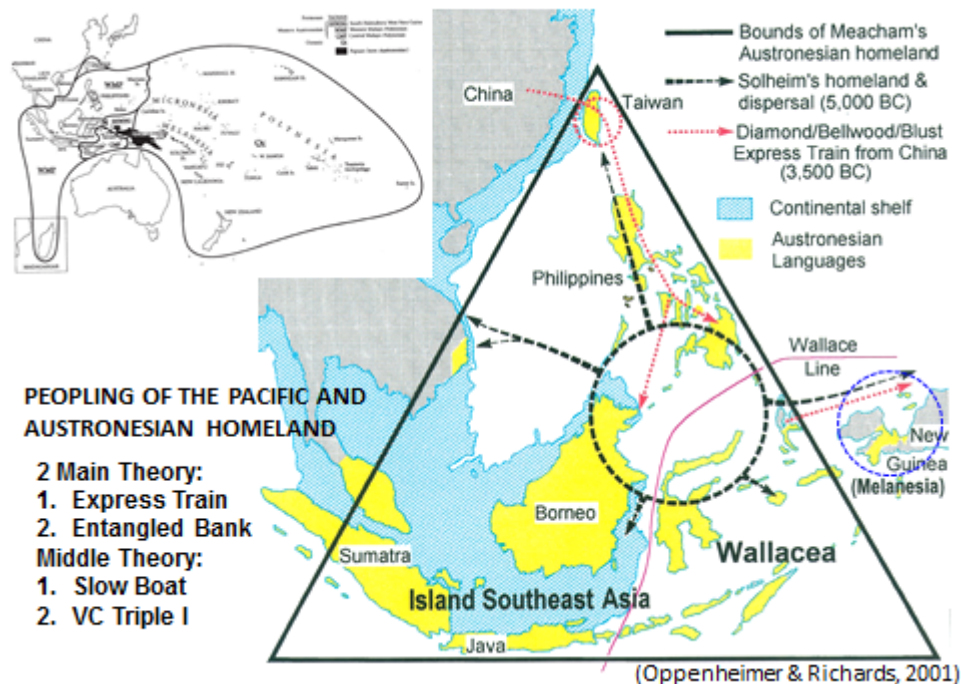


Early Peopling of the Pacific: Paleoanthropology, Genetic and Linguistic Perspectives

Sofwan Noerwidi
Balai Arkeologi Yogyakarta

The question about the origins of Polynesians people has been the subject of hot debate. There are two principal hypotheses concerning Polynesian ancestry, there are called as “Express Train” (Asia origin) and “Entangled Bank” (Melanesia origin). Several intermediate hypothesis exists between them are “Slow Train”, “Slow Boat” and “Voyaging Corridor”. To traces human migration and movement in prehistoric times is not easy case, it should used a comparisons study based on historical linguistic, genetic, and palaeoanthropological data. Results of those studies are able to evaluate some of the competing hypotheses that relate to the settlement and colonization of the Pacific Insular and the bio-cultural connections within another region that may inform on population movements.

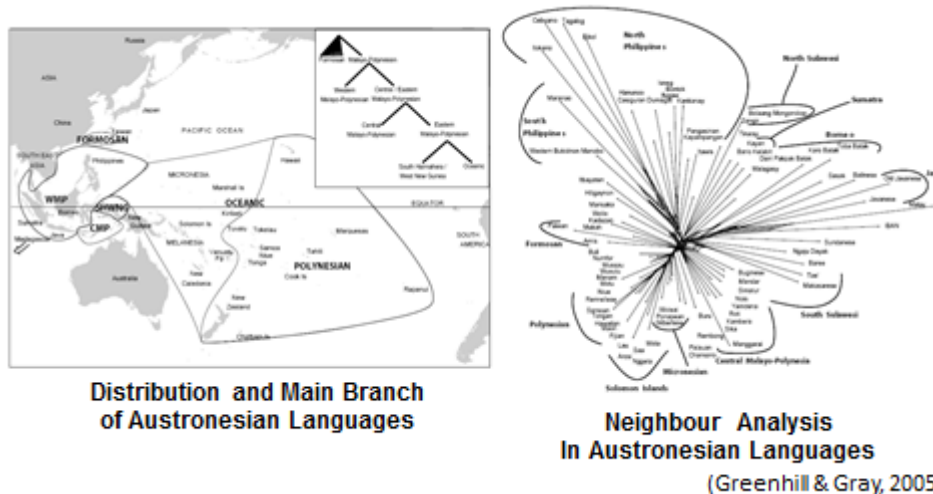


Linguistic

From linguistic perspective, the robust connection between Polynesia and Island of Southeast Asia at opposite ends of the chain would seem to be the Austronesian languages. Their language affiliations have been seen as an essential sign to the solution. The geographic and numeric centre of gravity of the Austronesian language family is in island Southeast Asia, which was therefore originally seen as their dispersal homeland. Linguistic study by Greenhill and Gray (2005) is to testing population dispersal hypothesis by phylogenetic tree of Austronesian languages. Their first preliminary attempt to test the Express Train scenario of Pacific settlement in a quantitative manner used parsimony methods derived from evolutionary biology to construct an optimal language tree. First the lexical data is grouped into cognate sets

using systematic sound correspondences. The second step is to translate this lexical data into a binary matrix. The next step involves expressing the dispersal hypothesis as precisely as possible. The final step is to generate some trees from binary data matrix.

Greenhill and Gray (2005) analysis results do not support the ‘Entangled Bank’ model of Pacific settlement. There is phylogenetic signal in the lexical data, which enables many of the major Austronesian subgroups to be correctly inferred. There is also some signal reflecting the sequence of movements predicted by the Express Train, also the Voyaging Corridor Triple I and Slow Train scenarios. However, when this signal is evaluated with an appropriate null model it appears relatively weak. The weakness of the signal is a consequence of both limitations in the database, and the presence of some borrowing word. With the present data it is unable to distinguish between the Express Train, the Voyaging Corridor Triple I, the Slow Train, and the Slow Boat scenarios. Then, only with historical language families can of themselves tell nothing about the spread of human population in prehistoric times.

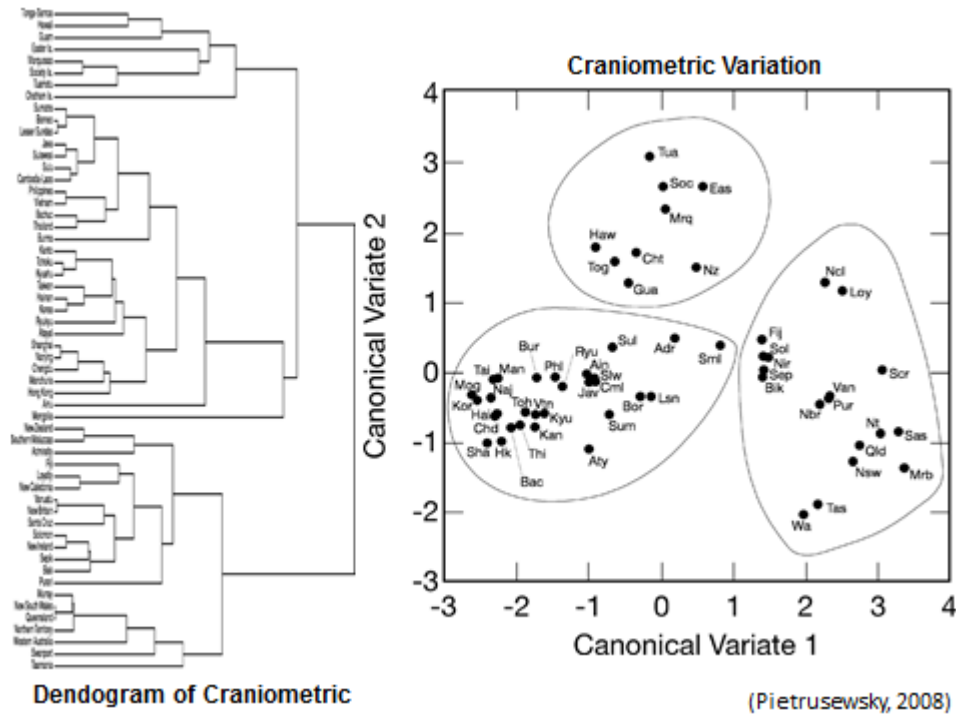


Paleoanthropology

The primary focus of paleoanthropological study by Pietrusewsky (2008) is using craniometric data to investigate the historical-biological relationships of the modern indigenous peoples of Southeast Asia, East Asia, Australia, and the Pacific Islands. A total of 2,595 male crania representing 56 cranial series are included in this study with stepwise discriminate function analysis and Mahalanobis generalized distance are applied to 27 landmark measurements recorded. The data used in this study are fifty six cranial series represent modern and recent indigenous inhabitants from Remote Oceania, Near Oceania, Australia, Island Southeast Asia, Mainland Southeast Asia, East Asia, and North Asia.

The results of Pietrusewsky’s (2008) study on multivariate analysis of craniometric data helps to explain the biological relationships of the modern and recent inhabitants of Pacific and surrounding regions. He uses several analysis methods including the inspection of jackknifed classification results, canonical plots, and the construction of diagrams of relationship based on Mahalanobis distances. The main result of his craniometric analysis are: Inhabitants of Australia, Tasmania, and Melanesia have a different character with the peoples of East Asia, Southeast Asia and Remote Oceania, and division that groups implies separate origins for the indigenous inhabitants of these two regions. The marked separation of East/North Asian and

Southeast Asian cranial series supports models that hypothesize long term continuity rather than population intrusion and/or replacement. Biological connections between Island and Mainland Southeast Asian cranial series are clearly in these results. The population of Remote Oceania, while part of the greater Asian division show connections with several Island Southeast Asian series supporting archaeological, linguistic, and genetic models for the peopling of Remote Oceania. Within Island Southeast Asia, a west to east patterning within the island chain is apparent. The cranial series from the Southern Moluccas reveals biological affinity with adjacent Melanesian as well as Polynesian series further to the east.

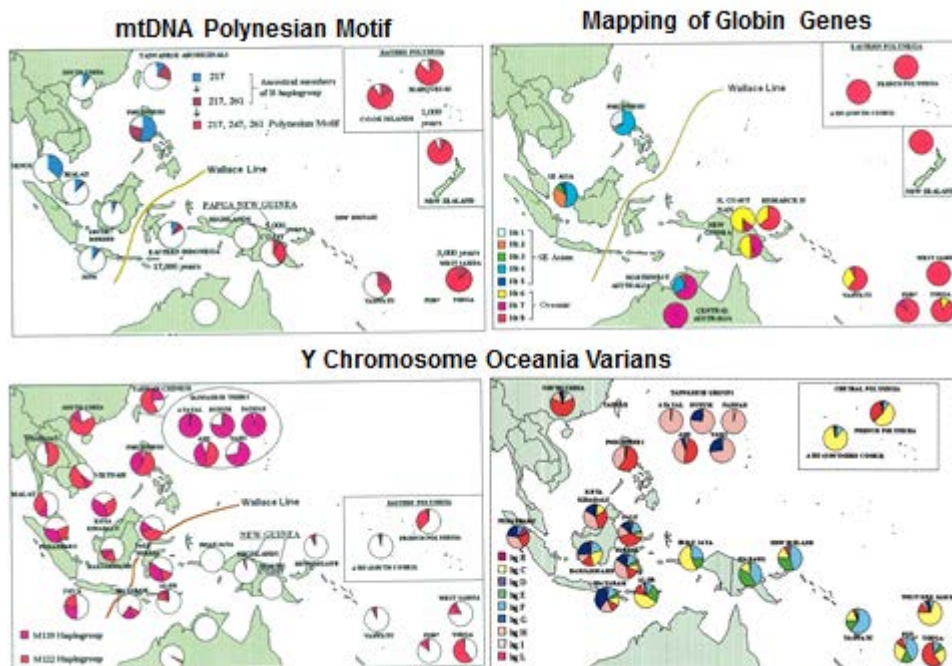


Genetic

Openheimer and Richards (2001) study on genetic data try to answer the question about the origins of the Polynesians people. Their genetic study based on distribution of ancient globin genes, mitochondrial DNA and Y chromosome. The mapping of globin genes in the 1980s suggested that there were two α -globin gene deletions ($\alpha^{3.7^{III}}$ and $\alpha^{4.2}$) resulting in two forms of α -thalassaemia, an inherited autosomal recessive blood disease. This character detected as migration markers found throughout coastal and lowland Melanesia, suggests an important places for migration of Polynesian people. These observations suggest that the Polynesians ancestor, if they were not local must have stopped at least long enough to intermarry locally. Based from mtDNA evidence in the Indo-Pacific region there are identified a nucleotide position of 16247, a sub-group of haplogroup B known as the “Polynesian motif”. This motif is not found in the Philippines, Taiwan or China, it does find in these regions its immediate ancestor type. Eastern Indonesia is the westernmost region in which the full motif type, then the 16247 mutation must have arisen in that region, approximately 17,000 years (5,500–34,500 years). There are two Y-chromosome haplogroups dominate the Polynesian scene. M122 marker is clearly derived from East Asia or Southeast Asia, since it is common throughout those regions

but absent in the New Guinea highlands. Another haplogroup defined as M119 marker may also be identified dispersal from or via Taiwan, although the evidence is even more ambiguous than for the M122 clade. This cluster is less common on the mainland especially in Indo-China, but occurs at extremely high frequencies in Taiwan and is also common in the Philippines.

For the conclusions Oppenheimer and Richards agrees if it is possible that there was a Neolithic dispersal from the Asian mainland, via Taiwan, into the Indo-Malaysian archipelago, but Y-chromosome evidence is equivocal and mitochondrial DNA is not yet match. Ancient Asiatic lineages mark a clear genetic trail out into the Pacific, their local derivative lineages are also very old, and considerable inter-mixing has taken place with indigenous New Guineans. On the available evidence, Oceanic and Central Malayo-Polynesian Austronesian speakers are considerably closer, genetically, to lowland Papuan speakers than they are to Western Malayo-Polynesian speakers. Southeast Asian lineages may have been spreading to lowland Melanesia from before the mid-Holocene. Polynesians in the late Holocene are connected their maternal and paternal lines of descent trace back mainly to Wallacea, and to some level also to Lowland and Island of Melanesia.



(Oppenheimer & Richards, 2001)

Discussion

A number of alternative hypotheses seek to explain the origins of the three groups of Pacific populations (Melanesians, Micronesians, and Polynesians), who speak languages belonging to the Oceanic subfamily of Austronesian languages. The main problem faced by Greenhill and Gray (2005) in their linguistic analyses is the lack of sufficient, evenly sampled data. This problem makes an origin for the tenth branch in Taiwan weakens the case for “Out of Taiwan” origin and enables us to discriminate between the Express Train and Slow Train scenarios. If Taiwan had simply been an Austronesian backwater, as argued on the basis of archaeological evidence, earlier levels of diversity might well have survived. Maybe the homeland of pre-Oceanic distribution of the Austronesian language family was in the broad

triangular area formed by Taiwan, Sumatra, and Timor, where the oldest Malayo–Polynesian languages are found and where no other languages are spoken today (Gibbons, 2001).

The Oceanic Austronesian languages are a form of larger subgroup known as Eastern Malayo-Polynesian. Direct relation of Oceanic languages in Island of Southeast Asia is a group spoken at the western end of New Guinea, around Cenderawasih Bay, and in South Halmahera known as South Halmahera-West New Guinea (Blust, 1978). Austronesian speakers probably first entered New Guinea from the Moluccas. The likeliest location of Proto Eastern Malayo-Polynesian close to where its two primary branches meet, on or near the north coast of New Guinea, in the area bounded by Cenderawasih Bay and the Bismarck Archipelago. A dispersal centre in or near Cenderawasih Bay is favoured by the fact that Eastern Malayo-Polynesian in turn has its closest relatives in the Moluccas and the Lesser Sundas. The Oceanic branch probably diverged from South Halmahera-West New Guinea when some speakers of Eastern Austronesian moved eastwards, either along the north coast of New Guinea or directly to the Bismarcks (Blust, 1984/1985).

According to a linguistic study by Pawley, there are a number of inferences about the linguistic sequence in the Pacific: The non-Austronesian families have been in Near Oceania for much longer than Austronesian (34.000 BP), but non-Austronesian languages probably did not reach Remote Oceania. And after, Austronesian languages entered Near Oceania from Wallacea (3.500 BP). When Austronesian languages speakers reached Remote Oceania (2.000 BP) they had the field to themselves (Pawley, 2007). This sequences makes of Wallace (Moluccas) and Near Oceania (Bismarcks) have important positions in Austronesian migration into Pacific as a “homeland” and “hybridization” place. According to Blust, languages can spread without preserving the genetic makeup of the original speakers, such as Latin (in Gibbons, 2001). Consequently, this condition makes a reconstruction of human migration in prehistoric times based on linguistic hypothesis alone has many limitation.

In physical anthropology, cranial morphology is a central role to understanding biological relationships and evolution of human populations. Pietrusewsky (2008) use cranial series from modern and recent indigenous inhabitants for examining relatedness between and within past and present populations. Question in this study is how modern and recent sample could explain level and process of human migration in the past. Another sample problem in his study is related to the inhabitants of the eastern Lesser Sunda (Nusa Tenggara) and Moluccas Islands to the west of New Guinea which shows considerable variation. Because of the limited number of specimens available for this region, they have been combined with specimens from the string of islands extending east of Java from Bali to Aru to represent a Lesser Sunda series. While, population group in this region shows variation culture who speak West Malayo-Polynesian, Central Malayo-Polynesian and Non-Austronesian (Papua phylum) languages.

Generally, broader palaeoanthropological multivariate comparison by Pietrusewsky grouped Polynesians with South-east Asian and East Asian groups well differentiated from Melanesian samples, and lending support to the view that Polynesians are not of Melanesian origin. His more specific study about a skeleton of a 40-50 year old male, associated with Lapita pottery dated back from 2700 BP from a site near Yalobi Village, Waya Island, Fiji suggest morphological similarities with Southeast Asia, the presumed homeland of Austronesian speaking people in Oceania (Pietrusewsky et al, 1997). But, another sample of human skeletal and dental remains from Watom Island, East New Britain Province, Papua New Guinea, dated

circa 2500 to 2100 BP and associated with the Lapita cultural complex were studied by same researcher telling different story. Multivariate analyses, using mandibular measurements, generally separate the Watom and Lapita mandibles from other Pacific and Asiatic groups but hint of a possible biological connection with eastern Melanesian and possibly Polynesian populations (Pietrusewsky, 1989). Result of this study indicating a significant contact between Austronesian and Papuan population in early stage of Austronesian migration into Pacific, especially in Island of Melanesia.

Genetic affinities between aboriginal Taiwanese and populations from Oceania and Southeast Asia have previously been explored through analyses of mitochondrial DNA (mtDNA), Y chromosomal DNA, and human leukocyte antigen loci. Studies of mtDNA variation in indigenous Taiwanese populations have suggested that they held an ancestral position in the spread of mtDNA throughout Southeast Asia and Oceania. mtDNA with a 9-bp deletion have considerable mainland-Asian diversity and have spread to Southeast Asia and Oceania through a Taiwanese bottleneck (Melton, et. al., 1998). From complete mtDNA sequencing information, B4a lineages were associated with the origin of Polynesian migration from Taiwan defined as B4a1a. Coalescence times of B4a1a were 13.2 ± 3.8 thousand years in Island of Southeast Asia or 9.3 ± 2.5 thousand years in Papuans and Polynesians (Trejaut, et. al., 2005). The high intervals of these calculations make them confused to compare with another data, because the expansion times of mtDNA B4a1a from Taiwan and Island of Southeast Asia seem very large when compared with the linguistic and archaeological evidence of early Austronesian languages expansion into Pacific about 3500 years ago.

Y chromosomes examined by Capelli et. al., 2001 from "East Asia" suggest that M9 marker defines a group that includes a large set of non-African types but that excludes ancestral lineages found only in Africa. This result argues strongly against a significant genetic contribution of *Homo erectus* to the *Homo sapiens* genetic composition of the region, at least on the paternal side (Capelli et. al., 2001). Analysis of autosomal microsatellites revealed a group including Polynesia, Melanesia and Australia and separated from East Asian populations, whereas mtDNA analysis of the same individuals grouped Melanesia, Australia, and East Asian populations in contrast with distribution of the Polynesian motif (Lum, et. al., 1998). While the ages for the expansion of the Polynesian motif in PNG and Polynesia proposed by Oppenheimer and Richards (2001) are date back to 17.000 years ago for eastern Indonesia is hard to reconcile with any inferred proto-Polynesian expansion event in that or any other region. Another view proposed by Hagelberg, et. al., 2008 makes the problem more confusing, that argue the Polynesian motif seems to be derived from an ancestral type in Taiwan, and its exact time of entry into the Pacific is unclear, but the genetic evidence is consistent with a route of migration through the Philippines and Micronesia.

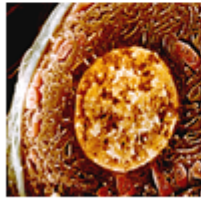
Consequently, early peopling of the Pacific is a hard question which tried answered by multiple points of view, and also require the combined efforts of archaeologists, linguists, and biologists perspective.

AUSTRONESIAN DIASPORA IN PACIFIC

- In some level there are a relationship between language family – genotype and phenotype population
- Two main stage of Pacific occupation

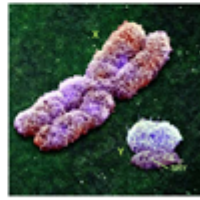
Mt-DNA

- Fast Train Model
- Massif migration from Taiwan to Southeast Asia and Pacific



Y-Chromosome

- Slow Boat Model
- Mixed with Australo-Melanesian genes in Voyaging Corridor



Early peopling of the Pacific is a hard question, even to answered by multiple points of view from of archaeological, linguistic, and biological perspective.

Reference

- Blust, Robert. 1978. Eastern Malayo-Polynesian: A Subgrouping Argument. *Second International Conference on Austronesian Linguistics: Proceedings*, pp. 181–234.
- _____. 1984/1985. The Austronesian Homeland: A Linguistic Perspective, *Asian Perspectives*, 26:1, pp.45-68
- Pawley, Andrew. 2007. Locating Proto Oceanic. *The Lexicon of Proto Oceanic: The Culture and Environment of Ancestral Oceanic Society. Vol. 2, The Physical Environment*, pp.17-34
- Greenhill, Simon J and Russell D Gray. 2005. Testing Population Dispersal Hypotheses: Pacific Settlement, Phylogenetic Trees and Austronesian Languages. *The Evolution of Cultural Diversity: A Phylogenetic Approach*
- Gibbons, Ann. 2001. The Peopling of the Pacific. *Science, New Series, Vol. 291, No. 5509 (Mar. 2, 2001)*, pp. 1735-1737
- Hagelberg, Erika et. al., 2008. A genetic perspective on the origins and dispersal of the Austronesians: mitochondrial DNA variation from Madagascar to Easter Island. *Past Human Migrations in East Asia: Matching archaeology, linguistics and genetics*. New York: Routledge
- Lum, J Koji et. al., 1998. Mitochondrial and Nuclear Genetic Relationships among Pacific Island and Asian Populations. *American Journal of Physical Anthropology* 63:613–624
- Melton, Terry et. al., 1998. Genetic Evidence for the Proto-Austronesian Homeland in Asia: mtDNA and Nuclear DNA Variation in Taiwanese Aboriginal Tribes. *Am. J. Hum. Genet.* 63:1807–1823
- Oppenheimer, Stephen and Martin Richards, 2001. Fast Trains, Slow Boats, and the Ancestry of the Polynesian Islanders. *Science Progress* 84 (3), 157–181
- Pietrusewsky, Michael. 1989. A Study of Skeletal and Dental Remains from Watom Island and Comparisons with Other Lapita People. *Records of the Australian Museum Vol. 41: 235-292.*
- _____. 2008. Craniometric Variation in Southeast Asia and Neighboring Regions: A Multivariate Analysis of Cranial Measurements. *Human Evolution Vol. 23 - n.1-2 pp.49-86.*
- Pietrusewsky, Michael et. al., 1997. A Lapita-Associated Skeleton from Waya Island, Fiji. *Micronesia* 30(2):355-388
- Trejaut, Jean et. al., 2005. Traces of Archaic Mitochondrial Lineages Persist in Austronesian-Speaking Formosan Populations. *Plos Biology* 3 (8)