WORKSHOP

BIOLOGICAL MARKERS OF CHANGE

IN SOUTHEAST AND ISLAND SOUTHEAST ASIA

29 – 30 JUNE
2017

Biological Markers of Change in Southeast and Island Southeast Asia

Max Planck Institute for the Science of Human History
Jena, Germany

Organized by Monica Tromp

29 – 30 June 2017

Despite widespread acknowledgement that Island Southeast Asia (ISEA) has been an important link between Southeast Asia and the Southern Hemisphere for at least 50,000 years, little is known about interactions both within ISEA and with Mainland Southeast Asia to the north, and Sahul (Australia and New Guinea) to the south. Due to the tropical climate of the Southeast and Island Southeast Asia region, organic materials are rarely preserved and traditional archaeological techniques have not been particularly successful when it comes to understanding how people interacted with and within their environments. In this workshop we will be discussing novel and innovative methodologies and ideas that might be applied to the region, while highlighting recent findings that have already employed some of these techniques such as genomic, isotopic, lipid, microparticle and proteomic analyses.

Day 1
Thursday, 29 June

9:30 – 10:00 Arrival and coffee at the Max Planck Institute for the Science of Human History

10:00 – 10:10 **Nicole Boivin (Max Planck Institute for the Science of Human History)**
Welcome

10:15 – 10:30 **Monica Tromp (Max Planck Institute for the Science of Human History)**
Broad themes and overview of workshop

Session 1: Back to the future: New methods, old questions

Chair: Nicole Boivin

10:30 – 10:50 **Jessica Hendy (Max Planck Institute for the Science of Human History)**
Ancient protein analysis: emerging methods and applications to ancient dietary studies

10:55 – 11:15 **Frederik Seersholm (Curtin University)**
Prospects for Bulk Bone metabarcoding in Southeast Asia

11:20 – 11:40 **Janelle Stevenson (The Australian National University)**
The pace and rhythm of climate: 600,000 years in a biological hotspot

11:40 – 12:00 Discussion

What is the potential for these new methods to address human interaction in this tropical region? How applicable might they be for samples that have been sitting in variable storage conditions for years? How can we bridge communication gaps between interdisciplinary boundaries – between the field and lab?

Session 2: Indo-Pacific Interactions and beyond

Chair: Monica Tromp

12:00 – 12:20 **Marlin Tolla (Regional Office of Archaeology for Papua-Indonesia)**
Tracking the interaction between Papua and Near Oceania in Holocene time

12:25 – 12:45 **Nicolas Brucato (Laboratoire d´Anthropologie Moléculaire et Imagerie de Synthèse (AMIS))**
Genomic admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean trading network

12:45 – 13:00 Discussion

How can we better integrate archaeological and both ancient and modern genetic data in this region? Should there be more interdisciplinary discussion between those working in the Pacific Ocean and the Indian Ocean?

13:00 – 14:30 Catered lunch at the Institute

Session 3: DNA and disease

Chair: Jillian Swift

14:30 – 14:50 **Hallie Buckley (University of Otago)**
Searching for the origins and antiquity of the Metabolic Syndrome in the Pacific Islands

14:55 – 15:15 **Anna Gosling (University of Chicago/University of Otago)**
Evolutionary explanations for high metabolic disease burden among Austronesian-descendent populations: Current evidence and future possibilities

15:20 – 15:40 **Kathrin Nägele (Max Planck Institute for the Science of Human History)**
Ancient DNA preservation in Southwest Pacific human remains

15:45 – 16:05 **Murray Cox (Massey University)**
A Genetics of social change

16:05 – 17:30 Discussion and recap of the day

How can palaeopathological studies and aDNA studies inform each other to better understand the change of the health and disease burden of the region through time? Should there be a greater focus on modern genetic studies in this region if bimolecular preservation is poor? If so, how can we create productive dialogue between archaeologists and geneticists?

18:00 BBQ at the Institute

Day 2
Friday, 30 June

09:30 – 10:00 Arrival and coffee at the Max Planck Institute for the Science of Human History

10:00 – 10:10 **Monica Tromp**
Review and announcements for the day

Session 4: Of biomolecules and bones…

Chair: Anna Gosling

10:10 – 10:30 **Patrick Roberts (Max Planck Institute for the Science of Human History)**
Unusable or under-explored? The potential for archaeologically-directed stable isotope studies in the Late Pleistocene and Holocene of Mainland and Island Southeast Asia

10:35 – 10:55 **Charlotte King (University of Otago)**
Using chemical analysis of human skeletal tissues as a proxy for environmental change

11:00 – 11:30 Coffee break

11:30 – 11:50 **Jillian Swift (Max Planck Institute for the Science of Human History)**
Investigating human-environment interactions through stable isotope analysis of Pacific rats (*Rattus exulans*)

11:55 – 12:15 **Stuart Hawkins (The Australian National University)**
Understanding human origins, Palaeoecological interactions, and dietary adaptations in the insular Wallacean region

12:20 – 13:00 Discussion

How much potential is there for new stable isotope techniques to build on the data that has already been generated in the region? How can field methods be improved to recover faunal material for traditional zooarchaeological analyses as well as biomolecular analyses in tropical regions?

13:00 – 14:00 Catered lunch at the Institute

Session 5: Plant potential

Chair: Patrick Roberts

14:00 – 14:20 **Monica Tromp (Max Planck Institute for the Science of Human History)**
Vietnam to Vanuatu: Dental calculus and the Austronesian expansion

14:25 – 14:45 **Cristina Castillo (Institute of Archaeology, University College London & Graduate School of Agricultural Science, Kobe University)**
Archaeobotany in Southeast Asia: Issues, results and prospects

14:50 – 15:10 **Aleese Baron (The Australian National University)**
A mixed method, multi-scalar approach to identify domesticated rice (*Oryza sativa*) in pottery sherds from early Neolithic sites (4150-3265 cal BP) in Southeast Asia

15:15 – 15:45 Discussion

What is the potential for finding plant biomolecular markers in addition to micro and macro fossils in the region? What field methods can be improved?

15:45 – 16:00 Coffee break

16:00 – 17:30 Overview of workshop and directions forward: Discussion led by Hallie Buckley

What are the "big questions" that might be answered as a result of both the new methods and sites presented?

17:30 End of Workshop

ABSTRACTS

(in alphabetical order of presenting author)

A mixed method, multi-scalar approach to identify domesticated rice (*Oryza sativa*) in pottery sherds from early Neolithic sites (4150-3265 cal BP) in Southeast Asia

Aleese Barron, Michael Turner, Levi Beeching, Tim Senden and Tim Denham

The Australian National University

While much archaeological literature has been dedicated to investigating the earliest origins of rice domestication in East Asia, relatively little attention has been given to exploring the spread of rice agriculture into Mainland and Island Southeast Asia. Unfortunately, due to the inconsistent application of archaeobotanical retrieval techniques, most archaeological rice remains from the region are in the form of rice tempered pottery, as both organic material and impressions, from which it has proved difficult to extract information about the domestication status of the rice plants represented. In this research, multiple analytical techniques were tested on a small sample of pottery sherds from Vietnam in order to assess whether the sherds firstly, contain rice temper, and secondly, if rice domestication traits can be observed within the clay matrices. Five imaging methods were tested, including macroscopic description, light reflected microscopy, scanning electron microscopy, 2D x-radiography and 3D computed tomography, in an attempt to apply spikelet base morphometric analysis in order to apply qualitative methods of determining domestication status in rice husks. It was found while both light reflected microscopy and SEM imaging could determine the presence of rice in pottery, only 3D tomography could provide the morphometric detail and appropriate orientation of view needed to identify domestication in spikelet bases.

Genomic admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean trading network

Nicolas Brucato[1], Pradiptajati Kusuma[1,2], Philippe Beaujard[3], Stéphane Mazières[3], Pascal Bailly[3], Jacques Chiaroni[3], Herawati Sudoyo[2,5], Murray P. Cox[6] and François-Xavier Ricaut[1].

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[5] Department of Medical Biology, Faculty of Medicine, University of Indonesia.

[6] Statistics and Bioinformatics Group, Institute of Fundamental Sciences, Massey University.

The Indian Ocean has long been a hub of interacting human populations. Following land- and sea-based routes, trade drove cultural contacts between far-distant ethnic groups in Southeast Asia, South Asia, Middle East and Africa, creating one of the world's first proto-globalized environments. The best examples of extensively admixed populations, resulting from overseas historical trading activities, are the Malagasy and the Comorian, the descendants of a unique admixture event between East African Bantu and Southeast Borneo individuals. Although these populations are a clear result of gene flow between distant geographical areas of the Indian Ocean rim, the extent of the diverse gene flows along the dense trading network of maritime routes, remains to be examined. Reconstructing admixture times from genomic data in 3,006 individuals from 187 regional populations reveals a close association between bouts of human migration and trade volumes during the last 2,000 years across the Indian Ocean trading system. Temporal oscillations in trading activity match phases of contraction and expansion in migration, with high water marks following the expansion of the Silk Roads in the 5th century AD, the rise of maritime routes in the 11th century and a drastic restructuring of the trade network following the arrival of Europeans in the 16th century. The economic fluxes of the Indian Ocean trade network therefore directly shaped exchanges of genes, in addition to goods and concepts.

Searching for the origins and antiquity of the Metabolic Syndrome in the Pacific Islands

Professor Hallie R Buckley

Department of Anatomy, School of Biomedical Sciences, University of Otago

Rates of Metabolic Syndrome (MetS) conditions, particularly hyperucaemia and gout, are extraordinarily high in some Polynesians populations. This high prevalence is due to a genetic predisposition for hyperuricaemia and other MetS conditions in these populations. Genetic and palaeopathological evidence trace the source of this predisposition to Austronesian peoples in Island Southeast Asia and show a gouty trail from Taiwan to New Zealand. This paper will discuss the palaeopathological evidence for this pattern and outline the importance of macroscopic analysis of skeletal collections alongside micro-techniques to aid in diagnosis.

Archaeobotany in Southeast Asia: Issues, results and prospects

Cristina Castillo

Institute of Archaeology, University College London & Graduate School of Agricultural Science, Kobe University

It is often suggested that archaeobiological investigations in Southeast Asia are limited because of preservation issues caused by the tropical climate. Whilst this is true to some extent, the retrieval of botanical macroremains has been successful in many sites across Mainland Southeast Asia consequentially we now have more information regarding the diet of prehistoric people and the ecology of the sites and their surroundings. Although most field archaeologists in Southeast Asia are still not routinely collecting samples for biological studies archaeobotanical data has grown considerably in the past 10 years with the use of flotation to retrieve macroremains and the collection of phytoliths. This growing dataset has resulted in different hypotheses about the emergence of rice agriculture in Southeast Asia, as well as a refined understanding of the 'beginnings of Indianisation.' I will present data from different sites I have worked in Southeast Asia which shape our understanding of Southeast Asian prehistory and relate some of the difficulties encountered when conducting research.

A Genetics of Social Change

Murray Cox

Statistics and Bioinformatics Group, Institute of Fundamental Sciences, Massey University

The history of the Indonesia – the extraordinary process of settling an island world – has long caught the attention of genetic researchers. More than ninety years after the first molecular anthropology was undertaken in the region, the broad outline of the archipelago's history has been sketched with some certainty. This talk will survey how genome-scale data is now both confirming and rewriting Indonesia's past.
In particular, using computer modeling and the latest genome scale data, we will consider the social actions of Indonesian peoples and how their genomes may have responded to them.

Evolutionary explanations for high metabolic disease burden among Austronesian-descendant populations

Anna L. Gosling

Department of Anatomy, School of Biomedical Sciences, University of Otago

Many Pacific populations have high rates of metabolic disease including diabetes and gout. This has often been explained as being the result of selection for a "thrifty genotype" in Polynesian populations, however examination of epidemiological data surrounding serum urate levels suggests that this phenotype may be common to Austronesian-descendant populations in general, not only those in Remote Oceania. Several alternative explanations including ancient ancestry and selection for a hyperuricaemic phenotype in malarial environments will be discussed.

Understanding human origins, Palaeoecological interactions, and dietary adaptations in the insular Wallacean region

Stuart Hawkins, Sue O’Connor, Julien Louys

The Australian National University

Wallacea (eastern Indonesian islands of Sulawesi, Halmahera and the Lesser Sunda Islands including Timor-Leste) is a unique region where some of the earliest human maritime adaptations to depauperate terrestrial islands have been reported. Hominins had to adapt to significant changes in climate and ecology over several millennia while traversing this archipelago using water-transport. Zooarchaeological data, as part of a large multidisciplinary project, is currently being used to reconstruct human subsistence adaptations to changing climate and environment conditions at key sites in Timor-Leste (Laili Cave, Uai Bobo, and Matja Kuru 2), and Alor Island, eastern Indonesia (Tron Bon Lei and Makpan). The data indicate that humans effectively adapted to faunally depauperate islands and climate change since the Late Pleistocene. However, clear knowledge gaps have become apparent due to limitations in archaeological sampling, preservation, and methodology. Researchers are still coming to terms with the timing and origins of human movements into the region. Issues of high level non-specific taxonomic identification of vertebrate remains, a lack of pollen core data and poorly understood palaeohabitats of extinct species have hampered palaeoenvironmental reconstructions. A lack of archaeobotanical data has limited our understanding of the full spectrum of hunter-gatherer and horticulturalist development with regards to socioeconomic activity. Multiproxy analyses of faunal material that include zooarchaeology, ZooMS, stable isotopes, dental calculus, archaeobotanical, palaeoecological (pollen), and aDNA studies are necessary to advance our knowledge of these critical issues.

Ancient protein analysis: emerging methods and applications to ancient dietary studies

Jessica Hendy

Department of Archaeology, Max Planck Institute for the Science of Human History

The analysis of ancient proteins is emerging as a new research field in archaeological science, with wide promise for understanding past diets, diseases, biomolecular taphonomy, phylogeny and evolution. In addition, analysis of collagen peptide mass fingerprints using zooarchaeology by mass spectrometry (ZooMS) is increasingly routinely utilized to expand zooarchaeological datasets and, in some contexts, provide taxonomic clarification. In recent work examining ancient dental calculus and ceramic residues, we have been able to detect species-specific dietary proteins of both plant and animal origin, and thus identify the processing or consumption of past foodstuffs with high taxonomic and tissue-specific resolution. This presentation will outline the methodological strategies of ancient proteomic techniques, and outline how such analyses may provide new insights into the dietary strategies of past populations, in the hope of seeding ideas for novel applications in regions where these techniques have not yet been applied.

Using chemical analysis of human skeletal tissues as a proxy for environmental change

Charlotte King

Department of Anatomy, School of Biomedical Sciences, University of Otago

In the Southeast Asian context, environmental change and its impact on human subsistence and social organisation is beginning to take a more prominent role in archaeological modeling. In particular, changes to monsoon strength in the Iron Age have been hypothesised to have triggered the emergence of fixed social hierarchy and water management strategies in northeast Thailand. Currently these models are primarily based on the few lake core sequences that exist for this important transitionary period (Lake Kumphawapi and Lake Pa Kho). These lakes, however, are geographically removed from the archaeological sequences they are used to explain. As a consequence, there is a general paucity of regionally-specific palaeoenvironmental data with which to quantify changes to the environment in prehistory. There are, however, numerous large δ^{18}O datasets which have been generated from the analysis of dental enamel carbonate in both human and faunal remains from archaeological sites. Usually generated for the purposes of assessment of human palaeodiet/mobility, δ^{18}O datasets have generally be dismissed as too complex to be of use in the Southeast Asian context. We suggest, however, that these are an untapped resource in terms of tracking environmental change. In this paper we will discuss how human/faunal bioapatite δ^{18}O data fits with current palaeoenvironmental modeling, and the data that needs to be gathered in the future to fully-explore site-specific changes in hydrological regimes.

Ancient DNA preservation in Southwest Pacific human remains

Kathrin Nägele, Cosimo Posth and Johannes Krause

Department of Archaeogenetics, Max Planck Institute for the Science of Human History

Whole genome analyses of ancient human remains are providing new insights into the understanding of human population history. The retrieval of ancient DNA (aDNA) is however limited not only by time but also by environmental conditions. While in temperate climate regions, nuclear aDNA has shown to survive under ideal conditions since the Pleistocene, tropical climates represent an obstacle for nuclear aDNA preservation even from much more recent times. For this reason, aDNA studies in the southwest Pacific have been until recently limited to mitochondrial DNA (mtDNA) analyses. Those have, however, limited power to infer detailed demographic processes compared to genome-wide data.

Sampling different skeletal elements paired up with next generation sequencing technologies have been investigated to maximize the yield of endogenous DNA. In particular, extracting DNA from the petrous portion of the temporal bone has recently allowed reconstructing genome-wide data from ~3,000-year-old Pacific human remains. We screened teeth and petrous bones from several individuals across the Southwest Pacific, ranging from approximately 5,000 to 200 years BP. We describe overall differences between petrous bones and teeth not only regarding DNA preservation but also in the relative proportion of mtDNA compared to nuclear DNA. We additionally performed targeted enrichment of genomic regions with the aim of genetically disentangle the succession of events in the peopling of the Southwest Pacific.

Unusable or under-explored? The potential for archaeologically-directed stable isotope studies in the Late Pleistocene and Holocene of Mainland and Island Southeast Asia

Patrick Roberts

Department of Archaeology, Max Planck Institute for the Science of Human History

Archaeologically-focused stable isotope studies of tropical environments have remained relatively limited due to the hostility of these settings to bone collagen preservation. Nevertheless, methodological advances and new applications have meant that novel information, relating to human diets, environments, and mobility, can be obtained through stable isotope studies in the tropics, including hyper-humid tropical forests. Here, I review three main potential avenues of stable isotope research in tropical Late Pleistocene and Holocene Mainland and Southeast Asia. These are a) the stable carbon and oxygen isotopic study of human tooth enamel to test hypotheses regarding changing human ecologies and adaptations, b) the stable carbon and oxygen isotopic study of faunal tooth enamel from an archaeological sequence to provide information relating to the fluctuating environments exploited by human populations, and c) the compound specific isotope analysis of leaf waxes in archaeological and natural sediment sequences to provide long-term, highly-resolved palaeoclimatic information. The potential benefits, and current limitations, of these methods are explored and general recommendations made for the factoring in of stable isotope analysis into multidisciplinary, biomolecular studies in Southeast Asia.

Prospects for Bulk Bone metabarcoding in Southeast Asia

Frederik Seersholm

Curtin University

The study of fossil assemblages is a valuable tool to gain insight into the biodiversity of the past. However, current morphological methods to study bone fragments are limited by low taxonomic resolution and relies heavily on the identification of well-preserved bone fragments. Bulk-Bone metabarcoding (BBM) is a DNA based method which effectively recovers the species composition from a given sample by converting non-diagnostic bone fragments into powder which is then genetically indexed, amplified and sequenced.

Due to the warm and humid climate in Southeast Asia and the associated poor DNA preservation, ancient DNA (aDNA) studies in this region has historically been limited. As opposed to traditional aDNA methods based on bone-by-bone analysis, BBM provides an alternative that allows for a characterisation of up to a hundred bones in one extraction. Hence, with the uncomplicated screening of thousands of bones in one batch of sample preparation using BBM, the chance of finding bones with well-preserved DNA is greatly increased.

BBM has been successfully applied at a number of sites with challenging preservation conditions in Australia, New Caledonia, Belize and Zanzibar. From the archaeological site at Mapangani in Zanzibar, BBM identified 40 different taxa, representing at least 31 different species. Among these were 5 species of fish and the lipspot moray eel (*Gymnothorax chilospilus*) all of which were not picked up by traditional morphological techniques. This demonstrates how BBM can be used to overlay genetic data over more traditional archaeological analyses in areas with challenging environments such as Southeast Asia.

The pace and rhythm of climate: 600,000 years in a biological hotspot

Janelle Stevenson[1], Marco J.L Coolen[2], Sarah Ivory[3] and Rebecca Hamilton[1],

1. Department of Archaeology and Natural History, Australian National University

2. WA-Organic and Isotope Geochemistry Centre (WA-OIGC), Curtin University

3. Department of Earth, Environment, and Planetary Science, Brown University

Utilising pollen and ancient chloroplast DNA coupled with a record of compound specific stable isotopes ($\delta13C_{\text{leaf wax}}$), this project aims to produce a record of terrestrial vegetation, fire and biodiversity that is innovative in its resolution of vegetation change and unrivalled in age depth for southeast Asia.

The project is part of a much larger international research effort being carried out in Sulawesi, Indonesia and supported by the International Continental Scientific Drilling Program (ICDP). The focus of the research program is Lake Towuti, the largest deep lake in Indonesia. Drilling took place in 2015, resulting in the collection of approximately 1000 m of sediment from eleven boreholes centred on three drilling locations. The maximum core depth recovered was 175 m below the lake floor, capturing the entire sedimentary infill of the basin and estimated to cover the last 600,000 years. While the analysis of the sedimentary sequence has only just begun, initial data from core and borehole logging reveals the evolution of a highly dynamic system.

The ultimate goal of the larger program of research is to better understand the timing, patterns and mechanisms of climate and rainfall in the Indo-Pacific Warm Pool, a significant driver of the Earth's climate.

Investigating human-environment interactions through stable isotope analysis of Pacific rats (*Rattus exulans*)

Jillian A. Swift

Max Planck Institute for the Science of Human History

Pacific rats are widely distributed throughout Oceania, and their remains are often recovered in abundance from even the earliest layers of archaeological sites. The rat's close commensal relationship with humans, along with their omnivorous and opportunistic feeding behaviors, allows rat dietary stable isotope analyses to provide new insight into local site activities and ecological change. Carbon and nitrogen stable isotope ratios from rat bone collagen serve as a proxy for understanding nutrient flows within anthropogenic food webs. Through this lens, variations in rat δ^{13}C and δ^{15}N values can inform on large-scale social-ecological processes including soil nutrient depletion, fire ecology, and species extinctions, as well as localized changes to human subsistence and site activities. Case studies from several Polynesian islands demonstrate the potential and interpretive challenges within this approach, and consider applications of this method to other regions and commensal taxa.

Tracking the interaction between Papua and Near Oceania in Holocene time

Marlin Tolla

Regional Office of Archaeology for Papua-Indonesia

The Lapita culture appeared on the Bismarck Islands 3500 and about 2500 Years BP and reached the area of Near Oceania and also Papua, which is partly an Indonesian island. In Papua, the influence of Lapita culture is strongly distributed in the northern coast, especially in the area of Geelvink Bay and Port Numbay. Based on the archaeological and ethnographical data, the appearances of Lapita culture in these areas has furthermore becoming a red line that shows the interactions occurred between the island of Papua and Near Oceania in the past, especially in Holocene time. Above all, it seems pertinent to remember that the interactions between the island of Papua and Near Oceania in the time of Lapita spreading was not just limited to pottery, the influence also included the introductions of other culture variants, such as plants and animals, between the islands. In Geelvink Bay and Port Numbay areas, the number of archaeological sites are rich with Lapita pottery associated with the marine and terrestrial biotas, *Canarium* nuts as well as human remains, teeth, marsupials, monetremes and Suidae bones. The variants of archaeological evidence are considerable and used to track the interconnections between the islands.

The analysis of archaeological findings through traditional way, for instance with morphological analysis, is limited in several ways, in precision and misleading interpretation. Thus this topic could be further developed by applying microbiological techniques.

Vietnam to Vanuatu: Dental Calculus and the Austronesian Expansion

Monica Tromp

Department of Archaeology, Max Planck Institute for the Science of Human History

The prevailing model for Austronesian expansion is the “Out of Taiwan” model that suggests an agricultural and ceramic maritime culture originating in Taiwan approximately 4,000 BP travelled through Island Southeast Asia (ISEA) and Melanesia before expanding into the wider Pacific by 3,000 BP. However, conflicting linguistic and genetic data suggest this model is too simplistic, not taking into account the influence of pre-Neolithic interactions between Mainland Southeast Asia (MSEA) and ISEA prior to and after the Austronesian expansion.

The Austronesian expansion is primarily linked with the spread of Austronesian languages from Taiwan but also with a MSEA and/or ISEA Neolithic cultural “package” that included commensal plants and animals. Genetic and cytological data show pre-Austronesian influences to the “package” from New Guinea (e.g. sugar cane and banana) and Vietnam (e.g. pigs) that eventually spread into Oceania. In contrast, the Neolithic Taiwanese parts of the “package” such as agricultural rice production appear to have been lost by the time the expansion reached SW Oceania. In ISEA the picture is murkier and it is unknown how much of an influence New Guinean (Oceanic) plants and animals may have had prior to and during the expansion compared to those derived from MSEA.

This project will use microfossil, proteomic and genetic techniques on human dental calculus spanning at least 3,000 years and twice as many kilometres to refine our understanding of the Austronesian expansion including not only the dispersal patterns of people, but also their domesticates, health and diseases from MSEA, ISEA and into Vanuatu.