much of this debate is a consideration of the megafaunal-rich region of Southeast Asia. Martin briefly mentioned Southeast Asia in his original framing of his hypothesis, but presented no data on this neglected region. While some of this information would have been available to Martin at the time of his writing, nevertheless since his original arguments were formulated much new data has come to light. With that in mind, I return to Martin's original megafauna extinction hypothesis and, in light of the predictions he made on the basis of his global model for overkill, I review extinction data from continental and oceanic islands in Southeast Asia. Continental island extinctions in Southeast Asia at the generic level are minimal and are not synchronous with the arrival of modern humans, contrary to Martin's hypothesis. Patterns of extinctions on oceanic islands also contradict Martin's predictions, in that they appear to occur before modern human arrival, or significantly after. The pattern of extinctions from Southeast Asia indicate that extinctions during the Quaternary are not easily pigeonholed into a single global model.