



Chiang Ching-kuo Foundation for
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EUROCORES Programme
European Collaborative Research

OMLL
**The Origin of Man, Language and
Languages**

*Language and Genes in
East Asia / Pacific*

Uppsala, Sweden, 12-13 December 2006

The central topic at the workshop "Language and Genes in East Asia / Pacific" is the extent to which genetic data reveal details of the history of our language, and the amount there is to learn from a comparison of genetic and linguistic variation among human populations. The focus at the workshop will be on the geography of East Asia, which is taken loosely to include the whole area stretching from the Arctic into the Pacific.

The workshop aims to be a melting pot in the true sense of the word. Not only does the workshop bring together linguists, archaeologists and geneticists, but it will also be a meeting place for experts from the East and the West. The main objective of the meeting is to serve as a potential starting point for further fruitful collaborations in the future.

The workshop "Language and Genes in East Asia / Pacific" is organized by the EUROCORES programme "On the Origin of Man, Language and Languages (OMLL)", supported by the Chiang Ching-kuo Foundation for International Scholarly Exchange (CCKF) and hosted by the Swedish Collegium for Advanced Study (SCAS) in Uppsala, Sweden.

<http://www.esf.org/omll>

Programme



Monday December 11th

19.00	Welcome Reception at the Swedish Collegium for Advanced Study
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Tuesday December 12th

Chair: Don Stilo (MPI for Evolutionary Anthropology, Leipzig)

9.00	Registration
9.15	<p>Welcome by Björn Wittrock (Swedish Collegium for Advanced Study)</p> <p>Workshop Opening by Ovid Tzeng (Chiang Ching-kuo Foundation for International Scholarly Exchange)</p> <p>Opening remarks by Rüdiger Klein (European Science Foundation)</p> <p>Introduction by Eva Lindström (Stockholm University)</p>
10.00	<p><u>Central Asia / the North</u></p> <p>Victor H. Mair (University of Pennsylvania) <i>Recent Research on the Genetics of Eastern Central Asia</i></p>
10.40	<i>Break</i>
11.00	<p>Brigitte Pakendorf (MPI for Evolutionary Anthropology, Leipzig) <i>Linguistic and genetic perspectives on the prehistory of the Sakha</i></p>
11.40	Gísli Pálsson (University of Iceland)

Workshop "Language and Genes in East Asia/Pacific", 12-13 December 2006, Uppsala, Sweden

	<i>Genomic Anthropology: Coming in From the Cold</i>
12.00	<i>Lunch</i>
Chair: Alain Peyraube (Centre National de la Recherche Scientifique, Paris)	
13.00	<p><u>China</u></p> <p>Yong-Gang Yao (Kunming Institute of Zoology) <i>Ethnogenesis and genetic relationship of Chinese ethnic groups: A matrilineal perspective</i></p>
13.40	Martha Ratliff (Wayne State University, Detroit) <i>Miao-Yao (Hmong-Mien) Prehistory: the linguistic evidence</i>
14.20	<i>Break</i>
14.40	Pan Wuyun (Shanghai Normal University) <i>On the Genetic Relationship between the Miao-Yao Languages and the Sino-Tibetan Languages</i>
15.20	Tracey Lu (Chinese University of Hongkong) <i>"Hand-axe" and Human Diaspora in Southern East Asia</i>
16.00	<i>Break</i>
Chair: Ovid Tzeng (Chiang Ching-kuo Foundation for International Scholarly Exchange)	
16.20	<p><u>Vietnam</u></p> <p>Vu-trieu-An¹, Laurent Sagart² and Alicia Sanchez-Mazas³ <i>Human populations diversity in Vietnam: a multidisciplinary study</i> ¹ HMU, Hanoi ² CRLAO, CNRS, Paris ³ University of Geneva</p>
17.10	<i>Break</i>
17.20	<p><u>The Pacific, Part I</u></p> <p>Erika Hagelberg (University of Oslo) <i>Genetic affinities of the peoples of the Pacific</i></p>
18.00	Pedro Moral Castrillo (Universitat de Barcelona) <i>A genetic view on the Polynesian population of Easter Island</i>
18.40	Alain Peyraube (Centre National de la Recherche Scientifique, Paris) <i>OMLL : New perspectives for interdisciplinary research into the Origin of Man, Language and Languages</i>
19.30	<i>Dinner at Bill & Bull Restaurant</i>

<u>Wednesday December 13th</u>	
Chair: Richard Villems (University of Tartu)	
9.00	<u>South East Asia & the "Out of Taiwan"-hypothesis</u> Stephen Oppenheimer (University of Oxford) <i>Mitochondrial DNA and prehistoric dispersals in Southeast Asia and the Pacific</i>
9.40	Jean Trejaut, (Mackay Memorial Hospital, Taipei) <i>mtDNA analysis reveals an unexpected large number of new M and N haplogroups in ISEA.</i>
10.20	<i>Break</i>
Chair: Christoph Harbsmeier (University of Oslo)	
10.40	Cheng-hwa Tsang (Academia Sinica, Taipei) <i>Recent archaeological discoveries in Taiwan and their implications for the Austronesian dispersal</i>
11.20	Paul Li (Academia Sinica, Taipei) <i>Formosan Subgrouping and Related Problems</i>
12.00	<i>Special Santa Lucia Lunch</i>
Chair: Laurant Sagart (Centre de Recherches Linguistiques sur l'Asie Orientale, Paris)	
13.30	Peter Bellwood (ANU, Canberra) <i>The Out of Taiwan hypothesis for Austronesian origins: new archeological evidence from Taiwan and the northern Philippines.</i>
14.10	<u>The Pacific, Part II</u> Glenn Summerhayes (University of Otago) <i>Recent advances in Melanesian archaeology</i>
14.50	<i>Break</i>
Chair: Françoise Friedlaender (Temple University, Pennsylvania)	
15.10	Michael Dunn (MPI for Psycholinguistics, Nijmegen) and Ger Reesink (Radboud University Nijmegen) <i>Contact and phylogeny in Island Melanesia linguistic prehistory</i>
15.50	Russell Gray (University of Auckland) <i>Out of Taiwan? Genes, languages and the peopling of the Pacific</i>
16.30	<i>Break</i>
Chair: Alicia Sanchez-Mazas (University of Geneva)	

16.50	Sean Myles (MPI for Evolutionary Anthropology, Leipzig) <i>Population history of the Solomon Islands - perspectives from mtDNA</i>
17.30	Jonathan Friedlaender (Temple University, Pennsylvania) and Françoise Friedlaender (Temple University, Pennsylvania) <i>The Peopling of the Pacific: Resolving the Genetic Puzzle</i>
18.10	Closing remarks by Eva Hoogland (European Science Foundation)

Participants

Peter	Bellwood	School of Archaeology and Anthropology, ANU, Canberra, Australia
Michael	Dunn	MPI for Psycholinguistics, Nijmegen, Netherlands
Jonathan	Friedlaender	Temple University, Pennsylvania, USA
Françoise	Friedlaender	Temple University, Pennsylvania, USA
Russell	Gray	University of Auckland, New Zealand
Erika	Hagelberg	University of Oslo, Norway
Christoph	Harbsmeier	University of Oslo, Norway
Eva	Hoogland	ESF, Strasbourg, France
Rüdiger	Klein	ESF, Strasbourg, France
Paul	Li	Academia Sinica, Taipei, Taiwan
Eva	Lindström	Stockholm University, Sweden
Tracey	Lu	Chinese University of Hongkong, CUHK
Victor	Mair	University of Pennsylvania, USA
Pedro	Moral Castrillo	Universitat de Barcelona, Spain
Sean	Myles	MPI for Evolutionary Anthropology, Leipzig, Germany
Stephen	Oppenheimer	University of Oxford, UK
Brigitte	Pakendorff	MPI for Evolutionary Anthropology, Leipzig, Germany
Gísli	Pálsson	University of Iceland, observer ESF Standing Committee for the Humanities
Alain	Peyraube	Centre National de la Recherche Scientifique, Paris, France
Martha	Ratliff	Wayne State University, Detroit, USA
Ger	Reesink	Radboud University Nijmegen, Netherlands
Laurant	Sagart	Centre de Recherches Linguistiques sur l'Asie Orientale, Paris, France
Alicia	Sanchez-Mazas	University of Geneva, Switzerland
Don	Stilo	MPI for Evolutionary Anthropology, Leipzig, Germany
Glenn	Summerhayes	University of Otago, New Zealand
Jean	Trejaut	Genetics, Mackay Memorial Hospital, Taipei, Taiwan
Cheng-hwa	Tsang	Institute of History and Philology, Academia Sinica, Taipei, Taiwan
Ovid	Tzeng	Academia Sinica, Taipei, Taiwan
Richard	Villems	University of Tartu, Estonia
An Vu	Trieu	Hanoi University of Medicine, Vietnam
Björn	Wittrock	Swedish Collegium for Advanced Study, Uppsala, Sweden
Pan	Wuyun	Shanghai Normal University, China
Yong-Gang	Yao	Kunming Institute of Zoology, China

Abstracts of Presentations

Victor H. Mair (University of Pennsylvania, USA) ***Recent Research on the Genetics of Eastern Central Asia***

This paper on the region just to the west of East Asia begins with a summary of published work on population genetics of the Tarim Basin and surrounding areas. Since East Asian genes and languages have spread into this region as well as into the Pacific, there is much that can be learned about the population dynamics of East Asia from studying the genetics and linguistics of Eastern Central Asia. The paper goes on to describe current work in DNA labs at Jilin University (in Changchun, Jilin) and Fudan University (in Shanghai). An account of the large-scale investigation of the National Geographic Society's Genographic Project is also presented. The implications of all this research for population movements and language spreads are considered.

The paper concludes with a discussion of problems and prospects in the study of the ancient and modern DNA of the peoples of Eastern Central Asia.

Brigitte Pakendorf (MPI for Evolutionary Anthropology, Leipzig, Germany) ***Linguistic and genetic perspectives on the prehistory of the Sakha***

The Sakha (also known as Yakuts) are a Turkic-speaking group living in north-eastern Siberia. They stand out amongst the peoples of north-eastern Siberia not only by their language but also by their subsistence pattern of cattle- and horse-breeding. The Turkic language and pastoral subsistence pattern of the Sakha are indications of an origin of this population further to the south, which is placed by archaeologists in the vicinity of Lake Baykal in southern Siberia. It is hypothesized that the Sakha migrated northwards from this area several centuries ago, possibly under pressure of the Mongol hordes. After colonization of the area by the Russians, the Sakha were able to expand demographically and geographically, displacing or assimilating the indigenous population groups. The historical and current neighbours of the Sakha are the Tungusic-speaking Evenks and Evens as well as the Yukaghirs (whose language is probably distantly related to the Uralic language family), all of whom are traditionally hunters and fishers, as well as nomadic reindeer-breeders.

In the absence of written records, the effects of such prehistoric migrations cannot easily be identified. For instance, it is not clear whether the expanding Sakha actually intermixed with the indigenous Tungusic-speaking groups they encountered, or whether the latter were primarily pushed to the peripheral areas of the Yakut settlement. In cases like these, genetic data can help clarify a population's prehistory, since the gene pool of the population is likely to retain traces of previous admixture, if this was substantial enough and if the sample size used in the analysis is adequate.

However, genetic analyses can only show prehistoric contact of a rather intimate kind, such that it leads to actual genetic admixture between two population groups. Groups of people that migrate to a new area of settlement experience less intimate kinds of contact too, that may well lead to influences on the language (up to a complete language shift to the language of the dominant group) without leading to detectable genetic admixture. Combining both linguistic and genetic analyses can therefore provide a more complete picture of the prehistoric contact situations that a group of people was involved in.

This study is an attempt at such an integrated analysis of Yakut prehistory, combining both molecular genetic analyses and linguistic studies in order to obtain a more fine-grained picture of the prehistoric contact they were involved in.

Gísli Pálsson (University of Iceland)
Genomic Anthropology: Coming in From the Cold

Anthropology tends to be thoroughly divided on the issue of genomic research. On the one hand, the new genetics is an important critical site for ethnography and theoretical reflection. On the other hand, the genome is a useful avenue into human history since historical information is necessarily embodied in it. This article discusses some of the implications of the new genetics for "genomic anthropology", a hybrid and broadly defined field that combine "social" and "biological" perspectives. I argue that collaborative genomic research in which subjects become consultants, even co-researchers and co-authors, is bound to play an increasing role. The discussion is partly framed within the context of research among Inuit in Alaska, Canada (Nunavut), and Greenland. Here as elsewhere, I suggest, genomic research raises larger concerns about the relevance of local notions of belonging and relatedness and the nature and degree of collaboration between researchers and the people providing genetic and ethnographic information. While the collaborative approach may invite particular problems, it does allow for responsible practice and sensitivity to local relations, both of which are central for post-colonial anthropology.

Yong-Gang Yao (Kunming Institute of Zoology, China)
Ethnogenesis and genetic relationship of Chinese ethnic groups: A matrilineal perspective

China has 56 officially recognized ethnic groups and many isolated populations. The origin and genetic relationship of these Chinese ethnic groups have not been satisfactorily resolved. Understanding the peopling of China also has special reference for us to reconstruct the demographic history in East and Southeast Asia (including the Pacific Islands). Based on a well-defined mtDNA phylogeny, we have systematically analyzed the matrilineal components and genetic relationship among more than 30 ethnic populations across China. In particular, we focused on four main questions: (1) Phylogeographic differentiation of Han Chinese regional populations; (2) Genetic admixtures in the Silk Road region; (3) Genetic structure of ethnic populations from southwest China with different ancient tribal origins; (4) Dissection of the matrilineal components of ethnic populations from north China. Our results showed that there is marked regional difference in Han populations across China. Han populations from south China and populations of ancient south Pai-Yuei origin contain higher frequency of ancient mtDNA haplogroups and genetic diversity compared with those populations from north China and populations with ancient Di-Qiang origin. Genetic admixture of western and eastern Eurasian matrilineal pools can be clearly discerned in populations from the Silk Road region; however, the amount of western Eurasian matrilineal contributions to genetic structure of each ethnic population varied. Overall, the current matrilineal genetic structures of Chinese ethnic populations bear the imprints of their ethnohistory more or less. The origin and development of ethnic groups is a complex and dynamic process, which was influenced by all kinds of genetic and demographic effects.

Martha Ratliff (Wayne State University, Detroit, USA)
Miao-Yao (Hmong-Mien) Prehistory: the linguistic evidence

Less has been written about the prehistory of the relatively small Hmong-Mien linguistic family (roughly 9 million speakers for all 30-40 languages combined) than the larger families of south China and Southeast Asia: Sino-Tibetan, Tai-Kadai, Austroasiatic, and Austronesian. Yet these speakers live in the centre of an area of primary agricultural origin south of the Yangzi River, and are thus of historical interest. I will present linguistic evidence showing that Hmong-Mien speakers have inhabited roughly the same "high-traffic" area for the past 2000 years. I will also report on attempts to identify a super-family that includes both the Hmong-Mien family and one (or more) of its neighbours.

Pan Wuyun (Shanghai Normal University, China)

On the Genetic Relationship between the Miao-Yao Languages and the Sino-Tibetan Languages

Benedict put forward Austro-Tai phylum including the Miao-Yao branch which traditionally is part of the Sino-Tibetan language family. However, the genetic structure of East Asians shows that both the Sino-Tibetan and the Miao-Yao populations have a remarkably high frequency of the O3-M122, while O1-M119 is found with high frequency among the Daic and the Austronesian populations, indicating that Sino-Tibetan populations and Miao-Yao populations have a closer genetic relationship. The paper examines some basic words in the Miao-Yao languages and compares them with those in Old Chinese and Tibeto-Burman, the result of which corroborates the genetic evidence.

Tracey Lu (Chinese University of Hongkong, CUHK)

"Hand-axe" and Human Diaspora in Southern East Asia

It has been argued that modern human beings (*Homo sapiens*) were from Africa and migrated to other continents in the late Pleistocene, but it is unclear when and how this migration took place, nor is it clear whether the indigenous were replaced by the African migrants. The discovery of "hand-axe" in South China in recent years seems to lend support to the above hypothesis. However, a careful examination of these "hand-axes" raises doubts. Based on recently discovered archaeological data, it is argued that there might have been human and cultural contacts in southern East Asia in the late Pleistocene, but local stone tools still illustrate cultural continuity. Thus it is unlikely that the indigenous in southern East Asia were replaced by the African migrants, and that the human and cultural dynamics in this region might have been a process of co-existence and cultural localization.

Vu-trieu-An¹, Laurent Sagart², Maria-Eugenia Riccio⁴, Jean-Marie Tiercy³, and Alicia Sanchez-Mazas⁴

Human populations diversity in Vietnam: a multidisciplinary study

¹ *HMU, Hanoi, Vietnam*

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Because of the war (1946-1975), Vietnam has been relatively isolated from abroad and, except for a few works done after 1954 with the liberation of the North, anthropological studies were published after the reunification of the country in 1975, and mainly in Vietnamese. Thus, to provide the scientific community with an overview of Vietnamese research in that field, we will first summarize some results of the main anthropometric studies performed during that period. While giving limited hypotheses on the history of the Vietnamese population, those works reveal a complex pattern of population relationships based on cranial measurements, suggesting that its numerous ethnic groups may have distinct origins.

We will then focus on linguistic and genetic diversity. Vietnam is also complex from a linguistic point of view. The 83 millions people now inhabiting the country are distributed into 54 ethnic groups speaking different languages. The vast majority (approximately 85%) belongs to the Viet Kinh population whose language belongs to Austro-Asiatic, a phylum of 168 languages also including Mon and Khmer as the most representative, but also northern Indian (Munda, Khasi) tongues. The history of this phylum is still poorly known. Moreover, Vietnam is also settled by populations speaking Tai-Kadai or Austronesian languages, and a coherent scenario for the peopling of this country has still to be found.

Due to the long Vietnam War, genetic studies have only recently been published by local researchers on blood groups, HLA and molecular markers. Within the scope of a funded research project, we are now studying the genetic diversity of several ethnic groups all over the country. We present here a set of results concerning the Kinh and Muong populations, as well as preliminary HLA data on the Khmer from southern Vietnam and the Munda from northeast India.

Erika Hagelberg (Dept. of Biology, University of Oslo, Norway)
Genetic affinities of the peoples of the Pacific

The quantity of genetic data on peoples of the Pacific, primarily on the uni-parentally inherited mitochondrial DNA and Y chromosome systems, has grown at an astonishing rate in the past few years. However, most published studies focus on large-scale pictures of Pacific settlement and ignore micro-evolutionary processes within geographical areas. Moreover, despite increasing sophistication, the analyses are often based on relatively simplistic views of Pacific settlement. The present state of research on the genetics of Pacific populations will be discussed, with arguments for a more meaningful cross-disciplinary discourse.

Pedro Moral Castrillo (Universitat de Barcelona, Spain)
A genetic view on the Polynesian population of Easter Island

A set of different kind of genetic markers (mtDNA sequences, Y chromosome STRs, and autosomal variation in Alu insertions and apolipoprotein, HMC, and immunoglobulin genes) have been analyzed in a n=88 sample from native Easter Island inhabitants (Rapanui). Available genealogical records allowed subdividing the total island sample into two groups, one representative of the native population living in the island around 1900, and another formed by individuals with some ancestors of non-Rapanui origin. Relatively high gene diversities and significant differences between the two sub-samples and from other population groups lead to biodemographic and historical inferences about the origin and evolution of this geographically isolated island population.

Stephen Oppenheimer (School of Anthropology, University of Oxford, UK)
Mitochondrial DNA and prehistoric dispersals in Southeast Asia and the Pacific

The prehistory of Southeast Asia is highly contested. The prevailing model, based primarily on linguistics and supported by many archaeologists, suggests that modern Southeast Asians are largely descended from expanding Chinese agriculturalists. These are thought to have dispersed from a homeland in the middle Yangzi around 7000 years ago as a result of the development of rice farming. By around 4000 years ago, these dispersals are held to have extended as far as the Malay Peninsula and most of Island Southeast Asia in the south, reaching Oceania in the east by around 3500 years ago. This model, although much discussed and questioned by some archaeologists, remains to be tested in the Southeast Asian heartland using a large, well-resolved mitochondrial DNA (mtDNA) data. Here mtDNA is used from populations in both Malaysia and Indonesia to examine this model. The results indicate that there is a substantial indigenous population stratum throughout Southeast Asia that extends back to the earliest modern human settlement, at least 50,000 years ago. The majority of lineages appear to mark dispersals in the late Pleistocene or early Holocene, most likely triggered by post-glacial flooding, and mid-Holocene arrivals from the north were rather minor, at least on the female line of descent. Lineages arriving in the Pacific during the Holocene derive from Melanesia and Southeast Asia rather than Taiwan.

Jean Trejaut, (Genetics, Mackay Memorial Hospital, Taipei, Taiwan)
mtDNA analysis reveals an unexpected large number of new M and N haplogroups in ISEA

mtDNA control and coding region np 9016-10900 were used to determine the maternal genetic structure and population relationship of 1200 individuals from the Philippines, Indonesia, Vietnam, Fujian and Taiwan Formosan and non Formosan speakers. This analysis was complemented by the introduction of informative restriction fragment polymorphism (RFLP) of the mtDNA coding region. Most lineages were classified without ambiguity. Ensuing searches in the literature and of our sequence database indicated that these lineages had highly confined regional dispersions with Taiwan and ISEA segregating from continental East Asia. In most instances, it supported the archaeological and linguistic history of the regions. The remaining lineages, situated among the deeper branches of a most parsimonious tree constructed with control and coding divisions were associated to either haplogroup M or N. Based on the whole mtDNA sequencing of these lineages, we characterized ~20 new branches of macrohaplogroup of M, seven of macrohaplogroup N (6N, 1 B), and many new twigs corresponding to subhaplogroups of M (G1, D4, M9, M13 and Z) and N (B4, B5, F1 and N9a). The diversification times obtained from coding region variations suggested existence of lineages that were among the earliest mtDNA variants to appear in ISEA, most likely relics of the genetic pool of a Pleistocene dispersion of human in the ancient continent of Sundaland.

The presence of an unexpected high number of new variant lineages in ISEA, with trunk rooting directly from superhaplogroups M or N may have strong implications on the time scale for the migration of human to eastern Asia and ISEA. Except for belonging to superhaplogroups M or N, there is no structural relationship between these ISEA lineages and those lineages seen in west Eurasia or India. In addition to isolation by distance and giving plenty of cleansing time to drift there is also one possibility that the migration of humans from the horn of Africa to Melanesia went much faster than initially thought.

Cheng-hwa Tsang (Institute of History and Philology, Academia Sinica, Taipei, Taiwan)
Recent archaeological discoveries in Taiwan and their implications for the Austronesian dispersal

The island of Taiwan lies 45 kilometres to the east of the Pescadores and 160 kilometres off the southeastern coast of China on the edge of the East Asian continental shelf. It marks the mid-point of an island arc extending from the Kamchatka Peninsula in the north to the Sunda Islands in the south. The size of Taiwan is approximately 36,000 square kilometres, extending 380 kilometres from north to south across the Tropic of Cancer, and 150 kilometres from east to west at its broadest point. The topography of this island includes hills, lakes, river terraces, basins, alluvial plains, and sea coasts. The climate of Taiwan is generally characterized by high temperatures, heavy rainfall, and strong winds, but with pronounced regional and vertical variations. Despite its' very complex natural environment, the history of human settlement on Taiwan is also of great complexity. A reliable documentary history of Taiwan began only after the early seventeenth century when, in 1624, the Dutch occupied the southwestern coastal region.

The four hundred years of recorded history of Taiwan saw the history of four main groups of literate people -- the Dutch, the Spanish, the Chinese, and the Japanese. Before these groups entered Taiwan, however, the island had long been inhabited by peoples speaking Austronesian (Malayo-Polynesian) languages. These native tribes were horticulturists, cultivating millet, taro, yams, rice, and beans, and they also engaged in hunting and gathering.

Since the historic period of the island of Taiwan spans no more than four hundred years, an investigation of the island's history before the seventeenth century must rely upon archaeological studies. So far, a great deal of archaeological materials have already been collected and studied on this island, indicating at least four major developmental stages for

the prehistory of Taiwan:

1. The earliest stage is represented by the pre-ceramic assemblage (named Ch'angpinian) uncovered from the cave site at Chang-pin on the east coast of Taiwan and dated between 30000 and 5000 years BP. This is characterized by a lithic industry consisting solely of chipped pebble and flake tools, as well as by the absence of pottery and evidence of farming.

2. The second stage is represented by the oldest ceramic culture of the island -- the so-called Tapenkeng culture or Coarse Corded Ware culture, which was uncovered mainly along the western coastal area of Taiwan.

Pottery of this culture is sand-tempered, rather thick and heavy, buff to dark brown in colour with coarse cord impressions on the exterior surface. Typical stone implements include rectangular and shouldered adzes, pecked river pebbles, perforated triangular slate points, and bark beaters. It was postulated that the people of the Ta-pen-keng culture were among the earliest horticulturalists in Southeast Asia. While still engaging in hunting, fishing, and collecting activities, they may have planted some roots, tubers, and fruits, adapting to marine, estuarine, riverine, and lacustrine microenvironments in a humid and warm subtropical-tropical region. But recent discovery of charred rice and fox tail millet grains from a few Ta-pen-k'eng culture sites reveals that people of the Ta-pen-keng culture had already possessed knowledge of cereal cultivation for their subsistence.

3. Subsequent to the Ta-pen-keng culture, a series of middle Neolithic cultures emerged in Taiwan around 2500 B.C. or shortly thereafter. They are the Yuan-shan, the Chih-shan-yen, and the Niu-chou-tzu cultures on the west coast, as well as the Ch'i-lin and the Pei-nan cultures on the east coast. This stage of Taiwan prehistory, as represented by these middle Neolithic cultures, is characterized by the development of intensive agriculture and larger settlement.

The settlement patterns among these middle Neolithic cultures show a great variation. For example, evidence from west-central Taiwan indicates that the settlements of the earliest phase appeared mainly on the coast and the lower terraces of the river basin, but the settlements of the subsequent phases were more widely distributed and extended further into the interiors of the valleys. This phenomenon seems to suggest that expansions of the population and adaptations to various ecological niches took place during this period between 4500 B.P. and 2000 B.P.

4. The fourth stage of Taiwan's prehistory enters into the Metal Age, whose inhabitants may have been the direct ancestors of some aboriginal tribes known in historical records. Although archaeological assemblages of this stage are scattered in widely divergent locations, they present some common traits: hard or soft paste pottery stamped or incised with geometric designs, the appearance of glass ornaments and iron implements, and the decline of stone tools.

One of the most important features of this stage is the development of the long-distance trade for exotic goods with Mainland Chinese and Southeast Asians. The items traded include carnelian beads and ornaments, bronze artefacts, glass beads, bracelets, gold ornaments, porcelain, and silver objects. The subsistence economy of the inhabitants of this stage appears to have been mixed. While cereal crops such as rice and millet formed a part of this subsistence base, hunting, fishing, and collecting of marine resources, were dominant characteristics of this subsistence economy.

As seen above, the prehistoric cultures in Taiwan present great variations both in time and in space. One of the most important significances of Taiwan's prehistory, however, is in the problem of the Austronesian origin and expansion. It is because of that Taiwan lies partially in its role as a land bridge between the Asian Mainland and the Pacific, as well as in its potential role in the connection between prehistoric cultures and modern Austronesian speakers on the island. Therefore, the island has long been recognized by some scholars as an area perhaps involved in the transmission of the Austronesian peoples and languages from South China into

the Pacific.

In recent years, several archaeological works, which yielded very important evidence relevant to the problem of the Austronesian dispersal, were conducted in Taiwan. They are:

1. The rescue archaeological work at the Tainan Science-based Industrial Park in southern Taiwan.
2. The discovery of the 4000-year-old stone tool manufacturing workshop sites on the Qi-meí Island of the Penghu archipelagos in the mid of Taiwan Strait.
3. The discovery of a metal age settlement site at Qiwulan of Yilan county on the northeast coast of Taiwan.
4. The discovery of a metal age settlement site at Jiuxianglan of Taitung county on the east coast of Taiwan.

The purpose of this paper is in an attempt to introduce the above mentioned archaeological discoveries and discuss their implications for the problem of the Austronesian dispersal.

Paul Li (Academia Sinica, Taipei, Taiwan)
Formosan Subgrouping and Related Problems

Taiwan is generally believed to be the most likely Austronesian homeland by comparative Austronesian scholars. Yet as of today, there is no generally accepted classification of Formosan languages. I shall discuss problems of some subgrouping hypotheses. Moreover, I'd like to say something about our on-going interdisciplinary research project: "Classification and Dispersal of the Austronesians: Anthropological, Archaeological, Genetic and Linguistic Studies Relating to Taiwan".

Blust's (1999) subgrouping hypothesis for the entire Austronesian language family is nine subgroups of Formosan languages plus the Malayo-Polynesian subgroup outside Taiwan. On the one hand, there are too many subgroups, ten in total. On the other, there is not much linguistic evidence for some of the subgroups he recognized or postulated. For example, there is little phonological or morphosyntactic evidence for a close relationship between Tsou and the so-called "Southern Tsouic", Kanakanavu and Saaroa. Tsou has undergone a number of morphosyntactic innovations of its own, including (1) Its focus system is different from all the other Formosan languages, (2) Each clause requires an auxiliary, (3) Verbs must agree in focus in the same clause, (4) Causative constructions are restricted to non-Agent focus, (5) It has completely lost the PAn perfective marker <in>, and (6) It is the only Formosan language that has developed bound nominative pronouns for the third person (Chang 2006). Nevertheless, Kanakanavu and Saaroa share none of these innovations with Tsou. In fact, they resemble the other Formosan languages much more closely in all these respects. In a recent paper by Malcolm Ross (2006), "Reconstructing the Case-marking and Personal Pronouns of Proto Austronesian", he has found no shared innovations for some of Blust's subgroups, such as "East Formosan". Above all, the most serious problem with Blust's subgrouping is that the nine subgroups are geographically spread all over the island of Taiwan, and there is no way to determine the centre of dispersal.

Starosta's (1995) binary subgrouping hypothesis seems to be more plausible: Rukai is the first offshoot from PAn, Tsou the second, Saaroa the third, and so on. A great advantage of his subgrouping hypothesis is that the centre of dispersal is clearly determinable in the southwestern plains of Taiwan. However, a strange result of his work is that Chamorro, an extra-Formosan language spoken in Guam and Saipan, is genetically closer to Kanakanavu, as shown in his subgrouping. As a matter of fact, Kanakanavu and Saaroa are more or less mutually intelligible. It is extremely unlikely that Chamorro would be even more closely related to Kanakanavu.

Scholars in different disciplines may come up with different results or suggestions. My colleagues in archaeology (such as Dr. Tsang) believe that southwestern China, more specifically Canton, is the Austronesian homeland, while my colleagues in genetics (such as Dr. Marie Lin) would suggest Indonesia rather than Taiwan as the more probable Austronesian homeland. How shall we reconcile these differences? Scholars in various disciplines should all aim at great accuracy as much as possible, and not worry about their differences at this stage.

Peter Bellwood (School of Archaeology and Anthropology, ANU, Canberra, Australia)
The Out of Taiwan hypothesis for Austronesian origins: new archaeological evidence from Taiwan and the northern Philippines.

'Authors: Peter Bellwood (School of Archaeology and Anthropology, ANU), Hung Hsiao-chun (Department of Archaeology and Natural History, ANU); Yoshiyuki Iizuka (Institute of Earth Sciences, Academia Sinica, Taipei); and Eusebio Z. Dizon (National Museum of the Philippines, Manila)

Linguistic, archaeological and genetic evidence indicate that Taiwan was a major origin region for the Austronesian-speaking peoples. Their major branch, that of the speakers of Malayo-Polynesian languages, has spread more than half way around the world, and today has over 350 million members. The archaeological roots of this dispersal can be traced in Neolithic cultures in Taiwan and the northern Philippines (Batanes Islands and northern Luzon) dating between 5000 and 3000 years ago. Archaeological excavations in Taiwan and the Batanes Islands will be discussed, as well as new sourcing research on Taiwan nephrite, that travelled between 4000 and 1500 years ago over huge areas of SE Asia (to Philippines, Malaysia, Vietnam, Thailand and Cambodia).

Glenn Summerhayes (University of Otago, New Zealand)
Recent advances in Melanesian archaeology

The results of recent fieldwork into the archaeology of Papua New Guinea will be presented. This will include:

1. recent fieldwork at a 35,000 year old occupation at Kosipe (Papua) and what it tells us about models on the initial human colonisation of Sahul, and
2. research at Lapita sites in the Bismarck Archipelago, and what it tells us about the nature of interaction with Lapita settlements from further east in Remote Oceania.

If time permits I can present the results from recent research in the Yaeyama Islands (southern Japan), just east of Taiwan, and their relationship to the Austronesian expansion out of Taiwan.

**Michael Dunn (MPI for Psycholinguistics, Nijmegen, Netherlands) and
Ger Reesink (Radboud University Nijmegen, Netherlands)**
Contact and phylogeny in Island Melanesia linguistic prehistory

The non-Austronesian languages of Island Melanesia present a difficult problem to linguistic prehistorians. Recurrent typological similarities between these languages suggest shared history, but the comparative method is unable to reconstruct shared ancestry. In this paper we investigate phylogenetic and phenetic relationships between these languages using computational methods from bioinformatics applied to language structure. We conclude that despite evidence for contact relationships, the most likely account for the deep similarities between the non-Austronesian languages of Island Melanesia is descent from a small number of ancestral languages.

Russell Gray (University of Auckland, New Zealand)
Out of Taiwan? Genes, languages and the peopling of the Pacific

Despite over hundred years of academic inquiry, and numerous recent genetic studies, the sequence and timing of Pacific settlement is still under substantial dispute. In this talk I will outline how computational phylogenetic methods can be used to test between three hypotheses about the settlement of the Pacific. These hypotheses differ in the predictions they make about how tree-like lexical data will be, where the root of an Austronesian language tree should be, and the age of proto-Austronesian. Lexical data drawn from our database of basic vocabulary for over 400 Austronesian languages (see <http://language.psy.auckland.ac.nz/>) will be used to test these predictions. Bayesian phylogenetic methods and rate smoothing enable us to estimate divergence dates without assuming constant rates of lexical replacement. The results from the linguistic data will be contrasted with the apparently conflicting evidence found in mitochondrial and nuclear DNA studies. I will suggest that recent evidence for a "J curve" in the rate molecular change affords a partial reconciliation between the linguistic and genetic evidence.

Sean Myles (MPI Evolutionary Anthropology, Leipzig, Germany)
Population history of the Solomon Islands - perspectives from mtDNA

In the Solomon Islands in Island Melanesia there are currently a large number of languages spoken which belong to the Austronesian family and a smaller number of Papuan languages which have no relationship to Austronesian languages and are even difficult to relate to each other. It is widely accepted that the Austronesian languages arrived in the region in a large migration which began in Taiwan ~5000 years ago. However, the Solomon Islands have been inhabited by humans for at least 30000 years and it is widely thought that the present day Papuan languages spoken in the Solomon Islands are descended from the original languages spoken by these early inhabitants. To investigate how language and genes have interacted in this part of the world, we collected ~700 DNA samples from both Austronesian and Papuan speakers in the Solomon Islands. Data collection is currently underway and results from the mtDNA HVR1 region will be presented.

**Jonathan Friedlaender (Temple University, Pennsylvania, USA) and
Françoise Friedlaender (Temple University, Pennsylvania, USA)
*The Peopling of the Pacific: Resolving the Genetic Puzzle***

J.S. Friedlaender¹, F.R. Friedlaender¹, J.A. Hodgson², L.B. Scheinfeldt³, K.K. Kidd⁴, J.R. Kidd⁴, M. Bauchet⁵, G. Chambers⁶, R. Lea⁶, G. Koki⁷, F. Reed⁸, D. A. Merriwether⁹.

1. Temple University, 2. New York University, 3. Children's Hospital of Philadelphia, 4. Yale University, 5. Pennsylvania State University, 6. Victoria University, 7. Papua New Guinea Institute of Medical Research, 8. University of Maryland, 9. University of Binghamton.

For the past decade, the genetic evidence concerning the origins of Polynesians and their relationships to Island Melanesians and Southeast Asians has been contradictory and puzzling. The mitochondrial DNA evidence has suggested the (maternal) ancestors of Polynesians primarily derived from Aboriginal Taiwanese populations (during the Holocene), and moved rapidly through Island Southeast Asia and Melanesia, retaining few signs of intermixture with local populations there, before commencing to colonize the formerly uninhabited islands of Remote Oceania. In the process, they do seem to have left a major (maternal) genetic imprint in Island Melanesian Populations.

To the contrary, the Y-chromosome evidence indicated extremely weak paternal ties between Polynesians and Aboriginal Taiwanese/Southeast Asian populations, and suggested instead that the ancestral Polynesians genetically derived primarily from Island Melanesians. Also, the Island Melanesian populations seem to show only very faint Y-chromosome influences from Taiwan/Southeast Asia.

Our genetic survey in 40 Pacific populations covers over 600 autosomal short tandem repeat polymorphisms and 200 insertion-deletions, in addition to variation in the mitochondrial DNA and Y-chromosome. It indicates a resolution of the contradictions of earlier studies. Polynesians do have genetic affiliations with both Island Melanesian and Taiwanese/Southeast Asian populations, but primarily the latter (more consistent with the mitochondrial DNA pattern). Within Island Melanesia, there is a very small but clear Southeast Asian genetic footprint in particular Oceanic-speaking populations (more consistent with the Y-chromosome pattern). Neither the mtDNA nor the Y-chromosome pattern by itself provides an adequate description of the overall population genetic relationships across the Pacific.

Our survey results also underscore the remarkable genetic diversity of Island Melanesian populations from one language group to another, and from island to island. A number of ancient genetic variants are autochthonous to this region. This is the result of the small sizes of the populations and the very long extent of modern human settlement there (over 30,000 years). The most singular genetic profiles occur in the more remote Papuan-speaking populations.

Therefore, while the correspondence of patterns of language and genetic variation across the region is hardly strong, taken together the patterns are highly informative with regard to reconstructions of ancient population movements.

Supported by grants from the US National Science Foundation, Wenner-Gren Foundation, National Geographic Exploration Fund, and the National Institutes of Medicine (to the Marshfield Clinic).

Lunch & dinner

Lunch

On Tuesday and Wednesday, lunch will be served at the Swedish Collegium for Advanced Study. On Wednesday there will be a special Santa Lucia surprise.

Aside – Santa Lucia

December 13th is a Swedish national holiday: the feast day of Santa Lucia, the Queen of Light. Traditionally, in the early hours of the morning of December 13th a young woman, dressed in a white gown would go from one farm to the next carrying a torch to light her way and bringing baked goods.

In Norway and Sweden it is still a custom on December 13th for a girl in a white dress to bring a tray of saffron buns and steaming coffee to wake the family with a song. She is called the Lussibrud (Lucy bride) and her pastry (saffron buns) is Lussekattor.

In schools people sing Santa Lucia's song. A famous song is the following:

The night goes with weighty step round yard and round earth. The sun's departure leaves the woods brooding. There in our dark house, appears with lighted candles Saint Lucia, Saint Lucia.

The night goes great and mute. Now one hears its wings in every silent room murmuring as if from wings. Look at our threshold. There she stands white-clad with lights in her hair Saint Lucia, Saint Lucia.

The darkness shall soon depart from the earth's valleys thus she speaks a wonderful word to us. The day shall rise anew from the rosy sky. Saint Lucia, Saint Lucia.

Dinner

On Monday evening December 11th all participants are welcomed at the Welcome reception, hosted by the Swedish Collegium for Advanced Study. Address:

Swedish Collegium for Advanced Study (SCAS)

Götavägen 4

Uppsala, Sweden

Phone: +46 (0) 18 55 70 85

<http://www.scasss.uu.se/>

On Tuesday evening, December 12th, dinner has been arranged in the restaurant Bill & Bull, conveniently located near the train station and a few blocks from the hotel. Address:

Restaurant Bill & Bull

Smedsgränd 9

Uppsala

Phone: + 46 18106680

Aside – Bill & Bull

The restaurant is named after Bill and Bull, two characters from the Swedish children's books series about Pelle Svanslös, a cat without a tail, by Gösta Knutsson. These characters were based on models from local politics and university people. Pelle was the writer himself, Bill and Bull were the ambassador Rydbeck and his friend Lindberg, a director of an airline company.

Further Information

Workshop "Language and Genes in East Asia/Pacific", 12-13 December 2006, Uppsala, Sweden



H = Hotel Linné
S = Station
M = Meeting place - Swedish Collegium
R = Restaurant Bill & Bull

Further information

For more information, contact the Coordinator for the EUROCORES programme "On the Origin of Man, Language and Languages (OMLL)", Eva Hoogland at omll@esf.org.