Speakers and Abstracts

<u>Adrian Viliami Bell</u>
Measuring Driving Factors While Capturing Uncertainty in the Settlement of Near and Remote Oceania
I present a new statistical model that measures the strength of competing theories in the settlement of Near and Remote Oceania. Using a model selection approach, I further utilize a Bayesian framework to incorporate the uncertainty in settlement times by introducing them as informed priors, thus reducing the strength of assumptions behind settlement chronology. This approach also allows us to test for the robustness of results by artificially increasing the uncertainty behind settlement dates. With this new approach, my collaborators and I show that models of exploration angles and risk performed considerably better than models using inter-island distance, suggesting early seafarers where already adept at long-distance travel. These results are robust even after substantially increasing settlement date uncertainty.

<u>Robert Blust</u>
Science, Language and Prehistory
I begin with a brief commentary on the commonly-perceived pecking order in the sciences (physical > biological > social), which is sometimes an obstacle to cross-disciplinary communication. Then a word or two on the Austronesian homeland as seen by linguists, archaeologists and geneticists. As an aside I will comment very quickly on the Austro-Tai hypothesis, and in particular on the position of the Kra-Dai languages vis-a-vis Austronesian. This will be followed by a few remarks on Austronesian culture history, and the way that some archaeologists, and even one linguist, have zealously over-interpreted negative archaeological evidence in an attempt to show that the achievements of Austronesian historical linguistics over the past 80 years cannot be trusted. Finally I will note why (cultural) anthropology needs (historical) linguistics.

<u>Nicole Boivin, Alison Crowther and the Sealinks Project team</u>
The westward Austronesian expansion – multidisciplinary perspectives
While Austronesian expansion into the Pacific is now increasingly well understood from decades of intensive, multidisciplinary study, the later westward movement of Austronesians into the Indian Ocean, which led to the colonisation of Madagascar, remains hazy. In particular, while linguistic, cultural and now genetic studies all confirm the movement of people from Southeast Asia to Africa, probably some time in the latter half of the first millennium AD, archaeological evidence for such a dispersal remains frustrating elusive. We present evidence for a potential Austronesian archaeological signature in the archaeobotanical record of eastern Africa. This provides insights into the timing and process of Austronesian expansion into the region. We also present multidisciplinary evidence from zooarchaeological, aDNA, proteomic and modern genetic studies of various domestic and commensal animal species to shed further light on patterns of past biological exchange across the Indian Ocean, and their relationship to the maritime activities of agents from Southeast Asia and elsewhere. Our results suggest the need for closer integration between researchers studying the various branches of the Austronesian expansion, as well as for further research in Island Southeast Asia to fully understand archaeological and genetic patterns emerging in eastern Africa.

<u>David Burley</u>
Polynesian Origins in the Fiji/Tonga Interface
The "Holy Grail" of research questions for the settlement of Remote Oceania has been Polynesian origins. At a conference that integrates archaeologists, linguists, geneticists and bio-molecular researchers, the question itself becomes complex, for our definitions of Polynesian and origins are not necessarily compliant. Archaeological data for the Fiji/Tonga interface now provide a well-defined chronology and specific insights into the historical relationships of peoples across the Melanesian/Polynesian divide. These data beg the question not of when or where Polynesians

became Polynesian, but of how. The implications for linguistic and bio-molecular interpretations of Polynesian genesis are posed.

Bethwyn Evans
Micro-processes and macro-patterns in understanding the past
Human history is often modeled from two perspectives: that of macro-evolution and general historical processes which can explain patterns of similarity and difference across populations, and that of micro-evolution and processes of social transmission among individuals within a population which can explain patterns of continuity and change. In historical linguistics these two perspectives can lead to quite different models of change and interpretations language history. This talk takes as a case study the investigation of the history of southern Bougainville (Papua New Guinea) through historical linguistics, cultural anthropology and population genetics, and asks how macro- and micro-evolutionary perspectives can be more tightly integrated in our understandings of the past.

Alex François
Subgrouping without trees - How the linkage model redefines language genealogy
Contrary to widespread belief, there is no reason to think that language diversification typically follows a tree-like pattern, consisting of a nested series of neat splits. Language evolution normally involves multiple innovations spreading across a network of idiolects, typically resulting in entangled isoglosses. Insofar as these events of language-internal diffusion are later reflected in descendant languages, the sort of language family they define – called "linkage" by Ross (1988) – is one in which genealogical relations cannot be represented by a tree, but only by a diagram in which genealogical subgroups may intersect.
We thus need non-cladistic models to represent language genealogy. This talk will focus on an approach that combines the precision of the Comparative Method with the realism of the Wave Model. This method, labeled Historical Glottometry (François 2014), identifies genea¬logical subgroups in a linkage situation, and assesses their relative strengths based on the distribution of innovations among modern languages. Provided it is applied with the rigour inherent to the Comparative Method, Historical Glottometry should help unravel the genealogical structures of the world's language families, by acknowledging the role played by linguistic convergence and diffusion in the historical processes of language diversification.

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Emily Gasser
Cenderawasih Bay and the Structure of SHWNG
Unlike its better-studied sister, Oceanic, little is known about the linguistic relationships within the South Halmahera-West New Guinea subgroup of Austronesian. Many of the languages comprising the group are themselves severely underdocumented; despite a few recent comprehensive documentation projects, the only data available for most SHWNG languages is a wordlist collected by late-19th-century Dutch missionaries, and for many even that does not exist. Comparative work is even rarer, and little exists by way of well-founded proposals for subgrouping within the family. David Kamholz's (2014) dissertation presents a thorough comparison of these languages based on the Comparative Method, and his results diverge significantly from prior assumptions by placing the Raja Ampat languages in a clade with those of South Halmahera, rather than the Bird's Head and Cenderawasih Bay varieties. This talk considers the results of applying statistical modeling of language change based on lexical data to compare Kamholz's tree to the more traditional model of the SHWNG group, to further illuminate the relationships between these little-known languages.

Michael Gavin
Why are so many languages spoken in the Pacific?: Exploring new frontiers with interdisciplinary research and synthesis

I will argue that some of the biggest and most interesting questions research can address require a synthetic and interdisciplinary approach. However, this can prove challenging given the structure of funding and research organizations. Synthesis centers provide a mechanism for overcoming these barriers. I will report results from research on the geography and evolution of cultural diversity from international and interdisciplinary working groups at a U.S. National Science Foundation synthesis center. One central question has been: why do Pacific islands that cover a small fraction of earth's surface and contain an even smaller portion of the population support over 25% of the world's languages? We have used analytical approaches developed in ecology to test answers to this question proposed by diverse fields. Our results demonstrate the role social and environmental factors have in creating language diversity patterns, and provide examples of the power of modeling approaches that shed light on underlying mechanisms shaping human diversity.

Simon Greenhill
Phylogenetic trees and the complexities of Austronesian prehistory

We are often told that language family trees tend to oversimplify the myriad complexities of human prehistory - trees are boring!
In 2009 we published a large Austronesian language phylogeny, however there were a number of shortcomings in both the data and the methods.
In this talk I will present some new phylogenetic analyses of the Austronesian language family, that fix these shortcomings. I will show how these trees provide
new insights, and, rather than oversimplifying human prehistory, reveal some of the complexities at play in the peopling of the Pacific.

Michiko Intoh
Cultural Role of Prehistoric Coral Islanders in Micronesia

Micronesia has a complex history of human dispersals. Linguistic studies have been successfully demonstrated a complex colonization scenario. Following the first movements around 1500BC into western Micronesia (i.e. the Marianas, Yap and Palau), the second movements were made by Nuclear Micronesian speakers around 2000 years ago from Melanesia to the central and eastern parts of Micronesia. The third movements were made by the Polynesian-speaking people to two atolls, Nukuoro and Kapingamarangi. Archaeological evidence has broadly agreed with this scenario.

Beside these major colonization movements, a number of interactions among islands after initial settlements have been demonstrated by archaeological evidence. Some of such evidence is significantly diverse compared to the linguistic model. This paper presents archaeological evidence obtained from Fais Island in the Central Caroline Islands that clearly shows a complex history of interactions of the islanders within and beyond the Micronesian islands. A number of items including pottery, fishing gear, animals and some technological knowledge were transported to Fais from different directions at different timings. A multi-disciplinary examination will be made to understand the nature of the prehistoric interactions in the region.

Albert Min-Shan Ko, Qiaomei Fu, Ying-Chin Ko, Mark Stoneking
**Genetic Perspectives on Formosan ancestry**

A skeleton was recently excavated from the Liang Island of Matsu Archipelago, located in the Taiwan Strait, between China and Taiwan. It is termed the Liangdao Man, who is AMS-C14 dated to about 8200 years ago. We sequenced the mitochondrial DNA of the Liangdao Man. The maternal lineage is haplogroup E, which has no detectable descendants in China but is found among Austronesian speakers from Madagascar to Near Oceania. Our analysis shows the specimen is closest to aboriginal Taiwanese, thus connects the Austronesian dispersal to coastal Fujian 8000 years ago. We also reconstructed the Formosan mitochondrial phylogeny to understand the Neolithic peopling of

Taiwan. It describes a rapid dispersal of early people from north to south of the island. We estimate the genetic formation of Formosan groups started about 3400 years ago in southern Taiwan. From there, we have also started to analyze the sources of Formosan genetic ancestry in China and their phylogenetic relationships with ethnic groups in China to see if there are any deeper structures to the origin and development of Austronesian peoples.

Stephen Lansing
Kinship practices explain the coupling of language and gene trees
Language trees have been observed to mirror gene trees from local to global scales. This suggests that languages and genes evolve in tandem as the communities that carry them split and diverge, but this model is inconsistent with the widespread mobility observed between communities. Instead we require a model that explains correlations between genes and languages, while accounting for high rates of migration and language adoption. Here we show that the critical variable is that human movements are not random, but highly structured. Finely resolved co-phylogenies of languages and genes from villages on the island of Timor reveal patterned movements between stable speech communities, causing language and gene trees to track each other.
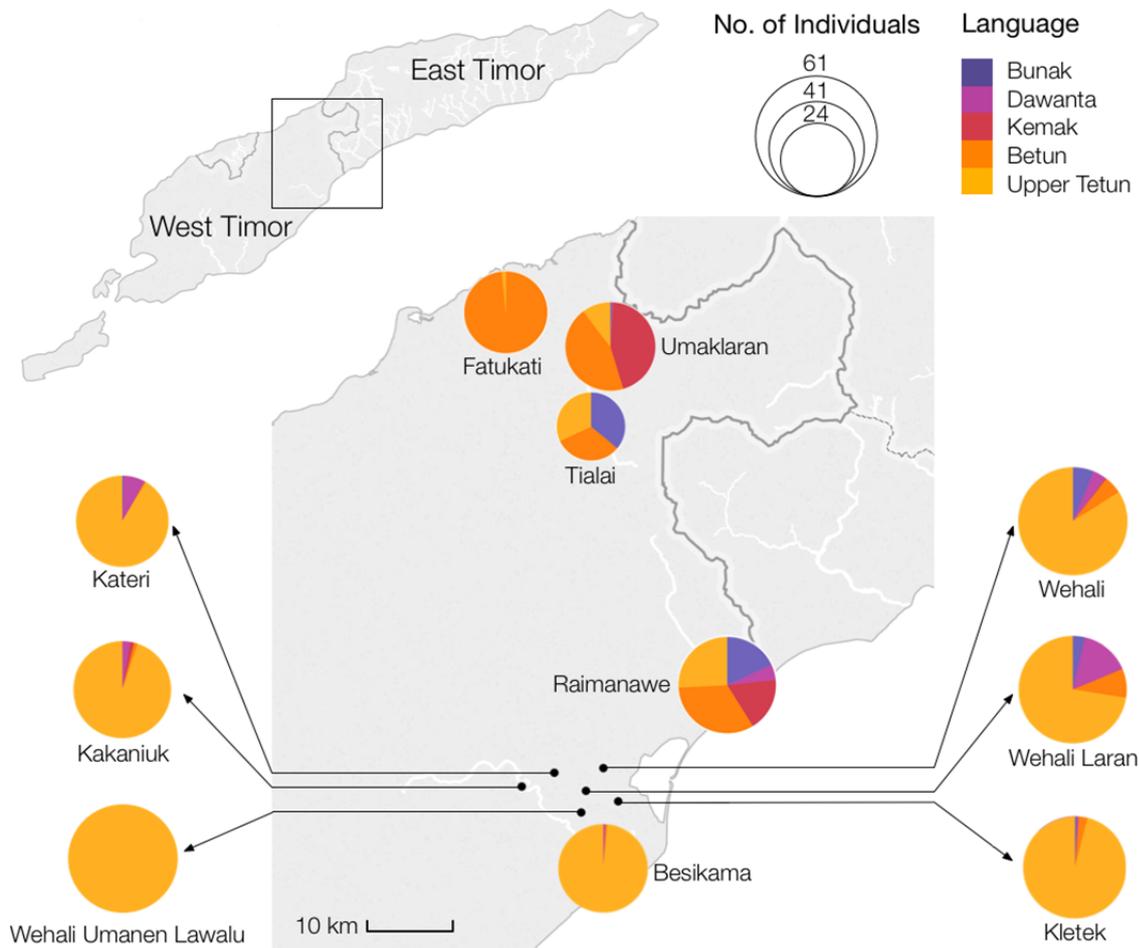
Johann-Mattis List
The Future of the Comparative Method
The comparative method is one of the most peculiar aspects of historical linguistics. Although termed a method, it does not constitute a formal procedure, but rather covers a bunch of techniques that historical linguists commonly use to reconstruct the history of languages and language families. These techniques are seldom explicitly taught to students of historical linguistics. It is rather expected that young historical linguists acquire them in practice (Schwink 1994), and the method has proven

very successful in resisting all major attempts of modification, be it simplification (Greenberg 1987), formalization (Hoenigswald 1960), or automatization (Holman et al. 2008): Throughout more than 150 years of research, the comparative method has remained the standard procedure to prove language relationship, carry out language comparison, and reconstruct proto-languages. And even the recent quantitative turn in historical linguistics has not been able to challenge its status. Not only is the comparative method still regarded as the sole method that can reliably prove that two or more languages go back to the same ancestor, it is also the main means by which datasets for quantitative approaches are produced: Since it is generally assumed that it is impossible for computational approaches to cognate detection to reach any near-human performance, the major work of cognate assignments in the large lexical comparative databases, like the Austronesian Basic Vocabulary Database or the Indo-European Lexical Cognacy Database, is still carried out manually by experts working in the framework of the comparative method.

Given the important role that the comparative methods plays in historical linguistics, it is important to keep in mind that it is not free from flaws and shortcomings. One major shortcoming is the speed by which it can be applied. Being a method that is basically carried out without any computational support, it takes scholars years and sometimes even decades to come up with convincing solutions for the history of a given language family. Due to the lack of a fixed formalized workflow and an agreed-upon norm for data representation and exchange, one can further note a significant lack of transparency regarding the presentation of the results. Thus, up to today, etymological dictionaries are the main form of data-presentation. Etymological dictionaries, however, are a very impractical form of data-presentation: it is difficult to query them for items of interest, there structure is basically left to the expert and can vary greatly among different scholars, and the underlying structures are very complex, containing many comments or intuitive assessments, so that it is incredibly difficult to investigate them quantitatively. As a result, etymological dictionaries are not only quite error-prone, but it is also very difficult and time-consuming to check their quality in an objective manner.

If we want to improve in integrating inferences about our past, be it for specific research questions regarding the peopling of the Pacific and South East Asia, or for more general questions regarding the methodological basis of historical linguistics, we need to enhance the transparency of the comparative method and find a way to smoothly integrate both the findings of different researchers and the findings of automated procedures. In the talk, I will address these issues in detail and with help of examples from actual research practice in the fields of Austronesian and Sino-Tibetan linguistics. I will propose initial solutions for certain shortcomings of the comparative method and point to questions which seem very hard to solve at the moment. In this way, I hope to instigate a vivid discussion among traditional and computational linguists and increase the awareness that transparency in research is the key for the integration of different findings and inferences about our past.

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Anna-Sapfo Malaspinas
Transpacific contact: a genomics perspective
The mode and tempo of the colonization of the Americas before it was discovered by Europeans remains contentious. After more than a century of study the majority of available genetic, archaeological and linguistic evidence supports one or more pre-Columbian migration event(s) from Siberia to North America around 15-30 thousand years before present, followed by an expansion into South America. Prehistoric or historic connections between South America and Southeast

Asia/Oceania have been noted including similarities in culture, human skull morphology and domestic breeds, but until recently no genetic evidence from humans has been found to support such contact.

We discuss two suggestive lines of evidence of a human transpacific contact. First we present morphological, isotopic, 14C dating, and genomic sequence data from two human skulls identified as belonging to the indigenous Botocudo peoples from the state of Minas Gerais, Brazil. We find that their genomic ancestry is Polynesian, with no detectable Native American component. Moreover, radiocarbon analysis of the skulls suggests a most likely date around 1650 AD, a time where Polynesia was still effectively unknown to Europeans.

Second, we present genome-wide data for 27 Easter Islanders. By using non-parametric multidimensional statistics and clustering methods, we show genome-wide patterns consistent with both Native American and European admixture. We infer local ancestry tracts and, by comparing their distributions, we find that the Native American admixture predates the European admixture event with Easter Islanders. Using a simple model of discrete pulses of admixture, we estimate that the Native American admixture happened around AD 1360 (21 generations ago) and the European admixture happened around AD 1870 (four generations ago).

We discuss possible scenarios and conclude that in both cases our findings could represent genomic evidence of Polynesians reaching South America during their Pacific expansion.

Lisa Matisoo-Smith
Reconsidering models for Pacific prehistory: Evidence from ancient and modern human and commensal studies
The initial settlement of Remote Oceania has been associated with the spread of the Lapita Culture and the Oceanic subgroup of Austronesian languages. But what is the actual biological evidence about the people who transported the Lapita culture and spoke these Austronesian languages? Mitochondrial DNA data, both ancient and modern, obtained initially from commensal animals (those transported by humans during colonisation) and more recently from human populations suggest that things may be slightly more complicated than the traditional two wave theory often presented. As genetic data accumulate, we are beginning to see that there is much more variation both in past and modern populations than previously thought, which I argue may indicate a more complex and dynamic history for Pacific peoples than often presented.

Weera Ostapirat
Linguistic inferences on Austro-Tai cultural history
This paper discusses the shared vocabulary items between Kra-Dai and Austronesian from a semantic field perspective. While Kra-Dai and Austronesian lack shared words of rice terms, they show related forms for taro, sesame, chaff, to plant and potentially the early etymon for cultivated field. For faunal terms, KD and AN share such words as bear, otter, bird, centipede, but they have a completely different set of etyma for domesticated animals such as dog and pig. The ancestral Austro-Tai people may have subsisted on tubers, collected edible seeds (including wild rice grain), and just practiced an early stage of cultivation. When KD and AN parted, the society they lived in might not be full-fledgedly agricultural. KD has a good word for 'boat' that can be related to AN *aluja 'paddle, canoe' but otherwise appears to be land-oriented contrasting to the sea-oriented AN, who has rich etyma in sea/navigation related fields. Related kinship terms, personal pronouns, deictics, numerals and body parts are well represented. The issues of homeland and language contact will be discussed.
Keywords: Austro-Tai, Kra-Dai, Austronesian, East Asian language families, cultural history

Adam Powell
Human demographic inference in population genetics

Genetic phylogeographic approaches to inferring human demographic history have proved extremely popular over the last few decades. It is, however, a seriously flawed methodology. In this talk I will summarize the problems of genetic phylogeography and then introduce some of the recent model-based approaches developed by population geneticists to overcome these limitations. Finally, I will demonstrate the gene-culture coevolution inference framework I have developed, which allows demographic inference from geographically-explicit simulation of both genetic and cultural systems.

Irina Pugach, Ana T. Duggan, Mark Stoneking
The gateway into Remote Oceania: new insights from genome-wide data

The widely accepted two-wave scenario of human settlement of Oceania involves the first out-of-Africa migration ca 50,000 ya and the last pre-European dispersal of people, known as the Austronesian expansion, which reached the coasts of Papua New Guinea by 3,000 ya. Earlier genetic studies provided evidence for the extensive sex-biased admixture between the incoming and the indigenous populations, which occurred prior to the expansion into the Remote Oceania. Some archeological, linguistic and genetic evidence however paint a more complicated picture of settlement, indicating that the two-wave scenario is incomplete. To study regional variation in Oceania in more detail, we have compiled a large genome-wide dataset of populations sampled across the Solomon Islands archipelago. The dataset also includes samples from Australia, Papua New Guinea, island of Santa Cruz (a known genetic outlier), Polynesians, as well as populations from East Asia, Taiwan and India. The Solomon Islands connect Near and Remote Oceania, and as such served as a gateway to settlement of the Pacific. With this dataset we are investigating the movements of people across the Solomons and their timing, as well as potential contact between populations following expansion into Remote Oceania.

Martine Robbeets
Austronesian influence and Transeurasian ancestry in Japanese

The Japanese language displays remarkable similarities with the Transeurasian (traditionally "Altaic") languages as well as with the Austronesian languages. This fact has given rise to a certain polarization in classification attempts between scholars who try to relate Japanese to the Transeurasian languages on the one hand (e.g. Miller 1971, Vovin 1994, Starostin et al. 2003; Robbeets 2005) and others who try to relate it to the Austronesian languages on the other hand (e.g. Kawamoto 1985, Benedict 1990), with consensus approaches such as the idea that Japanese is a language of Transeurasian ancestry on an Austronesian substratum (e.g. forword Poppe in Miller 1971) or a mixed language (e.g. Murayama 1976, Maher 1996, Sakiyama 1996). The aim of my presentation is to propose an alternative scenario that reconciles prehistoric Austronesian influence with Transeurasian ancestry and brings together data from linguistics, archaeology and genetics. To this end, I will propose a hypothesis that correlates the Transeurasian homeland with the early Neolithic Xinglongwa culture (6000-4800 BC) situated in Southern Manchuria in the sixth millennium BC and situates the homeland of Japanic on the Liaodong peninsula between the third and second millennium BC, with its speakers taking part in the Liaodong-Shandong interaction sphere. The Japanese-Austronesian linguistic similarities have often been viewed in the light of a possible Jomon-Pacific connection, but there is hardly any interdisciplinary support for such a scenario. However, situating proto-Japonic in the Liaodong-Shandong interaction sphere may leave room for a prehistoric contact scenario between Japanic and para-Austronesian when these languages were still spoken on the continent.

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Malcolm Ross
Comparing phylogenies: the Austronesian languages of Northwest Melanesia

Two phylogenies of the Austronesian languages of Northwest Melanesia are compared, one derived by the comparative method of historical linguistics, based on various shared innovations, the other by a Bayesian phylogenetic analysis of lexical data. Reasons for their differences are discussed, among them the difficulty entailed in assuming that a tree is a conceptually adequate model. In conclusion, implications are sketched for both approaches and for the history of languages in the Northwest Melanesian area.

Laurent Sagart
Why Tai-Kadai is Austronesian

This paper describes possible lexical and phonological innovations shared uniquely by Tai-Kadai and Malayo-Polynesian languages. It discusses a proposal that Tai-Kadai has inherited from Austro-Tai vowel distinctions which have been lost in Austronesian. Finally, in an attempt to clarify the way of life of the earliest Tai-Kadais, it examines the Tai-Kadai cultural vocabulary of Austronesian origin, pointing out the importance of fishing and questioning the centrality of cereal production.

Christophe Sand
One or a series of human movements into Southern Melanesia? Unsecure assumptions and real questions: the need for an interdisciplinary approach

The research on the long-term history of Island Melanesians remains influenced by a number of approaches that are not strictly archaeological. The identification of a chronological divide between Near and Remote Oceania has led to a puzzling assumption that the Lapita spread was associated to Proto-Polynesian populations, followed by a supposed "Melanisation" of Southern Melanesia and Fiji. Some teams have highlighted the absence of any clear cultural break in the archaeological data, favoring instead cultural continuity. This does not exclude a complex first Lapita settlement process, followed by secondary regional influences, be they cultural, genetic and/or linguistic. An ideal place to study these questions is the archipelago of New Caledonia, isolated at the southern tip of the Melanesian crescent. The unique linguistic aspects of a number of Kanak languages, the archaeological questioning around topics like the petroglyphs and the regional ties of the Plum ceramic tradition, as well as oral traditions recalling intrusion of news Oceanic groups during the pre-contact period, might signal a more complex human history than what archaeology alone can propose.

Paul Sidwell
Phylogeny, innovations, and correlations in the prehistory of Austroasiatic
Phylogenetic analysis of the Austroasiatic (AA) Language phylum suggests a complex regional prehistory punctuated by phases of rapid expansion and diversification in and out of Indo-China/Lower Mekong Basin. Of particular note:
• 13 branches become clearly distinguished between 5000 and 4000BP;
• From around 2500 years BP groups in Indo-China, Malay peninsula, and the western periphery, diversify rapidly;
• Northern groups share lexical innovations, while the periphery retains more archaic elements such as the rice related vocabulary.
Archaeology currently dates the arrival of rice (and brass) in the region at about 4200BP, which currently presents problems of interpretation for linguistics. Was there a deeper and more complex history for agriculture in MSEAsia, such as a relation between rice and tuber cultivation (Sidwell and Blench 2011); are we wrong about the phylogenetic structure of AA (e.g. the place/age of Munda)?

The significance of metals also invites discussion; does the Iron Age in SEAsian correlate with the increasing contact between AA, Austronesian, Tai or Tibeto-Burman speakers in the 1st Millennium BC?

It is clear that a combination of improved linguistic data and computational methods, in the context of an integrated multidisciplinary approach, hold the best prospects for advancing our understanding of these complex cultural transitions.

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Frederique Valentin
Is the biological origin of Polynesians solely Lapita derived?
The eastward expansion of Austronesian speaking people and bearing the Lapita culture complex within Remote Oceania is generally viewed as the source of the Polynesian peopling. However, evidence gained from the associated human skeletons appears to be in contradiction with this view. Pietrusewsky et al (2014) noted that "the results of this new biodistance analysis do not support Late Lapita people as ancestors of Polynesians" as a conclusion of their study of human skeletal remains recently uncovered on Watom (New Britain, PNG). The authors challenge the view that origin of Polynesians was solely Lapita-derived. They consider that an intrusion may be a more likely explanation to account for the observed pattern and suggest Micronesia as possible alternative route for the ancestors of the Polynesians. In this paper, we will revisit this proposition using data collected on human skeletons recently discovered on Tongatapu (Kingdom of Tonga) and associated with the emergence of the Ancestral Polynesian Society.