

OUT OF ASIA Peopling the Americas and the Pacific



Edited by Robert Kirk and Emöke Szathmary

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The Journal of Pacific History, Canberra

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Introduction

TWO VAST AREAS OF THE EARTH'S SURFACE RECEIVED THEIR FIRST HUMAN POPULations by migrations out of Asia. One of these areas comprises the North and South American continents, joined by the narrow isthmus of Central America. It was populated first by peoples who crossed from eastern Siberia to Alaska and penetrated southwards ultimately to the extreme tip of Tierra del Fuego. The other area comprises the myriad islands, some large, some very small, scattered across the expanse of the Pacific Ocean. These islands were colonized first by peoples who moved out from southeast Asia and who populated the domain of the Pacific progressively over a long period of time as their navigational skills improved from sight-of-land to long distance voyages.

The manner and the timing of the early colonization of both the Americas and the Pacific have long excited interest. Different theories have been advanced, some to be replaced as new evidence emerged, others to be resurrected after a period in oblivion. During the last two decades many studies in various disciplines have shed new light on these questions. For this reason it seemed opportune to use the occasion of the XIth International Congress of Anthropological and Ethnological Sciences, held in Vancouver during August 1983, to bring together archaeologists, linguists, physical anthropologists and geneticists to make a synthesis around two themes: 'Peopling the Americas' and 'Peopling the Pacific'. Much of what is known about the first inhabitants of both the Americas and the Pacific Islands is gleaned from the archaeological record. While stone tools and sherds, their ages, their pattern of distribution and the context in which they occur can tell us much about the lifeways and the cultural connections of these early peoples, artefacts alone yield no information about the ethnicity of the makers of either the tools or the pots. We need to add substance to this picture by studies of skeletal materials and to try to trace ancestral ties through investigations of the genetic structure of the living populations of these areas.

Linguistic studies are a valuable adjunct to those of the archaeologist, and through reconstruction of the protolanguages inferences can be made about the speakers of these languages in the past. Such studies, as is clear from some of the papers in this volume, have been important, particularly in the Pacific.

In the present volume Stephen Zegura paints the backdrop for discussion of the peopling of the Americas. He reviews the archaeological record and summarizes the palaeoclimatic data needed for deciding which were the most plausible routes which could have been followed by the first migrants to North America. He draws attention also to the long-standing dispute on the distinctiveness or otherwise of the American Indians and the Aleut-Eskimos, and concludes by presenting a speculative scenario for the origins of the diverse human groups among the aboriginal inhabitants of the Americas. Christy Turner lends support to Zegura's description, drawing on his own extensive studies of the structure of teeth recovered from crania of the Americas and from many parts of north and east Asia. The distinctive structure of the teeth of all native Americans places their biological relationship firmly in an east Asian setting.

The current status of the geneticists' view of the peopling of the Americas is indicated by Emöke Szathmary and Francisco Salzano. Szathmary focuses on populations in northern North America, the subarctic culture area populated by speakers of two large language families, Athapaskan and Algonkian. Some clues are provided by specific genetic markers which suggest that the Athapaskan genetic link is toward the Bering Sea area while the Algonkian connection is toward the south. Using multivariate statistical measures of genetic distance she finds that the Eskimos cluster with the Siberian Chukchi, whilst Athapaskans are closer to Eskimos than are the Algonkians. The South American genetic data is reviewed by Francisco Salzano against the background of archaeological remains, which point to early dates for the widespread dispersal of man in South America. He argues that, so far, neither archaeological, anthropometric or genetic studies can furnish unequivocal evidence about the routes travelled by the first colonizers within the continent. Although it seems that the main contribution to the Amerindian gene pool originated in Siberia, Salzano concludes that the genetic data do not contradict the possibility of other minor sources from the Pacific (Proto-Polynesians?).

Chapters 5 to 12 are concerned with the peopling of the Pacific. Kazuro Hanihara has summarized the extensive data on cranial measurements both from past and living populations in Japan. He concludes that variability in modern Japanese probably is the result of varying amounts of admixture between a basic Japanese Jomon population and later migrants through the Korean Peninsula.

During the Pleistocene period Japan was part of the east Asian landmass, but as sea levels rose the routes for new migration in became severely restricted. The Japanese islands, however, pointed southwards, providing a possible launching pad for movements further out into the Pacific. But the major thrusts into the Pacific came from further south, though the bases for these thrusts and their timing still remain obscure.

Among the present islands of the western Pacific world some were also part of the Asian landmass during the Pleistocene. These include much of Indonesia and the Philippines, and for this reason their populations have more ancient connections, frequently overlaid with peoples who arrived at later dates. In the Philippines the various Negrito populations may well represent descendants from such earlier groups and Keiichi Omoto's chapter reviews his detailed genetic studies of these peoples. Studies of six Negrito populations in various parts of the Philippines show them to be quite distinct, genetically, from any African populations. They are more closely related to Southeast Asian populations than to Australian Aborigines or New Guineans. Omoto suggests that one group, the Mamanwa, were derived from an ancestral Proto-Malay population of late-Pleistocene Sundaland from which the other Negrito groups also evolved but with a phenotypic specialization for small body size due probably to adaptation to life in the tropical rainforest.

Another sophisticated approach to tracing genetic ancestry is outlined by Rebecca Cann. The structure of the DNA in cellular organelles, called mitochondria, can now be determined precisely and variations in this structure from person to person can be traced back through the maternal line. Using samples from Australian Aborigines and other peoples around the world she concludes that mitochondrial DNA analysis shows that some of the maternal lines can be traced back to one with a worldwide distribution roughly 350,000 years ago. She finds also that multiple populations have contributed to the spread of peoples in the Pacific.

Susan Serjeantson has employed another powerful tool for analysing the genetic relationships between Pacific peoples. Making use of the genetic characteristics of the human leucocyte antigens (HLA) she has used HLA data not only to trace population movement but also to estimate the extent of admixture which has occurred in the past. For the Nauruans, for example,

she estimates a Melanesian admixture of nearly one-third. Similarly for Fijians she shows that there is a substantial Polynesian contribution of 21%. Of particular importance is her conclusion based on the HLA data that coastal and island Melanesians show evidence of intermarriage with Austronesians, but that the peoples associated with Lapita pottery further east in Samoa were virtually uninfluenced by Melanesian genes.

Recent theories on the peopling of the Pacific have drawn heavily on two sources of evidence: language diversity and archaeology, particularly evidence for the spread of the Lapita-style pottery. Three important chapters in the present volume address themselves to respective reviews of these studies. Darrell Tryon discusses first the distinctive languages of Australia and the possibility that these represent descendants of the Australoid languages spread across New Guinea and Australia before their landmasses became separated some 10,000 years ago. In New Guinea they were replaced by at least two waves of Papuan languages, and more recently by speakers of the Austronesian, or Malayo-Polynesian, languages which moved across the region from the northwest. Tryon draws attention to the difficulties of interpreting the diversity found within the large subgroup of Austronesian languages known as Oceanic. He believes that there is now general agreement that the reconstructed Proto-Oceanic language formed and consolidated in the New Britain/New Ireland area. Only a tentative account can be given of the way in which this language later spread, particularly into other parts of island Melanesia.

Another set of insights into the linguistic complexity of the Pacific region is provided by Andrew Pawley and Roger Green. In their view archaeological research now gives a clearer picture of the time depths and cultural continuity among sequences for some of the island groups associated with Oceanic languages. Increasingly, they state, linguistic evidence indicates that Proto-Austronesian dispersed from the Formosan-Philippine region and that the Oceanic subgroup of the Austronesian languages came from a movement of people speaking Austronesian languages along the north coast of New Guinea via eastern Indonesia. There was then a relatively swift spread of Oceanic speakers across Melanesia followed by a disintegration into regional languages or dialect chains.

Pawley and Green point out also that recent research has given a better understanding of the distribution of Lapita pottery and closely related traditions. Matthew Spriggs takes up the discussion of Lapita in greater detail. Spriggs raises questions about previous theories on Lapita culture and supports the view that Lapita was not basically derived from a southeast Asian tradition but may have developed in the northwest Melanesian area.

Finally, Patrick Kirch reviews recent archaeological research in the Polynesian Outliers, islands on the Melanesian 'fringe' which have long been regarded as a key to Oceanic origins and dispersals. Archaeological studies on two Outliers, Anuta and Tikopia, have revealed highly complex settlement histories extending over three millenia.

Clearly, the contributions to the present volume, which, with the exception of the chapters by Susan Serjeantson and Matthew Spriggs, are based on contributions to the symposia on 'Peopling the Americas' and 'Peopling the Pacific' at the XIth International Congress of Anthropological and Ethnological Sciences in Vancouver in August 1983, demonstrate the complementary nature of work in a wide variety of disciplines. Such an exchange of views is a valuable part of a symposium, and the organizers are to be congratulated on their choice of speakers.

No modern symposium can be staged without some financial resources. In the present instance the generous financial assistance of the Wenner Gren Foundation for Anthropological Research and the Canadian Association for Physical Anthropology is gratefully acknowledged. As well, individual participants and their parent institutions provided help which made possible the success of the symposia. The encouragement and assistance of Dr S. Pfeiffer and Mrs L. Osmundsen in the organization and execution of the 'Peopling of the Americas' symposium are greatly appreciated. We are grateful to the Board of Management of the *Journal of Pacific History* for allowing five of the chapters to be reprinted from Volume XIX, 1984, and for including this volume in the Journal's publication series. Also, we owe special thanks to Jennifer Terrell for her editorial guidance and assistance, and to Val Lyon for redrawing many of the figures.

Canberra and Hamilton, September 1984 Robert Kirk Emöke Szathmary proponents. Yet, a diverse body of genetic data points to Asia as the heartland of Homo sapiens. In 1976 Benveniste and Todaro used DNA hybridization to assess the similarity of type C viral gene sequences in a variety of higher primates and found that humans were identified as Asian rather than African by their technique.¹³ They therefore proposed an Asian origin for Homo sapiens and suggested a long history in Asia before our species migrated throughout the world. Subsequently, Guglielmino-Matessi and coworkers presented a speculative model for the Asiatic origin and subsequent spread of Homo sapiens sapiens that was concordant with gene frequency data.¹⁴ Then Denaro and coworkers studied ethnic variation in the cleavage patterns of mitochondrial DNA from a larger sample than Brown had used (235 vs 21) and concluded that the formation of human ethnic groups started in Asia probably within the last 50,000-100,000 years. Evidence for the centrality of Asia also comes from a study of the world distribution of 39 alleles from 10 loci by Piazza, Menozzi and Cavalli-Sforza. ¹⁵ They found that most genetic variation is associated with longitude and that central and especially south Asia appear as epicentres in terms of synthetic principal component variables constructed from the nuclear gene frequencies. On the basis of their genetic analysis they proposed the following migratory events: (1) major migrations to America and Australia from northeastern Asia and southeastern Asia, respectively; (2) the replacement of Neanderthals by Homo sapiens sapiens who were probably of Asiatic origin; and (3) the radiation of Neolithic populations from the Near East 10,000-5,000 years ago. Thus, according to their scenario over the last 40,000 years Asia has increasingly become the centre of both the New and Old Worlds.

Perhaps fossil material from China like the larger-brained late Homo erectus specimen from Zhoukoudian (ca. 230,000 BP), the newly discovered calvarium from Hexian in Anhui Province, the morphologically transitional Dali cranium, the various fragments from Xujiayao and Changyang and the more modern Mapa skull-cap represent samples from an evolving Asian population system more important for the origins of Homo sapiens and for the eventual appearance of Homo sapiens sapiens than previously realised. Unfortunately, except for Zhoukoudian precise dates for these Chinese remains are lacking with most of the specimens placed near the Middle-Upper Pleistocene boundary (late Middle Pleistocene or early Upper Pleistocene). ¹⁶

Obviously, the 'Big Picture' may be large, but it certainly is not clear. For instance, did our species arise through anagenetic transformation, or by a branching process associated with a true speciation event? Where and when did *Homo sapiens*, *Homo sapiens sapiens*, and the major geographic races originate? What is the relationship of present-day population systems to past population systems? Do subgroupings like races, ethnic groups, demes, or other subspecific distinctions help us to understand human evolutionary history when they are projected back into time? How do skeletal populations relate to the present distribution of genetic systems? How do all the above relate to culture? We simply do not have the answers for these conundrums. In some areas like place and time of origin we have at least begun to limit the range of possibilities, in others there is practically no agreement. For instance, Weiss and Maruyama feel strongly that it is futile to use racial classifications and population genetics models to study human racial ancestry because according to them: 'The present distribution of peoples is the result of the historical accidents of cultural evolution, and is not necessarily a representative reflection of populations at some hypothetical ancestral branchpoint.'¹⁷

On the opposite side of the ledger we find Nei and Roychoudhury stating that from their genetically based perspective 'the classification of human races is the first step in the study of human evolution' and furthermore that one of their most important conclusions based on genetic distance models involves the nondichotomous nature of human genetic differentiation due to gene flow.¹⁸ Still, we must not forget that human evolution was and is a biocultural phenomenon that takes place in a cultural context. Any so-called 'Big Picture' based on genes and/or skeletons is sorely deficient if it excludes the details of the cultural framework and environmental setting for our evolutionary history.

From the 'Big Picture' to the Americas: I would now like to focus on some of the evidence for the microevolutionary events associated with "The Peopling of the Americas.' First of all, there is absolutely no biological evidence for the presence of any hominid group other than modern Homo sapiens sapiens in the Americas. Despite some claims to the contrary, I believe this suggests that the peopling of the Americas occurred sometime after 40,000 BP.¹⁹ Although there is widespread consensus that the source of the migratory influx was northeastern Asia and that the route was across the now submerged Bering Land Bridge portion of Beringia, controversy rages concerning the number and especially the timing of these colonizing episodes. Between 12,000 and 11,000 years ago the earliest clearly defined, undisputed North American culture, the fluted projectile point Clovis or Llano culture, had already become established. Those who favour a late date for the peopling of the Americas on the order of 12,000 to at most 14,000 BP generally favour the hypothesis that the Clovis peoples or their contemporaries were the first inhabitants of the Americas.²⁰ Indeed, some have adopted a scenario for the demise of the American Pleistocene mammalian megafauna that involves a rapid spread of these Palaeo-Indian peoples throughout the Americas. According to proponents of this Pleistocene over-kill hypothesis, Palaeo-Indians traversed the entire length of the Americas in less than a millennium arriving in Tierra del Fuego by 11,000 BP and causing the extinction of the megafauna as they advanced.²¹

Those who favour an earlier date for the initial peopling of the Americas point to a substantial body of archaeological evidence dated before 12,000 BP from places as geographically diverse as the Yukon, Idaho, Pennsylvania, Mexico, Venezuela and Peru. While it is true that some of this evidence is questionable because of doubtful provenience, chemical contamination, redisposition and methodological uncertainties in the chronometric techniques, it seems most probable that the 12,000-year date is too conservative. Thus, I believe the initial human occupation of the Americas occurred somewhere between 12,000 and 40,000 years ago.²²

For Bada and Masters and indeed, for many traditional physical anthropologists 'the single most important piece of evidence necessary for establishing when human beings first migrated into the Americas is, not the antiquity or authenticity of "artifacts", but rather the ages of human skeletons found in the New World'.²³ The only human skeletal evidence from the Americas claimed to be older than 40,000 years of age on the basis of any absolute dating method are the La Jolla Shores, Del Mar and Sunnyvale remains from California (see Fig.1) dated by amino acid racemization at 44,000, 48,000 and 70,000 BP, respectively.²⁴ The recent archaeometric fate of the Del Mar and Sunnyvale specimens has been instructive. In 1981 Bischoff and Rosenbauer used uranium series analysis to redate the Del Mar and Sunnyvale remains at 11,000 and 8,300 years BP, respectively, and early in 1983 Taylor and coworkers used both decay and direct-counting ¹⁴C techniques on the Sunnyvale postcranial skeleton to arrive at an estimate of 3,500-5,000 radiocarbon years BP. Thus, the Sunnyvale female has somehow managed to grow 60,000+ years younger during the last decade!²⁵

A number of additional chronometrically dated American skeletal remains supposedly fall within the 12,000 to 40,000 year interval (see Fig.1); however, some residual uncertainties remain in practically every case. For instance, the Los Angeles skeleton has been dated at > 23,600 years by ^{14}C analysis of bone collagen and at 26,000 years BP by aspartic acid racemization.²⁶ Unfortunately, both non-finite bone collagen dates and amino acid racemization dates have proved to be unreliable in the past. A consistent date of around 20,000 BP for Yuha Man (discovered at a site near El Centro, California) has been obtained from indirect ¹⁴C,²³⁰Th, and amino acid racemization analyses. Additional confirmatory analyses are precluded at present because the skeleton has been missing since December 1980 and according to Bischoff and Rosenbauer is presumed stolen.²⁷ Finally, the Laguna skull and associated postcranial material have yielded collagen-based ¹⁴C dates of 17,150±1,470 years BP and greater than 14,800 years BP, respectively. This material was found at Laguna Beach, California in 1933 but subsequent attempts to relocate and date the site have yielded much younger dates and a confusing stratigraphic record.²⁸ Since the postcranial remains of both the Laguna and Los Angeles individuals were consumed for ¹⁴C

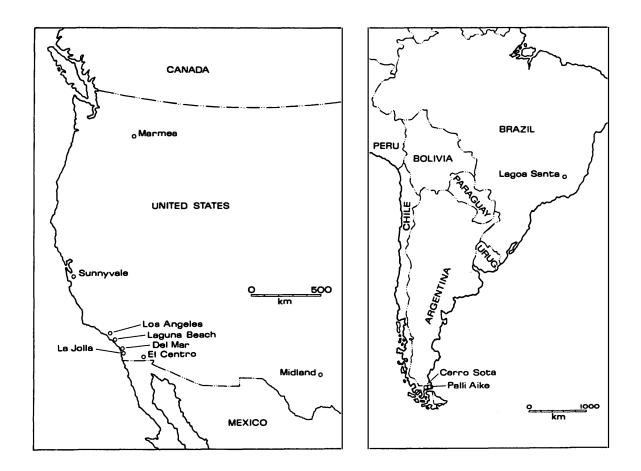


Figure 1 Important early human skeletal sites in North and South America

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analyses, only the cranial material of these two cases still exists for future analyses. Other skeletal candidates for a possible pre-12,000 year date include Midland Man from Texas, Marmes Man from Washington and a mandibular fragment from Old Crow Flats.²⁹

Taken in toto, the human skeletal record for the occupation of the Americas before 12,000 years ago is meagre at best and woefully inadequate to document or confirm anything according to skeptics. There are no stratigraphically secure, well-documented human skeletal populations that predate such Palaeo-Indian aggregates as the 11,000 year old cremations from the Cerro Sota and Palli Aike caves of Chile or the Lagoa Santa cave inhabitants of 10,000 years ago from Brazil (see Fig.1).⁸⁰ The best we have at present are bones of isolated individuals, often of uncertain provenience with highly questionable dates. In fact, we have better skeletal evidence for the origins of the genus *Homo* around two million years ago than we have for early Americans 20,000 years ago. Thus, the case for a pre-12,000 year date for the peopling of the Americas rests almost entirely on material culture.³¹ Among archaeologists specializing in areas germane to the topic of New World origins, the right to disagree is a fervently practised liberty. As a result no consensus has emerged concerning exactly when a band of transplanted Siberians actually became the first Americans, although it is generally agreed that these first Americans were the ancestors of the American Indians rather than of the later appearing Aleut-Eskimo population system.³²

Perhaps a look at the reconstructed palaeoecology of Beringia (see Fig.2) can help us focus on some physical and/or biological components of the land bridge environment that will increase the temporal resolution of our scenario. There are two extreme views concerning Pleistocene Beringia. One sees the Pleistocene Arctic steppe as a richly productive grassland similar in ecosystem dynamics to the present-day African Serengeti Plain while the other envisions a harsh polar desert with sparse, discontinuous vegetation less capable of supporting large, ungulate populations. Hopkins has provided a sequence of time-stratigraphic units for the interval between 120,000 and 8,000 years ago in unglaciated Beringia which can be used as a framework for discussing its palaeoecology and palaeogeography.³³ The sequence starts with a poorly dated periglacial/glacial period called the Happy interval followed by a warmer, more mesic interstadial called the Boutellier interval which probably began about 60,000 years ago and which ended 30,000 years ago. Then a severe periglacial/glacial episode, the Duvanny Yar interval, began and it continued until about 14,000 years ago when the Birch interval brought an end to the Pleistocene periglacial in Beringia. This period of rapid environmental change highlighted by the rise to dominance of birch pollen ended by about 8,500 years ago as peat accumulations became widespread and spruce and alder pollen became abundant.³⁴ Thus the periods of main interest for the peopling of the Americas are the Late Boutellier, the Duvanny Yar, and the early Birch intervals.

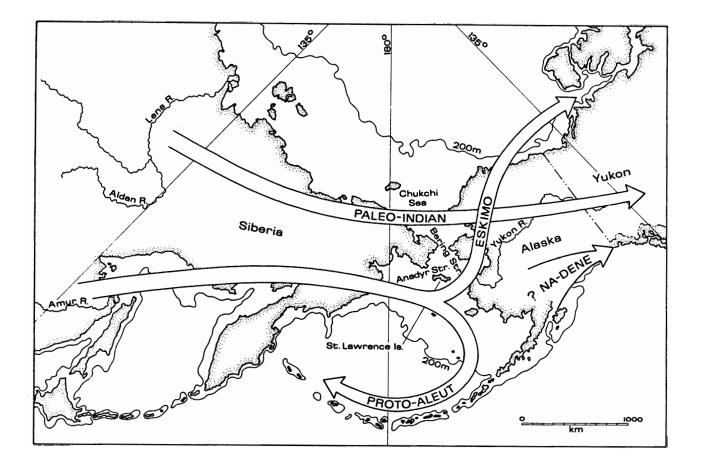


Figure 2 Beringia: Geography and possible migration routes

Climatic conditions began to deteriorate from the Boutellier interstadial maximum about 40,000 years ago and by 30,000 years ago Beringia was starting to become a cold, dry, treeless, sandy plain. In fact, the polar desert concept probably does apply to Beringia during the subsequent Duvanny Yar interval. By 18,000 years ago world-wide sea levels were at a minimum(120 metres below the present level) and in Beringia sea level was probably 90 metres lower than today (a drop in sea level of only 46 metres will create a dry land bridge between Siberia and Alaska). It was then that the Beringian land bridge was at its maximum, extending more than 1,000 km north to south and about 4,000 km east to west (see Fig.2). During the height of the Duvanny Yar much of Beringia was inhospitable. Wind-blown dune systems predominated on the Arctic lowlands and discontinuous herbaceous vegetation dotted the landscape. It is also highly likely, however, that there were some mesic refugia near the Bering Strait where cottonwood and aspen held on and where large ungulates like mammoth, horse, bison and caribou found forage. The existence of fossil bones from these large-bodied herbivores underscores a real productivity paradox. How could the barren steppe-tundra of Duvanny Yar Beringia support these animals? It seems necessary to postulate patches of high productivity or hot spots to account for the presence of these animals. Whether these hot spots actually existed and whether humans were part of the ecosystem of these patches of significant productivity are key questions for future research.³⁵

As the Duvanny Yar came to a close climatic changes caused sea levels to rise. As early as 15,500 years ago the Bering Strait became flooded and the land bridge was reduced to a narrow isthmus at the Anadyr Strait between St Lawrence Island and Siberia (see Fig.2). This isthmus was also flooded by about 14,400 BP, thereby effecting final separation of Siberia from Alaska and by 12,000 BP St Lawrence Island became separated from mainland Alaska. By the end of the Pleistocene about 10,000 years ago sea level was only 20 metres below its present position and the land bridge portion of Beringia was entirely submerged. The abrupt warming at the end of the Duvanny Yar also ushered in the Birch interval during which the floral landscape of Beringia was transformed to an open woodland habitat with flowing streams and numerous lakes fed by increased precipitation. By the end of the Birch interval around 8,500 BP the characteristic Holocene climate and landscape of the region took hold. The transition to the present-day regime of less lush and productive vegetation and a water-logged tundra without mammoth or bison was now complete.³⁶

Palaeoclimatologists generally agree that the ultimate cause of the end of the last ice age involved changes in the orbit and axial tilt of the earth.³⁷ On a world-wide scale the last Pleistocene glacial seems to have exited in two steps with the first phase of climatic warming starting sometime between 13,000-16,000 years ago. By 11,000 years ago ice sheet disintegration had reached a maximum rate. Then, according to data from the North Atlantic Ocean and continental Europe, there was a hiatus in the warming trend from about 11,000 to 10,000 BP. This colder period is called the Younger Dryas by European glaciologists. After this brief respite the warming trend resumed and deglaciation continued between 10,000 and 8,000 BP. Finally, pollen, fossil logs, and recent macrofossil data from Jasper National Park in Alberta, Canada show that timberlines were much higher than at present by 8,700 BP thereby implying the onset of the comparatively warm Hypsithermal which lasted until about 5,200 BP.³⁸

Using the palaeoecology of Beringia as a framework, the editors of a volume stemming from a 1979 Wenner-Gren Symposium on this topic adopted the following viewpoint for the role of Beringia in the peopling of the Americas. They stated that humans were widely distributed (though not necessarily numerous) in Beringia as early as 35,000 years ago and that they were present south of the ice sheets as much as 10,000 years earlier than the Clovis hunters whom they feel may represent the possessors of a variant technology rather than the arrival of a new human group.³⁹ Their scenario implies human penetration of eastern Beringia, including eastern Alaska and the Yukon Territory, sometime between 35,000 and 25,000 years ago. Important to their case are Mochanov's archaeological sites in the Aldan River Valley near the western extremity of Beringia (see Fig.2) which have been ¹⁴C dated at between 24,000 and 35,000 BP as well as the apparent hiatus in human activity east of the Aldan River from about 25,000-15,000 years ago.⁴⁰ Whether Beringia was abandoned during this portion of the Duvanny Yar or whether we just have not found the record of the hot spot refugia which may have sustained herbivores and their human hunters cannot be presently determined. Also critical to their scenario is the authenticity of the mounting archaeological evidence for pre-Clovis occupation in North, Central and South America. If humans reached Central and South America by 20,000 years ago as some maintain and if the Duvanny Yar climate prevented Beringian habitation from 25,000-15,000 years ago, then a late Boutellier date becomes reasonable. On the other hand the presumed existence of hot spots possibly occupied by humans during the Duvanny Yar could be interpreted as suggestive of a slightly later initial penetration of the Americas. Finally, if one does not find any of the evidence dated before 12,000 BP convincing, a late entry date during the Birch interval remains a possible alternative. Once again, resolution requires both confidence in the validity of a variety of archaeological sites of postulated antiquity and faith in the ultimate efficacy of future research. Klein has recently sounded a pessimistic message relating to both desiderata for a resolution to the problem of the timing of the initial peopling of the Americas when he stated: 'The time of earliest human colonization may never be fully resolved for either Beringia or the Americas as a whole, since archaeologists cannot

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agree on what constitutes reasonable evidence for ancient human presence'⁴¹ At issue is the interpretation of unstratified material and debris of dubious cultural origin. Also germane is the unfortunate possibility that the data critical to an understanding of this human migration and its microevolutionary implications have been destroyed or presently lie at the bottom of the Bering or Chukchi Seas.

Additional indirect evidence from physical anthropology for the initial peopling of the Americas comes from analyses of gene frequencies and dental data. Harper used contemporary Athabascan Indian and Aleut-Eskimo gene frequencies based on protein data to estimate that the North American native population system originated about 19,000 years BP, while Turner used a diachronic sample of over 9,000 American Indian and Aleut-Eskimo dentitions as the basis for his estimate of 15,000 years BP for the initial penetration of the Americas by American Indians.⁴² Both of these estimates would rule out a Late Boutellier date and are broadly concordant with linguistic evidence which suggests that the internal differentiation within Amerind requires a time depth of the order of 20,000-25,000 years.⁴³ Note also that these Duvanny Yar dates are consistent with Havnes' scenario of pre-Clovis peoples with roots in Europe about 28,000 years BP crossing Beringia in pursuit of big game between 20,000 and 15,000 years ago, as well as with an origin of the Microblade dominated Dyukhtai culture from the north Chinese Microlithic Tradition about 25,000 years ago followed by its eventual spread to East Beringia by 15,000 BP.44

Both the dental and genetic evidence, however, definitely favour an Asian origin for the Native American population system. Prehistoric Native American teeth are very similar to those of North Asians exhibiting what Turner calls a Sinodont pattern of dental trait intensification.⁴⁵ In addition, this Sinodont condition (characterized by frequent incisor shoveling, 3-rooted lower first molars, single-rooted upper first premolars and a variety of other traits) differs from the patterns found in all other populations. Likewise, the Asiatic kinship of the native populations of North America was succinctly summarized by Spuhler in his concluding statement after analyzing the variation in blood group gene frequencies from over 50 Indian, Aleut and Eskimo groups: 'On a world scale, the North American Indians, Eskimos, and Aleuts are a genetically distinct geographic race or breeding population, related most closely to the Mongoloid peoples of eastern Asia.'⁴⁶

The question of how many population systems are actually represented among the Native Americans today and whether they are descended from a single or multiple migrations is a topic beyond the intended scope of this presentation. I will, however, offer a few general observations pertinent to these issues. Physical anthropologists are vigorously debating the relationship between North American Indians and the Aleut-Eskimo population system. The traditional view emphasized the biological distinctiveness of these two groupings; however, recent skeletal, dental and genetic analyses have revealed surprisingly close phenetic and genetic similarities between Eskimos and Na-Dene Indians.⁴⁷ If these ties reflect close common ancestry rather than gene flow, one can start to reconstruct more explicit alternative phylogenetic scenarios for Native Americans. For instance, the traditional view of clear-cut biological distinctions between the American Indians and the Aleut-Eskimo group is represented in Fig.3, diagram C. The view that the closeness of the Na-Dene Indians and the Aleut-Eskimo group is due to gene flow is represented by diagram B while diagram A corresponds to the view that the Na-Dene Indians and Aleut-Eskimo group shared a common acestor not shared by the rest of the American Indians. This last hypothesis would make the Na-Dene Indians and Aleut-Eskimo closely related sister groups according to Hennig's systematic principles.

The origins of the Native Americans: The microevolutionary processes of gene flow and genetic drift have made the reconstruction of the more than 12,000 years of American population history from 20th century genetic data a highly speculative enterprise. The paucity of American skeletal remains predating the end of the Birch interval and the onset of the subsequent Hypsithermal warming 8,000-9,000 years ago, as well as the complete absence of any Aleut-Eskimo skeletal material before about 4,000 BP, have made it impossible to make direct correlations between archaeologically defined cultural traditions and the biological characteristics of the people responsible for the material culture. With these caveats in mind I will now offer an eclectic and admittedly speculative scenario for the origins of the diverse human groups known as 'Native Americans'.

Just as roots of Native Americans were Asian, I think it quite likely that the roots of anatomically modern Homo sapiens sapiens were Asian as well. It may even turn out that the transition between Homo erectus and Homo sapiens, whether anagenetic or cladogenetic, took place somewhere in south Asia. Dating these events is extremely problematic. One internally consistent chronology would place the erectus-sapiens transition in Asia between 125,000 and 200,000 years ago followed by the appearance of anatomically modern man 30,000-40,000 years ago. Then sometime between 30,000 and 15,000 BP during the Duvanny Yar the Asiatic forebears of the (non-Na-Dene) American Indians crossed Beringia and became the First Americans with their descendants subsequently populating all of North, Central and South America (see Fig.2). The ancestors of the Na-Dene Indians and the Aleut-Eskimo group were later (and perhaps separate) arrivals from Asia entering North America sometime during the Birch interval. Finally, the actual formation of the ancestral Eskimo population system by a fissioning of the Aleutian Island-Southwest Alaskan maritime population did not occur until about 4,000 years ago after a climatic maximum.⁴⁸

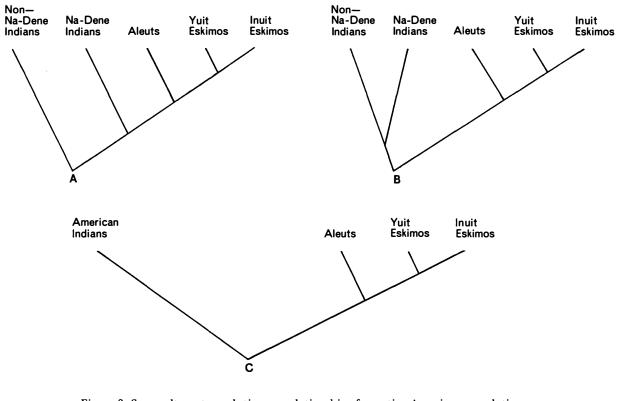


Figure 3 Some alternate evolutionary relationships for native American population systems

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It indeed seems ironic that this evolutionary scenario based primarily on Darwinian principles, genetic data, inferences from skeletal biology and palaeoanthropology, as well as on palaeoecological reconstructions would champion the pre-Darwinian idea of the central import of Asia for understanding human origins and human variation. Hopefully, Darwin's prediction about the legacy of his work, namely that 'light will be thrown on the origin of man and his history' will someday be considered a truism that has withstood the test of time. Remember, science yields proof without certainty. By its very nature science permits competing theories, hypotheses and interpretations and sometimes demands genuine and honorable disagreement.⁴⁹

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The peopling of the Americas as viewed from South America

Francisco M.Salzano

2

THERE IS GENERAL AGREEMENT THAT THE MAIN ROUTE OF ENTRANCE OF THE ancestors of the American Indians in the continent was through the Bering Strait; and it takes just one look at one Amerindian to be convinced that his (her) main origin should be Asiatic. This does not exclude, however, the possibility of other, minor migrations, that could have taken place, for instance, through the Pacific. Elsewhere I have reviewed some of the alternative (or complementary) hypotheses.¹ Most of the evidence gathered to develop them was of a cultural nature. The majority of the physical anthropological data refer to morphological characteristics observed in bones and was interpreted at a time when the 'racial type' concept was still prevalent. Knowledge of population genetics made such types obsolete and hypotheses based on them of dubious value. On the other hand, Matson and colleagues, after examining data on nine blood group systems concluded that Polynesians and Amerindians resembled each other more than either resembled the northeast Asian Mongoloids.² In what follows I will first examine some of the characteristics of extinct and extant Brazilian or South American Indians and then will consider how this information may help to clarify their origins.

What were the main routes travelled by the first migrants to South America? Fig. 1 summarizes some of the suggestions put forward by Brazilian archaeologists.³ At least three routes should have been taken by the people who crossed the Panama isthmus thousands of years ago. One went south by the

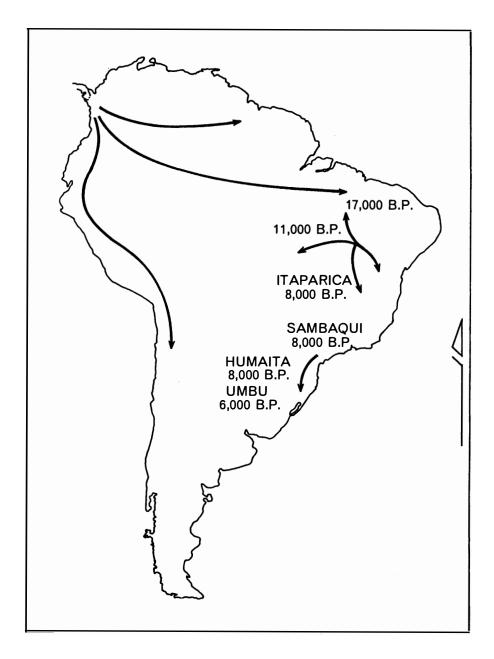


Figure 1 Map of South America showing some of the routes that may have been travelled by prehistoric Indians, as well as the antiquity of a few archaeological sites and the names of some cultural complexes.

Pacific coast, and the two others moved one to the Brazilian northeast, and the other to the northern part of the Amazonian region.

The oldest reliable datings in the northeast go as far back as 17,000 years before present (BP). From there groups radiated to other areas of central and southern Brazil. Another centre of internal migrations seems to have existed nearby the Sao Francisco River. The Itaparica tradition covers a large area of central Brazil, with datings from 11,000 to 8,000 BP. In the south, remains as old as 8,000 to 6,000 BP have been obtained from the Sambaqui (shellmounds) of the littoral and two other hinterland traditions. The tools here suggest migrations from populations different from those who colonized central Brazil and the northeast, indicating Pampa-Patagonian influences.

What were the physical characteristics of the people from these populations? We have information mainly from two groups: the remains discovered in caves near Lagoa Santa, in Minas Gerais (Brazilian southeast), as well as those recovered in the littoral (Sambaqui). Table 1 summarizes the scanty data available. Sambaqui Man generally presented higher measurements; in addition, they were mesocranic, mesorrhine and hypsiconch, that is, they had less dolichocephalic heads, a narrower nose and a higher orbit. Variation within the shell-mound populations also exists, mainly of factors of overall size, cranial height, and face.

Table 1 Physical characteristics of two groups of prehistoric Brazilian Indians.¹⁰

Characteristic	Lagoa Santa Man	Sambaqui Man	
Antiquity	10,000 years BP	7,000 years BP	
No. studied	10	ca 350	
Morphology Cranial index	Dolychocranic	Mesocranic	
Nasal index	Chamaerrhine	Mesorrhine	
Orbital index	Mesoconch	Hypsiconch	

Variation within the populations of Sambaqui Man can be synthesized in seven (males) and six (females) main components, of which three explain 70% of the variation (mainly factors of overall size, cranial height, and face).

Let us now consider the anthropometric variation of the extant populations. Table 2 informs about the ten better studied Brazilian tribes. The average Brazilian Indian male has a stature of 1.61 m, weighs 57 kg, and is mesocranic and mesorrhine. The average Brazilian Indian female does not reach the 1.50 m threshold (1.49 m), weighs 50 kg, and is also mesocranic and mesorrhine. No clear geographic trends appear on these traits, but there is wide dispersion in head form (the cephalic index varying from 75 to 83, indicating brachycephalic, mesocephalic and dolychocephalic groups). As for the nasal index, individuals from nine of the ten tribes would be classified on average as mesorrhine. The Yanomama of Venezuela and Brazil, with flat noses, provide the exception.

	Males (N=1,105)		Females (N=986)		
	Average	Range	Average	Range	
Stature (m)	1.61	1.53-1.69	1.49	1.44-1.55	
Weight (kg)	57	49-68	50	42-55	
Cephalic index	79	75-83	79	75-83	
Nasal index	81	70-89	81	75-90	

Table 2 Four anthropometric characteristics studied in ten Brazilian tribes.¹¹

Six of these tribes have been examined using mutivariate methods of comparison, which may be more helpful in discerning trends. The data for males are shown in Table 3 (females showed essentially the same pattern). The smallest D^2 difference (Cayapo vs Caingang, 2.1) is about ten times less than the highest (Xavante vs Tenetehara, 22.6). Again, no geographic gradients are observed, but there is a certain parallelism with language diversification. The Cayua and Tenetehara are both Tupi-Guarani, and the morphological distance between them is 5.9 only. The Caingang, Cayapo and Xavante all speak a Ge language, and the average distance among them is 8.0. The Yanomama belong to an independent linguistic group; if we compute the distances between them and the other tribes, as well as between tribes speaking languages of different families, the resulting average is 9.1. The differences are not large, but the values within linguistic groups are lower than those between groups.

How much of these differences are due to shape and how much to size? Information about this question is shown in the rows' second lines, Table 3. The shape component is more important than size in 12 of the 15 comparisons (1.2 to 4,195.0 times higher).

	Cayua	Cayapo	Tenetehara	Xavante	Yanomama
Cayapo	4.5				
	159.0				
Tenetehara	5.9	9.3			
	0.9	1.6			
Xavante	13.5	12.1	22.6		
	6.0	8.0	1.4		
Yanomama	4.9	7.1	3.6	19.4	
	0.9	1.2	298.0	1.2	
Caingang	4.2	2.1	6.8	9.8	3.9
	4,195.0	100.0	1.2	4.0	0.4

Table 3 Size (Si²), shape (Sh²) and within-sex morphological distances (Mahalanobis' D²) among six Brazilian Indian tribes (males).¹²

First line: D^2 ; second line: Sh^2/Si^2 . Characteristics compared: height, face height, nose height, nose breadth, head length and head breadth.

Table 4 shows the information concerning 13 genetic systems expressed in blood in ten Brazilian Indian tribes. In average these groups show high frequencies of L^{Ms} , P^1 , R^1 , Fy^a , Gc^1 , $Gm^{1,21}$, Hp^1 , PGM_1^{1} and ESD^1 , and low of L^{NS} , R^Z , R^o or r and ACP^A . But there is wide variation in the frequencies of the 20 alleles listed. For example, Di^a does not occur among the Yanomama, but has a frequency as high as 39% among the Parakana. These two tribes generally showed the most extreme values, while the Wapishana presented as a rule intermediate frequencies. No clear clines appear when the variation in these loci is considered.

Schanfield defined as highly polymorphic a system in which one or more alleles have frequency (ies) of 10% or more.⁴ They may be especially useful in characterizing populations. The HLA loci can be classified as such, and data about them are slowly accumulating for South American Indians. The available information is given in Tables 5 and 6. These populations present high frequencies of A2, A9, Aw19, A28, Bw35, B40, Bw16, B5 and B15, as well as reduced values of A1, A3, A10 and A11. World frequencies for these two loci, as listed by Schanfield, were more uniformly below 10%. The results for loci C and D are too scanty yet for any generalization.

WHAT does all the information summarized above have to do with the question of the origins of the American Indian?

System & allele	Average	Range	System & allele	Average	Range
MNSs			Gc		
L^{MS}	18	9-47	Gc ¹	78	31-94
$L^{M_{\mathcal{B}}}$	57	32-81	Gm		
L^{NS}	5	0-13	Gm ¹ ,21	71	57-87
L ^{N 8}	21	0-33	Gm ¹ , 2, 21	27	12-41
Р			Km		
P ¹	55	10-76	Km ¹	44	37-52
Rh			Haptoglobi	in	
R^1	66	49-82	"Hp ¹	67	25-72
R ²	25	6-45	PGM		
R^{Z}	6	0-12	PGM1	87	76-98
R^0 or r	3	1-16	Esterase I)	
Duffy			ESD ¹	71	36-86
Fy ^a	64	54-100	Acid phos- phatase		
Kidd Jk ^a :	47	37-63	ACP ^A	8	1-29
Diego					
Di ^a	17	0-39			

Table 4 Gene frequencies (%) in 13 polymorphic systems expressed in blood in ten Brazilian Indian tribes (N=7,404).¹¹

Two approaches can be envisaged in the examination of this problem: (a) comparison of the morphology of extinct and extant groups, as well as those of the living populations among themselves, to verify if there are geographical gradients corroborating the migration routes suggested by archaeologists; (b) by examining the frequencies of genetic markers in the presumptive ancestors and the groups under consideration it could be possible, making some assumptions (representative samples, genetic equilibrium, and equating genetic similarity with common descent) to verify if the observed values are in accordance with different hypotheses of ancestrality.

In relation to the first approach, the results obtained here were clearly negative. It was not possible to relate living groups with populations of the past, and no geographic trends appeared when the anthropometric character-

Number o studies	f Numbe trib		Number of individuals	, C	Countries	
9	15	; ;	1,610	Bra	Brazil	
				Chi	le	
					ench Guiana	
				Per	-	
				Ver	nezuela	
		Gene fr	equencies %			
Allele	s Mean	Range	Alleles	Mean	Range	
A1	0.4	0-5	B5	15.0	0-55	
A2	39.0	19-76	B7	0.4	0-3	
A 3	0.3	0-3	B8	0.2	0-2	
A 9	27.0	5-57	B12	0.4	0-2	
A 10	0.2	0-1	B13	0.1	0-1	
A 1 1	0.1	0-1	B14	0.6	0-8	
A 2 8	10.0	0-37	B15	12.0	0-46	
Aw19	23.0	0-48	Bw16	15.0	9-39	
			B17	0.2	0-2	
			B18	0.1	0-2	
			Bw21	0.2	0-2	
			Bw 2 2	0.1	0-1	
			B27	0.2	0-2	
			Bw35	23.0	0-56	
			B40	16.0	0-41	

Table 5 HLA studies performed in South American Indians (loci A and B).¹³

istics of the present communities were considered. But it should be stressed that the amount of information available is not large.

As for the second approach, recent analyses have been performed by several authors. For instance, Rychkov and Sheremetyeva, after considering the variability in 11 loci among Siberians and Amerindians decided in favour of the general similarity of these two groups of people.⁵ Kirk, on the other hand, studying 13 blood systems by the method of genetic distances, verified a close relationship between Noanama Indians of Colombia and the Samoans, with the Yanomama not very far away from the general cluster of central Pacific populations. This analysis also showed that the Maori from New Zealand clustered with the Maya from Central America. However, with 28 loci he found that the American Indians clustered more closely with the Japanese than they did with other Pacific populations.⁶

Subsequently, Szathmary, using Nei's genetic distances and 14 loci, observed three basic divisions among Siberian and northern North American populations. One included the Reindeer Chukchi, all Eskimos and Athapaskan speakers, a second only Asiatics, and a third the Algonkian speakers.⁷

Locus	Number of studies	Number of tribes	Number of individuals	Countries
HLA-C	4	7	828	Brazil
				Venezuela
HLA-D	1	1	121	Venezuela

Table 6 HLA studies performed in South American Indians (loci C and D).¹⁴

Gene frequencies %

Alleles	Mean	Range	Alleles	Frequency
Cw1	3	0-13	Dw8	15
Cw3	34	16-44	LD5a	30
Cw4	31	9-46		
Cw4	<1	0-3		

Finally, Nei and Roychoudhury performed the comparisons that are summarized in Table 7.⁸ Several observations can be made using the data presented there: (a) Polynesians (represented by the Samoans) and Asiatics (represented by the Japanese) do not differ much among themselves (average genetic distance: 1.7); if the differences were larger the analysis could have yielded more conclusive results; (b) in general the genetic distances are those expected considering geographic distances and a main migration route

	Asiatics	Eskimos	N.Am.Indians	S.Am.Indians
Eskimos	2.6			
N. Am. Indians	4.1	3.2		
S. Am. Indians	5.7	7.0	4.3	
Polynesians	1.7	3.2	4.0	3.7

Table 7 Average genetic distances based on 18 loci among Asiatics, Eskimos, North and South American Indians and Polynesians.¹⁵

Loci studied: A_1A_2BO , MSNs, Rh, Fy, Jk, P, Di, Hp, Tf, Gc, ACP, PGM₁, AK, PGD, ADA, ESD, K, Lu.

starting in the Strait of Bering (Asiatics vs Eskimos: 2.6; Asiatics vs North American Indians: 4.1; Asiatics vs South American Indians: 5.7; Eskimos vs North American Indians: 3.2; North American Indians vs South American Indians: 4.3; Eskimos vs South American Indians: 7.0); (c) comparisons with the Polynesians are profitable because they show a slightly lower distance with South American Indians (3.7) than with North American Indians (4.0). But the most interesting finding is a *lower* distance Polynesians vs South American Indians (3.7) than between Asiatics and South American Indians (5.7). Ideally, however, the comparisons should have been made with inhabitants of Siberia and not with Japanese when considering the putative Asiatic ancestors of the American Indians. Also, the number of populations chosen as typical of the different stocks were few, a risky procedure if we remember the large amount of variability that occurs in Amerindians and their putative ancestors.

What conclusions can be drawn from all these data and analyses? There is a conflict concerning the archaeological and palaeoanthropological datings in North and South America, if the only origin of the Amerindians was Asiatic. Laughlin and Harper favour a very late entry of the first Americans (15,000 years BP), and according to Dumond the results on northwestern North America do not provide evidences of human occupants before 11,000 years ago.⁹ But there exist remains of the same or greater antiquity in the south! There are at least three explanations for this paradox: (a) all the old date determinations in South America are wrong, which is difficult to believe; (b) lack of preservation of old sites in North America; (c) some of the old sites in South America may have originated from descendants of people from the Pacific (Proto-Polynesians?). The genetic data certainly do not disprove this last possibility. But much more information for highly polymorphic, polymorphic, private polymorphic and idiomorphic loci is needed, on a larger number of Asiatic, Pacific and Amerindian populations than those considered until now before a final decision can be made on this issue.

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3 The dental search for Native American origins

Christy G.Turner II

THIS CHAPTER ADDS NEW DATA FOR AND EXPANDS UPON ANALYSES PRESENTED IN four previous dental anthropological contributions to understanding the peopling of the Americas.¹ The main points were: (1) the population of East Asia possesses two significantly different dental patterns within the Mongoloid dental complex defined by Hanihara.² Addition and intensification of traits is characteristic of Sinodonty which occurs in the north. Retention of an older condition and simplification makes up Sundadonty in the south. (2) All Native Americans including Palaeo-Indians are Sinodonts. (3) There are three American dental sub-patterns with culture area and language correspondences: American Indian, Greater Northwest Coast Indian (Na-Dene), and Aleut-Eskimo. (4) The sub-patterns are temporally and spatially stable due to limited selection and time for dental microevolution in the New World. (5) A three migration hypothesis, with three possible variants, was proposed to explain the American dental variation. The population-culture relationships were: (a) Diuktai-like big-game-hunting Palaeo-Indians exited Arctic steppe Siberia by way of the LenaRiver basin-interior Beringian route to give rise to most post-Clovis North and South American Indians. (b) Ancestral Aleut-Eskimos entered Alaska along the southern coast of the Bering Land Bridge, as proposed by Laughlin,³ after developing a maritime adaptation in the lower Amur River basin. (c) Greater Northwest Coast Indians are descended from the forest and riverine-oriented Diuktai peoples between the Lena and Amur drainages. In North America these smaller-game

hunters and fisherfolk were bearers of the Palaeo-Arctic tradition. (6) The dentitions of European Upper Palaeolithic people had a Caucasoid pattern and could not have been the sole ancestors of Palaeo-Indians.

The following progress has been made in two years of analysis and three months of data collecting in South America and at the Smithsonian Institution: (1) the three migration hypothesis has been strengthened. (2) Another method of estimating the rate of dental microevolution has been developed, and like the older way supports a relatively late entry into North America by Palaeo-Indians. (3) The three New World dental groups remain the same. (4) Mal'ta, Kostienki, Sunghir and other European and central Asian Upper Palaeolithic peoples have no dental relationship to American Indians. (5) Recognition that the North China Microlithic Tradition and its bearers are the best potential Old World culture and population for the source of all late Pleistocene and early Holocene east Siberians and Americans.

With the exception of those who belong to the uncritical fringe, no serious Americanist doubts that the ancestors of Indians and Aleut-Eskimos originated in the Old World, arriving via the now submerged Bering Land Bridge route connecting Siberia and Alaska in late Pleistocene times.⁴ Force-ful argument for this position was developed as early as 1925 by Ales Hrdlička who also held that the initial migration could not have occurred more than 15,000 years ago.⁵ Hrdlička, solely on the basis of head form, proposed a four migration sequence of long-headed people first, then round heads, Athapaskans and possibly Eskimos last or accompanying the Athapaskans. Adams, Van Gerven and Levy provide a critical review of such abusive use of migrationism for explaining anthropological variation.⁶ I am acutely aware of their cautionary remarks and similar ones from Dekin.⁷

It is well established that the early Palaeo-Indian hunters of mammoth and other large animals were in North America by 12,000 BP. Their descendants reached the southern tip of Chile 1,000 years later.⁸ Evidence for human presence in the Americas prior to 12,000 BP is qualitatively poor, quantitatively insufficient or variously controversial.⁹ Determining precisely when humans first arrived is one of several interesting problems about the peopling of the Americas. One other is a two-part problem which, stated simply is, where precisely in the Old World did the first Americans originate, and was there more than one migration ?

Hrdlička¹⁰ was also a noteworthy early contributor to solving this problem by his rich and original documentation of the physical anthropological similarity between Native Americans and eastern Asians. Since then, something of a working consensus among Americanists sees two migrations as responsible for the New World early artifact and later physical anthropological variation. First to arrive were Palaeo-Indians, followed by ancestral Aleut-Eskimos.¹¹ Minority views at one extreme include West, who envisions only one Beringian population and culture, and Voegelin who, on the basis of language, proposed hundreds of groups from Asia. More in keeping with biological and archaeological data, Greenberg proposes only three linguistic waves. Ackerman sees three waves in northern archaeological remains and McGhee has four scenarios with two to four possible migrations¹²

Dental Morphology

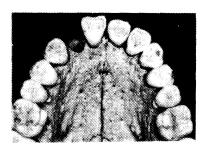
Sinodonty and Sundadonty. Two east Asian dental patterns exist within the Mongoloid dental complex.¹³ Table 1^{*}shows the northern Sinodont and southern Sundadont patterns based on the frequencies of 28 crown and root traits, some of which are illustrated in Figures 1 to 6. I have not considered tooth size, another distinctive trait set being studied by Brace.¹⁴ The crown and root traits have been assessed statistically (Spearman ranked correlation coefficient and chi square) and found to be largely independent of one another.¹⁵ Only shoveling and double-shoveling have a moderately strong relationship. Sex dimorphism is low to absent and dental genetics have been reviewed and found to be polygenetic.¹⁶ In effect, this battery of traits represents at least two dozen separate epigenetic systems and as such is an extremely powerful means for direct estimates of prehistoric population genetics characteristics and phenetic relationships. Tooth hardness facilitates long term preservation permitting diachronic evolutionary analysis.

Sample composition for Table 1 is provided in the appendix. Briefly the Sinodont set consists of northeast Asians, northeast Siberians, Aleuts, Eskimos, Greater Northwest Coast Indians and all other North and South American Indians since these groups are dentally all very similar on univariate (Table 1) and multivariate (Table 2 and Figures 7 and 8) bases.

The Sinodont pattern is a combination of trait frequency intensification and addition relative to Sundadonty or Caucasian. Sundadonty is thought to retain more of the ancestral qualities of earlier late Pleistocene teeth as well as having undergone some crown reduction.

The dental intensification in Sinodont populations includes greater frequencies of shoveling, double-shoveling, the tuberculum dentale complex, canine distal accessory ridge, parastyle, cusp 6 (entoconulid), cusp 7 (metaconulid) and the protostylid. These are all traits that add mass to the tooth crown, depending on their degree of expression, and presumably were selected for under the dentally demanding Arctic-like conditions of northeastern Asia in late Pleistocene times.¹⁷ The additions of Sinodonty for which no obvious selective mechanism can be identified include higher frequencies of winging, enamel extension, odontome, 1-rooted upper first premolar, and lower frequencies of the hypocone, cusp 5 (metaconule) of the upper molar, 3-rooted upper second molar, mutiple lingual cusps of lower second premolar, Y groove pattern and 4-cusped lower second molar (absence of entoconulid and hypoconulid). Only the increased frequency of 3-rooted lower first molar root specialization seems to have some potential

^{*} Numbered tables referred to in the text are at the end of this chapter.

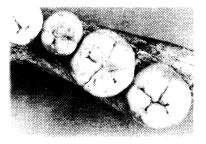


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(1)



(2)



(3)

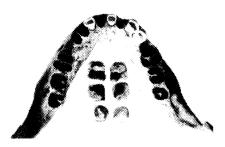


(4)



(5)

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(6)

Figure 1 North Chinese upper dentition showing incisor shoveling and Carabelli's cusp on the first molars. Shang Dynasty Chinese No. 50 from the An-yang site. Institute of History and Philology, Academia Sinica, Taipei (CGT neg. no. 3A 9-9-75).

Figure 2 North Chinese upper left molars showing peg-shaped third molar. An-yang No. 151 (CGT neg. no. 28 9-9-75).

Figure 3 North Chinese lower right teeth showing multiple lingual cusps on both premolars, and five-cusped first and second molars. First molar has a + groove pattern, the second has X pattern. An-yang No. 205 (CGT neg. no. 30 9-9-75).

Figure 4 Comparison of recent Chilean Indian (upper) and intentionally cremated 11,000 BP Chilean Palaeo-Indian (lower) from Palli Aike Cave discovered by J.Bird. The Palaeo-Indian had in life all three molars. The first had three roots. This is the oldest known example of a 3-rooted lower first molar in the New World and Asia. The upper specimen, from Cerro Sota Cave, also possessed the 3-root polymorphism. American Museum of Natural History, New York (CGT neg. no. 7 7-77).

Figure 5 Archaic Alabama upper dentition showing central incisor winging, lateral incisor with marginal interruption groove which is weak expression of the tuberculum dentale complex, and the Uto-Aztecan premolar on the right first premolar (viewer's left). Shoveling is pronounced on all incisors and the canines. Perry site (Lu 25) No. 11 Department of Anthropology, University of Alabama, Tuscaloosa (CGT neg. no. 26 6-15-80).

Figure 6 Aleut lower molar roots and sockets. First molars (upper pair) possess the 3-rooted trait; second (centre) and third (lower) have the 1-rooted polymorphic condition. In this female the 3RM1 morphogenetic field was especially strong causing all six molars to develop the supernumerary root. Oldest known Neo-Aleut (A.D. 780). Chulka site, Akun I. Department of Anthropology, Arizona State University, Tempe (CGT neg. no. 24 6-20-81).

for increased dental fitness, namely by better attachment of the key first molar.¹⁸

Retention or simplification characterizes Sundadonty. The traits that add to crown mass and presumed enhancement of tooth longevity, have lower frequencies in the Sundadont peoples. Also, some dental reduction has taken place as evidenced by fewer individuals with lower molar cusps 5 and 6 (4-cusped lower second molars are five times more frequent in Sundadonts than in Sinodonts), more examples of peg-shaped, reduced or congenitally missing third molars, fewer individuals with shoveling and much less doubleshoveling (less than one half that found in Europeans). Retained ancestral conditions are especially notable in the root traits. The specialized upper premolar and molar root number of Sinodonty is much less frequent in Sundadont crania. The specialized Sinodont 3-rooted lower first molar occurs in fewer Sundadonts (no known example of 3-rooted lower first molars is known for any primate or fossil hominid).¹⁹ As can be seen in Tables 1 and 2 and Figures 7 and 8, Sundadont peoples had nothing to do with the peopling of the Americas although they are clearly involved in the peopling of Polynesia.

Antiquity of Sinodonty. There are two sources of direct diachronic information on the antiquity of the Sinodont dental pattern. They are teeth of the 10,000 to 12,000 year old Palaeo-Indian remains from North and South America, and the $20,000 \pm$ year old late Pleistocene teeth from northern China. The former are at present a better resource for antiquity assessment because of the greater number of Palaeo-Indian teeth. Dating of them is relatively secure, and I have personally examined all the Palaeo-Indian dentitions reported here. I have had to rely on casts or illustrations of the Chinese specimens.

Using the Palaeo-Indian sample for Sinodont age assessment, Table 1 shows the main features of the pattern had been established by the beginning of the Holocene. Palaeo-Indian teeth exhibit Sinodonty as follows: marked frequencies of the 3-rooted lower first molar, shoveling, parastyle, 1-rooted upper first premolar and double-shoveling. Also conforming to later Sinodonty are the absence of 4-cusped lower second molars and the lack of examples of third molar reduction or congenital absence. If not due to small sample size, some degree of Sundadonty may be reflected in the frequency of the Y groove pattern, 3-rooted upper second molar, enamel extension, Carabelli's trait and incisor winging. But altogether, Palaeo-Indian teeth are much more Sinodont than Sundadont and far removed from the Northwest European pattern ('Western complex' of Zubov and Kaldiva).²⁰

These degrees of resemblance or dissimilarity can be appreciated more quickly in the multivariate mean measures of divergence (MMD) comparisons based on the procedures of Smith.²¹ Table 2 shows that Palaeo-Indians are

more like Sinodont Asians than Sundadonts, Europeans, Africans or Pacific Basin peoples. In terms of MMD values, Palaeo-Indian teeth are morphologically like those of Kets (0.062), almost as similar to North and South American Indians (0.088, 0.101), Greater Northwest Coast Indians (0.107) resemble each of the northern Asian series about the same (Northeast Siberia 0.195,Amur 0.221, Northeast Asia 0.250) and are quite unlike Northwest Europeans (0.414) and Australmelanesians (0.504).

From these comparisons it is evident that Sinodonty evolved before 10,000 BP and that the pattern is characteristic of all Native Americans and northern Asians. Considering the time involved Sinodonty is stable.

With only 19 traits available for the very small Chinese sample it can only be suggested that the Sinodont pattern is $20,000 \pm$ years old. The divergence values for this suggestion are: Upper Pleistocene China/Palaeo-Indian -0.159, Upper Pleistocene China/American Indian-0.080, Upper Pleistocene China/USSR Upper Palaeolithic 0.205, Upper Pleistocene China/Northwest Europe 0.617.²² Even though only the last value is significant, each is at the expected order of magnitude given what is presently known about Asian-American prehistory.

The rate of dental microevolution based on New World prehistory. As the fossil record shows, time and evolutionary divergence are not independent of one another. Even though local selection, population structure and geophysical factors can affect to varying degrees the strength of the timeevolution relationship, an averaging out of these variables can be expected for large regions such as eastern Asia and the Western Hemisphere. Quantification of human population evolutionary divergence is accomplished here with the mean measure of divergence statistic applied to dental morphology.

To obtain a multivariate-based rate of average dental microevolution all that has to be done is divide any MMD between two groups by the known time of genetic separation. For example, the MMD of the Palaeo-Indian/ North American Indian comparison is 0.088. Assuming the two groups have been separated for 10,000 years gives a rate of 0.008 MMD/1,000 years (0.088/10). For Palaeo-Indian/South American Indian, assuming the same amount of separation gives 0.010 MMD/1,000 years. The average of the two is 0.009/1,000 years. Unfortunately, I am skeptical about the precise dating of some of the dentitions assumed here to be Palaeo-Indian. Should these be more recent, they would decrease the real rate because of being more similar to recent Indians (i.e. less time for divergence). Because the dental microevolutionary rate has considerable potential as an additional means for estimating the antiquity of a skeletal series, I want to be as exact as possible. For this I need to use a better example, although as will be seen the Palaeo-Indian-based rate is apparently satisfactory. The isolated Aleutian Islands provides a better basis for establishing a working rate.

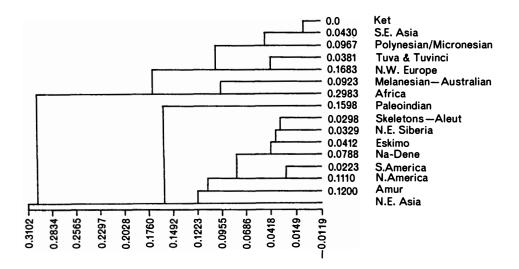


Figure 7 Relationships within and between Native American, Pacific and Old World populations based on 28 dental trait mean measures of divergence clustered by unweighted pair group, arithmetic averages method (reference: computer file HCLUS World 10).

Occupation of the Aleutians has probably been continuous for a minimum of 9,000 years. The archaeological sequence starts with the 8,700 to 7,200 year old Anangula blade tool site, bridges from 7,000 to 4,000 BP at the Anangula village site with its blade and bifacial stone tool 'Transitional culture', and continues without interruption to the present day at the 4,000 year old Chaluka midden in nearby Nikolski, Umnak Island, at Chulka-Islelo on Akun Island, and elsewhere in the Aleutians.²³ Since Anangula is located at the southeastern terminus of the now flooded Bering Land Bridge, it was likely reached earlier and occupied by ancestral Aleuts initially at a lower elevation now under water, that is, before the Land Bridge southern coast migration route was completely flooded 14,000 to 12,000 years ago. Access to Anangula before this time would have been severely hindered, even with the use of umiak-sized skin boats, because of glacial ice on and adjacent to the Alaska Peninsula.²⁴ Thus time as well as isolation, population structure and selection has contributed to the biological distinctiveness of the Aleut population. Excavations on the Alaska Peninsula and in the islands adjacent to the Peninsula show almost no external cultural or biological penetration of the Aleut population system.²⁵

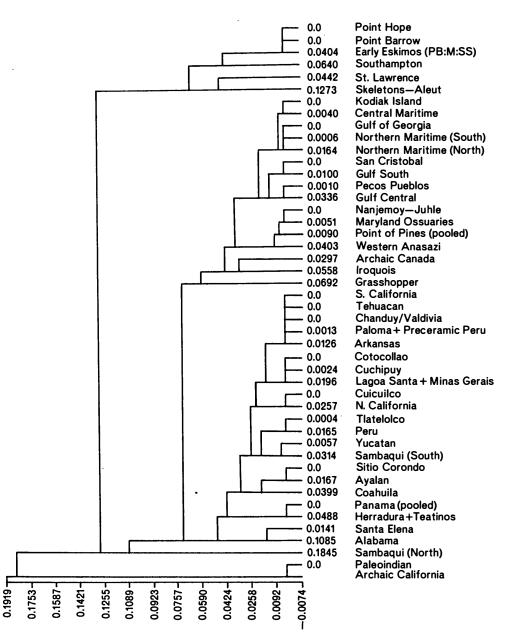


Figure 8 Relationships within New World groups based on 28 dental trait mean measures of divergence clustered by unweighted pair group, arithmetic averages method (reference: computer file HCLUS New World 2).

Because Aleuts and their ancestors have been genetically separated from interior Northeast Asians like Chinese, Japanese, Mongols and Buriats since at least the time of the flooding of the Bering Land Bridge, their divergence from these peoples can be employed to estimate the rate of northern Mongoloid (Sinodonty) dental microevolution (Table 2). Three estimates for Northeast Asian/Aleut separation can be offered, and the corresponding rates of dental microevolution determined. The best estimate can then be compared with other New World archaeological information to assess the reasonableness of the rate:

Aleut/NE Asia branching (MMD/time)	Prehistoric event	Comment	Rate of MMD/1000 years
<u>.115733</u>	Anangula blade	Too recent,	.01286
9,000 BP	site occupied	branched earlier	
<u>.115733</u>	Land Bridge	Probable best	.00964
12,000 BP	flooding	branch point	
<u>.115733</u> 15,000 BP	N.Japan & Amur blade culture origin of Aleut	Too old, incomplete branching	.00771

For the reasons indicated above, the rate of 0.00964MMD/1,000 years is preferred. Two independent test cases are available in New World prehistory for assessing the usefulness of the rate.

The first is that of the Indian migration into North and South America. Dividing the North American Indian/Northeast Asia MMD by the preferred rate (0.117/0.00964) gives an estimate of 12,000 years ago when these groups separated. For the branching between South American Indians and Northeast Asia an estimate of 15,975 years ago is obtained. This seems excessive, although not impossible if linked North American groups retained genetic connections with Northeast Asia up to or even after the Land Bridge flooding. The average MMD (0.135/0.00964=14,000 years BP) is in my view the best estimate of genetic branching given Siberian prehistory. Harper calculated 19,000 years of divergence on the basis of Alaskan genetic traits.²⁶ Compared to Harper's the rate of dental divergence is conservative. If the 0.00771 rate is used, then the time of divergence between North and South American Indians from Northeast Asia is 17,600 BP.

The second case involves northwestern North American Indians. Various studies suggest that some (Na-Dene-speakers), if not most, Northwest Coast and Alaskan interior Indians are descended from the 9,000 to 10,000 year old Palaeo-Arctic tradition-bearers of Alaska and their $12,000 \pm$ year old Diuktai counterparts in Siberia.²⁷ Using the Greater Northwest Coast/

Northeast Asia MMD (0.085), their branching occurred 8,800 years ago. Like the previous case, this too shows substantial correspondence with archaeological information. Swadesh calculated that Haida language separated from the rest of the Na-Dene languages about 9,000 years ago.²⁸ Here, what is important to note is that language, biology and prehistory show strong resemblance. None of the threee is, for example, suggesting 1,000 or 50,000 years of antiquity. Some other broad comparisons are supportive:

	Estimated time of separation (years)		
Rate=.00964	Dentochronology	Archaeology	
SE Asia/Poly-Micronesia	4,300	3,000+	
Australmelanesia/SE Asia	13,400	20,000+	
Africa/NE Asia	31,900	40,000*	
Europe/NE Asia	31,300	40,000*	
Palaeo-Indian/NE Asia	25,900	20,000	
Palaeo-Indian/N America	9,100	10,000	
Palaeo-Indian/S America	10,500	10,000	
N America/S America	2,300	10,000	
Aleut/Eskimo	3,700	4.000**	

* Assuming single common modern ancestral population.

** Based on language.

The correlation coefficient for these pairs of estimates is strong (r=0.934) and significant (P=0.004). These comparisons support a worldwide rate of dental microevolution at about 0.01 MMD/1,000 years. Other comparisons are desired and needed, but in the meantime, I suggest this rate be adopted. Dental change within the Americas is limited and supportive of Martin who rejects claims for Palaeo-Indian antiquity much before 12,000 BP²⁹ In the following section it will be shown that intra- and inter-hemispheric dental variation likewise is unsupportive of claims for great antiquity of Palaeo-Indians.

Asian-American regional dental variation. Comparative regional variation provides a means of assessing potential regional selection, population structure, isolation, antiquity of a given population and genetic homogeneity (here, epigenetic). Table 3 provides the regional internal divergences, based on mean measure of divergence, for Aleut-Eskimo, Greater Northwest Coast, North America, South America, Northern Asia and East Asia. Most apparent is that the latter two have much more internal divergence, that is, these Asian populations are more variable than are the four American regions or Indians taken as whole. Pan-Indians have less than half the average divergence of Northern Asians, and a quarter that of East Asians. Within the New World, excepting the Greater Northwest Coast, there are no significant differences in the average regional divergence. Given the long and linear population structure of Aleut-Eskimos, which would favour founder's effect, and their dentally severe Arctic lifeway, which would encourage selection, it is not surprising that they possess the largest average MMD of the four New World regions. It is not, however, significantly greater than that of Indians in North and South America. Thus, I view these dental traits as exhibiting substantial evolutionary conservatism and stability.

With respect to North and South American Indians, the average divergence is not significantly greater in the north. This argues against MacNeish's position that people were in North America for 100,000 years and in South America for 25,000 years.³⁰ Were this the case, and given what has been proposed for the rate of dental microevolution, would we not expect greater variation in the northern hemisphere than in the south? The similar average MMDs of North and South American Indians and Aleut-Eskimos suggests each has been in the New World about the same length of time, even allowing for the potentially greater divergence in the Arctic.

It is the Greater Northwest Coast Indians that are puzzling. They have the lowest amount of internal variation, even though I have included the maximal area and most remotely possible candidates for inclusion. In the north this includes Kodiak Islanders and the Kachemak Bay series, both considered to be Eskimos by most Alaskan archaeologists.³¹ In the south I have included crania from the lower Columbia River, which is near the southern limit of the Northwest Coast culture area,³² and the Apache of Arizona and New Mexico who had ample opportunity to admix with Pueblo and desert Indians. Despite this very broadly defined group, its samples are yet remarkably similar with one another, unlike the great genetic diversity found by E. Scott for Athapaskans alone.³³ If this is not an artifact of the MMD statistic, and if it is not an unexpected statistical quality of hybridized groups, then I can imagine only three other explanations for the very low variation.

First, the cultural and environmental characteristics of the Greater Northwest Coast peoples may have encouraged much internal migration and gene flow. This could arise from slaving, mating practices (exogamous clans), and high mobility along the Pacific coast in large boats. Northwest Coast ethnography would support this possibility.³⁴

Second, the low variation suggests a relatively recent common ancestor for most if not all the included samples. This could have come about by either a relatively recent entry into the Northwest Coast, which I feel the Alaska-British Columbian archaeology suggests, or to a rapid expansion from a single ancestral group some time after arrival. My understanding of the region does not favour this late cloning possibility.

The third explanation may be that the founders of the Greater North-

west Coast region were extremely few in number so that the gene pool for these dental loci was much less than that of either Palaeo-Indians or ancestral Aleut-Eskimo. Of my three proposed New World founding populations, all must have been small, but Palaeo-Indians (hunting large game), and Aleut-Eskimos (fishing and sea mammal hunting) would have been relatively more numerous because of more and more reliable resources than the later entering, smaller game hunting, forest and riverine-oriented Palaeo-Arctic people. Palaeo-Arctic sites, such as Healy Lake, Denali, Hidden Falls and so forth, are highly pauperized when constrasted with Anangula. Even today the human and animal population densities in the Alaskan interior are much less than those along its coasts. Initially the Northwest Coast might not have been as bountiful or economically varied as it was some time after deglaciation.³⁵ In sum, the testable explanation I propose for the low internal dental variation of the Greater Northwest Coast region is one that envisions a small founding population of closely related individuals, late entry into the New World, later entry onto the Pacific coast from the interior and subsequent cultural developments that maximized gene flow within the regional group.

It could be argued that the size and composition of the Greater Northwest Coast group is not comparable with the other regional groups because it contains mainly individuals from one culture area, and the low dental variation is an artifact of this inequality. To such criticism I can offer two counterpoints. First, Aleut-Eskimo has been assembled on a nearly identical basis, namely a common culture and closely related languages. Yet, Aleut-Eskimo dental variation is significantly more than that of the Greater Northwest Coast crania. Second, I can assemble another New World regional division with several features in common with the Greater Northwest Coast. Dental samples originating from the west coast of South America share with Greater Northwest Coast a coastal habitat, use of marine foods and a long linear population distribution. The amount of area involved is about the same, boats were used, and overland travel restricted (mountains block easy travel in the north, deserts inhibit travel in the south). Identifiable points of difference are that the western South American series is probably on the average older than the northern one (but this would mean they would have had less time for divergence), and sweetwater sources in the south would have encouraged greater localization of populations, although in the north limited suitable coastal settlement sites may have had a similar effect.

The statistical qualities of the ten west coast South American samples are: average MMD divergence 0.044, SD 0.034, SE 0.005; no. 45. The west coast South American average MMD divergence (0.044) is significantly (P<0.0001) greater than that of the Greater Northwest Coast (0.011). From this I submit there is no lack of comparability in the makeup of the Greater Northwest Coast group. Their low dental variation is real. It is the result of their incompletely understood population history.

Could Na-Dene/Greater Northwest Coast have formed by admixture between ancient Aleut-Eskimos and Palaeo-Indians? Because 50% (14/28) of Greater Northwest Coast dental traits have frequencies for occurrence intermediate between those of Aleut-Eskimo and North and South American Indians (Table 1), it can be hypothesized that Na-Dene/Greater Northwest Coast formed by admixture. To assess this possibility assume for the moment that the trait frequencies for Aleut-Eskimo and North and South American Indians are equivalent to those at the time of the admixture event(s). Further assume that gene flow to the new hybrid population was equal from the two contributing populations, and that the genetics of these dental traits behave in a simple additive manner. By adjusting the number of individual North and South American Indian trait frequencies to equal the number for each Aleut-Eskimo trait, an equally weighted frequency can be obtained to produce the expected frequency. Using winging as an example, it occurs in 49.9% of the pooled Indians (578/1158), and in 25.4% (45/177) of Aleut-Eskimos. The equally weighted hypothetical winging frequency is obtained as follows: [(0.499)(177) + 45]/(177)(2) = 37.7% (133.5/354 individuals).

Using these new frequencies, the 27 trait mean measure of divergence between the hypothetical population and Aleut-Eskimo is MMD = 0.0168; between North and South American Indian MMD = 0.0212; and between Na-Dene, MMD = 0.0139. In the first two comparisons the significant MMD values are close to what actually exists between Aleut-Eskimo and Greater Northwest Coast (MMD = 0.0347) and between the latter and pooled Indians (MMD = 0.0365), although in both, the expected values are slightly smaller than those observed. In the Na-Dene comparison the MMD is greater and not significant.

It is interesting that even with equal contributions from the parent populations to the hypothetical hybrid, the resulting mean measure of divergence is slightly less between the hybrid and Aleut-Eskimo than between it and Indian. This differential divergence actually occurs between Aleut-Eskimo and Greater Northwest Coast (MMD = 0.0347) when compared with the latter and Indian (MMD = 0.0365). The outcome of this simple exercise rather strongly suggests that Na-Dene and Greater Northwest Coast could have formed by this evolutionary process. However, as the following univariate comparisons show, the case for hybridization is not overly strong.

Univariate chi square comparisons between the hypothetical and actual Greater Northwest Coast trait frequencies show 26.7% (8/30) to be significantly different (P < 0.05). The summed χ^2 for 30 comparisons is 94.9. Since there are more than 5% significant differences it has to be concluded that the hybridization hypothesis is incorrect, or one or more of the assumptions is. If the univariate comparisons are done for 27 traits (removing Uto-Aztecan

premolar, metacone and anterior fovea as in the MMD analyses because there are no data for Na-Dene) then 29.6% (8/27) are significantly different.

Comparing only the Na-Dene set against the hypothetical one produces 7.4% (2/27) significant differences, close to the 5% that can be expected on the basis of chance alone. The summed χ^2 value is 33.3. Here it would have to be concluded that the hybridization hypothesis has not been disproven but because the Na-Dene sample size is small (see Table 1) it would be unwise to conclude at this time that the Na-Dene formed by admixture.

Something like this simple exercise probably underlies the essential fact that Greater Northwest Coast and Na-Dene have half their trait frequencies intermediate between those of Aleut-Eskimo and Indian. If so, then the population formation more likely occurred in late Pleistocene Siberia between the Lena and Amur basins than in Alaska as will be discussed shortly. If the hybridization event(s) or gene flow occurred in Alaska during the Holocene we should expect to see more similarities than exist today between the cultures, languages and genetics of Aleut-Eskimos, and Athapaskans or other northern Indians. Recall that language, teeth, genetics and prehistory all point to Na-Dene antiquity of greater than 9,000 years.

New World dental sub-pattern stability. Inspection of Tables 1 to 3 and Figures 7 and 8 will show that New World dental variation is significantly less than the external Asian variation. The American Indian sub-pattern of Sinodonty remains the same whether in North or South America. Indian Sinodonty differs from that of Asia in the slightly greater frequencies of Carabelli's trait, protostylid, Tome's root, double-shoveling, and canine distal accessory ridge, and in lower frequencies of enamel extensions, peg-reduced-congenitally absent upper third molars, Y groove pattern, multiplelingual cusps of lower second premolar and 3-rooted lower first molars. The Aleut-Eskimo deviate from Asians by having a greater frequency of 3-rooted lower first molars and lower frequencies of the hypocone, lower molar cusp 6 and 3-rooted upper second molars. None of the local samples of North and South American Indians have evolved Aleut or Eskimo characteristics. Likewise, Aleuts and Eskimos have not changed locally into Indians. When all 155 worldwide samples are compared, not a single Indian or Aleut-Eskimo sample clusters with any Pacific, African or European sample.

Stability can also be recognized by the fact that regional descent groups remain more like temporally earlier regional samples than like extra-regional groups. Thus, diachronic MMD comparisons of Palaeo-Indians with other groups show less internal divergence than external: North America 0.088, South America 0.101, Greater Northwest Coast 0.107, Eskimo 0.132, Aleut 0.184. Similarly low internal divergence occurs among the Northwest Coast peoples. The early (3,000 BP average?) Northern Maritime South crania (Namu and Prince Rupert Harbor) compared with others shows: Greater Northwest Coast 0.003, North America 0.042, South America 0.08, Eskimo 0.05, Aleut 0.052.

Synchronic intra-regional comparisons show the same degree of stability. Eastern and Western Aleuts are very similar (0.004), more so than the MMDs between all Aleuts and: Eskimos (0.036), Greater Northwest Coast (0.045), North America (0.093) or South America (0.109). Eastern Eskimos are more like other Eskimos (0.011) and all Eskimos are more alike than like Greater Northwest Coast (0.033), North America (0.093) or South America (0.093).

In sum, the regional variation of the Western Hemisphere indicates that North and South American Indians have been in place for about the same amount of time. Aleut-Eskimos would appear to have also been in the New World for about as long as Indians, although it could have been less since environmental conditions in the Arctic would have accelerated internal evolutionary divergence. The Greater Northwest Coast people seem to have entered after the other two main groups, if in fact they did not actually form in Alaska as a hybrid of these two. Greater Northwest Coast environmental and cultural conditions have inhibited internal divergence by migration and gene flow along the coast. Finally, the significantly less internal divergence within the American Indian population compared with northern or East Asian variation corresponds with findings made on other biological traits showing marked Indian genetic homogeneity.³⁶ Most Indians are likely descended from a single relatively late small founding population. I can identify no pattern of regional variation that would suggest much selection at play after arrival in North America. Internal divergence seems to be due to genetic drift in the Americas. Spuhler reached a similar conclusion for blood group variation in North American Indians and Aleut-Eskimos.³⁷

Univariate comparisons. Table 4 provides the number and percent of traits that are significantly different and the summed chi square values for 27 trait comparisons between the groups of Table 1. These values evidence no significant difference between the Na-Dene-speaking Tlingit and Haida, and Greater Northwest Coast Indians, but various levels of significant differences between all the other 18 pairs of comparisons. Aleut-Eskimo have fewer traits that differ significantly in frequency from North Asians than do American Indians. Na-Dene has slightly less difference with Aleut-Eskimo than with pooled American Indians, but it is not significant ($\chi^2 = 0.02$: P > 0.8). Greater Northwest Coast Indians have fewer traits that differ significant ($\chi^2 = 1.86$: P > 0.1). There is less difference between North and South American Indians (15/27) than between these Indians and North Asia (21/27) as expected.

Because both the multivariate (MMDs, Table 2) and univariate comparisons $(\chi^2 s)$ produce similar results relative to degrees of inter-group difference, I thought it interesting to see what the relationship is between the respective pairs of MMD and summed χ^2 values for each of the possible 15 inter-group comparisons. The correlation coefficient (r) is 0.8001, which is a moderately strong and significant (P < 0.001) relationship.

Of the 27 traits, with 19 possible inter-group comparisons (including pooled North and South America), the following is the ranked order of traits and number of times they are significantly different: 15, double-shovel, 3-root upper second molar; 14, Carabelli, 1-root upper first premolar, 3-root lower first molar; 12, winging; 10, lower premolar cusp number, lower molar groove pattern, lower molar cusp 6, distal trigonid crest, protostylid; 9, upper molar cusp; 5, enamel extension, Tome's root; 8, hypocone, peg-reduced-congenital absence upper third molar, 4-cusped lower second molar; 7, tuberculum dentale complex, canine distal accessory ridge, 1-root lower second molar; 6, deflecting wrinkle; 5, shoveling, parastyle; 4, canine mesial ridge, odontome; 2, 2-rooted lower canine; 0, lower molar cusp 7.

These values give a quick sense of which traits vary most within all Native Americans, and which vary least. Interestingly, most root traits have high amounts of significant difference excepting the 2-rooted lower canine which is almost non-existent in the Americas while relatively common in Europeans. The greatest amount of significant variability, and therefore that of greatest utility for inter-group discrimination, occurs in winging, double-shovel, Carabelli, upper premolar and molar root numbers, and lower first molar root number. These are most of the traits that distinguish readily between Aleut-Eskimos and American Indians.

The dental microevolutionary and peopling scenario.

Table 2 contains the Asian-American divergence values on which the following discussion is based. I assume that all groups diverged at about the same rate. Table 2 also contains comparative information to help the reader appreciate how closely the north Asians and Americans resemble one another, and to show that there is an ever-present danger in over-interpreting these values even though they are statistically significant. The following points are essential to the scenario.

1. Both Aleut and Eskimo are slightly more like Northeast Siberians than like any Indians.

2. Both Aleut and Eskimo are more similar to Greater Northwest Coast than to other Indians, Eskimo slightly more so than Aleut.

3. Both Aleut and Eskimo are three times more alike than either is like North or South American Indians.

4. As one proceeds further east into Asia, Aleut and Eskimo eventually differ about equally from Northeast Asian and Amur people as they differ with North and South American Indians.

5. Eskimo are slightly more like the Amur group than like Northeast

Asians. Aleut are equally similar to Amur and Northeast Asia.

6. Greater Northwest Coast is slightly more like Northeast Asia than like Amur, and more like Northeast Siberia than like either of the other two groups.

7. Amur is slightly more like Eskimo and Aleut than like Northeast Asia.

8. Northeast Asia is more like Greater Northwest Coast than like Northeast Siberia or Amur (does this add support for the Sino-Tibetan/Na-Dene link proposed on linguistic grounds?).

9. Combined, the closest Old World tie for North and South America is with Northeast Siberia. However, this link is about two times more divergent than that between Aleut and Eskimo and Northeast Siberia. The next closest Old World link with North and South America is Ket. Ignoring the spurious Ket/Southeast Asia value, the former is very close to hybrid Tuvan and Northwest European. The latter group also contains some people with Mongoloid admixture, namely the North Khanty and possibly the Lapp.³⁸ All of the groups in Table 2 are relatively similar to Ket. How much of this 'Ket effect' is due to sample size or some sort of hybridization effect cannot be determined at present. Palaeo-Indian is even more like Ket than like other Indians.

Unlike many genetic traits such as the blood groups, and PTC tasting, the function of the dentition is known, so dental variation can be assessed for evolutionary causality. On a worldwide basis most of the morphological variation seems to have arisen because of genetic drift, so most of the above divergences are thought to be the result of this random process. However, close inspection of the Sinodont variation suggests some low level selection also. Dental microevolution in the American Indian relative to Northeast Asia was towards an even more robust crown morphology. This I believe resulted from slightly additional selection for tooth longevity during the transit to and across Arctic Beringia. The frequency array remained about the same after leaving the Arctic since the size and form of the dentition then made less difference for survival as can be seen by comparing North and South American trait frequencies in Table 1. Some genetic bottlenecking may have occurred in the passage through Central America.

Admixture or gene flow must be implicated in the trait frequencies of the Na-Dene, since several traits have frequencies intermediate to those of Aleut-Eskimo and other Indians. This is apparently due to their history of always having lived in between ancestral Aleut-Eskimo and Indian whether in Siberia and/or North America. The Na-Dene can be viewed as either a hybrid or clinal population.

There is an odd mix of some increased robusticity and a fair amount of reduction in Aleut-Eskimo trait frequencies. This condition could be due to either or both selection or past population structure. The reductive selective mechanism might be the low amount of calcium in the Arctic diet.³⁹ How-

ever, there is no inter-group dental support for this mechanism since Aleut have on the whole more reduction than do Eskimo. As Laughlin, Harper and Thompson are showing,⁴⁰ osteoporosis correlates well with Arctic latitude, and it should be the Eskimo who have more dental reduction if a calcium saving was possible by reducing the complexity of the crowns and roots. Reduction arising from population structure is more appealing as an explanation because some reduction can be seen even in the Amur group who are not in the Arctic (compare Amur with Northeast Asia in Table 1). I propose that founder's effect underlies the Aleut-Eskimo dental reduction and that the pattern of a long linear population distribution of today was also true for their ancestors who migrated to Alaska along the narrow coastal strip of eastern Siberia from the lower Amur basin.

Even though three different evolutionary processes can be suggested as having had some effect on the dental variation of the three Native American groups, the effects were small since all remained much like Asian Sinodonts rather than being altered to resemble any other worldwide group. This evolutionary conservatism permits the use of the dental trait frequencies for the peopling scenario, keeping in mind, of course, these minor adjustments.

The homeland. Between 40,000 to 20,000 years ago a population in north China evolved the Sinodont dental pattern. Assuming a common origin for all Homo sapiens sapiens populations, the dentally more specialized late Pleistocene north Chinese would have had to have originated from the more generalized Southeast Asian population since the latter are whom they most closely resemble other than the derived eastern Siberians and Native Americans (see Table 2). The time is based on the fact that by 20,000 BP Sinodonty can provisionally be recognized in the Upper Cave, Dingum, Ordos and other teeth. The lower limit is set by an estimate of the average rate of dental microevolution of 1% per 1,000 years. This is also the generally recognized time for the beginning of modern human populations.⁴

It is not possible to employ the MMD dental rate of microevolution to estimate the time of separation between Southeast and Northeast Asia since gene flow and migration are still occurring between these regions. However, American Indian can be used as an estimator for the beginning of Sinodonty. In so doing, the mean time of divergence or beginning of Sinodonty would be 26,800 years ago (South America/Southeast Asia = 27,800 BP; North America/Southeast Asia=19,100 BP; Palaeo-Indian/Southeast Asia=33,600) which is consistent with the independent Chinese fossil evidence. Upper Cave dates at 18,000 BP.⁴²

Culturally, this late Pleistocene north China population possessed the generalized North Chinese Microlithic Tradition: a lithic technology that contained all of the typological components found later in Palaeo-Indian culture including microblades, blades, various core types (all the known Japanese types), scraper forms, 'adzes', bifacial points and knives, and other items.⁴³ The several typological resemblances of this Chinese industry to that of Palaeo-Indian and early Arctic cultures has not been previously appreciated, nor has much attention been given to Neumann's observation that Indian crania are similar to those of Upper Cave.⁴⁴

This early Sinodont population could expand with relative ease only northward since there were established groups to the south, including those with the 18,000 year old Son Vi culture in Viet Nam which was to evolve later into the Hoabinhian culture.⁴⁵ Nor was population growth possible to the west since it appears Upper Palaeolithic Europeans extended as far east as Lake Baikal. The 18,000 BP site of Mal'ta near Lake Baikal was culturally linked with Europe and my study of the older Mal'ta child's unerupted permanent teeth showed them to be Caucasoid rather than Mongoloid.⁴⁶ The nearby but older site of Krasny Yar is felt to exhibit strong European influence as do numerous sites along the headwaters of the Ob and Yenisey rivers to the west.⁴⁷ Expansion to the East China Sea coast may also have been restricted since a good case can be made that Sundadonts were ranging up the Asian coast at least as far as Okinawa by 18,000 years ago as evidenced by the Minatogawa skeletons, and they were certainly in the southern Japanese islands at the end of the Pleistocene when Jomon pottery appears.⁴⁸ Later Jomonese are Sundadonts as are their descendants, the Ainu,⁴⁹ so it is reasonable to assume that the earliest Jomonese were also. What emerges from this synoptic odontological reconstruction of East Asian population history is a potential explanation for the peopling of the Americas: the Sinodonts were simply unable to easily expand their population in any direction except northward.

To expand from the sub-Arctic conditions of late Pleistocene north China into the Siberian Arctic required two key inventions, tailored windproof fur clothing and tamed dogs for help in transporting the tents, bedding, cooking utensils and other gear necessary for a nomadic Arctic hunting and fishing lifeway. We can presume that tailored clothing was possible 18,000 years ago since a bone needle was recovered from the excavations of Upper Cave, and the 11,000 year old dog burial at Ushki in central Kamchatka evidences domestication of these valuable animals by at least that time.⁵⁰

Origin of North and South American Indians: migration one. Population growth out of north China would have been channelized by a number of easily identifiable topographic and landform features. I propose that the late Pleistocene north Chinese who were ancestors of Palaeo-Indians, expanded into eastern Mongolia around 20,000 BP, down the basin of the northward flowing Vitim River, reaching the upper Lena River basin. Proceeding northward in the Lena basin would eventually bring the small bands of

hunters and fisherfolk (large fish remains were recovered from Upper Cave)⁵¹ to the thickly-iced Arctic coast near the much reduced Laptev Sea. This would be western Beringia. At this time (Sartan) Beringia was intensely cold Arctic steppe-tundra with very little plant cover for animal feed and reduced stream flow for fish.⁵² Rare mammoth and other large dangerous animals could have supplemented their meagre seasonal fare of fish and smaller animals as at the 13,000 BP site of Berelekh.⁵³Why Palaeo-Indians turned east in Beringia instead of or in addition to going west is unknown. Perhaps Caucasoids were already there. A chain of glaciers separated Chukotka from the Lena basin and the Anadyr valley which according to Dikov seems to have been completely glaciated. So the only route to Alaska would have been largely along the now-submerged continental shelf which today lies beneath the Laptev, Eastern Siberian and Chuckchi seas. This Lena-Arctic route to Alaska is recognized as completely feasible. It appears that before deglaciation commenced there was a limited range of migratory opportunities in the very far north because of ice barriers, low productivity and reduced streamflow. For these reasons I have difficulty imagining ancestral Palaeo-Indians moving into Kamchatka as proposed by Dikov on the basis of the 14,000 BP carbon 14 bone-dated stemmed points of Ushki level VII which he sees as having correspondences with Palaeo-Indian points like those of Marmes and the now cautiously-viewed British Mountain complex. On the other hand, Dikov does recognize these Ushki level VII points as also having resemblance to points from Japan. Regardless of what one makes of the very controversial level VII, there is not much evidence of Palaeo-Indian in Siberia.⁵⁴

A similar situation exists in Alaska. No pre-12,000 BP site has yet to be convincingly established. The lower level of Dry Creek, Girl's Hill and other sites are reasonable candidates for Palaeo-Indian but solifluction, shallow deposits or lack of diagnostic tools makes identification difficult.⁵⁵ I recognise the reservation of much more knowledgeable Americanists like Dumond, West and others over the Yukon finds of the Irving and Morlan research teams.⁵⁶ Precisely how long Palaeo-Indians were in eastern Beringia is indeterminable at this writing, but the strongest evidence indicates not much before the introduction of Diuktai culture over all of northeastern Siberia and into Alaska. Somewhere between Beijing and Alaska I believe Palaeo-Indians developed their diagnostic fluted points for spearing thick-skinned animals like mammoth, possibly because fishing and smaller game hunting was so unproductive in the patchy Beringian environment. I agree with the Clarks that early fluted points will eventually be found in acceptable stratigraphic context in Alaska demonstrating the northern origin of this distinctive feature of the Palaeo-Indian tool kit. I take this position on the basis of the basally-thinned points or knives found at Hutouliang (Tigerhead Hill) in north China dating 11,000 BP.⁵⁷ Although too late to be a progenitor of the Clovis fluted point, the content of the Hutouliang assemblage closely resembles that of the north China Xiachuan culture whose dates range between 24,000 to 16,500 BP. As mentioned previously, these materials make up the North China Microlithic Tradition of Jia.⁵⁸

In sum, the Lena-Arctic route to Alaska was difficult, hazardous and must have been severely limiting on human population size. The harshness of life is evidenced by the increased robusticity and limited amount of Indian dental variation. The dental connection between Indians and north China is stronger than the cultural link.

Origin of Aleut-Eskimo: migration two. Manchuria offers another natural route out of north China. This route would funnel Sinodont expansion to and down the Amur eastward toward the lowered Sea of Okhotsk which in late Pleistocene times was pack-ice covered like the reduced Bering Sea. This ice cover would have depressed southward the main body of the north Asia-tic sea mammal herds. Millions of animals would have occurred along the ice front near the Amur delta, on linked Hokkaido-Sakhalin-mainland, and adjacent to the Kuril archipelago. The eastern branch of the Sinodont population, moving down the Amur, eventually encountered this cornucopia of sea mammals which triggered the beginning development of the northern maritime tradition. If seals went some way up the Amur after fish, sealing may have developed even before reaching the coast. This wealth of sea mammals might have extended as far north as the western end of the Bering Land Bridge south coast, but likely not eastward until deglaciation was under way.⁵⁹

Emphasis on blade tool manufacturing in the lower Amur basin, northern Japan and at Anangula is noteworthy for both cultural affinity and technical application considerations.⁶⁰ This maritime distribution of blade tools in Japan, the Amur and in the Aleutians is as strong an affinity indicator as the interior occurrence of the Mongolian Gobi, Siberian Diuktai and Alaskan wedged-shaped cores and microblades.

As can be seen in Figure 9 the Amur branch of the expanding Sinodonts might have met Southeast Asian Sundadonts (ancestral Jomonese) advancing northward in the Japanese islands. This is another possible source of explanation for the Aleut and Eskimo dental reduction in crown features, but it does not explain their root trait characteristics (rocker jaw is very common in Jomonese and Polynesians; its greatest but still low frequency in the Americas occurs in Aleuts.

Rapid population growth should have occurred in the Amur Sinodont population as a result of the sea mammal food, fuel and fabricational resources. This growth would have stimulated further exploration northward. Movement would have been along the west coast of the Sea of Okhotsk as in Figure 9, and possibly through the ice-packed Kuriles if skin boats had been developed. The difficult to interpret Ushki level VII (14,000 BP) to my mind serves as a better candidate for ancestral Aleut-Eskimo who after leaving the Amur surely spent as much time on the sea coast as in the interior of Kamchatka. What I sense of level VII is a cultural assemblage in transition from the north Japan and Amur tool kit to the fully evolved maritime industry of Anangula, as well as an incomplete assemblage reflecting an interior winter settlement by people who spent most of the year on the Kamchatka coast. Further, as Arutiunov notes, some allowance for local invention has to be given to the stone tool variation in northeastern Siberia and Alaska. It is worth remarking at this point about how unique and valuable is the coastal

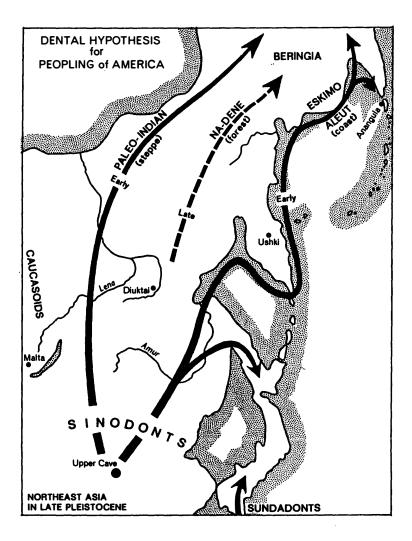


Figure 9 Proposed routes for the late Pleistocene peopling of the Americas.

Anangula site for reconstructing Bering Sea Mongoloid population history, even if the acidic soil did destroy all evidence of bone tools and food types. This can be most appreciated when one recalls that there are almost no Alaskan coastal sites that date before 5,000 BP because of the two metre rise in sea level during the 5-6,000 BP Hypsithermal.⁶¹ Only where coastal groups of 15,000 to 5,000 BP had alternative seasonal settlements away from coasts can we have any record of their lives. Such I think is the situation for Ushki level VII. Perhaps there is some hope for underwater archaeology along the Bering Sea coast, but I fear that winter ice scouring during deglaciation and the Hypsithermal left very little to recover. Thus, Dikov's 'Pri-Okhotsk' route to Alaska, when considered along with the distribution of dental variation, is an excellent choice for the ancestral Aleut-Eskimo migration. This scenario for ancestral Aleut-Eskimo and the up-coming Na-Dene is essentially the same as proposed by Vasilievsky; it and the one for Palaeo-Indian correspond with Hopkins.⁶²

Origin of the Na-Dene: migration three. The final third of the scenario is to account for the dental characteristics of the Greater Northwest Coast people. In Figure 9 these are indicated by the term Na-Dene. Perhaps they should be called Diuktaians after their Siberian culture named by Mochanov. Whatever, their intermediate dental qualities have already been discussed and what remains to decide is if the Na-Dene formed in Siberia or Alaska.⁶³

I fully agree with workers like Dikov, Dumond, Abramova, West and others, who recognize strong correspondences between the Siberian Duiktai culture of ca. 13,000 to 12,000 BP and the Alaskan Palaeo-Arctic tradition starting ca. 11,000 BP, as well as the lack of strong correspondence between Palaeo-Indian artifacts and those of these two.⁶⁴ The emphasis on big-game hunting that characterizes known Clovis Palaeo-Indian sites is not evident in Diuktai or Palaeo-Arctic finds, even though some mammoth remains are known for Siberian sites. More often smaller animals such as caribou, horse, bison and fish make up the food refuse accumulations, as in Ushki level VI (11,000 BP) sites. Pollen studies and site locations suggest a forest, foreststeppe and riverine adaptation for both Diuktai and Palaeo-Arctic. No harpoons or sea mammal remains were found in Ushki level VI sites even though bones and teeth were preserved. Bows and arrows seem to have been the preferred hunting weapons.

For several reasons I disagree with Dikov and Dumond in their shared opinion that Aleut-Eskimo originated with the Diuktai-Palaeo-Arctic population (at one time Dumond seemed to envision Palaeo-Arctic as ancestral to Na-Dene.⁶⁵ I have been unable to identify in his writings precisely what triggered his change of mind). First, all known Palaeo-Arctic sites occur in or very near the territory of modern Na-Dene-speaking Indians (all Alaskan interior and Alaska Peninsula sites) or near sites with Na-Dene dental remains

(all Northwest Coast sites). No accounting of this recognizable American dental group has been made in archaeological reconstructions of Alaska or western Canada. Second, in reconstructing Aleut-Eskimo prehistory, Dumond bases much of his scenario on the Kodiak Island archaeological sequence.⁶⁶ As shown elsewhere and in Fig. 8 the Kodiak dentition, as represented by more than 200 individuals from the Uyak site, are more closely related to those of Na-Dene Indians. The Kodiak sequence cannot be used to evolve Eskimos out of the Palaeo-Arctic tradition if the Uyak series is representative. Third, lumping Anangula with Palaeo-Arctic will not stand up to any manner of formal statistical analysis.⁶⁷ As Laughlin has pointed out, there are more artifacts from Anangula than from all Palaeo-Arctic sites combined.⁶⁸ Not a single wedge-shaped core or bifacial item exists in the thousands of Anangula specimens. Anderson quite correctly concludes that Anangula has nothing to do with Palaeo-Arctic tradition.⁶⁹ If Anangula cannot be included with Palaeo-Arctic, then Aleuts have to be excluded from the Palaeo-Arctic population. Fourth, Na-Dene dental characteristics are distinguishable and in place by about 4,000 BP at Namu on the central British Columbia coast at about the same or slightly later time in Prince Rupert Harbor sites.⁷⁰ The teeth from all these sites are very similar to more recent Northwest Coast Indian teeth (in Fig. 8 Namu and Prince Rupert Harbor are designated as Northern Maritime South). The Namu and general Pacific Northwest cultural sequence shows development from a Palaeo-Arctic (microblade) base to modern Northwest Coast material and economic culture with some southern influences.⁷¹ Directly supportive of long emplacement in Alaska by the Na-Dene, is the 8,800 year divergence estimate between them and Northeast Asians. Fifth, prehistoric human skeletal remains from the Alaskan interior are extremely rare. The one burial I have seen, although fragmented and cremated, showed no discrete traits that would lead to an Eskimo identification.⁷² Sixth, I have not found any explicit discussion of the relationship between Eskimo prehistory and the damaging effect on coastal sites during the Hypsithermal. The record of Alaskan coastal occupation before 5,000 BP is apparently destroyed except in regions where there has been tectonic activity or uplift following deglaciation. To jump from interior Palaeo-Arctic remains to post-Hypsithermal coastal sites ignores what cannot be known about possible Eskimo activity on the Alaskan Bering Sea coast before 5,000 BP?³

To sum up, I cannot identify any statistically sound basis for correlating Palaeo-Arctic tradition with Aleut or Eskimo. Palaeo-Arctic did not penetrate south of Canada where Palaeo-Indian culture and people can be recognised. Thus, there is both indirect and direct evidence to hypothesize that the bearers of Palaeo-Arctic traditon were Na-Dene people. Further, because there is good agreement on the Diuktai-Palaeo-Arctic correspondence, it is both parsimonious and logical to conclude that the Diuktai people were also Na-Dene. The Na-Dene formed in Siberia, not Alaska as a hybrid product of late-leaving Palaeo-Indians and early arriving Aleut-Eskimos.

Being terrestrially rather than coastally adapted when entering Alaska is possibly a contributing factor for the greater similarity Na-Dene teeth have with those of North American Indians than with those of Aleut-Eskimos. When the Asian influence on clustering is removed, the various sub-samples of Greater Northwest Coast link with Indians (Fig. 8). It is for this reason that I am unable to agree with Szathmary and Ossenberg who propose that Na-Dene (Athapaskan) shared an Alaskan acestor with Eskimo.⁷⁴ Brennan and Howells also found Na-Dene to cluster with Indians and not with Eskimos in their multivariate craniometric analysis of Siberia and North America.⁷⁵ It is very difficult to imagine the sort of strong and directional selection that could have driven the Na-Dene dental pattern towards that of Indians if the Na-Dene had branched from Eskimo. Other studies show no close relationship between Eskimos and Athapaskans.⁷⁶ However, other North American links with Athapaskans are hinted at by the dentition.

In tracing the distribution of northern North American side-notched points, Dumond and others proposed these were an indicator of Athapaskans.⁷⁷ These points occur around 1,500± years ago in the Barren Grounds, the northern Plains, the Yukon and in Alaska. Dumond further suggests that the arrival of Athapaskan-speakers in the Southwest and Pacific coast might also have been in this time range, but concludes that there is not much evidence for this possibility. Figure 8 may supply some. Note that Pecos and San Cristobal, both Pueblo period sites in New Mexico's oldest Apache territory, cluster with the more southerly of the Greater Northwest Coast groups (Gulf South and Gulf Central). This could be due to the occurrence of historic Apache genes in these Puebloans, but may be instead due to earlier Athapaskans as Dumond suggests. Note that all the other Southwest series (Point of Pines, Grasshopper, Western Anasazi) are also linked with the Na-Dene branch, as are the remaining Canadian Indians. This latter clustering is probably just the statistical effect of Pecos and San Cristobal pulling the others into the Na-Dene sphere, but it could be relic evidence of early Athapaskanspeakers in the respective areas. The two Maryland series are certainly chance convergences toward Na-Dene. However, is it just chance that has caused linkage between the Na-Dene and the prehistoric North American Indian series with known or possible Athapaskan contact?

To summarize, the key elements of this argument are: (1) the Na-Dene are distinct (serologically as well as dentally) and have been in place a long time, at least 8,800 years by dental microevolution assessment.⁷⁸ (2) There is only one known early tradition in Alaska to which the Na-Dene could be assigned, Palaeo-Arctic. (3) There is no statistically sound evidence linking Aleut or Eskimo to Palaeo-Arctic. (4) The record of Bering Sea coastal occupation before 5,000 BP has been largely destroyed. (5) Palaeo-Arctic

corresponds with Diuktai. Therefore, the Na-Dene most likely arose in Siberia as bearers of the Diuktai culture. Their dental trait frequency intermediacy between Aleut-Eskimo and Indian is a result of gene flow between them and the Lena Basin Palaeo-Indians and the Okhotsk coast Aleut-Eskimos.

Alternative explanations. My 1983 paper explicitly identified four possible migration scenarios for explaining New World dental variation:⁷⁹ (1) Three migrations: This is the model that has just been discussed. It is preferred because it is the simplest and provides the best overall fit with other sorts of independent evidence. (2) Two migrations: Here, the Na-Dene are envisioned as having formed in Alaska as a hybrid product between Palaeo-Indian and Aleut-Eskimo. As discussed, this model has no convincing support. It is especially weak when assessed by serological information.⁸⁰ (3) Three migrations with the Na-Dene forming in Alaska, Eskimo entering later after separating from Aleut in Siberia. This is rejected on the same grounds as model 2. (4) Four migrations: Palaeo-Indian, Na-Dene, Aleut and later-arriving Eskimo make up four migration waves. Until the problem of the Hypsithermal damage to Alaskan Bering Sea coastal occupation before 5,000 BP can be resolved, this model has to be allowed to stand as a possible explanation for New World dental variation. Its greatest strength is the appearance of Siberian Neolithic pottery in Alaskan Norton sites which suggests an immigration event.⁸¹ Unfortunately, what little Norton period skeletal material exists lacks teeth. A fourth migration or late appearance of Eskimo was proposed by Irving who had them arriving about 5,000 BP on the basis of the appearance of Arctic Small Tool tradition on the Bering Sea coast. Note that this is the issue I am concerned about with respect to the Hypsithermal event. Workman sees no Holocene migrations to Alaska.⁸²

Did Palaeo-Indians originate in Europe? Some prehistorians seem to directly envision Europe as the homeland of Palaeo-Indians, or indirectly by not discussing the archaeological sequence of north China when drawing Old World parallels with Palaeo-Indian stone tool technology. ⁸³A 23 trait MMD comparison between approximately 22,000 year old Upper Palaeolithic USSR teeth I have personally inspected, and those of similarly studied recent Northwest Europeans (Table 1) gives a value of 0.183. When the old Europeans are compared with Palaeo-Indians the MMD value is 0.438, much like the MMD of the old Europeans and North and South American Indians (0.529), when time is considered. The dental characteristics of recent Europeans had already evolved by 22,000BP. These characteristics are unlike those of all past and recent Native Americans.⁸⁴ Although it could be argued that the close resemblance between Palaeo-Indian and Ket is suggestive of at least some Caucasoid influence, this MMD is not significant. Furthermore, there are seven groups more like the Ket than Kets are like Palaeo-Indians. Now that we know somewhat more about dental variation in eastern Asia, I feel that my earlier suggestion that Palaeo-Indians might have been in contact with Caucasoids is an unnecessary inference to explain the dental characteristics of Indians. I no longer see any substantial dental basis to view early or later Indians as having been some manner of Mongoloid-Caucasoid hybrid and I certainly see no dental evidence for considering Palaeo-Indians as non-Mongoloids. Views such as these should not be given further encouragement.⁸⁵

APPENDIX

Sample composition. Full provenience treatment will appear later (Turner, n.d.). It is sufficient here to simply list the skeletal series and indicate the reasons for pooling. These were to (1) enlarge sample size for statistical reliability and (2) to generate regional dental characterizations rather than isolate or micro-racial characterizations. The organizational level the groupings are intended to approximate is that which S.M. Garn terms 'local race'.⁸⁶

Samples were pooled on three criteria: (1) strong inter-group multivariate similarity (for example, MMD=0.004 between eastern and western Aleuts so they meet this criterion); (2) common area of origin (all Aleut teeth originated from the same region with its single Aleut culture); and (3) known or presumed linguistic affiliations. Since this criterion's applicability decreases with time and migration factors, it could not be equally applied. For the most part there were no important problems in deciding how to pool the series to make up regional sets. However, six samples were troublesome and rearrangments in future analyses are possible. These are: Buriat. I have included the Buriats with the other Northeast Asians because of location and presumed language. But dentally, the Buriats are on the whole more similar to the Amur samples. The Buriat have a complex population history , which seems to align them with northeast Asians even though they are geographically closer to the Amur samples. An-Yang Chinese. This 3,100 year old north China series is dentally indistinguishable from recent Japanese (MMD=0.000). However, it is not especially like the Buriat (MMD=0.196) or the South Chinese (0.144) who have been included in the Northeast Asia series also. South China. This large series was excavated by A. Hrdlicka from an old Alaskan cannery cemetry on Kodiak Island. Chinese immigrants of this period (before 1900) left mainly from Canton (Kwangshow) in south China. The series is fairly like the Japanese (MMD=0.059) and Buriat (0.036), and decidedly different from any of the Southeast Asian samples. Kets. (More like American Indians than like any north Asians (for example, MMD=0.000 for Maryland, Pecos, Apache, Iroquois, Valdivia, etc.), the Kets are also very similar to the northwest Europeans. Kets are thought to be a hybrid population (Gokhman, pers.comm.), but recent research suggests strong biological ties with southern Siberians.⁸⁸ Kets mythology suggests some manner of American link or parallel. Kets are a linguistic isolate⁸⁹ Since they are the only series I have studied other than the Buriats that originated near the Lena River headwaters, which could serve as possible representatives for the Palaeo-Indian origin hypothesis, I have kept the Ket separate despite small sample size. Two series, Tuva and Tuvinci are almost certainly hybrid populations formed by European and Asian population mixture (A.Kosintsev; A.Zubov, pers.comm). The Tuva series originated from an Iron Age cemetery near Kyz'tl on the upper headwaters of the Yenesei River. The Tuvinci series is from near Krasnojarsk, also on the upper Yenesei. These Scythians are dentally similar (MMD=0.079) but both series have much missing data due to tooth loss or missing mandibles. Thus, sample composition is as follows: Northeast Asia, Urga and other Mongols, An-Yang Chinese, Buriats, Japan, Lake Baikal Neolithic and South China. Amur, Ulchi, Goldi, Orochi, Negedal and Tungus. Northeast Siberia, Ekven, Uelen, Chuckchi and 'Koryak'. Eskimo, early and late Point Barrow, Point Hope, Mackenzie River, Smith Sound, Southampton and St.Lawrence Island. Aleut, eastern and western Aleut. Greater Northwest Coast, Kodiak Island (Uyak), Northern and Central Maritime districts (of Kroeber),⁹⁰ Gulf of Georgia and Puget Sound, lower Columbia River, Inter-mountain and lower Fraser River valley, Apache, Yukon Athapaskans and Kachemak Bay. North American Indian, Cottonwood and Grand Gulch (Utah), southern California, Nanjemoy-Juhle (Maryland), Maryland ossuaries 2 and 4, San Cristobal and Pecos Pueblos (New Mexico), Archaic Saskatchewan and Archaic Quebec, Roebuck and Toronto Iroquois, Grasshopper and Point of Pines Pueblos (Arizona), Canyons de Chelly and del Muerto (Arizona), Kayenta Anasazi (Arizona), northern California (Humboldt, Sacramento and Alameda counties), Arkansas (Quapaw, Togo, Golightly, Wapanoca, Vernon Paul and Nodena), Alabama (Kroger Island), Tlatelolco, Coahuila, Cuicuilco, Chichen Itza, Tehuacan, North Dacota, and Archaic California (SJo-68). South American Indian, Preceramic Peru (Asia, Paloma and others), Patagonia, Bolivia, later Peru, Corondo (Brazil), Sambaqui north and south (Brazil), Minas Gerais and Lagoa Santa (Brazil), Ayalan, Cuchipuy, Santa Elena, Valdivia-Chanduy (Ecuador), Herradura and Punta Teatinos, Chuchipuy (Chile), Archaic and ceramic Panama. Palaeo-Indian, Old Crow, Sta. Maria Astahuacan, Melbourne, Del Mar, Minnesota Lady, Gordon Creek, Midland, Tepexpan, Cerra Sota and Palli Aike. Chinese Late Pleistocene, Dingcum, Upper Cave, Hsuchiayao (photos), Ordos (photos). Sundadonty, Thailand (Non Nok Tha, Ban Chiang, Don Klang, Ban Tong, (Bangkok), Niah Cave (west entrance), Malaya, Singapore, Philippines, Atayal (Taiwan), live Batak (Philippines), Japan (Ainu and Jomon). Northwest Europe, Lapps, Reindeer Island, Karilian Peninsula, North Khanty, USSR Upper Palaeolithic (Akhshtyr, Kostienki 14, 15 and 18, Mal'ta, Samarkand 1 and 2, Sunghir A, B, C and D). Ket, Ket (USSR). Upper Palaeolithic, same specimens listed in Northwest Europe extracted for appropriate comparisons.

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Table 1 Dental variation in Eurasian and American skeletal populations, grouped relative to hypotheses about Late Pleistocene origins of ancestral Aleut-Eskimos, Na-Dene Indians, and earlier Indians; migration number; and subsequent New World Dental microevolution. (Individual counts, sexes pooled).

.

	Trait Location Expression	UI	ging 1 1-4	Shov U11 2-7/	
Population sample	Dichotomy*	%	N	%	N
1. Sinodonty (poole	ed)	41.1	1954	98.8	1922
2. NE Asia		23.5	289	100.0	224
3. Amur Basin		50.0	34	100.0	15
4. NE Siberia		30.0	70	97.6	41
5. Eskimo		17.8	107	98.1	103
6. Aleut		37.1	70	97.5	40
7. Greater Northwes	st Coast	32.9	222	98.8	168
8. North American I	Indian	47.4	795	99.9	874
9. South American I	Indian	55.4	363	99.8	451
10. Palaeo-Indian		25.0	4	100.0	6
ll. China (late Plei	stocene)	33.3	3	100.0	3
12. Sundadonty (pool	led)	22.8	219	79.2	202
13. NW Europe		22.7	44	29.4	34
14. Ket		33.3	3	50.0	2
15. USSR (Upper Pala	eolithic)	0.0	5	16.7	6

* Scaling and observation procedures are given in references to Turner, 'Dental anthropological indications'.

****** New scale. Presence of tuberculum dentale includes any degree of cusp, cuspule, and/or marginal interruption grooves on the lingual surface.

Table	1 ((b)).
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	shov	Double- Tuberculum shovel UI2 dentale 2-6/0-6 UI2		ale	rid	ial ge UC /0-4	Distal accessory U 1-5/0-5	
	%	N	**%	N	%	N	%	N
SINO	71.0	1781	64.2	1990	1.2	2280	73.9	1073
NEA	40.6	239	51.8	220	2.2	275	68.9	138
AMUR	82.4	17	32.0	25	11.1	27	53.8	13
NESIB	59.1	22	72.5	51	0.0	83	55.0	20
ESK	59.3	91	76.2	105	0.0	173	58.4	77
ALEUT	50.0	38	60.6	66	0.0	76	86.2	29
NWC	57.7	156	73.7	194	0.4	265	81.6	109
NAMER	75.0	796	64.0	910	1.7	903	73.4	429
SAMER	90.2	417	65.2	414	1.7	474	79.5	254
PALIN	80.0	5	60.0	5	0.0	4	100.0	4
CHINA	50.0	2	66.7	3	-	-	-	-
SUNDA	14.9	201	58.1	186	2.0	245	65.0	139
NWEUR	39.3	28	64.0	50	4.8	62	31.6	19
KET	50.0	2	50.0	4	0.0	6	75.0	4
USSR	16.7	6	66.7	3	0.0	3	33.3	3

Table 1 (c).

	Az	Uto- Aztecan UP1 +/0 +		Hypocone UM2 1-5/0-5		p 5 M− /0-5	Carabelli trait UM1 2-6/0-6		
	% N		%	N	%	N	%	N	
SINO	1.0	2310	90.2	3639	19.0	2817	32.1	3194	
NEA	0.0	80	94.7	414	31.2	298	30.3	380	
AMUR	0.0	34	86.3	51	21.4	42	27.6	58	
NESIB	0.0	91	80.6	134	3.4	59	17.9	106	
ESK	0.0	192	79.8	257	23.1	182	17.5	211	
ALEUT	0.0	16	68.4	117	12.0	108	6.3	112	
NWC	0.6	166	91.8	451	21.3	376	24.8	386	
NAMER	1.6	1170	91.7	1358	18.4	1161	35.6	1282	
SAMER	0.5	557	92.6	852	13.6	588	41.9	655	
PALIN	0.0	4	100.0	5	33.3	3	100.0	4	
CHINA	-	-	66.7	3	100.0	1	0.0	1	
SUNDA	0.0	72	92.0	414	30.0	370	30.6	427	
NWEUR	0.0	91	81.7	115	15.5	97	33.9	115	
KET	0.0	11	93.7	16	25.0	12	53.8	13	
USSR	0.0	4	60.0	5	0.0	6	57.2	7	

Table 1 (d).

	Parastyle UM3 1-5/0-5		exte U	Enamel extension UM1 1-3/0-3		ntome 212 +/0,+	1-root UP1 1/1-3		
	%	N	%	N	%	N	%	N	
SINO	4.8	2400	68.5	5135	4.6	2738	87.8	4757	
NEA	8.3	145	73.7	518	4.0	249	75.0	428	
AMUR	0.0	26	86.4	81	5.1	39	98.1	103	
NESIB	1.0	99	79.7	227	0.0	50	90.8	251	
ESK	5.9	219	78.4	416	6.4	171	95.7	460	
ALEUT	6.3	79	68.8	231	3.4	116	93.3	252	
NWC	2.8	354	69.7	689	6.3	368	93.1	684	
NAMER	4.1	897	62.2	1849	3.7	1181	85.0	1534	
SAMER	6.3	575	68.5	1117	5.7	560	87.2	1033	
PALIN	16.7	6	57.1	7	0.0	4	100.0	12	
CHINA	0.0	2	-	-	-	-	100.0	2	
SUNDA	1.3	153	57.5	388	1.4	146	59.2	441	
NWEUR	1.4	71	47.3	167	3.2	63	64.7	167	
KET	16.7	6	83.3	18	0.0	9	73.7	19	
USSR	0.0	1	37.5	8	0.0	3	0.0	1	

Table 1 (e).

	3-r UM 3/1	-	cong UM3	educed . abs. C,norm	ling L	>1 .cusp P2 /0-3	Y groove pattern LM2 Y/Y,+,X		
	%	N	%	N	%	N	%	N	
SINO	51.8	3718	22.5	4623	47.2	2393	10.9	3783	
NEA	65.4	387	50.4	377	84.0	312	6.5	353	
AMUR	36.6	82	43.2	95	73.0	37	14.8	54	
NESIB	57.3	159	21.6	245	42.9	63	21.2	85	
ESK	34.6	396	20.6	472	37.4	123	20.1	214	
ALEUT	43.2	162	25.9	212	38.7	62	19.6	143	
NWC	41.7	513	18.6	566	48.9	274	11.0	491	
NAMER	60.0	1191	17.5	1551	41.5	1034	10.7	1631	
SAMER	49.9	817	20.9	1096	37.3	485	7.7	805	
PALIN	63.6	11	0.0	9	0.0	3	28.6	7	
CHINA	50.0	2	33.3	3	100.0	1	0.0	1	
SUNDA	73.9	333	44.0	300	79.1	278	19.6	342	
NWEUR	50.4	125	25.3	162	65.0	100	24.1	137	
KET	42.1	19	33.3	21	58.3	12	10.5	19	
USSR	100.0	1	0.0	4	25.0	4	16.7	6	

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Table 1 (f).
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	Cusp 6 LM1 1-5/0-5		LM	4-cusp LM2 4/4-6;or >4		cting kle l /0-3	Distal trigonid crest LM1 +/0,+		
	%	N	%	N	%	N	%	N	
SINO	47.8	2947	7.9	3583	70.7	1817	5.4	2825	
NEA	40.6	234	12.5	272	53.3	92	3.1	163	
AMUR	51.2	43	11.8	51	78.4	37	20.8	48	
NESIB	50.0	46	3.6	84	79.1	43	7.3	82	
ESK	39.9	178	3.8	209	65.7	102	14.4	180	
ALEUT	43.3	104	10.7	112	70.4	54	5.4	93	
NWC	40.6	406	4.2	471	57.6	191	7.5	292	
NAMER	49.2	1388	8.1	1597	73.3	923	3.3	1344	
SAMER	55.8	545	9.0	779	74.5	373	5.6	620	
PALIN	0.0	3	0.0	8	100.0	2	0.0	3	
CHINA	-	-	0.0	1	-	-	-	-	
SUNDA	35.5	282	40.4	317	55.3	161	7.3	96	
NWEUR	6.9	102	59.5	111	37.2	86	8.0	113	
KET	23.1	13	33.3	15	55.6	9	0.0	15	
USSR	0.0	7	80.0	5	33.3	6	0.0	6	

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Table 1 (g).

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	LM	stylid 1 /0-8	L	sp 7 M1 /0-5	L	root C 1-2	LM	root /1 L-3
	%	N	%	N	%	N	%	N
SINO	34.7	3739	9.8	3998	0.5	3722	13.8	5192
NEA	31.6	345	10.0	359	0.5	215	31.0	429
AMUR	7.7	52	5.7	53	0.0	74	31.1	71
NESIB	32.9	85	5.3	95	0.0	127	23.4	158
ESK	16.5	224	12.9	248	0.0	273	26.5	325
ALEUT	25.9	116	8.4	131	0.0	197	40.7	273
NWC	33.6	450	8.6	467	0.0	491	16.7	730
NAMER	41.9	1679	10.2	1788	0.5	1504	6.7	2077
SAMER	29.8	786	9.6	852	1.0	832	6.2	1117
PALIN	0.0	2	0.0	5	0.0	9	25.0	12
CHINA	0.0	1	-	-	-	-	0.0	1
SUNDA	30.0	337	7.4	367	0.0	207	9.3	343
NWEUR	20.0	125	7.0	143	4.7	169	0.6	178
KET	33.3	15	0.0	16	0.0	21	5.0	20
USSR	14.3	7	0.0	8	0.0	1	0.0	5

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Table 1 (h).

		root M2	root <u>Number of individu</u> LP1 3-5/0-5		of individu:	als w/ trait		
	%	N	%	N	mean	standard deviation	range	
SINO	34.5	4346	8.2	2883	384.8	145.4	2-2077	
NEA	38.3	381	2.6	117	283.3	113.3	80-429	
AMUR	62.2	74	2.8	36	49.0	23.7	13-103	
NESIB	20.1	139	1.6	62	99.2	62.1	20-251	
ESK	33.3	285	3.0	198	221.1	109.2	77-472	
ALEUT	31.2	237	0.6	181	122.4	71.4	16-273	
NWC	38.9	647	9.3	485	395.1	175.6	109-730	
NAMER	30.5	1672	13.0	1297	1279.1	383.9	429-2077	
SAMER	38.3	900	2.0	498	672.0	244.8	254-1117	
PALIN	27.3	11	11.1	9	6.0	3.0	2-12	
CHINA	100.0	1	-	-	1.1	1.1	0-3	
SUNDA	18.5	297	9.8	133	264.1	105.4	72-441	
NWEUR	30.5	164	1.8	114	105.4	46.4	19-178	
КЕТ	19.0	21	7.7	13	12.6	6.2	2-21	
USSR	50.0	2	-	-	4.4	2.3	0-8	

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	NE Asia		Amur		NE Siberia	ı	Eskimo		Aleut		NW Coast	
	Ket	.052	Eskimo	.100	Aleut	.030	NE Siber	.030	NE Siber	.030	Eskimo	.033
	NW Coast	.085	S. America	.102	Eskimo	.030	NW Coast	.033	Eskimo	.036	N America	.034
	SE Asia	.092	NW Coast	.107	NW Coast	.045	Aleut	.036	NW Coast	.045	Aleut	.045
	Aleut	.116	NE Siber	.114	N America	.057	N America	.093	Ket	.089	NE Siber	.045
	N America	.117	Ket	.116	Ket	.081	Ket	.099	N America	.093	Ket	.054
	NE Siber	.120	Aleut	.119	S America	.082	Amur	.100	Palaeoind	.101	S America	.057
	Amur	.122	NE Asia	.122	Amur	.114	S America	.106	S America	.109	NE Asia	.085
	Eskimo	.126	N America	.125	NE Asia	.120	NE Asia	.126	NE Asia	.116	Palaeoin d	.107
	S America	.154	Palaeoind	.221	SE Asia	.178	Palaeoind	.132	Amur	.119	Amur	.107
	Poly-Mic	.162	Tuva–Tuv	.253	Palaeoind	.195	Tuva-Tuv	.211	SE Asia	.195	SE Asia	.171
	Tuva-Tuv	.175	SE Asia	.254	Tuva–Tuv	.223	SE Asia	.216	Tuva–Tuv	.232	Tuva-Tuv	.205
	Palaeoind	.250	NW Europe	.347	Poly-Mic	.301	Poly-Mic	.315	Poly-Mic	.311	Poly-Mic	.268
	NW Europe	.302	Poly-Mic	.347	NW Europe	.305	NW Europe	.315	NW Europe	.329	NW Europe	.315
	Africa	.308	Africa	.541	Africa	.441	Africa	.473	Africa	.470	Africa	.403
	Aust-Mel	.350	Aust-Mel	.565	Aust-Mel	.474	Aust-Mel	.504	Aust-Mel	.506	Aust-Mel .	.462
					·							
	N Amorica		S America		Dalacoind	ion	SE Acia		Doly_Mic		Aust-Melan	ocia
	N America		S America		Palaeoind	ian	SE Asia		Poly-Mic		Aust-Melan	esia
	N America S America	.022	S America N America	.022	Palaeoind: Ket	ian .062	SE Asia	.000	Poly-Mic SE Asia	.041	Aust-Melan Poly-Mic	esia .057
		.022		.022		.062		.000		.041 .045		
	S America		N America		Ket	.062	Ket		 SE Asia		Poly-Mic	.057
	S America NW Coast	.034 .050 .057	N America NW Coast NE Siber Ket	.057	Ket N America	.062	Ket Poly-Mic	.041	SE Asia Ket	.045 .057 .112	Poly-Mic Africa SE Asia Ket	.057 .092 .129 .131
	S America NW Coast Ket	.034 .050	N America NW Coast NE Siber	.057 .082	Ket N America S America	.062 .088 .101	Ket Poly-Mic Tuva-Tuv	.041 .087 .092 .128	SE Asia Ket Aust-Mel	.045 .057 .112 .162	Poly-Mic Africa SE Asia	.057 .092 .129 .131 .206
-	S America NW Coast Ket NE Siber	.034 .050 .057	N America NW Coast NE Siber Ket	.057 .082 .087	Ket N America S America NW Coast	.062 .088 .101 .107	Ket Poly-Mic Tuva-Tuv NE Asia	.041 .087 .092	SE Asia Ket Aust-Mel Africa	.045 .057 .112	Poly-Mic Africa SE Asia Ket	.057 .092 .129 .131 .206 .262
	S America NW Coast Ket NE Siber Palaeoind Aleut Eskimo	.034 .050 .057 .088 .093 .093	N America NW Coast NE Siber Ket Palaeoind	.057 .082 .087 .101 .102 .106	Ket N America S America NW Coast Eskimo	.062 .088 .101 .107 .132	Ket Poly-Mic Tuva-Tuv NE Asia NW Europe	.041 .087 .092 .128 .129 .136	SE Asia Ket Aust-Mel Africa NE Asia Tuva-Tuv NW Europe	.045 .057 .112 .162 .174 .181	Poly-Mic Africa SE Asia Ket NW Europe Tuva-Tuv NE Asia	.057 .092 .129 .131 .206 .262 .350
-	S America NW Coast Ket NE Siber Palaeoind Aleut	.034 .050 .057 .088 .093 .093 .117	N America NW Coast NE Siber Ket Palaeoind Amur Eskimo Aleut	.057 .082 .087 .101 .102 .106 .109	Ket N America S America NW Coast Eskimo Aleut	.062 .088 .101 .107 .132 .184	Ket Poly-Mic Tuva-Tuv NE Asia NW Europe Aust-Mel	.041 .087 .092 .128 .129 .136 .171	SE Asia Ket Aust-Mel Africa NE Asia Tuva-Tuv	.045 .057 .112 .162 .174 .181 .268	Poly-Mic Africa SE Asia Ket NW Europe Tuva-Tuv NE Asia N America	.057 .092 .129 .131 .206 .262 .350 .445
-	S America NW Coast Ket NE Siber Palaeoind Aleut Eskimo NE Asia Amur	.034 .050 .057 .088 .093 .093 .117 .125	N America NW Coast NE Siber Ket Palaeoind Amur Eskimo	.057 .082 .087 .101 .102 .106 .109 .154	Ket N America S America NW Coast Eskimo Aleut NE Siber	.062 .088 .101 .107 .132 .184 .195	Ket Poly-Mic Tuva-Tuv NE Asia NW Europe Aust-Mel Africa	.041 .087 .092 .128 .129 .136 .171 .178	SE Asia Ket Aust-Mel Africa NE Asia Tuva-Tuv NW Europe	.045 .057 .112 .162 .174 .181 .268 .285	Poly-Mic Africa SE Asia Ket NW Europe Tuva-Tuv NE Asia N America NW Coast	.057 .092 .129 .131 .206 .262 .350 .445 .462
	S America NW Coast Ket NE Siber Palaeoind Aleut Eskimo NE Asia Amur SE Asia	.034 .050 .057 .088 .093 .093 .117 .125 .184	N America NW Coast NE Siber Ket Palaeoind Amur Eskimo Aleut NE Asia Tuva-Tuv	.057 .082 .087 .101 .102 .106 .109 .154 .263	Ket N America S America NW Coast Eskimo Aleut NE Siber Amur NE Asia SE Asia	.062 .088 .101 .107 .132 .184 .195 .221 .250 .324	Ket Poly-Mic Tuva-Tuv NE Asia NW Europe Aust-Mel Africa NW Coast	.041 .087 .092 .128 .129 .136 .171 .178 .184	SE Asia Ket Aust-Mel Africa NE Asia Tuva-Tuv NW Europe NW Coast	.045 .057 .112 .162 .174 .181 .268 .285 .301	Poly-Mic Africa SE Asia Ket NW Europe Tuva-Tuv NE Asia N America NW Coast NE Siber	.057 .092 .129 .131 .206 .262 .350 .445 .462 .474
-	S America NW Coast Ket NE Siber Palaeoind Aleut Eskimo NE Asia Amur SE Asia Tuva-Tuv	.034 .050 .057 .088 .093 .093 .117 .125 .184 .219	N America NW Coast NE Siber Ket Palaeoind Amur Eskimo Aleut NE Asia Tuva-Tuv SE Asia	.057 .082 .087 .101 .102 .106 .109 .154 .263 .268	Ket N America S America NW Coast Eskimo Aleut NE Siber Amur NE Asia SE Asia Tuva-Tuv	.062 .088 .101 .107 .132 .184 .195 .221 .250 .324 .340	Ket Poly-Mic Tuva-Tuv NE Asia NW Europe Aust-Mel Africa NW Coast NE Coast NE Siber N America Aleut	.041 .087 .092 .128 .129 .136 .171 .178 .184 .195	SE Asia Ket Aust-Mel Africa NE Asia Tuva-Tuv NW Europe NW Coast N America NE Siber Aleut	.045 .057 .112 .162 .174 .181 .268 .285 .301 .311	Poly-Mic Africa SE Asia Ket NW Europe Tuva-Tuv NE Asia N America NW Coast NE Siber Palaeoind	.057 .092 .129 .131 .206 .262 .350 .445 .462 .474 .504
	S America NW Coast Ket NE Siber Palaeoind Aleut Eskimo NE Asia Amur SE Asia	.034 .050 .057 .088 .093 .093 .117 .125 .184	N America NW Coast NE Siber Ket Palaeoind Amur Eskimo Aleut NE Asia Tuva-Tuv	.057 .082 .087 .101 .102 .106 .109 .154 .263	Ket N America S America NW Coast Eskimo Aleut NE Siber Amur NE Asia SE Asia	.062 .088 .101 .107 .132 .184 .195 .221 .250 .324	Ket Poly-Mic Tuva-Tuv NE Asia NW Europe Aust-Mel Africa NW Coast NE Coast NE Siber N America	.041 .087 .092 .128 .129 .136 .171 .178 .184	SE Asia Ket Aust-Mel Africa NE Asia Tuva-Tuv NW Europe NW Coast N America NE Siber	.045 .057 .112 .162 .174 .181 .268 .285 .301	Poly-Mic Africa SE Asia Ket NW Europe Tuva-Tuv NE Asia N America NW Coast NE Siber	.057 .092 .129 .131 .206 .262 .350 .445 .462 .474

NW Europe

Aust-Mel

Africa

NW Europe

Africa

.445 Aust-Mel

.378

.514

Poly-Mic

.574 Aust-Mel

NW Europe .414

. 399

.504

Amur

S America

Palaeoind

.254

.268

.324

Amur

S America

Palaeoind

.347

.368

.399

Aleut

S America

Amur

.322

.388

Table 2 Ranked ordering of mean measures of divergence (28 dental traits).

.506

.565

Table 2 (continued).

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Africa		NW Europe		Tuva-Tuvin	ci	Ket	
Aust-Mel Poly-Mic SE Asia Ket Tuva-Tuv NW Europe NE Asia N America Palaeoind NW Coast NE Siber Aleut Eskimo S America	.092 .112 .136 .151 .249 .250 .308 .388 .394 .403 .441 .473 .514	Ket Tuva-Tuv SE Asia Poly-Mic Aust-Mel Africa NE Asia NE Siber Eskimo NW Coast N America Aleut Amur S America	.007 .038 .128 .181 .206 .302 .305 .315 .315 .322 .329 .347 .378	Ket NW Europe SE Asia Poly-Mic NE Asia NW Coast Eskimo N America NE Siber Aleut Africa Amur Aust-Mel S America	.004 .038 .087 .174 .175 .205 .211 .219 .223 .232 .249 .253 .263	SE Asia Tuva-Tuv NW Europe Poly-Mic N America NE Asia NW Coast Palaeoind NE Siber S America Aleut Eskimo Amur Aust-Mel	.000 .004 .007 .045 .050 .052 .054 .062 .081 .087 .089 .099 .116 .131
Amur	.541	Palaeoind	.414	Palaeoind	.340	Africa	.151

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Statistic	Aleut- Eskimo	Greater NW Coast	North America	South America	Pan- Indian **	Northern Asia ***	East Asia ****
Mean MMD Standard deviation Standard error No. MMD comparisons Probability of signifi. difference: Aleut-Eskimo Greater NW Coast North America South America Pan-Indian Northern Asia East Asia	.068 .058 .009 45 <.0001 .06 .37 .27 <.0001 <.0001	.011 .017 .003 36 <.0001 <.0001 <.0001 <.0001	.051 .040 .003 210 .06 <.0001 .16 	.059 .050 .005 105 .37 <.0001 .16 <.0001 <.0001	.058 .048 .001 1035 .27 - - - - - - - - - - - - - - - - - - -	.133 .062 .009 45 <.0001 <.0001 <.0001 <.0001 - -	.220 .155 .012 153 <.0001 <.0001 <.0001 <.0001 - -

Table 3 Asian-American regional dental variation (intra-group MMD divergence*).

* Small sample size in some instances limited, so only 22 traits used. Excluded are Uto-Aztec premolar, parastyle, odontome, distal trigonid crest, Tome's root, and peg-reduced-congenital absence of upper third molars. I2 shovelling replaced I1.

- ** Excludes Aleut, Eskimo, and Palaeo-Indian. Kodiak included. See Appendix.
- *** Composed of recent Japanese, An-yang Chinese, South Chinese, Uelen, Ekven, Tungus, Mongol, East Siberia and Chukchi, Amur, and Buriat samples.
- **** Composed of above Northern Asians plus Niah, Non Nok Tha, Bangkok, Jomon, Don Klang and Ban Tong, Malay, Ban Chiang, and Ainu.

Group	North Asia **	Aleut- Eskimo	Na – Dene ***	Greater NW Coast	North America	South America	North & South America
North Asia	-	509.0	145.9	398.1	806.7	841.1	974.2
Aleut-Eskimo	14 (51.8%)	-	55.6	195.7	811.5	611.6	888.9
Na-Dene	9 (33.3%)	3 (11.1%)	-	28.6	69.9	82.6	65.0
Greater NW Coast	14 (51.8%)	10 (37.0%)	2 (7.4%)	-	309.1	326.9	324.1
North America	19 (70.4%)	17 (63.0%)	6 (22.2%)	17 (63.0%)	-	239.5	-
South America	14 (51.8%)	18 (66.7%)	4 (14.8%)	14 (51.8%)	15 (55.6%)	-	-
North and South America	21 (77.8%)	16 (59.3%)	4 (14.8%)	15 (55.6%)	-	-	-

Table 4 Univariate comparisons. Upper, summed chi square values (1 d.f.); lower, number of traits with significant differences (P>0.05); 27 traits*.

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* Uto-Aztec premolar excluded because of small sample size.

** North Asia includes Mongol, Buriat, An-yang Chinese, Japanese.

*** Na-Dene includes Haida, Tlingit, Yukon Athapaskan.

4 Peopling of North America: clues from genetic studies

Emőke Szathmary

TO MANY, THE RECENCY OF THE OCCUPATION OF THE AMERICAS AND THE RELATIVE 'sameness' of its peoples in traits of superficial morphology suggest that little can be learnt by studying Amerindian biology. Archaeologists, for example, who extol 'the richness and variety of prehistoric American cultures' and marvel at the linguistic diversity on the two continents seem unaware that considerable biological heterogeneity also exists in the Americas.¹ What appears to the same author, on the surface, to be 'a relatively uniform racial composition' masks a considerable amount of genetic variability.² Furthermore, even the superficial 'general sameness' refers only to features such as pigmentation of the skin, hair and eyes, hair form, the scantiness of facial and body hair, and dental traits.³ On the other hand, characteristics such as stature or craniofacial form and dimensions do show variation in both North and South America.⁴

What general interest most Americanists have in Amerindian biology is reflected in questions concerning the 'physical type' of the original immigrants.⁵ There is also some concern whether the diversity that is evident in their descendants resulted from successive population increments from Asia, or whether this was produced by evolutionary forces within the New World. Understandably, questions of the first sort are best satisfied by skeletal data, which, for the requisite time periods of first occupation, are vanishingly rare.⁶ However, genetic data obtained from the descendants can also be used to establish genetic relationships and there are many examples known where 'genetic distances reflect not only ethnology but also history and archaeology'.⁷

While it is fact that the question of Amerindian origins and affinities has long fascinated Americanists and continues to do so, this is not the only appeal the peoples of the Americas have for human biologists.⁸ Focus on genetic relationship, which is but one cause of genetic similarity distracts attention from the obverse, namely, genetic difference. The vast amount of genetic diversity in humans discovered by the application of improved biochemical detection methods begs explanation. Neel has been the most eloquent of all geneticists in articulating the importance of Amerindian studies, particularly on those groups that have maintained biological and sociocultural integrity, for making inferences about the evolutionary forces that maintain genetic variability in populations.⁹ This conviction has had the practical result that some South American tribal groups are better known genetically, liguistically and sociologically than most nation states. Studies on North American Indians have not been as detailed, in part because of the disruption most groups have experienced from post-Columbian immigrants. Nevertheless, it remains one of the tasks of human biologists to quantify the existing genetic differences within and between these populations as well. In addition, although the difficulties may be more severe, human biologists must provide explanations for how these differences arose and are maintained. Such explanations can be sought by testing the observed data against various models supplied by population genetics theory. The approaches would yield answers specific for the people of North America. However, their ultimate purpose for the human biologist would be to achieve a deeper understanding of how the evolutionary process operates on the human species.

This chapter provides a general framework for the interpretation of Amerindian biologic variability. It also supplies some examples of recent studies on the estimation of genetic diversity within groups of subarctic Amerindians. Lastly, it shows how such research can lead into deduction about Amerindian affinities with each other and with Asians.

Amerindian Biology: Current Perspectives

Few people growing up in North America have escaped the adage 'if you've seen one Indian you've seen them all.' The statement from which this maxim evolved has been attributed to Antonio de Ulloa, a Spanish scientific traveller writing in the year 1772. In 1951 Stewart and Newman documented how this opinion, espoused as it was by the most eminent men of 'early' anthropology, served to retard our understanding of Amerindian biological diversity. They concluded that (1) notions of Amerindian homogeneity, (2) the attribution of Amerindian variability to waves of migration, or (3) reluctance to interpret Amerindian diversity with the methods and theory of population genetics represented a failure of Americanists to keep apace with developments in the biological sciences. In their opinion 'data, old and new, will require interpretations set within the broad framework of modern biology, with special emphasis on population genetics, systematics and prehistory'.¹⁰

This dictum was certainly observed by Brues in her treatment of Amerindian variability.¹¹ She accepted as the baseline in her initial formulation a single archaeologically derived date (15,000 years BC) for first human entry into North America. With some simple calculations Brues showed that even with a very slow rate of population increase it would have been possible for a group of 100 'founders' to have 100 million descendants in 10,000 years. She saw no need to postulate mass migrations, certainly not to explain the distribution of culture traits, and argued that with the exception of the Eskimos and Aleuts the 'genetic make-up of the populations of the Americas was largely determined by the first migrants'. Diversification of this slowly expanding group, probably through the actions of genetic drift and natural selection produced what variability exists today.

The accuracy of Brues' interpretation is less dependent on the evolutionary mechanisms she postulated than on the archaeological context into which the interpretation must be cast. These include at minimum a correct estimate of the first occupation of the Americas, as well as the availability of a detailed, continents-wide prehistoric record. Nothing of this sort currently exists, hence the archaeologically derived baselines which form the initial assumptions for the biological model, are subject to modification and possibly even reversal.

This can be illustrated by contrasting the framework Brues employed with some recent developments in archaeology. Brues assumed an initial time depth of 15,000 years BC, a conservative, non-controversial estimate available more than a decade ago. This time depth meant entry into the New World towards the end of the climax of the Late Wisconsin glaciation, when the Bering land bridge was at its greatest extent. By 13,000 to 14,000 BP the Bering Strait had reappeared, and by 11,800 BP it became an unfordable barrier between Asia and America 'to any except skilled boatmen'.¹² Accordingly, the isolation of the first Americans from Old World contacts occurred within one or two thousand years after arrival of the 'founders'. Their southern expansion coincided with the retreat of the glaciers.

The new prehistoric evidence shows that humans were present as far east as the Old Crow basin of Canada's Yukon Territory as early as 27,000 years ago.¹³ Furthermore, it can no longer be doubted that people were present south of the Late Wisconsin ice sheets by 21,070 BP (Meadowcroft Rock Shelter, 40°17"N, 80°29"W).¹⁴ How these hunting bands got south of the ice is a biologically important issue, as well as a matter of some archaeological controversy. The pivotal problem is whether it was always possible for

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groups to move from Beringia to the central Great Plains, or whether the coalescence of the Cordilleran and Laurentide ice sheets effectively isolated the people south of the ice from those north of the ice for several thousand years. If the former possibility existed, then Brues' model needs little revision beyond a greater time depth. If the latter is correct, then there may indeed have been different 'waves of migration' into and across the Americas, not necessarily the Palaeoindian equivalent of organized convoys, but certainly, as the ice retreated, the gradual southward (and northward) movement of peoples that differed to some degree genetically.

The evidence for an ice-free corridor out of Beringia along the Mackenzie River and continuing south along the eastern foothills of the Rocky Mountains is accumulating. Detailed geomorphologic, climatic, and floral and faunal studies provide environmental reconstructions that suggest strongly that the corridor was inhabitable for periods of time between 25,000 to 15,000 BP. However, the so-called 'ice-free' corridor was not open continuously. Fladmark suggests that ice between latitudes 55°-60° N. probably blocked the corridor at the height of the glacial climax in west central North America, that is, between 18,000 to 15,000 BP.¹⁵ In such a case people north of the ice were separated from those to the south by a minimum of 3,000 years.While such a period may be insignificant geologically¹⁶ it is of some consequence for genetic differentiation. Three thousand years approximates 120 generations. Not an insignificant amount of genetic difference can accumulate in small populations isolated from each other for such lengths of time.

Indians of Subarctic North America

(a) Linguistic Relationships: The current distribution of indigenous people in Canada and Alaska shows that the entire subarctic culture area (Fig.1) is populated by speakers of either Athapaskan or Algonkian Amerindian languages. Athapaskan languages are confined to the west, while Algonkian languages are spoken in the central and eastern regions.¹⁷

From where and when did the Athapaskans and Algonkians come to inhabit such a vast territory? Algonkian and Athapaskan are distinct language families, with no known connections between them.¹⁸ Neither language family is confined to the subarctic, but by far the greatest number of Athapaskan tongues are spoken in the north, while the greatest number of Algonkian languages are spoken south of the subarctic.¹⁹

Opinions concerning the origin of these people are mixed. Linguistic analysis suggests the ancient homeland of Athapaskan speakers was probably located in Alaska, in its eastern interior and may have extended a considerable distance into Canada. Modern descendants of these ancestral Athapaskans speak a minimum of eleven languages in Alaska and likely another twelve in Canada. Greater precision regarding the exact number of languages is not possible, because Athapaskan, like many other language families, is a language and a dialect complex in which it is not always simple to determine boundaries.²⁰

Current classification of the Algonkian languages lists 26, although earlier works included only 17.²¹ The problem here also is the difference between a dialect complex and a distinct language. Algonkian languages like Athapaskan, are not confined to the subarctic culture area. However, while all extra-subarctic Athapaskans are thought to be descendants of people who had moved south from the northwestern region of the continent, the same cannot be said for Algonkian. The central and eastern subarctic currently includes the dialect continuum Cree-Montagnais with numerous dialects between, as well as Ojibwa in northwestern Ontario.²² The latter, however, is part of the Ojibwa-Potawatomi continuum that extends south of the western Great Lakes. All other Algonkian languages are spoken, and

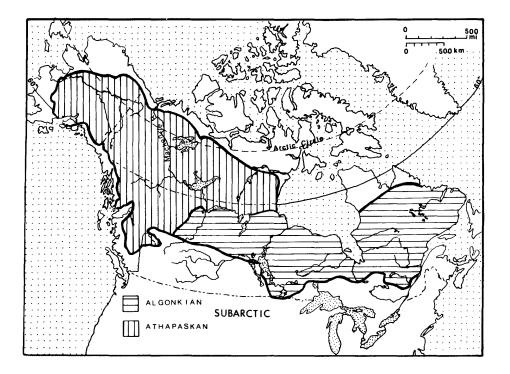


Figure 1 The subarctic culture area and languages spoken within it. (After J.Helm, (ed) Handbook of North American Indians. 6. Subarctic (Washington 1981) p.IX, and J.G.Taylor Canadian Geographic 100:52-58 (1980/81).

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other dialect continua are located south of the subarctic culture area, reaching as far west as the Rocky Mountains and along the eastern seaboard as far south as the Carolinas.

Identification of the ancient homeland of Algonkian-speakers has not been done with the linguistic criteria employed by Krauss for Athapaskans, that is, the region of greatest linguistic diversity. However, Siebert has argued cogently that reconstruction of proto-Algonkian words from floral and faunal word lists of several Algonkian languages and the correlation of these with ancient ranges and climates place the proto-Algonkian homeland in a restricted region of south central Ontario, between Lakes Huron and Ontario. This suggests that Algonkians are of a southern derivation, unlike the Athapaskans.²³

(b) Archaeological Relationships: The archaeological record is not particularly helpful in addressing questions of ultimate origin raised by current language distributions. The 'in-situ' hypothesis prevails, whereby living peoples are thought to be the lineal descendants of people whose prehistoric remains are located in the regions the living now occupy. Because skeletal data are either completely missing from the ancient time periods (e.g. Alaska), or are rare (e.g. Archaic samples from the Great Lakes)²⁴, and because such data are almost non-existent for historic sub-arctic peoples the archaeological record depends completely on items of material culture.²⁵ These have been used successfully to trace the modern peoples back in time for a matter of a few thousand years. Thus, the earliest sequence thought to show continuity in lithics with any historic Algonkian is the Laurel tradition (earliest date 200 BC) of northwestern Ontaria. For Athapaskans, agreement among archaeologists stops for sequences earlier than 1,000 AD.²⁶

The roots of the earliest Algonkian and Athapaskan traditons are thought to lie in the various Archaic cultures that antecede them in the subarctic area.²⁷ Some of these in turn are believed to have developed out of the earlier Palaeo-Indian big-game-hunting stage identified by the use of various kinds of laceolate points. Wright and Harp, for example, both agree that Palaeo-Indians from the central Plains (Plano tradition) moved north and southeast as the Laurentide glaciers retreated, ultimately to give rise to the Shield Archaic people (5,000 - 1,000 BC). Wright has suggested, on the basis of the continuity he sees between lithics and inferred lifeways between Shield Archaic and ensuing Laurel culture, that the Shield Archaic people may have spoken an Algonkian language. Harp, however, while seeing 'considerable merit' in this argument, thinks that the Shield Archaic was the foundation for all Indian groups which had a 'basic taiga economy' and this includes Athapaskan as well as Algonkian peoples.²⁸

It is worth noting that Dumond in his summary of the Northern Archaic tradition (4,000 - 2,000 BC), more commonly thought to be ancestral to Athapaskans does not derive them from a Palaeo-Indian base. Rather, he notes that others have tried to link the Northern Archaic sequence with the earlier occurring indigenous Alaskan Palaeo-Arctic tradition, even though the continuity between the two traditions is not satisfactorily demonstrated. Accordingly, Dumond repeats the conventional view that the Northern Archaic reflects a forest-adapted tradition that was carried northward by migrants 'after the end of the Pleistocene glaciation'.²⁹

The Northern Archaic, according to Dumond, is linked by virtue of the most commonly occurring artifact in it (the side-notched point) to the Archaic of eastern North America. This Archaic stage, called the Boreal (earliest sites c.4,000 BC) by Harp and Laurentian, by Wright, does not appear to have any connection to an earlier Palaeo-Indian projectile point tradition. Nevertheless, Harp thinks the Boreal Archaic 'gave rise to the early cultures of the Quebec-Labrador peninsula' Montagnais and Naskapi, both groups being Algonkian speakers. Wright, who also sees the Boreal (Laurentian) Archaic as very different from the Shield Archaic, suggests that the former represents a second Archaic population with a different technology and 'different antecedents'. What existed between Boreal and Shield Archaic peoples may have been interaction based on trade, much as existed between historic Algonkian and Iroquoian speakers of the northeast. Implicitly in Wright's view, these Laurentian (Boreal) Archaic people were not ancestors of the Algonkians.³⁰

I think it is safe to say that given the sparseness of the evidence, it is risky indeed to draw correspondences between the direct antecedents of historic peoples and the earlier Archaic cultures. Thus, 'although it seems eminently logical to assume that it (i.e. the Archaic) evolved into the various Indian cultures that occupied the region at the time of European discovery' indubitable continuities are not established between Archaic and subsequent traditions for any part of the subarctic culture area. Furthermore, the validity of inferring ethnicity from stone tools is questionable. Tools have functions. Pursuit of similar subsistence activities may require stone tools of similar size and shape (e.g. reflecting a 'taiga economy'), in which case similarity does not indicate anything about linguistic or biological relationship.^{\$1} Setting these difficulties aside, were the various archaeological speculations accepted, then all subarctic Indians would be derived from two interior Indian groups. The Algonkians would stem ultimately from Palaeo-Indians who moved northeast from the region of the central Great Plains, with a possible increment in the east from people of the pre-projectile point stage. The latter moved north with the spread of the forests. The same group is thought to have led to the appearance of the Athapaskans across the continent in Alaska and adjacent Canada.

(c) A Hypothesis of Population Relationship: A more critical observer might state, as has Dumond when discussing the archaeology of a better known area than the subarctic, the Pacific rim, that it is still not clear whether the different archaeological assemblages of different time periods indicate mass migrations from the north to the south and vice versa, or simply the transmission of tool-making ideas both northward and southward.³² This must also apply to the occupation of the subarctic. Given that people were present both north and south of the glaciers and that the late Wisconsin glaciers did recede thereby exposing enormous tracts of land for habitation, both movements of people and transmission of ideas are possibilities. The linguistic data suggest that ancestors of the Algonkians were the northward bound migrants, while the ancestors of the Athapaskans merely shifted their range south and southeast. If any tool-making ideas spread with the growth of forests, there were already people present in the northwest to whom these new ideas could be transmitted.

Genetic Studies on Subarctic Indians

In recent years several publications have summarized genetic data available on subarctic peoples of North America: Athapaskan and Algonkian.³³ These papers attest that the data gathering stage of subarctic genetic investigation is well under way. At least two different genetic systems have been described in 17 Algonkian-speaking populations and a similar number of systems have been described in some 15 Athapaskan-speaking groups. However, the summaries also show how little of the existing information can be used for comparative or interpretative purposes. Accurate genetic description requires information from more than just one or two loci. Many population geneticists (e.g. Nei and Roychoudhury) consider 20 loci as minimally adequate.³⁴ In fact, most studies on humans provide data on far fewer systems than this, and subarctic studies are no exception. Older works emphasized data on six to nine blood group systems. More recent ones may augment this with protein and enzyme data, but the trend has been to emphasize the latter to the exclusion of blood groups.³⁵ The result, when populations have been described for differing lists of genes, is that comparisons between groups are obviouosly impossible.

An additional problem that plagues northern studies is that of small sample size, a situation often unavoidable simply because the actual number of inhabitants in northern settlements may be absolutely small. Very likely smallness of local samples, as well as the notion that the only real biological difference between native North Americans is between Eskimos and Indians have led to the lumping of primary data under linguistic labels, for example, 'Athabascan'.³⁶ While the need for such approaches is understandable, they do ignore ethnic differences and thus prevent documentation of intra-Indian variability.

In sum, the existing genetic data on subarctic peoples allow some description, comparison and interpretation. However, the limited nature of the data in terms of numbers of systems tested in common, the total number of populations examined, and the size of the samples does not allow judgments to be definitive. What is known overall about the genetic traits of Athapaskans and Algonkians and the relationships within each group is based on information gleaned from disparate samples of five Northern Athapaskan and seven Algonkian 'tribes' (languages). These have been described for eight and nine blood group systems, respectively, and for each system sample sizes exceed 70 persons in all 'tribes'. To include more genetic information in testing of specific hypotheses, or in even providing description, means a reduction of the number of populations used to characterize the whole.³⁷ When questioning whether fewer 'tribes' are enough, it is worth keeping in mind that there are 22 Athapaskan-speaking languages ('tribes') in northwestern North America, at least 15 of these within the subarctic. The situation for subarctic Algonkian-speakers is not as dismal: of the five 'tribes' in this culture area reasonable data are available for four. It is only against the totality of the Algonkian distribution (26 languages or 26 'tribes') that the seven tribal data sets are judged insufficient.

(a) Genetic Diversity in Subarctic North America: Genetic variation within populations is influenced by aspects of population structure. These include phenomena such as the number of subdivisions within a group, the demographic features of the population, the degree of intragroup migration as required by mate exchanges, as well as details of population history.³⁸

The hunting and gathering populations of the subarctic were distributed very sparsely over large areas. For example, Roth estimated a population density of 1.7 per 100 square km for the Kutchin of the northern Yukon Territory.³⁹ The band level of social organization exhibited by such dispersed northern hunters maximized the chance of survival in a harsh environment. Fluctuations in local resources were met by movement of people out of and into other bands as needs demanded.⁴⁰ Meiklejohn has suggested that in the precontact period the high mobility and flexibility of hunting bands was probably accompanied by band exogamy. Major crises in food supply, expected every two or three generations would lead to major restructuring of groups through fissions and fusions. The consequences of such processes would be gene-flow preventing the 'appearance of major defineable population units'. Rather, only 'slight differences in gene frequencies over space' would be present. Meiklejohn has directly proposed that Athapaskans comprised such a single 'biological unit with changing internal structure of a fleeting nature'.41

Hypotheses of this sort require testing, ideally by examining the evidence for genetic variation in subarctic peoples. As a point of departure, it is worth noting that the band level of social organization did not preclude some degree of socio-geographic differentiation in the subarctic. Some of this evidently occurred else there would not be distinct languages or dialect continua within the Athapaskan and Algonkian subarctic regions. More directly, anthropologists such as Helm have documented the existence of regional bands, socio-territorial divisions defined by 'terms which refer to locus of occupation or area of exploitation in which a substantial number of the group can be found during a significant part of the year'. Group identification could extend through several generations and persons within groups were linked by primary consanguineal and affinal ties.⁴² Among the Kutchin, for example, there were ten regional bands, each comprised of several local bands. The temporal duration of such local bands varied, but among the Peel River Kutchin the modal span was three generations. Superimposed on this were three matrilineal clans that functioned to regulate In the eastern subarctic named groups also occurred (Montagmarriage. nais-Naskapi). In these populations bilateral cross cousin marriage was the form of mating preferred into the 1920s. There was, among the Mistassini Cree, no evidence for either band exogamy or endogamy, although the most common marital alliances were contracted between families whose hunting territories were geographically close.43

The existence of regional bands and mating rules in pre-contact days suggests that some degree of genetic differentiation probably accompanied socio-geographic differentiation. Whether the extent of that biological diversity can be deduced from modern genetic data depends on the specific population and its contact history. Sedentism has come to all subarctic groups: its pace accelerated after 1950 (in Canada) as a matter of government However, there are populations, for example the Athapaskan policy. Dogrib, for whom life before the turning point of the 1950s was not much different than it had ever been.⁴⁴ The sedentism that occurred among the Dogrib did not mean that all people left regional band areas to settle into permanent residences at Rae, the principal village. Rather, some modern settlements came into existence within regional band areas through a process of consolidation: people already members of the regional band through ties of blood or marriage built permanent houses at a spot favoured for a particular reason (e.g. proposed school site). Examples of this sort of settlement formation include the hamlets of Lac La Martre and Rae Lakes located within the hunting territories of the 'Filth Lake People' and the 'People Next to Another People', respectively. Dogrib regional bands recognized in the 1960s were already in existence in the 1900s and there is evidence that the Lac La Martre band existed even earlier.⁴⁵ Sampling of adults in such communities would certainly show the extent of gene diversity in the modern population, and there is little reason to think it would have been any different in any Dogrib regional band in precontact times.

The statistic used here to assess genetic variation is the gene diversity measure H, developed by Nei.⁴⁶ H was obtained for 11 blood group loci, ABO, Rh (C), Rh (D), Rh (E), MN, Ss, Diego, Duffy, Kell, Kidd and P. The Rh and MNSs 'loci' were considered separately because of the need to maximise the number of systems tested. Calculations show that very little difference in the value of H occurs when Rh and MNSs are treated as single or multiple loci.⁴⁷ Protein loci, although they are more suitable for theoretical reasons for the calculation of H, were not available for all the populations among whom comparisons were intended.

Gene diversity was estimated for each of three groups of Dogrib sampled over two northern settlements, Lac La Martre and Rae Lakes and the main village, Rae. H was also obtained for each of three villages of Kutchin (Arctic Village and Fort Yukon, Alaska, and Old Crow, Yukon Territory). All three villages are located within different Kutchin regional band areas. These villages, plus Rae, had their origins as points of European trade, missionary activity and ultimately government service. Such villages are large and contain people of European origin, as well as Indians from other 'tribes'. Lastly, gene diversity was estimated for three Ojibwa (Algonkian-speaking) samples. The village of Pikangikum is within the subarctic culture area. However, the Wikwemikong and Minnesota samples are drawn from reservation populations (i.e. several hamlets, as well as rural families in a specified area) that lie outside the subarctic in the Northeastern (Woodland) culture area.⁴⁸

Table 1 shows that, in all groups, even the smallest samples drawn from hamlets within regional band areas, H is considerably greater than zero. This suggests that there probably was significant gene diversity present within subarctic groups in precontact times. Table 1 also shows that Ojibwa, whether in the subarctic or not, display greater gene diversity than the Athapaskans. Some of this is clearly the consequence of European admixture, but the diversity that remains after correction for gene flow is still substantial. To what the greater diversity can be attributed is problematic. Gene diversity is known to increase with population size and geographic area inhabited.⁴⁹ The Woodland Ojibwa samples were obtained from larger populations distributed more densely over smaller geographic areas. This, however, is not true for the Pikangikum population. What seems a common element for the Ojibwa that sets them apart from these Athapaskans, is their history. Although some ethnographers, such as Rogers, maintain that the northern Ojibwa were always residents of the subarctic, others, like Dunning, Hickerson and Bishop think that the branches of this far-flung group migrated to their current locations from the northern rim of the Central Great Lakes around 300 years ago.⁵⁰ The histories of all three Ojibwa populations considered here, marked in particular for the extra-subarctic Ojibwa, attest to migration into their current territories by multiple independent family groups over a period of many years.⁵¹

		•				
Population	Location	Sample Size	Detectable European Admixture	н	±	s.e.
Dogrib	NWT, Canada					
Lac La Martre	63°08'N,117°16'W	19	0	.190	±	.059
Rae Lakes	64°10'N,117°20'W	32	.055 ^a	.181	±	.053
Rae	62°50'N,116°03'W	107	.082 ^a	.206	±	.046
Kutchin	Alaska & Yukon T.					
Arctic Village	68°08'N,145°19'W	78	. 128 ^b	.213	±	.056
Old Crow	67°35'N,139°50'W	92	.071 ^b	.201	±	.060
Ft. Yukon	66°34'N,145°17'W	110	.178 ^b	.228	±	.060
Ojibwa	Ontario and Minnes	ota				
Pikangikum	51°30'N,94°00'W	96	.030 ^c	.349	±	.056
Wikwemikong	45°29'N,81°26'W	105	.292 ^c	. 335	±	.065
Minnesota	47°13'N,94°21'W	491	. 272 ^c	.366	±	.049
Ojibwa - data com	rrected for admixtur	е				
Pikangikum		96	0	.347	±	.056
Wikwemikong		105	0	.302	±	.068
Minnesota		491	0	.323	±	.061

 Table 1 Gene diversity within subarctic and northeastern woodland Indians, based on genes at eleven blood group loci*

* The subarctic culture area includes the Dogrib, Kutchin and Pikangikum Ojibwa, whilst the northeastern culture area includes the Minnesota and Wikwemikong Ojibwa.

a. Mean value extrapolated from maximum admixture based on three blood group systems, one serum protein and two red cell enzyme systems. b. Mean extrapolated from maximum admixture based on three blood group systems.

c. Weighted single locus mean values, or mean extrapolated from maximum admixture (Pikangikum). For calculations see Appendix No. 38.

Perhaps what is more at issue than the extent of gene diversity within regional bands or within villages, is the extent of genetic differentiation between subgroups of the same population. Was there less differentiation between regional bands of precontact times than is seen between large postcontact villages, or between far-flung branches of a group whose structure was disrupted by historic events?

Such a question can be addressed by assessing gene diversity within and between population subdivisions, and then seeing what fraction of the total

population gene diversity can be attributed to between-group differences.

Nei has shown that the total gene diversity in a subdivided population can be apportioned into diversity within (H_S) and diversity between (D_{ST}) subdivisions, such that $H_T = H_S + D_{ST}$. The ratio D_{ST}/H_T measures the extent of genetic differentiation between subdivisions relative to genetic diversity in the total population. Nei represented this ratio by G_{ST} , which he called the coefficient of gene differentiation. For two allele loci, G_{ST} equals Wright's F_{ST} , the statistic that measures the correlation between two gametes drawn at random from each subdivision relative to the total population.⁵²

Table 2 shows that when gene diversity is considered in this fashion, the bulk of the genetic variation exists within groups rather than between groups. Moreover, the magnitude of genetic differentiation, G_{ST} , hardly differs among the Dogrib, Kutchin and Ojibwa. This suggests little change in the pattern of gene diversity from that of the past.

Whether G_{ST} is unusually low in these Indians could be addressed by examining, for the same systems and the same number of population subdivisions, genetic data from other peoples. Szathmary and coworkers found that G_{ST} was essentially the same for the Dogrib and the South American Macushi who are sedentary village horticulturalists (GST calculated over 36 blood group, protein and enzyme loci: Dogrib G_{ST}=0.0083±0.0022, Macushi $G_{ST}=0.0087\pm0.0025$.⁵³ Indeed, the existence of considerable within-group variation compared to between-group variation appears characteristic of our species. Others have documented this in South American tribal societies, in Pacific island villagers as well as human races.⁵⁴ Study of G_{ST} (or F_{ST}) values from many subdivided populations shows that G_{ST} increases with increase in number of subdivisions, and appears to decrease with increase in population size.⁵⁵ This suggests that in the subarctic under aboriginal conditions those groups that were small but had a number of regional bands were more diverse genetically (greater G_{ST}) than larger populations with fewer regional bands. However, in both of these instances, the bulk of the variation existed within bands rather than between them.

(b) Genetic Affinity and Clues to the Peopling of the Americas: Until this point the discussion has focussed on the assessment of genetic variation within populations. However, genetic diversity is the obverse of gene identity. It is, therefore, logical to ask what genetic similarities exist among subarctic Indians and their nearest neighbours, and to what these similarities are attributed. I will consider only two approaches here: (i) identification of 'marker genes' and (ii) similarities estimated by genetic distance measures.

(i) 'Marker Genes' in Northern North American and Asian Populations: Amerindians and Eskimos share genes that are indicative of an Asiatic origin.

Population	Number of Sub- divisions	н _т	н _s	D _{ST}	G _{ST}	Ref'ce
ATHAPASKANS						
Dogrib	3	.199 (±.050)	.197	.002 (±.001)	.012 (±.003) ^b	14
Kutchin	3	.219 (±.055)	.216	.002 (±.001)	.011 (±.003)	11
ALGONKIANS						
Ojibwa	3	.363 (±.054)	.359	.004 (±.001)	.012 (±.004)	This study
Ojibwa (corrected fo gene flow)	3 r	.335 (±.060)	.332	.003 (±.001)	.009 (±.002)	"

Table 2 Genetic differentiation among subdivided populations

(Standard errors calculated according to the method in Appendix No. 37)

These genes occur presumably by virtue of common descent from the Asiatic populations that gave rise to the Americans. Table 3 shows the known frequencies for Di^a (Diego blood groups), T_f^{DChi} (transferrins) and S-GOT² (soluble glutamic oxaloacetic transaminase). The distribution of $S-GOT^2$ is known the least, but it is clear the allele does occur in widely scattered groups of Algonkians, Athapaskans and Eskimos as well as Americans of Oriental ancestry.⁵⁶ Transferrin D Chinese is widely distributed in western Siberia but is rarer towards America.⁵⁷ The variant has not been observed in any Athapaskan or any non-Asian Eskimo population. It does occur in polymorphic frequences in the Northern Ojibwa and Cree, but is absent in other Algonkians. The Di^a allele is perhaps the best known of the Mongoloid marker genes by Americanists, in part because it was first identified in an Amerindian population, and also because it is said to distinguish Eskimo from Indians. The former lack the gene, while the Indians have it.⁵⁸ The data in Table 3 show this is not quite correct. In six of seven northern Athapaskan populations Di^a is either absent or attains a maximum of 0.006. It is polymorphic in the Slave only, as it is in the Navajo and Apache (southern Athapaskan) from the American southwest. The distribution of Di^a in Algonkians differs from the Athapaskans. Firstly, nine of ten groups tested have the gene and in these the frequency ranges between 0.024 and 0.188. Among the Eskimos, the occurrence of Di^a is said to represent gene flow

Population	Gene		Gene		Gene	
*=Subarctic Group	Di ^a	Ref'ce	Tf ^D Chi [.]	Ref'ce	s-g ot ²	Ref'ce
ALGONK I ANS						
Blackfoot	.030024	1,2	.000	2	nt(not t	ested)
Blood	.040	1	nt	-	nt	-
Cree [*]	.042064	3,4	.026	10	.015	4
Montagnais [*]	.101	5	.000	11	nt	-
Naskapi [*]	.049	5	.000	11	nt	-
Ojibwa ^{*(†)}	.000188	6,7	.040	12	.03801	7 12
Penobscot	.052	8	nt	-	nt	-
ATHAPASKANS						
Chilcotin	.000	13	nt	-	nt	-
Dogrib [*]	.000	14	.000	14	nt	-
Kutchin [*]	.000005	15,16	nt	-	nt	-
Slave [*]	.012	17	.000	10	nt	-
Tuchone [*]	.006	17	nt	-	nt	-
Alaskan "Athaba	.scan" [*] nt	-	.000	20	.022	22
Apache	.017	18	nt	-	nt	-
Navajo	.024	19	.000	21	nt	-
ESKIMOS						
Siberian	.020	23	.000	23	nt	-
St. Lawrence Is	013	24,26	.000	24	nt	-
Mainland Alaska	.000009	26,16	.000	26	.015	22
Canadian	.000	26	.000	26	. 02	27
Greenlandic	nt	-	.000	26	nt	-

Table 3 Distribution of Mongoloid marker genes in Athapaskan andAlgonkian Indians

† Northern Ojibwa alone are 'subarctic' occupants.

* Reference No.s are in the Appendix.

from mainland Asia, the gene probably transmitted by the Chukchi with whom Siberian Eskimos have intermarried. Perhaps a similar process explains the relatively high frequencies (for Athapaskans) of Di^a among the Apache and Navajo, the gene diffusing into the group from adjacent Indians (e.g. Pima: $Di^a=0.028$), with whom admixture is thought to have taken place.⁵⁹

Table 4 shows the distribution of another Mongoloid marker gene,

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 $Gm^{za;b03st}$ of the immunoglobulin system. The Gm immunoglobulins are extremely useful for anthropological purposes because so many haplotypes have limited distribution. $Gm^{za;b03st}$, for example, is a marker which originated in north east Asia.⁶⁰ The Athapaskan frequencies of this gene are well within the range of frequencies found in Chukchi and Eskimo populations.

Language Family and						
Population	Location	Gm ^{za;b03st}	Ref'ce			
<u>Chukotan</u>						
Reindeer Chukchi	Inland Chukotka	.153	28			
Coast Chukchi	Chukot Peninsula	.099	28			
Eskimoan						
Eskimo	New Chaplino, Siberia	. 205	28			
	St. Lawrence Island, U.S.	.306	24			
	North Alaska	.254	29			
	Igloolik, Canada	.171	27			
	Thule, W. Greenland	.121	30			
	East Greenland	.191	30			
Athapaskan						
Kutchin	Arctic Village & Ft. Yukon, Alaska	.143	29			
Dogrib	NWT, Canada	.158	31			
Chipewayn	Alberta, Canada	.135	32			
Navajo	Southwestern U.S.	. 174	32			
Algonkian	/					
N. Ojibwa	Pikangikum, Ontario	.070	12			
S.E. Ojibwa	Wikwemikong, Ontario	.005	12			
Cree	Alberta	.031	33			
<u>Uto-Aztecan</u>						
Zuni	New Mexico, U.S.	.049	34			
Papago	New Mexico, U.S.	.020	34			
Pima	Arizona, U.S.	.006	29			
South American						
28 tribes	Central and South America	.000060	35			

Table 4 Distribution of the immunoglobulin gene $Gm^{za;b03st}$ in some Siberian and native American populations

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However, Algonkian frequencies are much lower and fall in the frequency ranges for the southern United States, Central American or South American Indians.

The pattern in the frequencies of $Gm^{za; b 03st}$ and Di^{a} shows that Athapaskans are more similar to Eskimos than to Algonkian-speaking Indians. This is contrary to expectations arising from the premise that all Indians are the descendants of a single group of immigrants who arrived earlier in the New World than did the ancestors of the Eskimos. The pattern is also different from what would be expected if $Gm^{za;b03st}$ and Di^{a} were each under selection pressure in the subarctic. Were selection operating, convergence of subarctic Indian frequencies rather than divergence would be predicted from the following observations: (1) the archaeological evidence indicates similar depth of occupation of the subarctic for the two linguistic groups, Athapaskan and Algonkian (1,000 AD; Alaska; 200 BC: central and eastern North West Territory; 810 AD:Northwestern region; 620 AD:Southwestern region; 710 AD: Southeatern region; 1,000 AD:Northeastern region).⁶¹ Thus. the length of time over which selection could have operated is approximately the same for Algonkians and Athapaskans. (2) These Indians share a common environment. The subarctic is a single biotic province (i.e. the Hudsonian province) characterized by the presence of the boreal forest. There is no evidence suggesting that there are major ecological differentials between Hudsonian physiographic zones occupied by the named (tribal names) subarctic Athapaskans and Algonkians in Tables 3 and 4. The former groups inhabit the Cordilleran and Shield and Mackenzie Borderlands zones, the Algonkians are found in the latter only. Gardner notes that in these regions depth of snow cover is the single most important ecological variable, but this is markedly different only in the eastern part of the Shield and Mackenzie Borderlands zone, the area occupied by the Montagnais and Naskapi.⁶² Nevertheless, there is no evidence at all in any of the genetic traits known for these people that suggests they differ from more western subarctic Algonkians. Montagnais and Naskapi differences are with the Athapaskans.⁶³ In sum, the ecological data suggest that selection, were it operating on $Gm^{za,b\,03st}$ and Di^a , should have operated in the same direction in both the Athapaskan and Algonkian occupied subarctic regions for approximately similar lengths of time. Nevertheless the distribution patterns of these genes differ between these peoples.

To invoke chance as the mechanism whereby the different distribution patterns of $Gm^{za;b\,0\,3st}$ and Di^a arose in the subarctic zone is to provide no explanation. The probability that drift of Di^a produced a pattern shared by ten Indian groups on the one hand from which six Indian groups on the other hand differ, and that this difference should correspond to known lingguistic differences is very remote. The same could be said about the discreteness of the $Gm^{za;b\,0\,3st}$ distribution. What is more plausible is that the basic differences in the distribution of these genes reflect different population origins. If so, then clearly Athapaskan genetic links are towards the Bering Sea area, while Algonkian connections are towards the south.

(ii) The Evidence from Studies of Genetic Distance: Assessments of genetic similarities between populations are commonly done with statistics that measure genetic distance. This is less a contradiction than it seems, for the smaller the 'distance' the greater the genetic similarity. The advantage that distance statistics have over information provided by the distribution of marker genes, is that the distance measures can make use of all genetic data available in common for the populations compared. Thus, genes whose frequencies differ in quantitative fashion, and whose frequencies on scrutiny do not necessarily fall into any easily detectable patterns are nevertheless informative when used in conjunction with many such genes.

The statistic that has been used most often to detect genetic differences among northern North American and Asian populations is Nei's standard distance, D. Szathmary has also used Cavalli-Sforza and Edwards' chord distance measure, and found a significant and very strong positive correlation between the two statistics.⁶⁴ This was an interesting finding, for neither the mathematics nor the theoretical formulations of the evolutionary process in the two approaches are the same. Cavalli-Sforza and Edwards assume that evolutionary divergence between populations over time is modulated chiefly by the processes of genetic drift and selective drift, that is, natural selection operating differently in different places and times. Nei's approach, however, assumes that populations diverge through time through the accumulation of new and different mutations in each of the descendant groups. Accordingly, Nei's standard distance D, for protein and enzyme loci, measures the number of codon differences per locus that are detectable by the laboratory methods (electrophoresis) used to determine genotype. When blood group genes are used in the computation of D the statistic loses its biological meaning. However, it still provides a statistical estimate of the amount of difference present between two populations.

Customarily a matrix of genetic distances between pairs of populations is displayed visually as a dendrogram, that is a 'tree' of genetic differences, and therefore inferred similarities. The shorter the branch lengths between a pair of populations, the greater the similarity between them. A number of procedures are available for the construction of dendrograms. The one most commonly used with Nei's standard distance, because it tends to obtain correct branch lengths, is Sneath and Sokal's unweighted pair group average method.⁶⁵

Whether a tree of genetic differences should be interpreted as a depiction of human phylogenetic relationships is currently a matter of considerable controversy. Livingstone has argued strongly against the plausibility of genes affording accurate phylogenetic reconstruction. Nevertheless he has allowed that the concept of a 'marker gene' is useful, and the framework of population history and population structure are 'major determinants of present gene frequency differences at some loci'. In his view, 1,000 to 2,000 years of history is the maximum amount that could be reflected by gene frequency differences.⁶⁶

This time span happens to be sufficient to encompass all that the archaeological record and modern history can tell us, without controversy, about the origins of Algonkians and Athapaskans. Two thousand years also comfortably accommodates Eskimos and their Thule predecessors, although archaeologists trace Thule connections to the Arctic Small Tool Tradition that first appeared about 4,000 years ago.⁶⁷

Dendrograms depicting the genetic similarities among Eskimos, Indians and various groups of Asian populations have been published. The Indian groups sometimes include non-Athapaskans and non-Algonkians. In some the Indians are not pooled, but are compared as single tribes with the Eskimos. In these studies the number of systems used in the derivation of the distances varies from 8 to 14 and the latest papers use corrected data obtained from more reliable laboratories. The findings that emerge from these studies are four: (1) Eskimos are identifiable as a group because they cluster together; (2) Athapaskans, or discrete members of the Na-Dene language phylum either fall into the Eskimo cluster or are linked at the next highest level; (3) Northern Algonkians are more remote from Eskimos than the Athapaskans; (4) when Siberian Chukchi, linguistic relatives of Eskimos, are compared, the Chukchi and the Northern Athapaskans (pooled data) fall into the Eskimo cluster.⁶⁸

Fig.2 shows the dendrogram that was produced from the matrix of genetic distances obtained among 13 populations. Nei's standard distance D was calculated over 14 loci, the maximum data set held in common for all 13 populations. The loci were the following: ABO, Rh, MNSs, P, Kell, Duffy, Diego, Kidd, Gc, Hp, PGM, ACP, AK, and PGD. In this tree, subarctic Indians are not pooled, and each Indian pair includes one tribe that shared a contiguous border with Eskimos as well as one tribe from the subarctic interior. What emerges resembles what has been described: Eskimos and Chukchi cluster together, and among the Indians, the Athapaskans are closer to the Eskimos than are the Algonkians.

To what can this pattern be attributed? Few would disagree that the Eskimo cluster, even with the Chukchi included, reflects phylogeny. This interpretation is valid, even though the North American history of Eskimos appears to span 4,000 years, and the Chukchi-Eskimo connection must be more ancient. Similarly, the Athapaskan pair and the Algonkian pair of tribes reflect their internal phylogenetic connections. It is the more ancient connections between Eskimos and Indians that elicits doubt, particularly when everyone 'knows' that Eskimos (and Chukchi) are supposed to link with the classic Mongoloids of Asia, and not with the Indians.

The correctness of phylogenetic reconstruction is based partly on the accuracy with which statistical methods can deduce the likely paths that led to modern populations. Until very recently it was thought that a minimum of 20 loci were sufficient to produce reliable dendrograms, that is, trees with high reproducibility. However, more simulations show that for intra-species comparisons (i.e. smallest pairwise genetic distances are between 0.004 and 0.100) more than 30 loci are desirable, and the greatest accuracy is obtained when comparisons are restricted to eight or fewer populations.

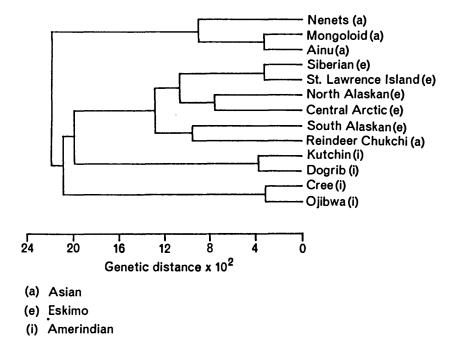


Figure 2 Dendrogram showing genetic similarities among Asian and American arctic and subarctic populations. Genetic distance is measured with Nei's standard distance, D, obtained over 14 loci. For sources of data see Appendix No.s 6, 7, 12, 14, 31, and 36.

Fig.2 was based on genetic distances computed from only 14 loci, the maximum currently available for all members of this population set. This falls far below the number of loci required for greatest accuracy, hence the

Athapaskan-Eskimo genetic connection remains an intriguing possibility that is not yet proven.

Nei and Roychoudhury have pointed out that the 'genetic differentiation of human races is not always correlated with the degree of morphological differentiation'. This observation is worth knowing, because so many judgements about population affinity are based on morphological stereotypes. Eskimos, whatever their external appearance are genetically (25 loci considered) different from Malay, Bhutanese, Chinese, Japanese and Ainu populations.⁷⁰ The array of genes currently known suggests very strongly that Eskimos and Athapaskans are more alike than would have been predicted from conventional views on the peopling of the Americas. This paper shows that their unexpected congruence is in fact interpretable if one allows that (1) populations north of the late Wisconsin ice sheets may have included a group that ultimately led to Athapaskans, (2) the roots of the Eskimos reach back to a population of Asiatic Beringia, (3) populations south of the Wisconsin ice sheets may have been ancestral to Algonkians.

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5

Origins and affinities of Japanese as viewed from cranial measurements

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FOR MORE THAN A HUNDRED YEARS SEVERAL DIFFERENT THEORIES ON THE ORIGINS of the Japanese have been proposed by anthropologists both in Japan and overseas.¹ However, no theory gives satisfactory explanations which cover all the various kinds of evidence available. Most of them tell some of the truth but do not explain all of the facts.

Particularly, recent findings in physical anthropology, archaeology, environmental sciences, etc., show that the origin of the Japanese is so complicated that simple theories such as those so far proposed cannot explain the complete history of the Japanese. For instance, fairly large geographical variations are recognized in Japanese populations, both physically and culturally, and these variations quite likely are connected with the origins and subsequent secular changes of the Japanese people. One of the basic studies needed for analyzing the origins of the Japanese, therefore, is to accumulate data of variability in their physical characteristics from palaeolithic to modern ages.

In this regard, a research group of anthropologists and anatomists obtained metric and non-metric data for more than a thousand modern Japanese skulls whose origins were known with certainty.² The hypothesis I am presenting here is based on statistics provided by this research project as well as metric data of skulls so far reported by a number of anthropologists. THE scattergram shown in Fig. 1 was made by the first and second factor scores computed from nine cranial measurements of Japanese populations from the earliest period to modern times. The measurements involved are: maximum cranial length, maximum cranial breadth, basion-bregma height, bizygomatic breadth, upper facial height, orbital breadth, orbital height, nasal breadth, and nasal height. These were selected from the data provided by Howells³ through a principal component analysis.

The secular changes in cranial measurements gradually proceed from upper right to lower left sides, and the populations form almost a straight line in chronological order. This result strongly supports the hypothesis proposed by Suzuki⁴ who emphasized morphological continuity from the neolithic Jomon people to modern Japanese.

The gradual changes in cranial morphology are quite evident in eastern Japan, but the picture is rather complicated in some parts of western Japan after the end of the Jomon age (ca. 10,000 - 2,300 years BP), or during the aeneolithic Yayoi age (ca. 2,300 - 1,600 years BP) which followed the Jomon age.⁵

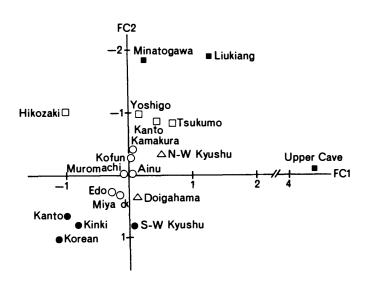


Figure 1

Secular changes in Japanese crania drawn from the first and second factor scores. (After Suzuki *Racial History of the Japanese* 1981).

Fig. 2 represents a two-dimensional scattergram of Japanese and neighbouring populations. The data used are Q-mode correlation coefficients computed from the nine cranial measurements described above, and the scattergram was drawn by the method of quantification theory model IV devised by Hayashi.⁶

First of all, it is important to note that Jomon people probably changed to Ainu in one direction, and to modern Japanese in another. Onkoromanai⁷ and Bozuyama⁸ are early sites in Hokkaido, and their age, the so-called epi-Jomon age in Hokkaido, is almost parallel to the Yayoi age on the main island of Japan. Therefore, the fact that Onkoromanai and Bozuyama remains show intermediate morphology between Jomon people and modern Ainu clearly shows phyletic relationship between both populations.

On the other hand, Yayoi people from sites in western Japan, particularly those from Mitsu⁹ and Doigahama, ¹⁰ are very close to the populations in north-eastern Asia, ¹¹ and they probably mixed with Jomon people, who were aboriginals in this area. This finding strongly supports the hypothesis proposed by Kanaseki. ¹² Possibly, the difference between modern Japanese and the Ainu is due to whether admixture took place

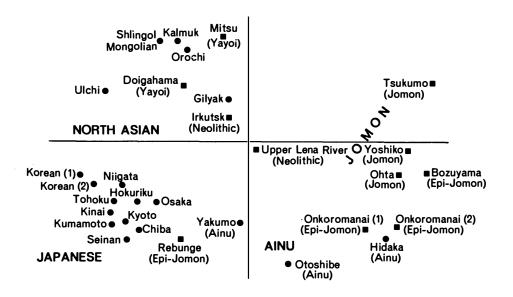


Figure 2

Scattergram of early and modern Japanese and neighbouring populations based on Q-mode correlation matrix and quantification theory model IV.

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between the Jomon people and the Yayoi people who migrated from the Korean Peninsula to the main island of Japan. In fact, the Yayoi people show several characteristics which are similar to those of the populations in north-eastern Asia. For example, Yayoi people in western Japan have a larger facial height, narrower nose, higher orbits, flatter face and rounder head in comparison with Jomon people.

However, Yayoi people in other parts of western Japan, as well as those in eastern Japan, are quite similar to Jomon people in cranial morphology.¹³ According to the traditional history of Japan, the migration from the Korean Peninsula continued until around the 8th century A.D. Japanese who lived on the main island, particularly those in western Japan, were likely to be affected by such migrants both physically and culturally, although the Ainu in Hokkaido seemed to remain unmixed.

Fig. 3 is a dendrogram drawn from the same data used in Fig. 2. One can recognize affinities between populations or between groups of populations more clearly. The populations shown here are roughly divided into four clusters: modern Japanese, Yayoi people in western Japan and north-eastern Asians, Ainu, and Jomon people.

If the general trends in secular changes of Japanese as shown in Fig. 1 are taken into consideration, we are able to understand the cause of the morphological difference between modern Japanese and Ainu, and to recognize the physical impact which the migrants had on the Jomon people.

The influence of the admixture which took place after the Yayoi age is still evident in western Japan. However, the eastern Japanese maintain some charcteristics which are similar to Ainu to a greater or lesser extent. For example, eastern Japanese are shorter in stature, slightly longer headed, with a lower face and broader nose compared with western Japanese.

Fig. 4 was constructed using the same statistical method noted above but with Chinese neolithic populations,¹⁴ and modern Pacific populations¹⁵ added. Here again, the populations are divided into four main clusters. In the first cluster are the Jomon people, the epi-Jomon people in Hokkaido, the Yayoi people in eastern Japan and the Ainu. The secular changes within this cluster seem to have taken place in the direction shown by the arrow on the right side. In the second cluster are the Chinese neolithic populations, modern Chinese, modern Japanese and Koreans. The secular changes in China probably occurred in the direction of the left arrow, but changes in Japan seem to have been affected by the populations in the third cluster, which consists of western Yayoi people and north-eastern Asians. As a result it is suggested that the Japanese have changed in a different direction, along the diagonal in this scattergram.

The modern Pacific populations, including Melanesians, Polynesians and Micronesians represent the fourth cluster. Although several pieces of evidence point to some phyletic relationship between Pacific peoples and

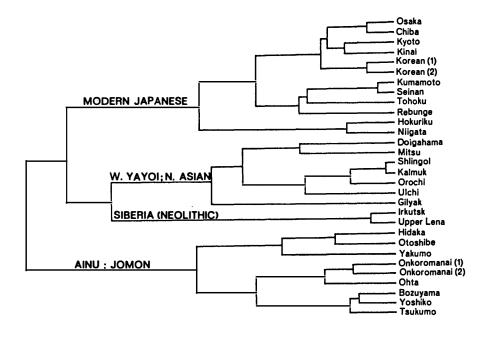


Figure 3

Dendrogram drawn from the same Q-mode correlation matrix used in Fig. 2.

east Asians, this evidence will not be discussed here.

Fig. 5 is a dendrogram of the same populations shown in Fig. 4. The morphological affinities among the populations are basically the same as in the dendrogram in Fig. 3. It is of interest to note, however, that the Chinese neolithic populations are included in the same cluster as the modern-type Mongoloids, whilst the Pacific populations are included in the cluster of early-type Mongoloids. The same cluster includes the Jomon people, Yayoi people in eastern Japan, epi-Jomon people in Hokkaido, and the Ainu.

This result seems to be very suggestive for the analysis of Japanese origins. In this regard, we are preparing to make overseas researches in China and the Pacific area, and if possible, in Siberia as part of our international cooperative studies. At the same time we are also planning more detailed interdisciplinary studies with investigators in different fields.

BASED on the statistical analyses described above, in conclusion I would like to propose tentatively the following points as working hypotheses.

- 1) Jomon people form the basis of the later Japanese population.
- 2) The populations which migrated to the Japanese islands from the

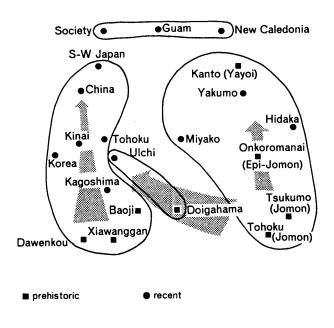


Figure 4

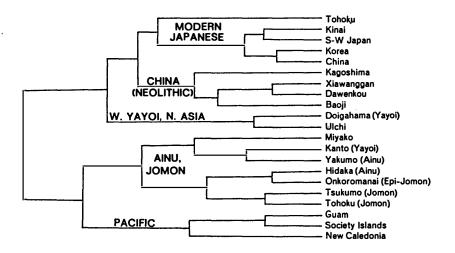
Scattergram of early and modern Japanese and neighbouring populations based on Q-mode correlation matrix and quantification theory model IV.

Asian continent via the Korean Peninsula during the Yayoi and protohistoric ages made a very large impact on the Jomon people, especially on those who lived in western Japan. The geographical variations in modern Japanese ¹⁶ probably are caused by different amounts of admixture between the Jomon people and these migrants.

3) The Ainu quite likely are the direct descendants of the Jomon people. This possibility also is supported by evidence from different fields of research, such as dental morphology, blood groups, red cell enzymes and serum protein types, finger and palm print patterns, and so forth.¹⁷

4) The ancestors of the Jomon people, or Japanese palaeolithic man, seem to have inhabited the Japanese islands probably only from the Upper Palaeolithic age at the latest.¹⁸ Otherwise it would be difficult to explain the large difference between the Jomon people and Chinese neolithic populations.

5) Needless to say, microevolutionary changes should be taken into consideration in addition to the effect of admixture which took place during the course of Japanese history.





Dendrogram drawn from the same Q-mode correlation matrix used in Fig. 4.

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6

Mitochondrial DNA variation and the spread of modern populations

Rebecca Cann

MOLECULAR APPROACHES TO EVOLUTIONARY PROBLEMS CARRY THE IMPLICIT recognition that modern populations reveal the past in genes they have inherited from their ancestors.¹ At present, most of our information about genetic divergence of human gene pools comes from the detection of substitutions in the amino acid sequence of proteins in gel electrophoresis. In contrast, by examining mutations in the DNA contained in mitochondria, my colleagues and I at Berkeley have suggested that the roots of human genetic diversity may be two to four times as old as the estimates made by protein electrophoresis.² This chapter summarizes work in progress towards understanding human mitochondrial DNA (mtDNA) evolution, and allows a fuller discussion of what implications these results might have for the spread of human populations and the peopling of the Pacific.

MITOCHONDRIA are organelles in the cytoplasm of eukaryotic cells that contain the molecular machinery for energy production. Closed circles (about 16.5 kilobases) of DNA in the mitochondria encode a small number of proteins and components of the translation apparatus that will function within the mitochondria itself. Unlike most genes, which are contributed to the embryo by both parents, mitochondrial genes are apparently transmitted only by the female, with no recombination.³ We now have complete mitochondrial genomic sequences for one human, cow, mouse, frog, and fruit fly, and recent advances in the field of animal mtDNA evolution are reviewed by Brown.⁴ Using a variety of techniques over 300 humans have been studied, and each individual appears homogeneous for one mitochondrial genotype. By following these genotypes, or lineages, it may be possible to trace the movement of individual females and their maternal relatives in populations.

IN order to measure mitochondrial variability we use an approach which takes advantage of restriction endonucleases, or enzymes which cut DNA at specific sequences, usually four to six nucleotides in length. The resulting fragments are examined by gel electrophoresis and autoradiography to see changes which alter those target sequences, called restriction sites. Mutations can make sites appear, and more commonly, disappear. This technique detects mutations on a very fine scale if high resolution polyacrylamide gel electrophoresis is coupled with labelling of the restriction fragments by radioactive nucleotides.

Fragments produced and labelled in this manner are shown in Fig. 1. Visible on this autoradiograph are most of the 28 restriction fragments that commonly result when human mtDNA is cut with the enzyme Taq 1, corresponding to the target sequence TCGA. This one enzyme gives us information on 112 nucleotides per individual. We map the location of these restriction sites by comparison to those produced in the one known human sequence, and by cutting the DNA with a battery of different restriction endonucleases which recognize a variety of base sequences we can see into every region of the mitochondrial genome.⁵

Fig. 2 shows a linear drawing of human mtDNA, divided into functional regions. 163 polymorphisms due to point mutations were found in a collection of 112 individuals when tested with 12 different restriction endonucleases.⁶ This technique was applied to many mammals at first, and led to the discovery about 5 years ago that mtDNA has an astonishing rate of change.⁷ Rapid evolution of genes in animal mitochondria relative to those in the nucleus was therefore noted before DNA sequencing became practical in many laboratories.

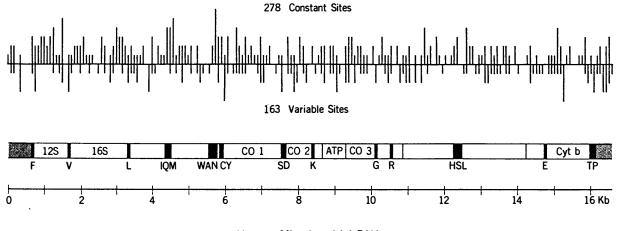
Most mutations which are fixed in human mtDNA are single base changes, and for the group we can infer directly, most of these do not cause amino acid substitutions.⁸ Mutations which alter mitochondrial protein sequences have been detected, however, as have polymorphisms caused by small additions and deletions.⁹ We have no information as yet on the association of mtDNA polymorphisms with human diseases, but mitochondrial genes may be implicated in one condition recently noted, mitochondrial cytopathy.¹⁰ So little is known about the majority of proteins encoded by mtDNA that it may be premature to speculate on advantageous versus neutral mutations. Many mutations may in fact be slightly deleterious, a reflection of the operation of Muller's ratchet in asexually evolving sequences.¹¹ The question of dispensability of these sequences due to high •

10 11

Figure 1 Fragments Produced by Digesting Human MtDNA with the Restriction Enzyme Taq 1

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Digestion of mtDNA from two Australians (individuals 10 and 11) with Taq 1 results in the patterns shown on this 3.5% polyacrylamide gel run under the conditions stated in Cann and Wilson (1983). The arrows show the fragments affected by the length mutation mapped to nucleotides 5877-5978.



Human Mitochondrial DNA

Figure 2 Location of Cleavage Sites and Functional Regions in Human MtDNA

The 16,569 bp circular genome is drawn in linear form. The major bar shows the regions of known function: 22 tRNA genes, each represented by a single letter and black shading, two rRNA genes (12s and 16s), and 13 genes coding for proteins, 8 of which are unassigned and 5 of which are known (three cytochrome oxidase subunits, one ATPase subunit and cytochrome B). Diagonal lines represent the large non-coding region, extending from 16,024 to 576 bp. The upper panel shows the locations of cleavage sites found in mtDNAs from 112 humans plus the Cambridge reference sequence with the aid of 12 restriction enzymes. Vertical lines below the horizontal line show the variable sites, or those present in some but not necessarily all of these mtDNAs. The vertical lines above the horizontal show those sites present in all the human mtDNAs examined. Height of the vertical lines is proportional to the number of sites found within an 80 bp segment. This Figure appeared previously in Cann et al. (1984).

copy number, small size, rapid turnover, coevolving modifiers from the nuclear genome, and lack of repair enzymes will no doubt make these issues difficult to resolve.

THE degree of mitochondrial polymorphism found among only a small. group of Aborigines from Western Australia compared to the rest of the individuals sampled on a worldwide basis can be seen in Table 1. About 75% of these mutations are shared by more than one major group of people, when the divisions are made on the basis of broad geographic origin. Fig. 3 shows where these polymorphisms are situated in the mitochondrial genome, along with their frequency in the Australians sampled. Polymorphisms unique to Australia so far include both length and point mutations, and do not seem to be unduly concentrated in any one functional region, with the exception of the region surrounding Urf 6, an open reading frame which has no assigned function at this time. Two phylogenetically informative mutations (those shared by two or more individuals) apparently unique to Australia are noted in Table 1, although the number of these private mutations is not significantly different from levels found in the other three major geographic regions. From the number of informative mutations inferred by a phylogenetic parsimony analysis (Wagner) of the entire data set, many of these polymorphisms appear to have arisen multiple times independently in the human population.

One of the most notable features of the phylogenetic treatment of 89 informative restriction polymorphisms is that patterns of association among maternal lines do not follow racial subdivision.¹² As we did not have extensive ethnographic information for the majority of our donors, we grouped them into one of four areas of geographic origin, corresponding to Australia, Asia (including China, Japan, Korea, Philippines, Polynesia, Vietnam and Indonesia), Africa (including Black Americans and individuals from sub-Saharan Africa), and Europe (including Europe, North Africa and the Middle East). Our conclusion that mitochondrial diversity shows no strong racial correlation is supported by sequence data from 7 individuals, in contrast to the findings of Johnson *et al.*¹³ Despite their confidence in the ethnographic and racial affinities of their samples it is probable that the low resolution of their methods and the small number of informative mutations rigourously mapped has contributed to this difference in interpretation.

DIRECT sequencing of mtDNA in hominoid primates has established an absolute rate of nucleotide substitution at around 2% per million years (i.e. two changes in 100 base pairs per million years of divergence).¹⁴ Such a value is about 10 times the rate of change for the 'average' single copy nuclear gene. One of the reasons we have worked so hard to define the exact nature of the mutations detected in mtDNA is that by understanding the mechanisms

Table 1 Mitochondrial Polymorphisms

POSITION refers to the nucleotide at which the polymorphism is mapped to the light strand reported in the Cambridge reference human mtDNA sequence as given in Anderson et al. (1981). REGION refers to the gene or functional area in which these polymorphisms are placed, and in the case of length mutations, more than one region may be covered. The NUMBER OF INFERRED MUTATIONS corresponds to the tree topology shown in Fig. 5 of Cann and Wilson (1983). CONTINENTAL DIS-TRIBUTION plots the presence of a particular polymorphism in four major areas where 1 refers to sub-Saharan Africa, 2 to Asia as broadly defined in this chapter, 3 to Australia, and 4 to Europe as also defined here. Numbers of individuals in each of these categories are listed at the bottom of this column. Length mutations are denoted by LM.

Position	Region	Distribution in Australia		Distribution Worldwide		Number of in- ferred mutations	Continental Distribution*			
		number	8	number	x		1	2	3	4
16049-52	D loop	1	8.3	1	0.9	1			+	
16130-33	н .	1	8.3	24	21.4	16	+	+	+	+
16208-11	н	1	8.3	6	5.4	4		+	+	+
16311		3	25.0	36	32.1	14	+	+	+	+
16390-94		1	8.3	11	9.8	5	+	+	+	
16491		1	8.3	1	0.9	1			+	
16519		4	33.3	39	34.8	17	+	+	+	+
9	*1	1	8.3	11	9.8	6	+	+	+	+
37-585, LM		1	8.3	12	10.7	9	+	+	+	+
37-585, LM		4	33.3	16	14.3	12		ŧ	+	+
1404	12sRNA	3	25.0	17	15.2	8		ŧ	÷	+
1463-66		1	8.3	1	0.9	1			+	
1484	11	9	75.0	34	30.4	19	+	+	+	+
1715-19	16sRNA	2	16.7	2	1.8	2			+	
2734-37	"	1	8.3	6	5.4	5		+	÷	+
3250	Leu tRN/		8.3	9	8.0	6	+	+	+	
3899-902	Urf 1	4	33.3	9	8.0	9		+	+	+
3958-4428,		1	8.3	2	1.8	2		+	+	
4411-14	Met tRN/		16.7	4	3.6	4		+	+	+
5552-56	Trp tRN/		8.3	1	0.9	1			+	
5261-5552,	LM	3	25.0	5	4.5	2	+	+	+	
5978-81	CO 1	1	8.3	1	0.9	1			+	
5877-5978,	LM	2	16.7	2	1.8	1			+	
7897-900	CO 2	1	8.3	10	8.9	6	+	+	+	+
7912-15	"	1	8.3	3	2.7	2			+	+
7986-90	н	1	8.3	7	6.3	5	+	+	+	
8167	**	1	8.3	1	0.9	1			+	
8592-95	ATPase (51	8.3	2	1.8	2		+	+	
9053-56		1	8.3	12	10.7	8	+	+	+	+
10398	Urf 3	5	41.7	47	42.0	18	+	+	+	+
10725-28	Urf 4L	1	8.3	3	2.7	3	+	+	+	
12560-63	Urf 5	1	8.3	3	2.7	3		+	+	
13031-35	"	11	91.7	49	43.8	19	+	+	+	+
13051-54	н	1	8.3	5	4.5	3	+		+	
14015-19	н	1	8.3	1	0.9	1			+	
14281	Urf 6	1	8.3	1	0.9	1			+	
14398		1	8.3	1	0.9	1			+	
15172-75	CytB	1	8.3	1	0.9	1			+	
15250-54		1	8.3	13	11.6	7	+	÷	+	
15883-86	н	1	8.3	4	3.6	3	+		+	+
15883-1599	4, LM	1	8.3	8	7.1	6	+	+	+	+
15925 1630	3, LM	3	25.0	4	3.6	1	+		+	
					<u></u>					
			6	ciao 112		t due la	10	25	12	16

Sample size 112 individuals

19 35 12 46

generating them we have more insight into their rate of appearance in different lineages. Many restriction sites must be mapped because of the wide range of functional constraints on various mitochondrial genes. Some types of mutation occur more frequently than would be predicted on the basis of information from nuclear genes. Limited sequence data also suggest a high level of parallel and convergent mutations in this genome. Given these uncertainties, if we assume an individual carries one type of mtDNA and that it is passed only through the germline of the mother, we may ask what is the

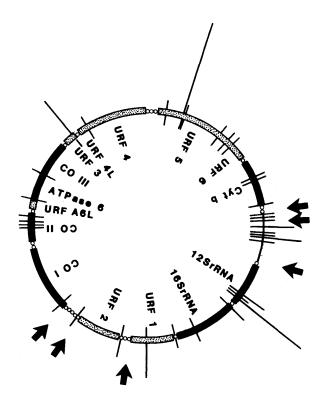


Figure 3 Polymorphisms and their Distributions in the MtDNA of 12 Australians

Mitochondrial polymorphisms reported in Table 1 are shown here in their map positions corresponding to their location in the genome, as illustrated in the centre circle. Thirty five of the polymorphisms attributed to single base substitutions are indicated, and their frequencies in the population sampled are shown as solid lines radiating from the mapped position. Three polymorphisms (1484, 12s RNA; 10398, Urf 3; and 13031-35, Urf 5) are found at high frequencies. All genes of assigned function are indicated by dark shading, with the exception of the tRNA genes, shown here only as small circles. The six regions of length mutation, listed in Table 1, are shown in Fig. 2 of Cann and Wilson (1983) by arrows on the outside of the circle.

REBECCA CANN

amount of time elapsed since two individuals last shared a common maternal ancestor. By measuring the number of mutations that have accumulated in two different lineages and estimating the rate at which those mutations arise, we trace mitochondrial relatives back in time to a point at which they would have intersected in one female.

The average amount of sequence divergence detected between any two individuals in this sample is about 0.7% by phylogenetic reconstruction using the Wagner method, which allows us to see the parallel and convergent acquisition of restriction polymorphisms. This is about twice the difference originally reported in a subset of 21 individuals.¹⁵ Such a number translates into the suggestion that the human gene pool contains mitochondrial lineages tracing back at least 350,000 years. Some female lineages will be more ancient, and some more modern. MtDNA sequence data from two Australian Aborigines in four different mitochondrial genes support this estimate, and lead to greater confidence in the data derived by indirect measurement.¹⁶

IN order to account for the distribution of mtDNA polymorphisms in modern humans, a model of extensive movement throughout the Old World must be considered. Such a model is supported by observations of the level of polymorphism found within as opposed to between geographic areas, when sampled by nuclear genes.¹⁷ The hunter-gatherer mode of life, with frequent long range treks as resources were depleted, left its mark on descendant populations. Particular groups which eventually reached Australia carried a significant portion of the total mitochondrial pool, and not just genes restricted to Southeast Asia. While the age of some mitochondrial lineages in all geographic groups may be quite ancient, the reticulate pattern of human population expansion has blurred the distinction of race as an indication of geography. Passage of women between groups reflects the enlarged social networks which spread property, maintain alliances, and transfer technology. This movement was apparently a characteristic of populations from which our own species emerged, leaving us the task to identify its effects on the genetic and cultural development of modern populations.

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7 The Negritos: genetic origins and microevolution

Keiichi Omoto

THE NEGRITOS OF SOUTH-EAST ASIA AND THE WESTERN PACIFIC POSE INTERESTING anthropological problems. One of the classic questions is whether they are racially related to the African Pygmies, the Negrillos. If they are, it is likely that they represent an evolutionary early stratum of modern man who once inhabited a broad zone in the tropics extending from Africa to south-east Asia. On the other hand, if they are not closely related to each other genetically, the similarities they share at the phenotypic level, such as small body size and frizzly hair, are explained by the result of adaptation to the similar environmental conditions or convergent evolution.

In order to shed light on this problem, a population genetic study of the Negrito groups of the Philippines has been undertaken. This study, starting in 1975, aimed at obtaining blood samples from the Negritos inhabiting mostly the remote areas of the Philippines, and through examination of genetic markers finding clues relevant to the problem of the genetic origins of the Negritos. Some results have been published earlier,¹ and the preliminary dendrogram based on genetic distances for 20 polymorphic loci indicated that the Negritos of west-central Luzon, the Aeta, are more closely related to Asian-Pacific groups than to Africans.² In this report the results of genetic distance analyses based on further examination of various Negrito groups in the Philippines are presented, and have been used for a hypothetical reconstruction of the early peopling of the western Pacific.

IN the Philippines there are at least six geographically separated groups which are usually classified as Negrito. From 1975 to 1982 a total of 1,027 blood samples were collected from these groups, most from the Aeta of westcentral Luzon and the Mamanwa of north-eastern Mindanao (Fig. 1). Only small series of samples could be obtained from the other groups, the Agta (Atta) and the Dumagat of northern Luzon, the Ati of Negros and the Batak of Palawan. Also, control samples were obtained from two Mongoloid slashand-burn agriculturalist groups, the Ifugao of northern Luzon and the Manobo of northern Mindanao, the two groups of Filipino lowlanders, the Tagalog (Manila) and the Visayan (Bacolod).

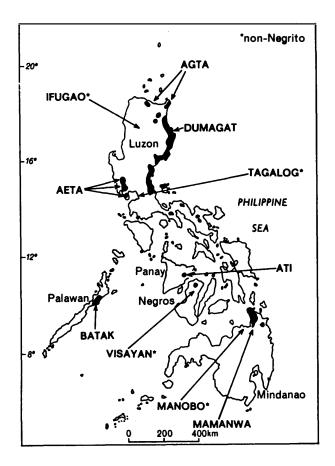


Figure 1

Map of the Philippines indicating the populations and the localities of sample collection. The populations marked with an asterisk are non-Negrito groups.

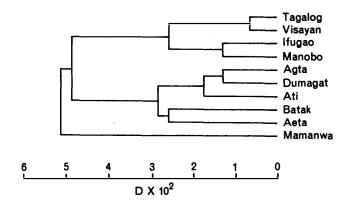
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Twenty five red cell enzymes (ACP, ADA, AK, CA1, CA2, DIA, ESD, GLO, GOT, GPI, GPT, ICD, LDHA, LDHB, MDH, PEPA, PEPB, PEPC, PEPD, PGD, PGK, PGM1, PGM2, SOD, UMPK), 11 proteins (HB α , HB β , HP, TF, GC, PI, BF, C3, C6, GM, KM), nine red cell antigens (ABO, MNS, Rh, Fy, Di, Jk, K, Lu) and three HLA systems (HLAA, HLAB, HLAC) were examined for genetic variation.

Eight red cell enzymes (CA2, ICD, LDHA, LDHB, MDH, PGK, PGM2, and SOD), two red cell antigens (K and Lu) as well as HB α and HB β , were found to be monomorphic. In this report the data for the polymorphic red cell enzyme and serum protein systems examined by electrophoresis, as well as the red cell antigen systems are used. For computation of genetic distances and construction of dendrograms the method of Nei was used throughout.³

THE distribution of alleles of common polymorphic loci indicates that the six Negrito groups share certain similarities, for example, a low frequency of ACP*A, GPT*1 and GC*2 alleles, and a high frequency of PGM1*2. The frequency of HP*1 tends to be low, except in the Mamanwa group (Table 1). As shown in Fig. 2, the dendrogram based on the data of 11 polymorphic loci (ACP, AK, CA1, ESD, GPT, PGM1, HP, GC, ABO, MNS, Rh) reveals that five Negrito groups form one cluster, contrasting with a cluster of four non-Negrito (Mongoloid) groups, while the Mamanwa are separate from both groups.

		Alleles								
Populations	N	ACP*A	ESD*1	PGM1*1	GPT*1	HP*1	GC*1F	GC*2		
Aeta, W.C.Luzon	443	.108	.778	.506	.173	.179	.530	.128		
Batak, Palawan Is.	59	.144	.712	.644	.195	.250	.348	.093		
Ati, Negros Is.	35	.186	.700	.629	.412	.118	. 357	.129		
Agta, N.Luzon	123	.138	.764	.687	.285	.146	.720	.024		
Dumagat, N.E.Luzon	40	.113	.763	.600	.288	.171	.563	.013		
Mamanwa, N.E.Mindanao	327	.143	.701	.519	.150	.667	.471	.248		





Dendrogram showing genetic affinities between 10 Philippine populations based on gene frequency data of 11 protein and blood group polymorphic loci.

Four kinds of unusual protein variants attaining polymorphic frequencies have been found (Table 2).⁴ The carbonic anhydrase-1 variant called CA1-3N, which has been identified by peptide mapping and amino-acid analysis as CA1-3Guam, has a remarkably high frequency among the Mamanwa of north-eastern Mindanao.⁵ It was absent from the Aeta of west-central Luzon but was recently found to occur among the Dumagat and the Agta of north-eastern and northern Luzon, indicating a south to north gene flow from Mindanao along the eastern coast of the Philippines. The esterase D variant called ESD-3N has so far been found exclusively in the Aeta. 'The GC variant GC-1N is common among the Aeta, and was recently found also in the Batak of Palawan. The distribution of these variants is useful for tracing migrations of the Negrito groups, and will be discussed later. The occurrence of the AK*2 among the Negrito is puzzling, since it is known to be a Caucasoid marker gene. Its frequency in some Negrito groups showing no obvious sign of Caucasoid admixture is too high to be ascribed to gene flow from Spanish colonists. Therefore it is probable that the variant is derived from a mutation independent from that leading to the Caucasoid AK*2 variant.⁶

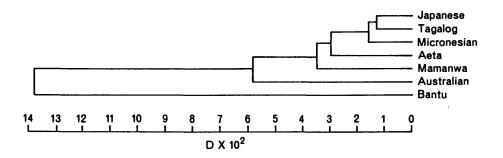
To examine possible Negrito affinities with Negroids in Africa a dendrogram was constructed using gene frequency data for the following 21 polymorphic loci: ACP, ADA, AK, CA1, CA2, ESD, GPT, PGD, PGK, PGM1, PGM2, GC, TF, ABO, MNS, Rh, Fy, Di, Jk, and P (Fig. 3). The topology of this dendrogram clearly suggests that the Philippine Negrito groups, in this case the Aeta and the Mamanwa, genetically belong to the Asian-Pacific

	Alleles						
Populations	N	AK*2	CA1*3N	ESD*3N	GC*1N		
Aeta, W.C.Luzon	443	.048	-	.098	.123		
Batak, Palawan Is.	59	-	-	-	.025		
Ati, Negros Is.	35	-	-	-	-		
Agta, N.Luzon	123	.037	.057	-	-		
Dumagat, N.E.Luzon	40	-	.075	-	• _		
Mamanwa, N.E.Mindanao	327	-	.217	-	-		

Table 2 Allele frequencies of the four private variants found in the Negrito groups

group and not to the African group, confirming the preliminary result published previously.⁷ The African Pygmy (Negrillo) could not be compared directly, but it has been shown to have genetic affinity with the Bantu population.⁸ Also, a recent study by Nei and Roychoudhury showed a distant relationship between the Negrillo and the Negrito populations.⁹

One of the advantages of using Nei's method for the computation of genetic distances is the feasibility of estimating the effective (minimal) divergence time between two populations, provided that conditions such as

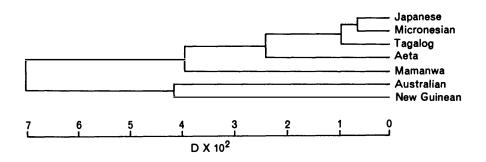




Dendrogram testing the African affinity of the Negrito groups based on gene frequency data of 21 loci which are polymorphic at least in one of the populations examined.

the random sampling of genetic loci, neutrality of alleles and independent evolution of the different populations are accepted. Since only polymorphic loci are used in the present study, the standard genetic distance of Nei's D is exceedingly large. The average heterozygosity per locus is about 25% for the Japanese data used, which is probably 3 to 5 times larger than the actual value. Nei and Roychoudhury, in the paper noted above, estimated the effective divergence time of Negroid from Mongoloid populations to be approximately 116,000 years, using the data of 62 protein loci and the formula t = $3.75 \times 10^6 \times D$. If it is postulated that the 21 loci used in the present study were only one-fourth of the randomly examined 84 loci, the other 63 loci being monomorphic throughout the world populations, the effective divergence time between Bantu and the Asian-Pacific populations would be 129,000 years, which is not too different from the estimate of Nei and Roychoudhury. It should be noted, however, that the inclusion of blood group loci may not be appropriate in such an estimation.

Fig. 4 shows a dendrogram for seven Pacific populations using data for 14 polymorphic loci, excluding those of blood groups: ACP, ADA, AK, CA1, CA2, ESD, GPT, PGD, PGK, PGM1, PGM2, HP, TF, GC. The average heterozygosity for the Japanese sample in this case is about 19%, which is probably 2-3 times larger than the actual value. Therefore, hypothetical values for effective divergence time between populations may be obtained using the genetic distances divided by a factor of 3. This gives divergence times for the New Guinean-Australian cluster from the Asian of 87,000 years, the New Guinean from the Australian 50,000 years, the Mamanwa from the Aeta 49,000 years, the Aeta from the Tagalog-Micronesian-Japanese cluster 30,000 years, the Tagalog from the Micronesian-Japanese cluster 10,000 years, and the Micronesian from the Japanese 7,500 years. Although such





Dendrogram comparing seven Pacific populations on the basis of 14 polymorphic protein loci.

estimates should be regarded as very tentative, the overall proportion for the different time-depths may help in developing a working hypothesis about the genetic origins of the Pacific peoples.

That two groups of the Philippine Negritos, the Aeta and the Mamanwa, are distinguishable by the gene frequency distribution is an interesting finding. These two groups are also remarkably different in the occurrence of private variants as mentioned above and also in the linkage disequilibrium pattern between HLAA and HLAB loci.¹⁰ Furthermore, the evidence of the occurrence of the CA1*3N gene in the Dumagat and the Agta on the one hand, and of the GC*1N gene in the Batak on the other, suggests that there were at least two streams of migration of the aboriginal groups in the Philippines, one being on the western part, perhaps from Borneo via Palawan to Luzon, and the other on the eastern part to Mindanao. The latter migration, which may be the older one, probably went further north along the shoreline, affecting to some extent the Negritos of northern Luzon.

The western group represented by the Aeta is phenotypically the true Negrito. They may have shared an ancestral stock with the Semang of Malaysia and evolved in the upper Pleistocene times, probably during 20,000 to 30,000 years ago, in the tropical rain-forest of Sundaland and developed phenotypic peculiarities through genetic adaptation. Although no experimental evidence is available, selective advantage of small body size in the tropical rain-forest appears to be obvious because of smaller calorie needs, a more efficient body cooling, and the relative ease of moving in a dense vegetation.

On the other hand, the Mamanwa do not seem to have developed this phenotypic specialization. With the average stature for male adults being approximately 157cm, they are definitely taller than the Aeta, who have a mean stature of approximately 150cm. It is tempting to speculate that the Mamanwa are descended from a generalized early population of the late Pleistocene Sundaland, which may properly be called the Proto-Malays. The aboriginal groups of the Moluccas, Timor and other marginal islands of Indonesia who are called Proto-Malays by anthropologists,¹¹ may also be the marginal remnants of this common stock, similar to the Mamanwa. Widespread occurrence of CA1*3 in the western Pacific suggests that the mutation leading to this variant was an old event which took place in this ancestral population. Further search for this variant is needed, particularly among the aboriginal Proto-Malay groups in Indonesia, to support this hypothesis.

Fig. 5 shows a hypothetical reconstruction of the microevolution of the western Pacific populations based on the speculations and the estimates for divergence time mentioned above. Until the time of the late Pleistocene lowest sea level, some 20,000 years ago, the early Australians and Papuans may have diverged already from the ancestral 'Proto-Australoid' population

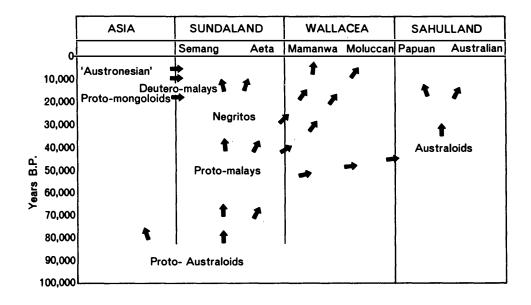


Figure 5

A hypothetical schema showing racial diversification in the western Pacific during late Pleistocene times.

of south-east Asia and moved into Sahulland. The Proto-Malays inhabited the more open inland and the shores of Sundaland and Wallacea, while some groups of them entered the rain-forest and evolved phenotypically into what we call the Negritos today. Their geographical distribution was fragmented by the rising sea level during post-glacial times and probably also by the intrusion from the Asian mainland of the Proto-Mongoloid hunter-gatherers, some 10,000-20,000 years ago, followed by the large-scale migrations of the Austronesian-speaking slash-and-burn agriculturalists, starting about 6,000 years ago.

The present study supports the view that the Negritos are neither an old stratum of *Homo sapiens* nor a racial stock closely related to African Pygmies. Rather, they represent groups of Proto-Malays who acquired a phenotypic specialization, particularly that for small size. Therefore, any theory postulating a Negrito racial element in Australia or New Guinea is not supported by the present view. On the other hand, it is suggested that in any Australoid groups the formation of Negrito-like phenotypes may have occurred, given the environmental condition and a sufficient time-depth, say, 20,000 years or so. It is probable that this will explain the occurrence of the phenotypically Negrito-like groups among Australian Aborigines, both at present and in the past.

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Migration and admixture in the Pacific

insights provided by Human Leucocyte Antigens

Susan W.Serjeantson

THE HUMAN LEUKOCYTE ANTIGEN (HLA) SYSTEM IS A HIGHLY INFORMATIVE genetic complex that provides a new and powerful tool for studying the ancestral relationships between populations. The HLA gene frequency distributions in 17 populations are here examined for the light they throw on current theories regarding the peopling of the Pacific.

It is generally accepted that the earliest arrivals in Sahul land, the single continent of Australia-New Guinea, were Australoids, migrating from the west about 50,000 years ago.¹ Certainly, the first Australians were in residence by 40,000 years B.P.² The archaic languages of the Australoids have evolved into languages now spoken by Australian Aborigines, but in New Guinea they have been overlaid by Papuan elements.³ Linguistic prehistory suggests at least three major waves of Papuan migration from the west. The first of these may have occurred 15,000 years ago, but most Papuan migration occurred 5-10,000 years ago, increasing the linguistic and genetic differentiation of New Guinea and Australia at a time when they were physically separated by the rising seas at the end of the Pleistocene.

Linguistic and archaeological evidence suggests that the first Austronesian speakers migrated into Melanesia between 3,500 and 5,000 years ago,⁴ intermarrying with coastal Papuans in New Guinea, the New Hebrides and New Caledonia. By 3,000 years ago, further groups of Austronesians arrived in Melanesia, some travelling east to Fiji and western Polynesia and carrying Lapita-style pottery as far as Samoa.⁵ Following 1,000 years of consolidation in the Samoa area, a few Austronesian settlers colonized the Marquesas Islands, 3,000 km to the east, before dispersing to the Society Islands, Easter Island, the Hawaiian Islands and New Zealand between 1,200 and 1,600 years ago.⁶

Meanwhile, western Micronesia (Palau and Marianas) had been settled at least 3,000 years ago by groups with cultural and linguistic affinities with northeastern Indonesia and the Philippines.⁷ The origins of nuclear Micronesians (Caroline, Marshall, Nauru and Gilbert Islands) are less clear. Howells argues for affinities with Polynesians on the basis of physical anthropometric characteristics while linguistic data suggest settlement from the New Hebrides.⁸

This simple version of the history of colonization of Oceania is widely accepted but is not without critics. For instance, major technological changes occurred in Australia 4,000 to 5,000 years ago, and although many attribute the new developments to a response to environmental changes, others argue for two Late Pleistocene populations.⁹ In island Melanesia, Wurm¹⁰ claims on linguistic grounds that Papuan speakers did not predate Polynesians, and argues that the first settlers in the New Hebrides and New Caledonia were Polynesians who were replaced later by Melanesians. This may well have been the case in Fiji, where archaeological findings¹¹ suggest an initial Lapita settlement with later Melanesian intrusion. Another unresolved question is whether the Lapita potters were derived from the earliest Austronesian-speakers in eastern Melanesia or represent a second wave of Austronesians from eastern Indonesia.¹²

Analysis of genetic relationships between populations in the Pacific has contributed important insights into the history of early Pacific migrations¹³ when interpreted within the framework of linguistic, archaeological and anthropological knowledge. The strength of genetic analysis is that genetic profiles cannot be altered by dictates of fashion, as can culture, cannot be casually acquired, as can useful foreign words and even language, and are not readily exchanged and spread as are trade goods. The weakness of genetic data is that substrata cannot be identified; only the contemporary genetic profile is observed. Thus genetic analysis can reveal, for example, that present-day Fijians have both Melanesian and Polynesian elements,¹⁴ but can make no statement regarding the first arrivals in the Fijian Islands.

Description of intergroup genetic relationships has been much enhanced by the recent definition of the HLA system. Human leukocyte antigens are markers on the surface of cells of most tissues but can be conveniently detected on white cells in peripheral blood. The antigens are intimately involved in immune response functions, including rejection of organ transplants, and specific antigens confer inherited susceptibility to a range of autoimmune and other diseases.¹⁵ For these reasons, the HLA system is of considerable interest to biological researchers and clinicians, but it has several features which make it a powerful tool in the hands of anthropologists also. These features include the large number of alleles at each of the HLA loci, the occurrence of populationspecific genetic variants and linkage disequilibrium or the tendency of HLA alleles to be inherited as clusters.

The HLA system comprises at least five loci, HLA-A, B, C, DR and DC. Serological definition of HLA-DC is in its infancy, but the other loci include between 10 and 30 alleles. This provides a minimum estimate of the potential number of genetically different individuals as 2,500 million, since the antigens are inherited codominantly, so that most individuals have two antigens detectable at each HLA locus.¹⁶ This extreme polymorphism can be compared with variation at the ABO blood group locus, where the four common alleles, A1, A2, B and O give rise to only six phenotypes.

Not all of the known HLA antigens occur in all populations, and Pacific groups have a comparatively restricted range of HLA alleles. Many alleles which are common in Caucasians, such as A1, A3, B5, B7, B8 and Bw44, do not occur in traditional Pacific populations and this feature of the HLA system can be exploited to estimate the proportion of foreign genes in any group. Since the combined frequency of Caucasian alleles that do not occur in the Pacific is 53% at HLA-A, 60% at HLA-B and 30% at HLA-DR, there is only a 13% chance that a Polynesian or Melanesian with a European parent will not be identified as such.¹⁷ Of course, in the next generation only 50% of the offspring will inherit the Caucasoid haplotype, but when the population as a whole is examined, the proportionate genetic contributions of different ethnic groups can be determined.

Some HLA alleles are unique to specific populations, where they may attain comparatively high frequencies. HLA-Bw46, for instance, is common in Chinese where it occurs in nearly 50% of Cantonese, is found in Thais¹⁸ but is absent from all other groups including Malays and Filipinos. HLA-Bw42 occurs in nearly 25% of Africans¹⁹ but not in other populations, although there are some instances of this antigen in Nauru in descendants of two American blacks.²⁰ In Polynesians and Melanesians there are variants of HLA-A10 and HLA-Bw22 which occur in Filipino and Malay groups also,²¹ but extensive comparative work on the distribution of these alleles has yet to be undertaken.

Another feature of the HLA system is linkage disequilibrium. The HLA loci are physically close to each other on human chromosome 6, so that they tend to be inherited as a cluster. Occasionally, however, during the cell division which produces sperm or ovum, the parental chromosomes may recombine to provide a reassortment of the HLA genes. If the parent carries A2.B40 on one chromosome and A9.Bw22 on another, then offspring will inherit A2.B40 or A9.Bw22 unless a reassortment, or recombination event, occurs. In the case of recombination, which occurs within the HLA region at a rate of about 1%, the offspring would inherit A2.Bw22 or A9.B40. This close association between HLA loci means that some alleles will appear conjointly in individuals more often than expected by chance, so that similarity in HLA an-

tigen clusters can be sought in different populations. There is an inevitable rate of decay in the strength of linkage relationships but, in some instances, they may persist for more than 10,000 years. For example, the rate of recombination between HLA-B and HLA-C loci is estimated as 0.2%,²² so that reassortment of HLA-B and -C antigens rarely occurs. Most Australian Aborigines positive for HLA-B13 are also positive for HLA-Cw4.²³ The B13.Cw4 combination occurs in Papua New Guinea Highlanders,²⁴ in coastal Melanesians including those from New Caledonia,²⁵ but not in any other populations yet examined. The exception to this is Nauru, where only two of 178 persons tested were B13 positive but both were also positive for Cw4.

Linkage disequilibrium values which measure the strength of the B13.Cw4 associations are provided in Table 1 for Papua New Guinea Highlanders from Asaro, for New Caledonians, Wallis Islanders²⁶ and Caucasians. The concept of linkage disequilibrium can be explained by following the numerical examples in Table 1. The gene frequency of B13 in New Caledonia is 0.063 and of Cw4 is 0.095, so that the expected joint occurrence of these two antigens in any individual is 0.063×0.095 or 0.6%. However, 3.6% of the population is positive for both B13 and Cw4 and this is the observed haplotype frequency. Then linkage disequilibrium simply measures the deviation of the observed

Deputation *	Gene Frequency		B13.Cw4	Frequency	Linkage	
Population*	HLA-B13	HLA-Cw4	Observed	Expected	Disequilibrium	
PNG Highlands	0.072	0.118	0.078	0.008	0.070†	
New Caledonia	0.063	0.095	0.036	0.006	0.030†	
Wallis Island	0.023	0.087	0.001	0.002	- 0.001	
Europe	0.028	0.121	0.007	0.003	0.004	

TABLE 1-Estimates of Linkage Disequilibriuim Between HLA-B13 and HLA-Cw4

• HLA-B13 and -Cw4 are in significant linkage disequilibrium in Australian Aborigines, but precise figures are not available.

† P<0.01

haplotype frequency from that expected, which is 0.036 - 0.006 = 0.030, the statistical significance of which can be tested by chi-square.

It is of interest to note in Table 1 that the gene frequencies of HLA-B13 are similar in all four populations, as are the frequencies of HLA-Cw4. Only the linkage disequilibrium values, which are significantly positive in Papua New Guinea and New Caledonia, indicate the ancestral relationship between these non-Austronesian and Austronesian speaking Melanesians.

The following analyses use the polymorphism of the HLA system together with linkage disequilibrium values to examine the genetic relationships between groups in the Pacific. The phylogenetic relationships between 17 populations have been calculated from HLA-A and -B gene frequencies and are given in Figures 1 and 2: These update the analyses given by Serjeantson *et al.*²⁷ by using more recently published series for New Zealand Maoris and Papua New Guinea Highlanders,²⁸ by including Nauruan, Filipino and Chamorro²⁹ (Mariana Islands) populations and by including data for HLA-Bw35. HLA-Bw35 is very rare or absent from Melanesian and Polynesian groups, but occurs in 36% of Nauruans. Data from duplicated series, from Fiji and Western Samoa, have been excluded. The method of calculating genetic distances is provided by Nei.³⁰

Micronesian populations from Nauru and Guam are well separated from the remainder of the groups studied (Fig. 1) with Nauruans showing close

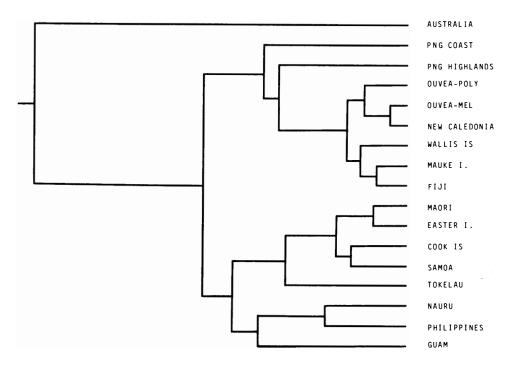


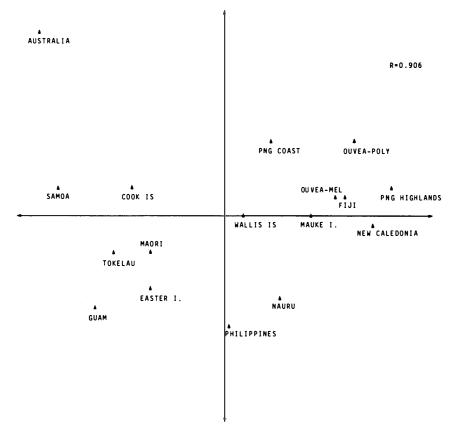
FIGURE 1

Diagrammatic Representation of Genetic Distances between 17 Populations based on HLA Gene Frequencies.

affiliations with Filipinos. Chamorros of the Mariana Islands have an HLA profile distinct from Nauruans, but since the Chamorros have considerable European admixture³¹ it is interesting that their Micronesian affinities can still be clearly depicted in the dendrogram.

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Australian Aborigines do not cluster with any other groups in the sample. Aborigines have a comparatively restricted range of HLA antigens and differ from Papua New Guinea Highlanders in several respects. They lack HLA-B27, which is present in 13% of Highlanders, and have only sporadic occurrences of HLA-B15 (Bw62), which is common throughout Melanesia but occurs in more than 40% of Highlanders. More intriguing is the occurrence of HLA-A2 in nearly 30% of Australians. HLA-A2 is absent from New Guinea Highland populations and this has been confirmed in the Fore, the Dani and in the Asaro.³² In general, the Australoid genome is a subset of the Papuan genome, with Aboriginal groups lacking, for example, the B antigen of the





Two-Dimensional Representation of Genetic Distances between 17 Populations based on HLA Gene Frequencies.

ABO blood group system and the S antigen of the MNS system. The HLA-A2 in Aborigines is unlikely to have arisen by recent mutation or by Caucasoid admixture because it is randomly distributed on haplotypes, indicating a long

presence in the population. It seems likely that the Papuan invaders of New Guinea lacked the A2 antigen and so outnumbered the remaining Australoids that HLA-A2 was lost in genetic drift. Genetic drift is chance variation in gene frequencies from generation to generation and has its greatest impact when groups are small. Through genetic drift the least frequent allele can reduce in frequency in successive generations to the point of irreversible loss. An alternative explanation is that there was a second wave of migration to Australia, by groups carrying HLA-A2, which by-passed New Guinea. This seems improbable, since the migrants would have been in all other aspects of the HLA system genetically compatible with the existing population.

HLA-A2 has a low gene frequency in coastal and inland Melanesia, ranging from 4-8%, but increases appreciably in Polynesia to 18-30%. In all these groups, HLA-A2 is in significant linkage disequilibrium with HLA-B40, indicating a common source of origin of the A2 allele. In Aborigines, HLA-A2 and -B40 tend to be negatively associated, implying a different origin for the Australoid A2 antigen.

The dendrogram (Fig. 1) shows close affinities between New Caledonia and Ouvea (Loyalty Islands) with no significant genetic differences between the Polynesian (Uea) and Melanesian (Iai) speakers of Ouvea. This suggests that the arrival of a few Polynesian immigrants in Ouvea had a far greater impact on language than on genetics, a situation commonly observed in Melanesia.³³

Fiji clusters with Mauke Island (Cook Islands) and Wallis Island in the dendrogram, indicating a strong Polynesian genetic influence in Fiji. One feature that Fiji and Wallis Island share is the HLA-B18 antigen. The early Austronesians carried HLA-B18 into coastal and island Melanesia, but this antigen was lost from groups colonizing Samoa and islands further east.

Western Samoa and the Cook Islands show close affinity with each other and split from the Maori-Easter Island branch in the dendrogram. Two antigens, HLA-B13 and -B27, which are present in all other Melanesian and Polynesian groups, are absent from both Maoris and Easter Islanders. This finding strongly supports the theory that a small group of colonizers left Samoa for eastern Polynesia before further dispersal to New Zealand and Easter Island. The group leaving the Samoa area lacked, by chance, the two HLA antigens, so that these antigens were irretrievably lost to any descendant populations. In all other respects, as is evident from the dendrogram, Maoris and Easter Islanders are similar to Samoans and Cook Islanders in their HLA profile.

Although Australian Aborigines failed to cluster with any other group in the genetic distance analyses, HLA linkage relationships clearly indicate the persistence of Australoid elements in Melanesia as previously discussed with respect to linkage disequilibrium of HLA-B13 and -Cw4. Table 2 provides haplotype frequencies and linkage disequilibrium values for A11.B40 and A9.Bw22. HLA-A11 and -B40 are significantly associated with each other in Australia, in Melanesia and in Nauru. In contrast, these antigens have a different source of origin in Polynesian populations, where they are not significantly linked. HLA-A9 and Bw22 are tightly linked in Polynesia and also in Fiji, clearly indicating that Fiji is a mixture of both Melanesian and Polynesian genetic influences. Data for Japan³⁴ have been included because there is a

	A11	. B4 0	A9. Bw 22	
POPULATION	HF	ã	HF	ã
Australia	89	51*	126	25
New Caledonia	18	65	236	32
Nauru	96	53 *	73	18
Fiji	29	61*	251	74*
Wallis Island	28	- 22	179	59 *
W. Samoa	41	6	105	59 *
Japan	16	- 42	370	114*

TABLE 2-Haplotype Frequencies (HF) and Linkage Disequilibrium Values (Δ) per 1,000 in Selected Populations

* P<0.05

paucity of information regarding HLA distributions for populations in Southeast Asia, but it is of some interest that the Polynesian linkage relationships are found in this group also. Japanese have many antigens, such as Bw51 and Bw52, that do not occur in the Pacific.

Nauru shows close affinities with Micronesia and Filipino groups in the genetic distance analysis but Table 2 is highly suggestive that there is a Melanesian genetic component in Nauru. This proposition can be investigated further by estimating the proportion of Melanesian admixture with respect to HLA-A and HLA-B antigens. Admixture coefficients can be determined by establishing a series of equations for the HLA alleles, such that for HLA-A2,

$$A2_{NAURU} = \alpha_M A2_M + \alpha_P A2_P + \alpha_F A2_F$$

where $A2_{NAURU}$ is the frequency of HLA-A2 in Nauru and $A2_M$, $A2_P$, $A2_F$ are the observed frequencies of HLA-A2 in Melanesian, Polynesian and Filipino populations respectively. α_M , α_P and α_F are the proportionate contributions of Melanesian, Polynesian and Filipino elements to the Nauruan gene pool. Similarly, equations can be established for each HLA-A and -B antigen so that the 16 simultaneous equations can be solved using standard iterative techniques to find the most likely estimates of α_M , α_P and α_F .

The validity of the solutions is dependent upon proper selection of the parental populations as well as assumptions that the parental groups have not themselves been subject to genetic drift and immigration. Since these assumptions are rarely true, admixture coefficients should be considered approximate rather than precise estimates. Table 3 provides estimates of the proportionate genetic contributions of Melanesian (represented by New Caledonia), Polynesian (Western Samoa) and Filipino groups to the gene pool of Nauru. This analysis shows a Melanesian admixture coefficient of 30%, which is compatible

	NAURU		FIJI			
Parental	Contribution	Standard	Parental	Contribution	Standard	
Population	(%)	Error	Population	(%)	Error	
Melanesian	30.3	± 7.8	Melanesian: NAN*	58.1	± 8.8	
Polynesian	4.5	± 6.4	Melanesian: AN	20.9	± 6.7	
Filipino	65.2	+ 8.1	Polynesian	21.0	+ 7.6	

TABLE 3-Estimates of Triracial Admixture in Nauruan and Fijian Populations

*NAN: non-Austronesian speakers; AN: Austronesian speakers.

with the linkage analyses given in Table 2, with virtually no Polynesian influence.

Similar calculations can be undertaken for Fiji, using HLA gene frequencies for non-Austronesian speaking Papua New Guinea Highlanders, for Austronesian speakers from New Caledonia and for Polynesians from Western Samoa. Table 3 shows that here the Polynesian contribution is substantial, at 21%.

The same technique can be used to estimate the genetic impact of recent foreign admixture in the Pacific, to determine the Caucasian, African and Asian contributions. However, there may be variation in the enthusiasm with which various investigators exclude from their sample people with known foreign parentage, so only a broad comparison between groups can be justified.

The population with the highest proportion of recent admixture is that of the Marianas. As early as 1783, 25% of Guamanians were descended from Spanish-Chamorro unions and 20% from Filipinos, as determined by pedigree data.³⁵ Today, the gene pool reflects 36% Caucasian and 17% Filipino genes, when admixture is calculated from observed HLA-A and -B distributions.³⁶ For other Pacific populations, the foreign contribution ranges from 0-10%, with the lowest rates in Papua New Guinea and the highest rates in New Zealand Maoris.

It would be of considerable interest to compare HLA gene frequency distributions in the Pacific with those of the various hill tribes of Southeast Asia, but unfortunately there is, as yet, very little data available for Southeast Asian populations. HLA gene frequencies in the Aeta and Mamanawas hill tribes of the Philippines have been provided by Horai *et al.* and the Aeta cluster very closely with Nauru in genetic distance analysis.³⁷ As yet, HLA profiles of the Malayan Aborigine, Senoi and Negrito have not been determined, but these groups are known to have a high frequency of oval-shaped red cells, a trait which also occurs in the Toradja, the land and sea Dyaks, and in coastal and low lying areas of Papua New Guinea.³⁸ We have not detected oval cells in small numbers of individuals examined in Fiji and New Caledonia.

The genetic analyses provided here reflect the interrelationships between modern populations. Extrapolation from these observations to conclusions regarding past migrations must be undertaken with some care. Many antigens of the HLA system are associated with disease susceptibility, so that selection for favourable alleles may cause some groups to be more similar to each other than would otherwise be expected. For example, there is no evidence as to whether infectious diseases that caused severe mortality in many Pacific groups in the last century caused higher mortality rates in people with certain HLA phenotypes, but such a phenomenon is possible, given the role of HLA antigens in immune response.

Another powerful genetic force is that of random genetic drift. As noted above, gene frequencies can fluctuate due to chance events, especially when the population is small. This may account for the clustering of Mauke with Wallis Island and Fiji in the genetic distance analysis, rather than with the Cook Islands.

Despite these reservations, the HLA system has described interrelationships between Pacific populations which are compatible with theories of colonization based on other disciplines.³⁹ As summarized in Figure 3, the Australoid HLA profile is very restricted and has been overlaid by Papuan elements in the New Guinea Highlands. Australia and New Guinea must have maintained contact with each other until at least 10,000 years ago since the HLA-A11.B40 linkage relationships persist today in both populations. The linkage disequilibrium values are compatible with the time of separation given by Golson,⁴⁰ who holds that the pig reached New Guinea about 8,000 years ago, but did not enter Australia due to its geographic isolation at the end of the Pleistocene.

THE first Austronesian speakers carried HLA-A2 into Melanesia on the haplotype HLA-A2.B40, together with HLA-B18. These Austronesian elements did not penetrate the New Guinea interior, although numerous Austronesian loan words have been incorporated into Papuan languages.⁴¹ Coastal and island Melanesians show evidence of intermarriage with Austronesians, with the HLA-A2 frequency ranging from 4-8%, but the Lapita potters who continued east to Samoa were virtually uninfluenced by Melanesian genetic elements. Rather, these early Polynesians had haplotypes HLA-A9.Bw22 and HLA-A2.B40 that are found in contemporary Mongoloid populations and the HLA data cannot support the theory of Polynesian evolu-

Population	A2 ^a	А9	A1 0	A11	B13	B15	Bw22	B40	B27	B16	B18	Bw35
Australia												
PNG Highlands		·· ·· ·										
Austronesia												
W. Polynesia												
E. Polynesia												
Micronesia												



a-indicates presence of HLA antigen

b-Australia has sporadic instances of A11

c-Austronesian-speaking Melanesians of coastal and Island Melanesia

tion within eastern Melanesia.

The group of colonists who left the Samoa area for eastern Polynesia about 2,000 years ago may have been small in number. By chance, the antigens HLA-B13 and -B27 were not represented in the migrating group or else were soon lost in genetic drift. The absence of either antigen in Maoris or Easter Islanders strongly supports the view that these two groups were derived from a common source, possibly in the Marquesas. The dendrogram (Fig. 1) also shows the split between the Samoa-Cook Islands branch of the Polynesian family and the Easter Island-New Zealand branch. Thus the HLA data is not consistent with linguistic analysis⁴² that clusters Cook Islanders with Maoris in the Tahitic subgroup of Polynesian languages.

In nuclear Micronesia, the only population with HLA data available is Nauru. There is no evidence for close affinity with Polynesians, as suggested by Howells,⁴³ but Melanesian elements can be detected. In addition, Micronesia has had an independent source of HLA genes, probably coming from the Philippines, as indicated by the high frequency of HLA-Bw35 which is absent from Melanesian and Polynesian groups.

This analysis has provided a broad overview of the relationships between Pacific populations. As more details of HLA antigen distributions and their linkage relationships become available, further insights into the origins of the Pacific peoples may well be possible.

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9 The peopling of the Pacific: a linguistic appraisal

Darrell T.Tryon

DURING THE PAST 20 YEARS OR SO MUCH PROGRESS HAS BEEN MADE IN SURVEYING and classifying the 1,800 odd languages in the Pacific area.¹ Although progress has been rapid, there are still big gaps in our knowledge of these languages which will prevent the formulation of definitive statements, especially detailed appraisals, for some years.

It is a sobering thought that of the 200 odd Australian languages² we have detailed information on only about half; of the 741 Papuan languages³ we are reasonably certain of one large genetic grouping (linguistically speaking), the Trans-New Guinea Phylum, but not really certain as to the genetic affinities of the not inconsiderable remainder (33%). Indeed fewer than one-third of all Papuan languages have been studied in any depth at all. On the Austronesian scene we appear to be moving towards a consensus on highest order subgroupings. However, one of the largest subgroups of Austronesian, the Oceanic subgroup, with more than 400 member languages, is still very problematic in that at present we are still not sure what its component first-order subgroups are. Currently we have only an unstratified collection of languages broken up into roughly 20 subgroups.⁴ Of the 400 or more Oceanic languages we lack any but the most fragmentary data on more than half. Even in Polynesia, where subgrouping has appeared secure for some time, there are still a number of unresolved issues.⁵

Nevertheless while many problems remain to be solved and unqualified generalizations are to be avoided, the work of linguists, particularly in the last few decades, allows some confident statements and appraisals to be made concerning language relationships in the Pacific area.

There are three unrelated language categories or 'families' in the Pacific area.⁶ These are:

- 1. The Australian Aboriginal languages.
- 2. The Papuan languages of the Papua New Guinea region.
- 3. The Austronesian or Malayo-Polynesian languages.

Australian Aboriginal languages are estimated to number between 200 and 300, depending on the criteria used,⁷ with around 260 distinct languages at the time of first European contact. In their major classification published in 1966, O'Grady and C. F. and F. M. Voegelin recognized 228 discrete languages.⁸ Most recently Dixon concluded that there were around 600 distinct tribes in Australia, speaking between them about 200 different languages.⁹ What do we know of these languages and how do they relate to the other languages of the Pacific?

The languages of Australia are all considered by most observers to be ultimately genetically related. However, Dixon considers that at present two of the languages, Tiwi, from Bathurst and Melville Islands, and Djingili, from the Barkly Tableland, cannot be demonstrated to be genetically linked with other Australian languages.¹⁰ The Aboriginal languages of Tasmania, all of which died out in the 19th century, remain unclassified, since the data available for those languages are too scanty to allow any positive demonstration of their relationship or otherwise with the languages of the Australian mainland.

The Australian languages are believed to be unrelated to any other language family in the Pacific area or anywhere else in the world as far as has been discovered.¹¹

Some observers believe that the languages of Australia comprise about 25 'families' or higher order subgroups.¹² One of these 'families', called Pama-Nyungan, covers nearly seven-eighths of the continent, while all the remaining 'families' are bottled up in the north, in the Kimberley/Arnhem Land area.

The languages of the north are characterized by prefixes to the noun or verb stem, among other things, while the Pama-Nyungan group, and one isolated group in northeast Arnhem Land,¹³ are characterized by an extensive suffixing system. Capell, among others, maintained that the prefixing and suffixing typologies have the same origin, the differences in system resulting from a gradual process of fixing an originally elastic word order in an utterance, so that certain elements came to fall into fixed positions, resulting in what are known as 'prefixing languages' existing in one part of Australia and 'suffixing languages' in the remainder.¹⁴ It is believed that the suffixing languages were the original type. Capell cites the Western Desert languages as an example of the most primitive system, for in these the original flexibility of word order is preserved.¹⁵ Capell's contention concerning the common origin of the prefixing and suffixing systems was vindicated by Hale, when during fieldwork in the Barkly Tablelands in 1959-60 he discovered a language family in which neighbouring languages, both prefixing and suffixing, used the same grammatical morphemes.¹⁶

Capell also recognized 'regional vocabularies', words particular to certain geographical areas.¹⁷ These are words which have survived regionally but not universally. Often there are lexical agreements over long distances which cannot be explained as coincidental, for example between the extreme north and south of the continent, but without cognate forms in the intervening areas. These are now considered to be remnants of very early speech, pushed out to the margins of the country by later-comers. Indeed, it is generally accepted that one of the languages or 'language families', which is thought to have developed in the north, spread throughout the continent, pushing existing elements out to the edges and superimposing itself until only vestiges of the original language remained.¹⁸

In more recent times Dixon has cast doubt on a number of issues which had previously won fairly general acceptance. He points out, for example, that it should not be inferred that Pama-Nyungan is in any sense a genetic unity, stating that the 'grouping' has probably been strongly affected by the phenomenon of 'areal diffusion'.¹⁹ At the same time he observes that traditional comparative linguistic methods have not been applied to Pama-Nyungan, and that diagnostic innovations for the establishment of a Pama-Nyungan subgroup have not been produced.

In fact Dixon considers that our present knowledge of the relationships between Australian languages is not sufficient to justify any sort of fully articulated 'family tree' model.²⁰ The modern languages can be arranged in lowlevel genetic subgroups, each involving eight or nine members, but little work has yet been attempted on higher-level subgroups, in terms of shared innovations. In fact in spite of the presumption that all Australian languages have developed from a single proto-language, formal linguistic proof has not yet been worked out, in terms of traditional historical-comparative methods. Indeed, the most urgent need is to discover whether presently identified low-level subgroups can be linked together to form larger genetic groupings.

The Australian languages are thought to have entered Australia from Papua New Guinea via the land bridge which linked the two countries until approximately 10,000 years ago.²¹ How or where they came from before then is unknown and probably beyond the reach of linguistic methodology.

THE Papuan languages constitute the second major language division in the Pacific. They occupy nearly all of West Irian/Papua New Guinea, together with northern Halmahera, parts of Timor, and parts of New Britain, New Ireland, Bougainville, and scattered parts of the Solomon Islands as far southeast as Santa Cruz.²²

Wurm reports most recently that there are 741 known Papuan languages, 507 of which (about 80% of all Papuan speakers numerically) belong to a single language group, the Trans-New Guinea Phylum.²³ Wurm lists the Papuan groups as follows:

Language Grouping	No. of Languages	No. of Speakers
Trans-New Guinea Phylum	507	2,307,000
West Papuan Phylum	24	217,000
Sepik-Ramu Phylum	98	194,000
Torricelli Phylum	48	80,000
East Papuan Phylum	27	69,000
Minor Phyla:		
 – Sko phylum-level Stock 	8	6,600
– Kwomtari phylum-level Stock	5	3,300
-Arai (Left May) phylum-level Family	6	1,600
–Amto-Musian phylum-level Stock	2	300
– East Bird's Head phylum-level Stock	3	17,000
– Geelvink Bay Phylum	5	12,000
Isolates	8	5,000

The Papuan languages are far and away the most complex, morphologically, of the Pacific area. While they are much better known today than even 10 years ago, fewer than half have been studied at all, and comparative linguistic techniques have not been applied to them to nearly the same extent as to the Austronesian or even the Australian Aboriginal languages. The tentative nature of remarks as to detailed subgrouping and/or migrations of Papuan language groups goes without saying. While the general picture has been worked out,²⁴ the details and revisions will take a decade or two before more definitive statements may be made.

The first immigrants into the island of New Guinea were probably Australoids, at a time when New Guinea and Australia were still a single continent, perhaps some 60,000 or so years ago. They spread south and east and into Australia until approximately 10,000 years ago, when Australia and New Guinea became separated by water.²⁵

The first Papuans entered New Guinea at a much later date, also coming from the west, and overlaid the Australoid population still in New Guinea. Blood group studies show there are genetic links between Papuan populations and Aboriginal groups in Australia.²⁶ Kirk suggests that the immigration of the first ancient Papuans into New Guinea took place either shortly after or not long before the isolation of New Guinea from Australia.²⁷ In support of his contention he points out that Papuans have not entered the Australian continent, certainly not in significant numbers. This means that the first Papuan immigration into New Guinea would have taken place at least 10,000 and at most 15,000 years ago. This migration seems to have spread right across New Guinea. Wurm considers that some of the language isolates surviving today may be remnants of that migration.²⁸ A few millenia later, a second Papuan migration appears to have entered New Guinea, overlaying the first migration and following much the same route. Surviving descendants of the second migration, which has clearly identifiable structural features, are found in the far west of the New Guinea area, although traces of their earlier presence are found in many parts of New Guinea as substratum features.²⁹

The main Papuan migration is considered to have taken place about 3000 B.C., when a group which was assumed to have lived in an area immediately to the west of the New Guinea mainland moved right through the island.³⁰ The languages involved in this migration are members of the huge Trans-New Guinea Phylum referred to above. The approximate date of 3000 B.C. for the main migration is deduced from the presence of Austronesian loanwords which the Papuans picked up west of the New Guinea mainland before the migration began. These indicate that speakers of ancestral forms of the Trans-New Guinea Phylum languages had been in close contact with Austronesians speaking an early form of Austronesian. Since the Austronesians are believed to have reached the area west of New Guinea about 5,000-5,500 years ago,³¹ a date of about 3000 B.C. for the beginning of the Trans-New Guinea Phylum migration is not unreasonable.

The Trans-New Guinea Phylum languages, then, overlaid the earlier languages in their path, traces of those languages remaining as substratum features. Yet earlier material culture and other cultural features remained largely unaffected.³² The main Papuan language migration also reached Timor, most probably from the New Guinea mainland. It is estimated to have taken about 1,000 years to have spread right across the mainland. Wurm is of the opinion also that the main Trans-New Guinea Phylum migration may have displaced an earlier language group in the south eastern tip of Papua New Guinea. He considers that this language group moved out to the Rossel Island area, leaving behind a lexical and structural substratum.³³ At the same time Papuan languages displaced in southeast Papua are considered to have reached New Britain and New Ireland, perhaps overlaying even earlier languages there.³⁴

From Rossel Island it appears that Papuan speakers moved to the western and central Solomons, perhaps as a result of having learnt seafaring techniques from the Austronesians, reaching as far east as Santa Cruz. The existence of Papuan languages southeast of Santa Cruz has not been demonstrated, although there has been some speculation that they may once have extended as far as southern Vanuatu and New Caledonia.³⁵

A retrograde east to west migration also appears to have taken place within the Papuan language area, possibly about 2000-1500 B.C., after the Austronesians had reached New Britain and New Ireland. Wurm considers that the migration began in the Markham Valley, spreading 'relatively recent Eastern Austronesian loans' within a considerable part of the Trans-New Guinea

Phylum.36

A final note on the Papuan languages concerns the Sepik-Ramu area, outside the Trans-New Guinea Phylum, but quite a large subgrouping in its own right. This language group appears to share a number of cultural and genetic traits with the Australian Aborigines. The cultural traits include the use of spear-throwers, the technique of painting on flat surfaces (like Aboriginal bark paintings) and slit-gongs, used in pairs, tuned to an interval identical with the natural over-blowing interval of the Australian didgeridoo.³⁷ Laycock, too, has indicated some lexical similarities between the two groups.³⁸ It is tempting to see the Sepik-Ramu Phylum language speakers as remnants of the original Australian Aboriginal migration which passed through Papua New Guinea at a much earlier period.

THE Austronesian (Malayo-Polynesian) language family, with approximately 800 languages and 120,000,000 speakers, extends from Madagascar in the west to Easter Island in the east. Austronesian languages are currently spoken in Madagascar, the Malay peninsula, southern Vietnam, Indonesia and the Philippines, and by the aboriginal populations of Taiwan, until about 500 years ago almost the entire population.³⁹ The Austronesian family had its beginnings, it is currently agreed, about 7,000 years ago.⁴⁰

Although there are still many unknowns, especially at lower levels of the 'family tree', the higher order subgrouping of the Austronesian languages and its attendant implications in terms of migration theory have made considerable progress in recent years. The higher order relationships between the Austronesian languages may be represented as shown in Fig. 1.

Briefly, the aboriginal languages of Taiwan are considered to constitute three of the four first order subgroups of Austronesian recognized by most linguists today. In fact Taiwan (and before it the South China area) is favoured by most as the most likely Austronesian homeland.⁴²

It has been demonstrated that all of the Austronesian languages outside Taiwan constitute a single first order subgroup, called Malayo-Polynesian.⁴³ This huge subgroup, whose speakers, hereafter, are referred to as Austronesians, moved south from Taiwan to the Philippines and eventually spread right through them. From the Philippines one group apparently moved southwest, through Borneo and subsequently Sumatra and Java, with branches penetrating the Malay Peninsula and eastern parts of Indochina.⁴⁴ This migration corresponds to the Western Malayo-Polynesian subgroup (Fig. 1). The other major migration from the Philippines carried the Austronesians first to northern Sulawesi. From there it is believed to have followed two paths; one south through Sulawesi and into the Ceram-Ambon area and Timor, corresponding to the Central Malayo-Polynesian subgroup (Fig. 1); the other towards southern Halmahera and the northwestern part of the New Guinea mainland, corresponding to the Eastern Malayo-Polynesian subgroup (Fig. 1).

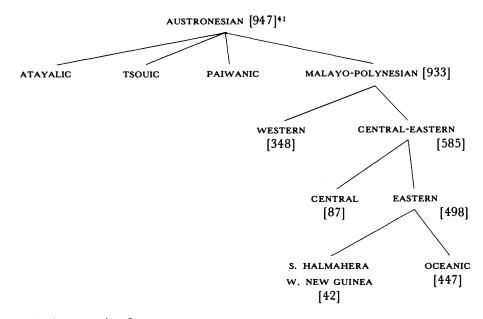


FIGURE 1: Austronesian Languages

Numbers in square brackets represent 'speech communities', i.e. communities recognizing that their speech differs from their neighbours, either at language or dialectal level; M. Ruhlen, 'Austronesian', mimeo. 1982.

It is currently held that the Austronesians reached west New Guinea by about 3500 B.C.⁴⁵ Blust has convincingly demonstrated the validity of the Eastern Malayo-Polynesian subgroup and its division into a South Halmahera-West New Guinea and an Oceanic subgroup.⁴⁶ This latter subgroup encompasses all of the Austronesian languages of Melanesia, Polynesia and Micronesia.⁴⁷

Besides the migrations discussed above, there were apparently numerous smaller scale migrations which criss-crossed the Austronesian-speaking area west of New Guinea, especially in the Philippines and western Indonesia. In these areas relatively recent migrations appear to have covered up and obliterated earlier language diversity, producing a regional homogeneity not commensurate with the estimated age of the known Austronesian settlements there. At the same time the languages of this region appear to have changed much more slowly than member languages of the Eastern Malayo-Polynesian subgroup.⁴⁸ In addition, as Dahl has shown, Madagascar was settled by an Austronesian migration from Borneo, somewhere around 2,500 years ago, after the primary migrations.⁴⁹

Speakers of the Oceanic languages probably moved from the Halmahera/West New Guinea area, certainly from eastern Indonesia, passed along the northern coast of New Guinea and settled in the New Britain/New Ireland area about 3000 B.C.⁵⁰ Here they appear to have remained for some time relatively undisturbed, to judge from the number of phonological and

morpho-syntactic innovations shared by the Oceanic subgroup of Austronesian. It was in this area that they came into contact with Papuan language speakers, whose linguistic influence is discussed below.

From the New Britain/New Ireland area migrations radiated in several directions, westwards to the north and northeast coast of the mainland of Papua New Guinea (a coast difficult of access for much of the year), and south to various parts of the coast of that huge island.⁵¹ Other migrations moved southeastwards, filtering through the Melanesian chain-the Solomons, Vanuatu and New Caledonia-and reaching Fiji by about 1500 B.C.⁵²

About this time, a set of migrations apparently began in the northern/central Vanuatu region, one moving north, spreading the Austronesian languages throughout Micronesia (for which there is evidence of an east to west spread),⁵³ another moving southeast to the Fiji group. From there, after a period of consolidation, the Polynesian languages evolved, moving out from the Tonga-Niue area sometime around 1000 B.C.⁵⁴

The languages of Polynesia have been intensively studied over the past two or three decades, and their migration history fairly clearly established. From the Tonga-Niue area, they spread first to the Samoa area and the Tokelau group, about 500 B.C. A little later some of the Polynesians drifted back to Melanesia and Micronesia, from islands near and around Samoa.⁵⁵ This resulted in the so-called Polynesian Outlier languages scattered throughout Island Melanesia and Micronesia.⁵⁶ From Samoa the Polynesian languages are also thought to have spread eastwards, to the islands of eastern Polynesia, namely the Marquesas, Easter Island, the Society Islands, the Tuamotus, Mangareva and Hawaii. From the Society Islands the Polynesians and their languages/dialects moved on to the Cook Islands, and to far away New Zealand. The eastward expansion of the Polynesians from the Samoa area is believed to have taken place between 100 A.D. (the date of settlement for the Marquesas) and 900 A.D. (when New Zealand was first settled).57 One particular problem area has been Easter Island, for while it is generally accepted that Rapanui, the language of Easter Island, was the first to part company from the Polynesian languages/dialects east of Samoa, the details of its development within Polynesian are still not clear.58

In terms of the Austronesian languages, then, the migration picture based on linguistic evidence may appear to be uncontroversial and settled. In some respects it is indeed so. One considerable problem which remains unresolved, however, concerns the huge subgroup of Austronesian languages known as Oceanic.

First there is the great number of languages, nearly 450 in all, within the Oceanic subgroup. Several reasons for the development of such a large number of different languages have been advanced. Most recently Pawley has argued that the degree of linguistic speciation in Oceania is a function of time, rather than isolation and other geographical factors.⁵⁹ Another problem is not so much the number as the heterogeneity of language types in Melanesia. Lynch

makes a good case for the 'many-groups-per-region' kind of diversity characteristic of the Melanesian region being to a large extent due to external contact and in particular to contact with Papuan languages.⁶⁰

There is, however, a central problem which must be resolved before we can discuss the peopling of the Pacific in general, and of Melanesia in particular. This problem concerns the subgrouping of the Oceanic group within the Austronesian languages.

Grace divided the Oceanic languages into 20 subgroups, presumed by nearly everyone to be first order subgroups of Oceanic,⁶¹ as follows in Fig. 2.

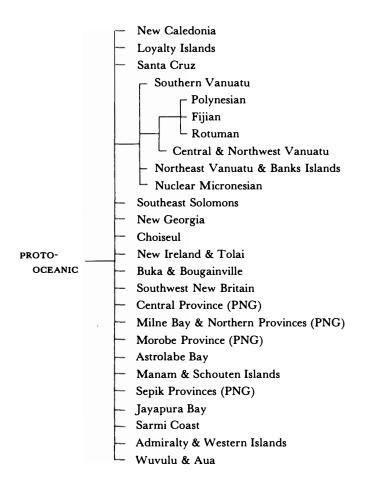


FIGURE 2: Oceanic Subgroup of Austronesian

The fact that many scholars presumed Grace's subdivisions to be first order subgroups of Oceanic has important implications for any discussion of migrations. Indeed Pawley has assumed that Proto-Oceanic, the ancestral form of the Oceanic languages of today, was spoken over a wide area, a view based on the wide-ranging geographic distribution of first order subgroups of Oceanic as found in Grace's 'family-tree'.⁶² The principal point at issue is to what extent the 'tree' is an accurate representation of current subgrouping hypotheses. Many scholars (including Pawley) have treated the Grace tree as largely unstratified, the branchings on that tree representing primary branches of Oceanic. This is now known not to have been Grace's intention.⁶³

Grace intended that the interrelationships between the subgroups which he identified be a matter for further investigation. Indeed, recent research has shown that the unstratified nature of what for want of a better term we shall call the 'Oceanic tree' is unlikely to be entertained seriously for much longer. A number of combinations of subgroups or parts of subgroups listed in the Grace tree have been proposed in recent years, many of which are believed by a number of linguists to be reasonably secure. These include:

- (a) A Papuan Tip group, consisting of the languages of Milne Bay and the Central Province of Papua New Guinea.⁶⁴
- (b) A Siassi group, consisting of the languages of the north coast of Papua New Guinea together with the offshore islands from the Papua New Guinea border to the Huon Peninsula, plus the Bariai group of west New Britain and the languages of the Vitiaz Strait.⁶⁵
- (c) An Admiralty group,⁶⁶ the languages of the Admiralty Islands, together with Wuvulu and Aua.
- (d) A Western Solomons group, consisting of the languages of Choiseul, New Georgia and all of Santa Ysabel except Bugotu.⁶⁷
- (e) An Eastern Oceanic subgroup, comprising the languages of the southeast Solomons, north and central Vanuatu, Fijian and Polynesian.⁶⁸
- (f) A Central Oceanic subgroup, consisting of the Eastern Oceanic subgroup languages as defined by Pawley,⁶⁹ together with the languages of the Eastern Outer Islands in the Solomons, and the languages of southern Vanuatu and New Caledonia.⁷⁰

While there may be no general agreement on the acceptability of all of the subgroups mentioned above, it seems certain that some stratification of the Oceanic tree is possible. Indeed it would not be surprising if the Austronesian languages of New Ireland, Bougainville and the western Solomons were shown to form a single subgroup of Oceanic.⁷¹

So far Proto-Oceanic has been reconstructed on the basis of those languages which are well known, rather than on any well defined subgrouping hypothesis. What is particularly needed, as we move towards a more detailed picture of Oceanic migration, is the reconstruction of interstage languages and comparison across subgroups.

In terms of the Austronesian languages, then, while consensus has been largely reached with regard to higher order subgroupings, we are still some

way from producing a generally accepted picture of Oceanic linguistic prehistory. While there is general agreement that Proto-Oceanic formed and consolidated in the New Britain/New Ireland area, any detailed account of later migration must still be regarded as very tentative, especially where the Island Melanesia world is concerned.

What emerges from the linguistic evidence in the Pacific region is that while our collective knowledge of Pacific languages and their histories has improved dramatically during recent years, great gaps still need to be filled before we are in a position to make definitive statements about the linguistic prehistory of this vast area.

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10 The Proto-Oceanic language community

Andrew Pawley and Roger C.Green

THE COLONIZATION BY AUSTRONESIAN SPEAKERS OF THE INDO-PACIFIC ISLANDS scattered almost two-thirds of the way round the tropical and subtropical world—was a feat with only one parallel in human history: the expansion of West European peoples after Columbus. In each case advances in sailing methods by maritime peoples, speakers of a single language family originally living on continents or continental islands, enabled them to undertake long ocean voyages to explore and trade, and led to their rapid colonization of farflung lands.¹ Yet the Austronesian expansion was more or less completed long before Columbus, and the challenge of reconstructing its course is more akin to that of reconstructing the original Indo-European expansion across Eurasia after 3500 B.C. We are dealing with prehistoric events and circumstances whose outlines may be recovered only by careful application of the methods available to prehistorians, especially those of archaeology and comparative-historical linguistics.

This paper will focus on one stage in the Austronesian settlement of the Pacific – that associated with the reconstructed language known as Proto-Oceanic (POC). What makes this stage of particular importance is that Proto-Oceanic is regarded by linguists as the immediate ancestor of a subgroup which contains more than 400 languages, or about half the Austronesian total. The subgroup coincides almost exactly with those members of Austronesian that are spoken in the southwest and central Pacific. Into Oceanic fall nearly all of the so-called Melanesian languages,² plus the Polynesian group and the Microne-

sian languages other than Chamorro, Belauan (Palauan) and possibly Yapese. No Oceanic languages are found west of New Guinea. The boundary line between the Oceanic group and the rest of Austronesian runs through the north coast of New Guinea between 136° and 138° E (east of the Bird's Head, between Sarera Bay and the Sarmi Coast), and curves through the western islands of Micronesia between 132° and 140° E (see Figure 1).

The main questions to be addressed here are the following: What do we know of Proto-Oceanic culture and society? What circumstances led, first to the formation, and second, to the disintegration of the Proto-Oceanic language community? Where, when, and why did Oceanic diverge from other branches of Austronesian? Where, when, and why did Proto-Oceanic itself break up?

THE IDEA that most of the Austronesian languages of Melanesia fall into a subgroup with all Polynesian and some Micronesian languages was first developed by Otto Dempwolff in the 1920s. The case was argued in detail in 1937 in the second book in his three volume *Vergleichende Lautlehre des austronesischen Wortschatzes*, a work that remains the cornerstone of Austronesian comparative linguistics. Not until the 1950s, however, did a small group of Oceanic specialists emerge who began to build on and refine that portion of Dempwolff's work which dealt with the Oceanic languages.³ Over the last 30 years the Oceanic hypothesis has provided the impetus for a considerable body of comparative research. Some of this work has been concerned with establishing the exact membership of the Oceanic group and with determining the internal relationships of its members.⁴ A number of revisions to Dempwolff's reconstructions of the Proto-Oceanic sound system have been made,⁵ while his lexical reconstructions have been greatly extended.⁶

The key that can unlock the prehistory of a language family has no better name than the 'comparative method' of historical linguistics. It has, however, no connexion with what is often termed the comparative method of ethnological or sociological reconstruction. The linguistic method is not concerned with language types or with structural similarity in a general sense, nor does it make any reference to evolutionary grade or progress. The crucial discoveries that led to the development of the linguistic comparative method, and its application to the tasks of reconstructing Proto-Indo-European, Proto-Germanic, etc., belong to the most impressive scientific achievements of the 19th century.⁷

What the Indo-Europeanists discovered is that sound changes (changes in pronunciation) in a particular speech tradition (dialect, language) are regular. That is to say, during the period when a sound change is taking place, pronunciations change not one word at a time but in classes of words defined by systematic contextual conditions. In fact, the regularities are such that 'laws of sound change' can be discovered, for the historical development of particular languages, that have something of the character of laws of physics or genetics.

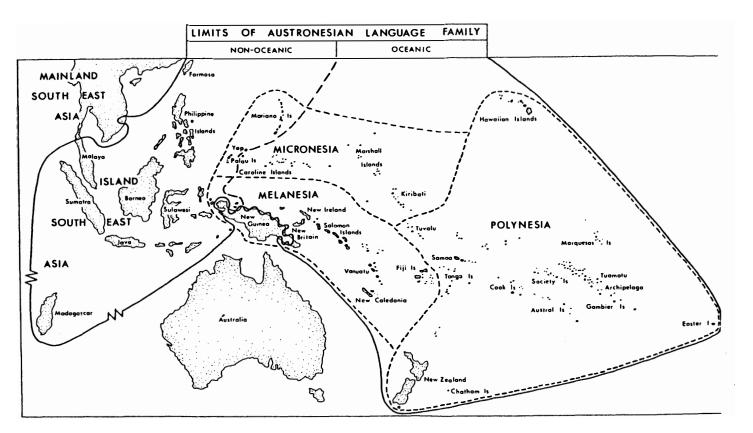


FIGURE 1.

Once the linguist identifies the (often complex) conditions of a sound change, he expects it to recur in all words which meet these conditions.⁸

From the fact that sound correspondences between earlier and later stages of a language are regular, it follows that correspondences between sister languages will be regular in that portion of their vocabularies that is genetically related ('cognate'), i.e. directly continues the common parent tradition. Taken together with the fact that word forms have an arbitrary relation to their meanings, the phenomenon of regular sound change makes possible the demonstration of genetic relationship among languages, the distinction between cognate words and resemblances due to accident or borrowing, and the reconstruction of the word-forms of earlier stages (proto-languages) ancestral to a group of genetically related languages. For example, the comparison of Tongan 'eiki 'person of chiefly rank' and Samoan ali'i 'chief' shows the correspondences: Tongan '(glottal stop) to Samoan zero; Tongan zero to Samoan l; Tongan k to Samoan '; and Tongan e to Samoan a in an unstressed syllable preceding a stressed syllable containing i, as well as the correspondence Tongan i to Samoan *i*. These correspondences are repeated throughout the lexicons. Taken together with material from other Polynesian languages, the sound correspondences allow us to reconstruct a Proto-Polynesian word having the form *qariki, with the approximate meaning 'chief'. When cognates diverge in meaning precise semantic reconstruction is not always possible.9

The 'comparative method', then, is a theoretical framework which demands that certain comparative procedures be applied in order to yield the kind of data that can be explained in a principled and regular manner by the theory. The method provides not only for establishing genetic relationship but also for determining degrees of relationship among sister languages, i.e. for subgrouping or family trees. Evidence for a subgroup is provided by the discovery that a subset of languages in the family share common innovations – have changed the parent language in identical ways. The strength of the case for a subgroup rests on the number of innovations and on their quality (how unusual they are as changes, and how well established the facts of change are).

Among the high-order branches of Austronesian, Oceanic is relatively welldefined. In spite of their great internal diversity, the Oceanic languages share an impressive mass of changes to the Proto-Austronesian (PAN) sound system and other common developments that set these apart from the rest of Austronesian. In phonology, for example, it is characteristic of Oceanic languages that they merge the two PAN stops, voiced *b and voiceless *p, into a single sound (reconstructed as POC *p), and that all other pairs of voiced and voiceless obstruents having the same point of articulation are similarly merged. PAN *d and *r also merge in POC. So do PAN *s, *z and *c. In the PAN vowel system, *e and *aw fall together in Oceanic (as POC *o), as do PAN *i and *uy (as POC *i).

Beyond these regular changes, which apply to the entire lexicon, Oceanic

languages agree in various other innovations, such as a restructuring of PAN patterns of word formation, the addition of some new consonants (principally POC *m^w and *p^w), and certain sporadic sound shifts, affecting particular isolated words. The latter are exemplified by POC *au '1st person singular, topic', which shows irregular loss of *k compared with PAN *aku, POC *mai 'come, hither', which shows irregular loss of *R compared with PAN *maRi, POC *moli 'citrus', which shows metathesis from PAN *limaw, and POC *-akin 'suffix deriving transitive verbs', which shows *i for expected *o in comparison with earlier *aken. Numerous common Oceanic words are traceable no further back than Proto-Oceanic, e.g. POC *kia(n)jo 'outrigger boom', *m^wata 'snake', *mana 'effective, powerful', *pai 'where?', *ka- 'edible possession marker'.

There are few if any scholars now active in Austronesian comparative linguistics who doubt the essential correctness of the Oceanic hypothesis.¹⁰ Some of Dempwolff's original arguments for Oceanic have been discarded in the light of more detailed evidence, but a solid core has remained and a good deal of additional evidence has been uncovered. This consolidation of opinion (and evidence) has come about slowly and unspectacularly enough to have escaped the attention of many scholars who are outside the immediate field.¹¹

WHAT manner of people were the speakers of Proto-Oceanic? The 1,500 to 2,000 lexical reconstructions so far attributed to Proto-Oceanic represent only a fraction of the total vocabulary of the language community, but tell a good deal about the culture. A selection of reconstructions for a number of cultural domains is given in the tables that follow.¹² In these tables PMP stands for Proto-Malayo-Polynesian, a reconstructed stage slightly later than Proto-Austronesian but ancestral to Proto-Oceanic (see Figure 2). A slash between two glosses or forms indicates an indeterminacy in reconstruction between the glosses or forms. Indeterminacy in reconstructing particular segments of forms is shown by parenthesizing the segment(s) in question. Comma between glosses indicates that both glosses are reconstructible.

These reconstructions indicate that POC speakers had an economy based jointly on gardening and fishing. The major root and tree crops of contemporary Oceanic economies, other than sweet potato and cassava, are represented: yam, taro, breadfruit, coconut etc. A variety of fishing techniques were exploited, including nets, lines, basketry traps and plant poisons. An extensive comparative study of terms for fish and fishing techniques, now being undertaken by Richard Walter, has so far yielded some 50 POC reconstructions for kinds of fish.

The list of artifacts in Table 4 is not very impressive. In part its brevity reflects a lack of careful searching for cognates. (Oceanic comparative linguists have been mainly interested in formal linguistic problems – phonological and grammatical change, and subgrouping; few are engaged in systematic

GLOSS	PMP	POC
boat, vessel	waŋkaŋ	waŋkaŋ
boat/sea travel	paraSu	podau
sail	İayaR	layaR
outrigger	katiR	nsaman
outrigger boom		kia(n)jo
sticks connecting outrigger and boom		patoto
side of canoe opposite outrigger/larger hull of	of	-
double canoe	-	katae/katea
rollers to beach canoe	laŋe(n,N)	laŋon
cross-seat/ribs of boat	seŋkar	so(ŋ)kad
caulk, splice, patch	. —	njema
load, cargo	-	Rujan
paddle	besay	ponse
to steer, rudder	quliŋ	quliŋ
bail out	limas	limas
fishing net	-	kupeŋa
basketry fish trap	buqubuqu	pupu
float of net	<u> </u>	uto
fishhook	kawil	kawil
Derris fish-poison	tuba	tupa
fish-bait, lure, trolling hook	-	mpaya

TABLE 1-*POC and PMP lexical reconstructions associated with sailing and fishing

* Note: q indicates a glottal stop and * a reconstruction.

wao	forest/bush/uncultivated land/weeds
topa	cultivated land
poki	clear the ground for garden-site
quma	garden, to make a garden
pa(n)si	to plant
ntiu	replant a garden without fallowing it
talun	fallow
ta(m)puki	yam mound
(m)pula(m)pula	seed yam/seedling
upe	taro top for planting/seedling
suli(q)	shoot, sucker (esp. banana, taro)
(n)suki	dig up, transplant
matuqa	mature, ripe, full-grown
dada	turn yellow in ripening
mena	ripe, full-grown
kono	long pole for harvesting fruits, nuts
kawit	to hook, catch by a hook; fruit crook
pale	hut, shed, garden shed or storage place
pata	stage, shelf, platform for storing food
paRa	platform, rack for storage
ko(n)so	husking stick; to husk coconuts

GLOSS	PMP	POC
taro	tales	ntalos
yam	qubi	qupi
Alocasia	biRaq	(m)piRaq
Cytos perma		
banana	pun(t,T)i	punti
Saccharum edule	_	tampukal
sugar cane	tebuS	(n)topu ·
coconut	niuR	niuR
sago palm	rumbi(a)	d(a,u)mpia
breadfruit	kuluR	kuluR
citrus	limaw	moli
Terminalia	(t,T)ali(c,s)ay	talinse
Inocar pus	qipil	qipil
Pandanus	panDan	pandan
Areca	bu(q)a	mpua
Casuarina	aRuqu/aRuSu	(y)aRu
Syzygium	_	kapika
Zingiber	leqia	laqia
Cordyline	siRi	nsiRi
Piper methysticum	-	kawa
Pometia		(n)tawa
Spondias	-	quRi
Barringtonia	butun	putu
Canarium	kaŋari	kaŋadi
melon/cucumber	timun	tim(o,u)n
breadfruit/fermented breadfruit	kama(n)(c,s)i	masi
pig	babuy	_
pig	beRek	mpoRok
domestic fowl	manuk	_ 15
cassowary		ka(n)suadi
megapode	_	malau
cuscus (Phalanger)	<u> </u>	kandoRa
bandicoot	_	mansad
Polynesian rat (Rattus exulans)		k(au)nsupe

TABLE 3-POC and PMP lexical reconstructions associated with edible plants and animals¹⁴

reconstruction of lexical terminologies.) But partly it is a function of the limitations of the lexicon. The fact that only two POC terms to do with pottery have so far come to light is no guarantee that POC speakers did not use a variety of vessel forms and decorative styles. Some significant features of material culture, e.g. different styles of ceramic decoration or vessel forms, tend not to be distinguished in the vocabulary. Here we must look to archaeology for evidence which linguistics is unable to provide (see below).

With Milke's work in the 1930s kinship terminology became the first POC lexical domain to receive systematic attention from a linguist¹⁶ (though Oceanic kin terms had much earlier been the subject of comparative

sociological study). The following table draws on Milke's work and recent additions and revisions.¹⁷

GLOSS	РМР	POC
clay/clay pot	daReq	daRoq
earthenware pot	ku(dD)en	kudon
ladle/dipper	ka(ŋ)buq	kampu(a)
axe-adze handle	paŘáRa	paRaRa
axe/adze	kiRam	kiRam
to adze	(tT)aRaq	taRaq-i
file/rasp	parut	pad(ou)t
hunting bow	busuR	pusuR
to shoot	panaq	panaq
ring (shell) bell/strike slit gong	girin	nkiriŋ
broom	sapu	sapu
needle	zaRum	(n)saRum
sharpened pole/stake	pa(ŋ)can	pasan
sharpened stake set in ground to stop or		-
wound animals or enemies	suja	su(n)ja
lever, stick for lifting	sual	sual

TABLE 4-Other POC and PMP reconstructions associated with material cultures

TABLE	5 - POC	kinship	terms
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1. consanguineous kin	
2nd generation up:	
grandparent	tumpu
1st generation up:	
father, father's brother	tama
mother, mother's sister	tina
mother's brother	matuqa
father's sister	(?) aya
Ego's generation:	
older sibling same sex	tuqaka tansi
younger sibling same sex	m ^w aqane ¹⁸
brother (woman speaking)	papine
sister (man speaking)	papine
1st generation down: child	notu
	natu (qa)lawa
sister's child (man speaking)	(qa)iawa
2nd generation down:	makumpu
grandchild	tumpu
2. Affinal kin	
1st generation up:	
parent-in-law	puŋao
Ego's generation:	•
wife's brother, husband's sister	ipaR

The terminology reconstructed here distinguishes the mother's brother from the father and father's brother, and sister's child from brother's child. This assymetry suggests the possibility that POC society had descent groups in which landrights were invested. Goodenough and Blust have elaborated arguments for attributing descent groups to early Malayo-Polynesian society.¹⁹ The term **kaiyana* 'clan, land-owning descent group' has been reconstructed as far back as the immediate common ancestor of the Polynesian and Nuclear Micronesian groups, a stage which either coincided with Proto-Oceanic or was close to it.²⁰

There is a small but rather powerful set of comparisons indicating that Proto-Oceanic society had hereditary chiefs.²¹ Specific lexical agreements between Polynesian and Solomon Islands languages point to the following pair of POC terms:

*qa-lapa(s) 'chief, senior person of a descent group' (lit. 'Great One') *qa-diki 'first-born son of chief' (lit. 'Little One')

In Polynesian only the second form survived (as Tongan 'eiki, Maori ariki, Hawaiian ali'i, etc.), and took on the meaning of *qa-lapa(s). The (probably obligatory) distinction between older sibling (POC *tuqaka) and the younger sibling (*tansi) of the same sex is consistent with a rank system emphasizing primogeniture.

Among the various terms for other social categories attributable to POC, *ntauta(n)si 'mariner, expert fisherman or sailor' is of some interest. This term is reflected in Polynesian and Nuclear Micronesian, and is analysable into *ntau'expert, specialist' and *ta(n)si 'sea'.

We will return later to the matter of cultural changes associated with the development of Proto-Oceanic.

THE COMPARATIVE method yields knowledge of prehistoric languages but does not place those languages in time or space. Several procedures are used to estimate the geographic locations of prehistoric language communities. One is the *Wörter und Sachen* method, which draws on the reconstructed vocabulary to make inferences about the environment familiar to speakers of a language.

The limited range of certain indigenous animal genera in the Pacific makes the distribution of cognate terms for these animals of considerable historical interest. Among the terms represented in two or more first-order branches of Oceanic, and so attributable to Proto-Oceanic, are POC *ka(n)suadi 'cassowary', *kandoRa 'cuscus' (Phalanger sp.), *mansad 'bandicoot', *malau 'megapode', *puqaya 'crocodile' and *dui 'dugong'.²² Of these, the cassowary is native to New Guinea, though transported by man at least to New Britain and possibly to other islands near New Guinea. The two marsupial types comprise genera that are represented in eastern Indonesia (bandicoots are found at least in the Moluccas and Lesser Sundas, and phalanger species occur in Sulawesi as well as further east),²³ New Guinea and the Bismarcks; phalangers extend into the Solomons, as far as San Cristobal. Crocodiles and dugongs have a still wider distribution, but are absent from Polynesia, Fiji, and most of Micronesia (and in the case of the crocodile, Vanuatu and New Caledonia).²⁴ Megapodes are absent from most of Micronesia and Polynesia.

This line of evidence, then, points to a location which includes New Guinea and/or eastern Indonesia, without excluding the Bismarck and Solomon archipelagoes.²⁵ Remote Oceania—the islands of Melanesia east of the Solomons, plus Micronesia and Polynesia—is virtually excluded.

A second widely used procedure is a version of the Age-Area method. A proto-language is placed most probably in that region where its genetically most diverse descendants (first-order branches) are concentrated, according to the principle of least moves²⁶ needed to account for the dispersal of the daughter branches. The principle of least moves favours a Melanesian location in general and the northwest (New Guinea and the Bismarcks) in particular. To see why, it is necessary to look at the structure of two different sections of the Austronesian family tree, above and below the Proto-Oceanic stage.

Figure 2 shows a classification about which there is a reasonable measure of agreement on certain points.²⁷ Some details are controversial, e.g. the number

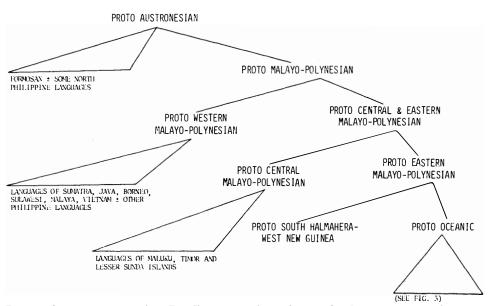


FIGURE 2: An Austronesian Family Tree (after Blust, 'The Proto-Austronesian pronouns . . .', *The Proto-Oceanic Palatals*; Dahl, *Proto-Austronesian*; Reid, 'The demise of Proto-Philippinic').

of first-order branches found in Formosa, and the position of the Philippines languages. However, the last decade has seen increasing consensus on the following: (1) Oceanic is no higher than a third or fourth order branch of Austronesian. The old notion of a primary split into Western and Eastern Austronesian (where Eastern = Oceanic) now appears untenable. (2) The immediate relatives of Oceanic are to be found at the western end of New Guinea and in south Halmahera, and, at a slightly higher level, in the zone of eastern Indonesia comprising Timor, the Moluccas and the Lesser Sundas. (3) The centre of genetic diversity within Austronesian as a whole is in the area comprising Formosa and the Philippines.

If we apply the principle of least moves to this classification, the conclusion must be that Proto-Austronesian was spoken in the Formosa-Philippines region, and that Austronesian speakers expanded from there in two main directions: southwest into Borneo, Java, Sumatra, etc., and southeast into eastern Indonesia and New Guinea. As the two major branches of the Eastern Malayo-Polynesian group are contiguous, and have their seam on the north coast of New Guinea between 136° and 138° E, it is most economical to conclude that the divergence of the Oceanic branch began when a group of Eastern Malayo-Polynesian speakers moved east of this seam to a region somewhere in western Melanesia.

The external relationships of Oceanic give some idea of the direction from which pre-Oceanic speakers entered the territory now occupied by the Oceanic group. But to say more about the location of Proto-Oceanic itself we must look at the internal classification of the Oceanic languages, indicated in Figure 3. This figure packs something of a surprise.

What is surprising is that there are close to 30 subgroups that have claims to being first-order branches of Oceanic. Furthermore, these form a chain of contiguous groups (separated only by ocean gaps) stretching from New Guinea through New Britain, New Ireland and the Solomons southeast to Vanuatu and New Caledonia. Only in the marginal regions of Oceania, in the central Pacific, do we find languages of a single first-order subgroup occupying very widely separated island groups. There is, then, no single region within western and central Melanesia that is clearly the centre of genetic diversity within Oceanic.

It is hard to see how Proto-Oceanic could have diversified more or less simultaneously into a large number of branches scattered from New Guinea to Vanuatu unless it was already spoken over a wide area, encompassing the seams of most if not all of the first-order branches. Thus, Figure 3 is consistent with the view that, at least in the final stages of its development, Proto-Oceanic was spoken by a widely dispersed population, centred in the chain of intervisible islands running from New Guinea, New Britain and New Ireland in the northwest to Malaita and San Cristobal in the southeast. Figure 3 does not indicate whether or not the initial dispersal of Proto-Oceanic was swift or slow, or

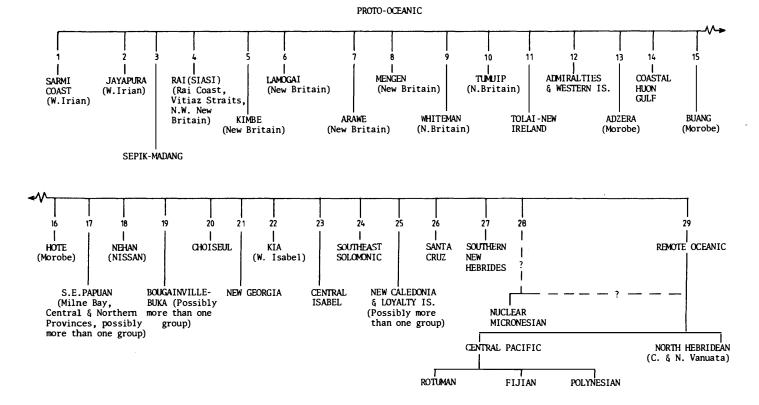


FIGURE 3: A subgrouping of the Oceanic Languages

whether regional dialects existed. We return to these issues shortly.

Of course, it is possible that the subgrouping in Figure 3 is badly astray. One or two scholars have recently suggested that further research ought greatly to reduce the number of first-order groups.²⁸ But even if this were to happen, it would not necessarily contradict our conclusions about the distribution of Proto-Oceanic. For one thing, it is not so much the number of first-order branches that is significant, as the pattern of their geographic spread. If there were, say, six first-order subgroups, but with widely dispersed seams, then there would still be no clearly defined centre of diversity or most probable dispersal centre.

Ten years ago a dramatic reduction in the number of first-order divisions of Oceanic seemed on the cards. Better data were appearing and subgrouping work was swinging into high gear. Now, prospects seem dimmer. A fair amount of searching has been done and no very striking evidence for more inclusive groupings has turned up. Slender evidence for some larger groups in western Melanesia has been brought forward, ²⁹ but no evidence indicating a marked pause of Oceanic speakers in northwest Melanesia after the breakup of Proto-Oceanic and before the expansion into the Solomon Islands and Remote Oceania. Evidence of such a pause would be provided by the discovery that one of the first-order subgroups in northwest Melanesia also includes most or all of the subgroups of the Solomon Islands and Remote Oceania. The discovery of a weakly defined sequence of this kind would do no more than indicate a brief pause. The period of time attributable to the formation of a subgroup is indicated in a rough way by the number of (well-attested) innovations attributable to the group. It seems that if any such sequence exists in northwest Melanesia it will turn out to be weakly defined.

A third line of evidence bearing on the location of a proto-language lies in the existence of innovations which cut across the lines of first-order subgroups. Such intersections point to the continued spread of innovations along a chain of languages *after* the first-order subgroups had begun to diverge. In certain circumstances it is possible to date the spread of the intersecting innovations to a period that is very early in the divergence of the proto-language. The implications then are, first, that the proto-language consisted of a number of dialects; second, that after the first-order subgroups began to diverge they remained in contact at certain points, allowing some interchange between contiguous dialects; and third, that the relative locations of the first-order subgroups at the time they were beginning to diverge is indicated approximately by the distributions of the intersecting innovations among contemporary languages.

This line of evidence is as yet little explored in work on Proto-Oceanic. There are, however, a few indications that some of the first-order subgroups of Oceanic, after they began to diverge, formed a chain of closely cohering dialects occupying roughly the same territories as their present-day descendants. For instance, the innovation of adding an 'echo' vowel after POC wordfinal consonants (e.g. Roviana onomo from POC *onom '6', gaili from POC *kawil 'fishhook') is an isogloss linking several otherwise separate subgroups occupying a more or less continuous region from (parts of) New Ireland through Bougainville and Choiseul to New Georgia and western Santa Isabel. But a subgrouping based on this isogloss is contradicted by other isoglosses which link different sets of neighbouring groups.

To sum up, we read the evidence as indicating (1) that the separate development of Oceanic began with a movement of Eastern Malayo-Polynesian speakers eastwards along the north coast of New Guinea to a point east of Sarera Bay, (2) that relatively unified development continued for several centuries—long enough for many changes to take place in the language, and (3) that at the time Oceanic speakers moved southeast to Vanuatu, after settling the Bismarcks and the Solomons, a relatively unified Proto-Oceanic language or dialect chain still existed.

BEFORE taking up the question of when Proto-Oceanic was spoken, it is appropriate to comment on two different conceptions of how subgroups were formed.

In work on Austronesian subgrouping since the 1950s there has been a tendency to conceive of subgroups as being formed by what we will call the *radiation* model. This model posits an initial period of unified development undergone by a localized, homogeneous language community, followed by a period of geographic expansion, leading to the creation of dispersed, isolated daughter communities which develop independently from the time of dispersal. The radiation model has, for instance, been much used by those of us working in Polynesian linguistics.

In some cases this model may reflect historical events fairly accurately. But as more detailed evidence comes in for various Austronesian-speaking regions, we find time and time again that things did not happen exactly that way. It begins to look as if linguists have underestimated the capacity of the early Austronesians to spread quickly over a vast area, and to maintain a fairly unified speech tradition across a network of local communities dispersed across an archipelago—a unity that may last for many centuries, even millenia, before there is a decisive divergence of local dialects. In some cases it is clear that the location of the ancestral language was approximately equal to the area now occupied by all of its daughter languages. That is to say, it is not necessary for there to be a geographic expansion for the proto-language to break up. A gradual weakening of ties between the network of sister dialects suffices: eventually, sharp language boundaries appear. Call this the network-breaking model.

How, in the network-breaking model, does a proto-language form and break up? The model assumes a flow of innovations across the dispersed local communities in the network. The flow need not be constant or perfectly even, but as long as it continues to be fairly even the entire dialect chain will continue to change as a unity, or as a partial unity. In these circumstances, there is no single point in time that can be equated with the breakup of the protolanguage. Instead, there is a period during which unity declines; when one dialect has ceased to be intelligible to the rest, or has ceased to take part in the flow of innovations, the breakup may be said to be complete.

If pressed, most linguists would probably have always conceded that subgroups are sometimes formed in this general manner. But scholars doing reconstructive work have generally been reluctant to admit that the chainbreaking model applied in *their* domain, because to do so would make the business of reconstruction much messier. It is more convenient to assume that each descendant of the proto-language is an independent witness to the form of the parent stage.

To account for the full range of evidence having to do with the Oceanic group it is necessary to employ both the radiation and the network-breaking models (for different stages).³⁰ Both permit the construction of family trees and proto-languages. The point that should be stressed is that reconstructions of Proto-Oceanic and many lower-order interstages arrived at by the comparative method may represent (a) a dispersed dialect chain rather than a localized homogeneous language, and (b) a period rather than a point of diversification.

A SUBGROUPING amounts to a *relative* dating (giving sequential order) of the branchings on a linguistic family tree. Estimates of *absolute* dates are given by the method of glottochronology but such dates are not regarded as being very reliable. To obtain reliable absolute dates, linguists must find a means of connecting the linguistic sequence with archaeologically dated events.

A secure correlation between linguistic and archaeological materials can be achieved only under certain rather rare conditions. In an earlier paper³¹ we argued that such conditions applied at one time in a few regions of Oceania, where the people who founded a continuing archaeological sequence in a given region can be strongly associated with the speakers of an Oceanic language ancestral to the present-day language or subgroup of that region. A set of principles was proposed for determining (a) when such an association can be made, and (b) the latest possible dates for the divergence of sister speech traditions associated with different regions.

In the course of a detailed review of current linguistic and archaeological knowledge of the Fiji-west Polynesia region, Green has recently applied these methods to the dating of Proto Central Pacific and Proto-Polynesian.³² The languages of Fiji and Polynesia all belong to Central Pacific, itself a branch of a subgroup of Oceanic (termed Remote Oceanic in Figure 3) which includes most of the languages of Vanuatu. The early Eastern Lapita assemblages of the Fiji-west Polynesia region, dating to 1600-1200 B.C., can be securely connected with the Central Pacific branch, and give a latest possible dating for the

divergence of Central Pacific from the rest of Oceanic.

In New Caledonia both the Lapita and the roughly contemporaneous Podtanean pottery assemblages, dating between 1600 B.C. and A.D. 300, may be associated with the New Caledonia languages, which are generally regarded as forming a single, closed subgroup.

In the New Guinea-Bismarck area it is more difficult to connect linguistic and archaeological traditions. While pottery is linguistically attested as a Proto-Oceanic trait, and some assemblages with pottery in that region may be reasonably associated with speakers of Oceanic languages, it is not always possible to do this with full confidence. The association is strongest in the case of cultural assemblages with pottery of a Far Western Lapita type, because of the clear connexions of this cultural complex with Oceanic subgroups in Fiji, Polynesia and New Caledonia. A less rigorous but probable case involves other early pottery assemblages in the Admiralty Islands which exhibit a continuity of the tradition that extends back to nearly 1700 B.C. and includes some levels with a few Lapita sherds of only slightly later date.³³ But there may be other assemblages there without pottery that in time will also qualify for inclusion, and others with pottery that will not qualify.

In northwest Melanesia the distinctive Lapita pottery style first appears in the Bismarck Archipelago, in some rather insecurely dated assemblages from Talasea locality on the Willaumez Peninsula of New Britain, Eloaue on Mussau Island in the St Matthias group and Malakolon on Ambitle Island in the Feni group of New Ireland. These have been convincingly shown to cluster together stylistically as an apparently ancestral Far Western Lapita group for which Anson argues an age of several hundred years prior to the 1600 B.C. date usually cited for Lapita beginnings.³⁴ This would be in line with the earlier $(3900 \pm 260 \text{ B.P.})$ of two radiocarbon dates accepted by the authors as more reliable for one oven at the Eloaue site.³⁵ It would also be in line with the view that the Lapita homeland was centred in the Bismarcks.³⁶ Having developed there for some centuries, the Lapita cultural complex³⁷ then rapidly spreads to the southeast Solomons, Vanuatu, New Caledonia, Fiji and west Polynesia in a dispersal that Irwin has described as 'virtually instantaneous' from an archaeological standpoint.³⁸ No pre-Lapita sites, other than the very problematic and insecurely dated New Caledonian tumuli,³⁹ have been found east of the Bismarcks as yet. As far east as San Cristobal in the Solomons such sites almost certainly exist, awaiting the archaeologist's trowel, for it seems to us unlikely that the non-AN languages of the Solomons all represent post-Lapita movements.

If the assumption is correct that the archaeological traditions that by 1600 B.C. were distributed as far apart as the Admiralty Islands on the one hand and Fiji-west Polynesia and New Caledonia on the other – a distance of more than 3,000 km and encompassing several ocean gaps of 300 km or longer – were carried by Oceanic speakers, we can safely conclude that 1600

B.C. is the latest possible date for the dissolution of Proto-Oceanic. Indeed, by this date a lower-order group, Remote Oceanic, had probably begun to diverge into a Central and North Vanuatu branch versus a Fijian and Polynesian branch. Thus, the indications are that Proto-Oceanic itself began to break up somewhat earlier than 1600 B.C.

To put an earliest possible date on the breakup of Proto-Oceanic is harder. Archaeological work in Island Southeast Asia shows ceramic traditions, likely to be associated with Austronesian languages, appearing widely in Indonesia and the Philippines during the latter part of the 3rd millenium B.C.⁴⁰ An Austronesian entry into northwest Melanesia earlier than 2000 B.C. is thus possible, though unattested. The discovery of Austronesian-associated assemblages earlier than 2000 B.C. in, say, the Bismarcks, would indicate that by this time the Oceanic branch had started to diverge from its Eastern Austronesian congeners further west. It would not, however, by itself say anything about the breakup of Oceanic. (It is necessary to distinguish between a 'pre-Oceanic' or developmental period in the formation of the Oceanic branch and a 'Proto-Oceanic' stage, representing the end of this formative period. It is the latter which is recoverable by the comparative method.) As already noted, evidence for dating the breakup of Proto-Oceanic resides in the discovery of two or more archaeological traditions from widely separated regions within the Oceanic-speaking zone, both of which can be strongly associated with Oceanic speech traditions.

The arguments for connecting bearers of the Lapita cultural complex with the dispersal of speakers of dialects of Proto-Oceanic now seem much stronger than they did a decade ago. This is not to say that by 2000 B.C. there may not have been significant local variation in material culture and some dialect diversity within the Proto-Oceanic community. For example the Lapita ceramic tradition seems now to have been as geographically variable as the rest of the Lapita material inventory,⁴¹ and the possibility of paddle-impressed and incised and appliqué ceramic assemblages contemporary with Lapita (Podtanean, Mangaasi and Mangaasi-related) at opposite ends of Island Melanesia (New Caledonia, Vanuatu and the Admiralties) must be seriously considered.42 Thus the spread of Oceanic need not have been carried out exclusively by Lapita potters. But it does seem that the latter were the spearhead of an Oceanic expansion into Remote Oceania. Further archaeological research throughout Melanesia is needed to choose from among several options answers to the twin questions: (1) when did AN speakers enter northwest Melanesia, and (2) when did they spread beyond the Bismarck-north New Guinea region?

THE LINGUISTIC record indicates (see above) that much of Proto-Oceanic culture continued earlier Austronesian traditions. What can be said about changes in lifestyle undergone by Austronesian speaking peoples in the period between their entry into Melanesia and the dissolution of Proto-Oceanic? It seems likely that, apart from drift or internally-generated cultural change, modifications of lifestyle would have been induced by at least two external causes: contact with alien cultures already resident in western Melanesia and adaptation to new environments.

There is a methodological problem in picking up such changes in the linguistic record. Comparative linguists focus their attention on continuity in vocabulary within a language family. The comparative method allows one to detect some of the losses in and additions to vocabulary, and some of the changes of meaning that occur between stages in the history of a language, but such changes tend to receive less attention than the continuities and to be more difficult to demonstrate.

A few plant names appear to be innovations of Proto-Oceanic, e.g. *kawa 'kava (*Piper methysticum*)' *tampukal 'Saccharum edule', *quRi 'Spondias sp.', *kapika 'Malay apple (Syzygium sp.)'. Of these plants, the first two are New Guinea or Oceanic natives and presumably were unknown to Austronesian speakers before they entered Oceania. No doubt there are other distinctively Oceanic plant terms awaiting discovery; this is a domain yet to receive specialist attention.

It is one thing to detect words that probably entered the Oceanic languages before the breakup of Proto-Oceanic; it is another thing to discover the source of these additions. No doubt there was some borrowing from non-Austronesian languages during this period. Certainly there are several well-documented cases of influence by non-Austronesian languages on particular Oceanic languages in more recent times.⁴³ But the enormous diversity of the non-Austronesian languages of Melanesia, which has so far prevented reconstructive work in that field from getting past the embryonic stage, makes it extremely difficult to find possible non-Austronesian sources for Proto-Oceanic innovations. McElhanon and Voorhoeve and Lynch have argued that a number of Austronesian words were borrowed in the other direction, by speakers of Trans-New Guinea Macrophylum languages, several millenia ago.⁴⁴ It will remain difficult to say much on this topic until the histories of the various non-Austronesian language families are understood better.

IN THE preceding discussion we have drawn attention to the importance of the Oceanic hypothesis in Austronesian comparative linguistics and to the methods used to reconstruct the Proto-Oceanic stage. Our main concern, however, has been to review the evidence accumulated so far concerning the Proto-Oceanic language community.

Linguistic and archaeological research over the last two decades has steadily added to this evidence. One result of the new material has been to make it easier than before to choose between competing hypotheses about the nature of Proto-Oceanic culture and society, and about when and where the language was spoken. A second result of recent work, perhaps of wider significance, has been a better understanding of the *processes* that produced the historical events and relationships inferrable from the evidence; that is, it is becoming easier to recognize recurrent patterns and to suggest general explanations for these.

The subgrouping evidence summarized above indicates that, at the time it broke up, Proto-Oceanic was spoken by a network of local communities spread over a considerable part of Melanesia, perhaps extending from New Guinea and the Bismarck Archipelago to the southeast Solomons. On archaeological grounds, the disintegration of Proto-Oceanic can be dated to not later than about 1600 B.C., and probably began somewhat earlier. In due course further linguistic partitioning took place within each of the major branches of Oceanic, eventually yielding the 450 or so distinct Oceanic languages that exist today.

Some 400 of these are located in Melanesia. The diversity of Austronesian languages in that region has puzzled linguists for a long time, and various explanations have been advanced. In the last 20 years the puzzle has been partly solved. More accurately, perhaps, part of it has vanished: there have been changes in our perception of the facts.

The received impression of Melanesian diversity has at least three different components: (1) quantitative diversity—the total number of languages in Melanesia, or in particular regions; (2) typological diversity—the differences between languages as measured by comparisons such as phonological and grammatical structure and lexicon; and (3) genetic diversity—the genetic distance between languages measured by their positions on the Austronesian family tree.

The genetic diversity of Austronesian languages in Melanesia is in fact less than was once thought. All are members of the Oceanic subgroup, which turns out to be no higher than a third or fourth order branch of Austronesian. At one time Grace⁴⁵ considered the possibility that certain typologically 'aberrant' languages in Melanesia are branches of Austronesian which have been in their present locations for much longer than more 'exemplary' Oceanic languages have. However, he favoured the view that unusually rapid change was what made the aberrant languages very different from the rest. Increasingly, the indications are that Grace was right. It is not just that the aberrant languages meet the phonological requirements for inclusion in Oceanic. When detailed work on them has been carried out, it has frequently turned out that they are closely related to certain neighbouring languages that are of a more exemplary Oceanic type, with fairly straightforward phonological histories.⁴⁶

Why have some descendants of Proto-Oceanic changed much more than others? This question has begun to receive considerable attention. Modifying ideas proposed earlier by Ray and Capell, Lynch has pointed to contact between Oceanic languages and non-Austronesian languages as one likely cause, attested by several recent studies in western Melanesia.⁴⁷ The effects of lexical tabus and of random variation in rates of change have also been suggested as important factors.⁴⁸

The sheer number of distinct Oceanic languages in most regions of

Melanesia is impressive, but should not be confused with deep genetic diversity. In many cases the various languages found on an island or in an island group are more closely related to each other than to languages of other regions – suggesting diversification *in situ* – and are typologically similar. For example, the island of Malaita contains some 13 languages but all are very much alike, to a degree which suggests that until a few centuries ago many were dialects of a single language. The 20 or so New Caledonian languages are lexically more diverse but structurally very alike. The indications are that for the first couple of millenia after the breakup of Proto-Oceanic, Austronesian language communities in Melanesia were typically much larger in geographic extent than today. Several recent studies have examined the combination of typological homogeneity and a large number of discrete languages found in many regions of Melanesia, and have proposed explanations for this phenomenon.⁴⁹

The lexical evidence presented here concerning Proto-Oceanic culture and society is regrettably incomplete. In particular, there are several relevant domains which we have said nothing about -e.g. warfare and politics, magic and religion, house construction, and food preparation and cooking techniques, among others. The reason is not only lack of space. The fact is that most of the work of identifying terminologies in the existing lists of lexical reconstructions, and of making careful semantic reconstructions for reconstructed forms, has not yet been carried out. A good deal has been accomplished; much remains to be done.



REFERENCES AND NOTES

1 There are of course many differences between the two cases, e.g. the Austronesians settled regions never previously inhabited by man, and their expansion was a good deal slower than the post-Columban one.

2 Unlike Polynesian, or Nuclear Micronesian, there is no such thing as a Melanesian branch of Austronesian. While the various Austronesian subgroups of Melanesia fall into the large Oceanic group, at a lower level some are more closely related to Polynesian than to other groups in Melanesia (see Fig. 3). The locution 'the Melanesian languages', unfortunately, remains in currency; it should be read as a geographic not a genetic categorization.

3 It was principally the subgrouping and reconstructive work of George Grace (e.g. 'Subgrouping of Malayo-Polynesian: a report of tentative findings', American Anthropologist 57:337-9 (1955); 'A Proto-Oceanic finder list', University of Hawaii Working Papers in Linguistics, 1: 39-84 (1969) and Wilhelm Milke (e.g. 'Zur inneren Gliederung und geschichtlichen Stellung der ozeanische-austronesischen Sprachen', Zeitschrift fur Ethnologie 83:58-82 (1958); 'Ozeanische Verwandtschaftsnamen', ibid., 226-9, 'Beitrage zur ozeanischen Linguistik', ibid., 86:162-82 (1961) that led to a wider acceptance of Dempwolff's Oceanic hypothesis and to the development of a fairly unified branch of Austronesian studies, Oceanic comparative linguistics, in the 1960s. The terms 'Oceanic' and 'Proto-Oceanic' were put forward by Milke, Proto-Oceanic being essentially equivalent to Dempwolff's 'Urmelanesisch'

THE PROTO-OCEANIC LANGUAGE COMMUNITY

Grace ('Subgrouping of Malayo-Polynesian...') presents an early comprehensive classifica-4 tion. See also Milke, 'Zur inneren Gliederung'. Numerous studies dealing with particular regions and subgroups have appeared since, e.g. B.Biggs, 'Direct and indirect influence in Rotuman', Lingua 14:383-415 (1965); I.Dyen, A Lexicostatistical Classification of the Austronesian Languages International Journal of American Linguistics Memoir 19 (1965); A.Chowning, 'Milke's "New Guinea cluster": the evidence from northwest New Britain' Oceanic Linguistics 12:189-243 (1973), 'Austronesian languages: New Britain', in S.A.Wurm (ed.), New Guinea Area Languages and Language Study Austronesian Languages Pacific Linguistics C40 (Canberra1976), and 'Rapid lexical change and "aberrant " languages: Sengseng and its neighbours', Pacific Linguistics in press; A.Pawley, 'On the internal relationships of Eastern Oceanic languages', in R.C.Green and M.Kelly (eds), Studies in Oceanic Culture History (Honolulu 1972) 1-142, 'The relationships of the Austronesian languages of Central Papua: a preliminary study', in T.E.Dutton (ed.), Studies in Language of Central and South-East Papua Pacific Linguistics C39 (Canberra 1976) 5-103, 'On redefining "Eastern Oceanic", mimeo. 1977, 13 pp, 'The New Guinea Oceanic hypothesis', Kivung 21:99-151 (1978), 'New evidence on the position of Rotuman', Dept of Anthropology Working Paper No. 52, University of Auckland; B.Bender, 'Micronesian languages', in T.E.Sebeok (ed.), Current Trends in Linguistics, 8, Oceania (The Hague 1971) 426-65; G.Grace, 'Notes on the phonological history of the Austronesian languages of the Sarmi coast' Oceanic Linguistics 10:11-37 (1971), 'Indirect inheritance and the aberrant Melanesian languages', in J.Hollyman and A.Pawley (eds), Studies in Pacific Languages and Cultures (Auckland 1981) 255-68; B.Hooley, 'Austronesian languages of the Morobe District, Papua New Guinea', Oceanic Linguistics 10:79-151 (1971); W.Milke, 'Comparative notes on the Austronesian languages of New Guinea', Lingua 14:330-48 (1965); D.T.Tryon, New Hebrides: an Internal Classification Pacific Linguistics C50 (Canberra 1976); M.Ross, 'Relationships of the Austronesian languages of the Sepik and western Madang coast of New Guinea', mimeo (1977), 'The Austronesian languages of Papua: towards a family tree', mimeo (1979); J.Lynch, 'Proto-South Hebridean and Proto-Oceanic', in S.Wurm and L.Carrington (eds) Second International Conference of Austronesian Linguistics: Proceedings Pacific Linguistics C61 (Canberra 1978) 717-79; F.H.Jackson, 'The internal and external relationships of the Trukic language of Micronesia', PhD thesis, University of Hawaii (Honolulu 1983).

5 See especially R.A.Blust, *The Proto-Oceanic Palatals* Polynesian Society Memoir 43 (Wellington 1978). Also Biggs, op. cit.; Grace, 'A Proto-Oceanic finder list'; Milke, 'Comparative notes....'; Pawley, 'On the internal relationships....'; Lynch, op. cit.; R.A.Blust, 'Some remarks on the labiovelar correspondences in Oceanic languages', in Hollyman and Pawley, op. cit., 229-53; F.Lichtenberk, 'Further evidence for Proto-Oceanic *ñ, *Oceanic Linguistics* 18:171-201 (1982); P.Geraghty, *The History of the Fijian Languages* Oceanic Linguistics Special Publication 23 (Honolulu 1983).

6 There is no single published work which lists all known Proto-Oceanic etymologies, although a fairly extensive compilation appears in a University of Hawaii printout (G.Grace (ed), Proto-Oceanic lexical reconstructions'. Computer printout, Dept of Linguistics, University of Hawaii).

7 The key theoretical synthesis was achieved mainly by Indo-Europeanists working at or in association with the University of Leipzig in the 1870s and 80s, drawing on the enormous store of comparative data that had been compiled during the 19th century.

8 These expectations are not always borne out completely; sporadic irregularities are encountered. Such exceptions do not invalidate the principle that sound change is perfectly regular. A change is regular in a particular community during the period when it is taking place [L.R.Palmer, *Descriptive* and Comparative Linguistics (London 1978), 210]. The results of the change may later be disturbed by separate historical events. Such disturbances in the pattern are detectable and often explainable.

9 See I.Dyen and D.F.Aberle, Lexical Reconstruction: the case of the Proto-Athapaskan kinship system (Cambridge 1974), and R.A.Blust, 'Early Austronesian social organization: the evidence of language', Current Anthropology 21:205-26 (1980) for discussions of problems and methods of semantic reconstruction.

10 Such has not always been the case. Conflicting ideas about the history of the Austronesian languages of Oceania were put forward by S.H.Ray, *A Comparative Study of the Melanesian Island Languages* (Cambridge 1926), and A.C.Capell, *The Linguistic Position of South-Eastern Papua* (Sydney 1943), and by Dyen, *A Lexicostatistical Classification....*, and given a wide airing in discussions of Oceanic culture history. However, Dempwolff's evidence for Oceanic was never challenged by proponents of competing hypotheses. Instead, they worked with methods designed to account for different facts from those addressed by the comparative method. But confidence in the reliability of

these other methods, never high in orthodox linguistic circles, has steadily faded and alternative explanations have been proposed for the facts in question.

11 In the 1960s and early 70s several factors combined to obscure to outsiders the central role of the Oceanic hypothesis in Oceanic comparative studies. One factor was the attention attracted by Dyen's lexicostatistical classification of Austronesian (op. cit.). Another was the longstanding idea (Ray, op. cit.; Capell, op. cit.) that the Austronesian languages of Melanesia are the product of not one but of many separate linguistic movements from Indonesia into Melanesia (each resulting in a mixed Austronesian-Papuan language following contact between Indonesian colonists and aboriginal populations). Thirdly, a lot of archaeological and linguistic research in the 1960s dealt with the question of the immediate origins of the Polynesians, leading to something of a preoccupation with the hypothesis of an Eastern Oceanic subgroup [Biggs, op. cit.; Pawley, 'On the internal relationships....'; R.C.Green, 'Languages of the Southeast Solomons and their historical relationships', in R.Green and M.Cresswell (eds), Southeast Solomon Island Cultural History, Royal Society of New Zealand Bulletin 11 (Wellington 1976), 47-60].

12 To qualify as Proto-Oceanic, a reconstruction must be represented by cognates in at least two first-order subgroups of Oceanic. Cognation is acknowledged only when the words show the forms predicted by the rules of historical phonology determined for each language, as well as showing connected meanings.

13 Based mainly on R.French-Wright, 'Proto-Oceanic horticultural practices', MA thesis, University of Auckland (Auckland 1983).

14 Based mainly on R.French-Wright, 'Some Proto-Oceanic animals', TS (1980), and op. cit.

15 There are at least two possible POC reconstructions for 'fowl' but each is problematic in certain respects. Standard Fijian toa, W. Fijian $t\bar{o}$, together with Mota, Sesake toa 'fowl' indicate Proto Remote Oceanic *to(q)a. But languages of diverse subgroups in central and western Melanesia show forms of the type of Roviana, Bugotu kokorako, Motu kokoroku, Kuanua kakaruk; apart from irregularities in the sound correspondences, the onamatapoeic nature of these forms reduces confidence in their cognation. POC *manuk is reconstructible but with a broader meaning, 'bird'.

16 Milke (1938, revised as 'Ozeanische Verwandtschaftsnamen....').

17 Blust, 'Early Austronesian social organization....', A.Chowning, 'Comment' on R.Blust, op. cit., *Current Anthropology* 21:231-2 (1980); A.Pawley, 'Melanesian diversity and Polynesian homogeneity: a unified explanation for language', in Hollyman and Pawley, op. cit., 259-309; Mac Marshall, 'Structural patterns of sibling classification in Island Oceania: implications for culture history', *Current Anthropology* 25: in press, provides extensive comparative data without applying the comparative method.

18 $*m^w aqane$ 'brother of a woman' and *papine 'sister of a man' (next term) were reconstructed by Milke, op. cit. There is considerable evidence for a competing reconstruction, *lopu 'sibling of opposite sex' (see data in Marshall, op. cit.).

19 W.Goodenough, 'A problem of Malayo-Polynesian social organization', American Anthropologist 57:71-83 (1955); Blust, op. cit.

20 A.Pawley, 'Rubbishman commoner, Big-man chief? Evidence for hereditary chieftainship in Proto-Oceanic', in J.Siikala (ed.), Oceanic Studies: Essays in Honour of Aarne A.Koskinen (Helsinki 1982); Goodenough, op. cit.

21 Pawley, op. cit.

22 French-Wright, 'Some Proto-Oceanic animals'; R.A.Blust, 'The linguistic value of the Wallace Line', *Bijdragen* 138:231-50 (1982).

23 Blust, op. cit.

24 Marine crocodiles have been sighted in Vanuatu but do not breed there.

25 Plant terms so far reconstructed for Proto-Oceanic generally do not indicate a specific region of the Indo-Pacific area, and mostly consist of terms for plants likely to be carried by man. Two items worthy of note here are POC *waiwai, 'Mangifera indica, mango', and *tampukal, 'Saccharum edule', plants that in pre-European times probably did not occur east of the Solomon Islands. See also Chowning, 'Proto-Melanesian plant names', in J.Barrau (ed.), Plants and Migrations of Pacific Peoples (Honolulu 1963), 39-44.

26 I.Dyen, 'Language distribution and migration theory', Language 32:611-26 (1956).

27 The classification is based on R.A.Blust, 'The Proto-Austronesian pronouns and Austrones-

ian subgrouping', University of Hawaii Working Papers in Pacific Linguistics. 9(2):1-15 (1977), 'Eastern Malayo-Polynesian: a subgrouping argument', in S.A.Wurm and L.Carrington, op. cit., Fascicle 1, Western Austronesian, 181-234, 'The Linguistic value....'; O.Dahl, Proto-Austronesian (Lund 1973); L.A.Reid, 'The demise of Proto-Philippinic', in A.Halim, L.Carrington and S.A.Wurm (eds), Papers from the Third International Conference on Austronesian Linguistics Pacific Linguistics C75 (Canberra 1982), 145-70.

28 J.Lynch, 'Melanesian diversity and Polynesian homogeneity: the other side of the coin', *Oceanic Linguistics*, 20:95-112 (1981), J.Lynch and D.T.Tryon, 'Central Oceanic: a subgrouping hypothesis', Paper presented at the 15th Pacific Science Congress, Dunedin, Feb. 1983.

29 Lynch and Tryon, op. cit.; Pawley, 'The New Guinea Oceanic hypothesis'; Ross, op. cit., 1977 and 1979.

30 The network-breaking model appears to fit the evidence for the formation and breakup of Proto-Fijian (A.Pawley and T.R.Sayaba, 'Fijian dialect divisions: Eastern and Western Fijian', Journal of the Polynesian Society 80:405-36 (1971); Geraghty, op. cit.), Proto Central Papuan (Pawley, 'The relationships of Austronesians....'), Proto Central and North Vanuatu (Tryon, New Hebrides....), Proto Southeast Solomonic (Pawley, 'On the internal relationships....') and Proto Trukic (Bender, op. cit.; Jackson, op. cit.), among other cases. The radiation model applies rather well to some of the Polynesian interstages (A.Pawley and R.Green, 'Dating the dispersal of the Oceanic languages', Oceanic Linguistics 12:1-67 (1973)).In many cases both models are needed to account for different phases of the sequence, e.g. Proto Central Pacific (Geraghty, op. cit.; Pawley, 'New evidence on the position of Rotuman') and Proto Remote Oceanic (Pawley, 'On the internal relationships', 'On redefining ...') seem to have persisted as dialect chains until one or more parts of the population moved to a distant island group, creating a sharp break.

31 Pawley and Green, op. cit.

32 R.C.Green, 'Location of the Polynesian homeland: a continuing problem', in Hollyman and Pawley, op. cit., 133-58.

33 Ibid.

34 D.Anson, 'Lapita pottery of the Bismark Archipelago and its affinities', PhD thesis, University of Sydney (Sydney 1983).

35 F.Bafmatuk, B.Egloff and R.Kaiku, 'Islanders - past and present', *Hemisphere* 25(2):77-81 (1980).

36 R.C.Green, 'Lapita sites in the Santa Cruz group', in Green and Cresswell, op cit.; J.P.White and J.Allen, 'Melanesian prehistory:some recent advances', *Science* 207:728-34 (1980).

37 A description of the elements characterizing the Lapita cultural complex is given in R.C.Green, 'Lapita', in J.Jennings (ed.), The Prehistory of Polynesia (Canberra 1979), 27-60.

38 G.J.Irwin, 'The prehistory of Oceania: colonisation and culture change', in A.Sherratt (ed.), *The Cambridge Encyclopaedia of Archaeology* (Cambridge 1980), 324-32.

39 R.C.Green and J.Mitchell, 'New Caledonian culture history: a review of the archaeological sequence', New Zealand Journal of Archaeology 5:19-67 (1983).

40 P.Bellwood, Man's Conquest of the Pacific (Auckland 1978), 153-80, 'New perspectives on Indo-Malaysian prehistory', Bulletin of the Indo-Pacific Prehistory Association 4:71-83 (1983).

41 Anson, op. cit., 274.

42 Green and Mitchell, op. cit.; R.C.Green, 'Cultural sequences from the Southeast Solomons to New Caledonia: a preliminary overview', in symposium on Recent Advances in Pacific Prehistory, XIth International Congress of Anthropological and Ethnological Sciences, Vancouver, Aug. 1983; J.Kennedy, 'Archaeology in the Admiralty Islands: some excursions', Bulletin of the Indo-Pacific Prehistory Association, 3:22-35 (1982), 'On the prehistory of Western Melanesia, the significance of new data from the Admiralties', Australian Archaeology 16:115-22 (1983).

43 T.E.Dutton, 'Magori and similar languages of south-east Papua', in Wurm, New Guinea Area Languages..., 581-636, 'Borrowing in Austronesian and non-Austronesian languages of coastal south-east mainland Papua', in Halim, Carrington and Wurm op. cit., 109-77; Lynch, 'Proto-South Hebridean....'; W.R.Thurston, A Comparative Study in Anem and Lusi Pacific Linguistics B83 (Canberra 1982). Cf also Capell, op. cit.

44 A.McElhanon and C.L.Voorhoeve, The Trans-New Guinea Phylum: explorations in deeplevel genetic relationships Pacific linguistics B 16 (Canberra 1970), J.Lynch 'Austronesian "loanwords"(?) in Trans-New Guinea Phylum vocabulary' Pacific Linguistics(A 61 (1981), 165-80. 45 G.W.Grace, 'Austronesian linguistics and culture history', American Anthropologist, 63:366 (1961). The possibility that Proto-Austronesian was spoken in Melanesia was argued by Dyen ('The lexicostatistical classification....' and A Lexicostatistical Classification....). J.Terrell ('Linguistics and the peopling of the Pacific Islands', Journal of the Polynesian Society 90: (1981) has argued a common origin for Austronesian and other Pacific Basin languages as the result of a sole initial settlement thousands of years ago, with later differentiation, in Melanesia, of Austronesian and non-Austronesian languages. However, recent developments in Austronesian subgrouping (summarized in Fig. 2) strongly favour an Austronesian dispersal centre in or near Formosa.

46 Dutton, op. cit. 1976 and 1982; J.Guy, 'Proto North New Hebridean reconstructions', in Wurm and Carrington, op. cit.; Lynch, 'Proto-South-Hebridean....'; A.Pawley, 'The relationships of the Austronesian languages....'; Chowning, 'Milke's "New Guinea cluster"....' and 'Rapid lexical change....'.

47 Ray, op. cit.; Capell, op. cit.; Lynch, 'Melanesian diversity'.

48 R.Keesing and J.Fifi'i, 'Kwaio word tabooing in its cultural context', Journal of the Polynesian Society 78:154-77 (1969); Chowning, 'Rapid cultural change...'.

49 G.Grace, 'Indirect inheritance and the aberrant Melanesian languages', in Hollyman and Pawley, op. cit., 255-68, 'Oceanic subgrouping: retrospect and prospect', *Pacific Linguistics*, in press; Pawley, 'Melanesian diversity....'; S.P. Harrison, 'Recent directions in Oceanic linguistics: a review of the contributions to *Studies in Pacific Languages and Cultures'*, *Oceanic Linguistics*, 20:151-231 (1981).

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11 The Lapita cultural complex

origins, distribution, contemporaries and successors

Matthew Spriggs

LAPITA POTTERY ASSEMBLAGES ARE NOW KNOWN IN AN AREA FROM THE ADMIRALties in the west to the Marquesas in the east, from New Caledonia in the south to the Caroline islands in the north. 'Classic' Lapita can be recognized by the distinctive pottery decoration produced by impressing with a series of toothed stamps. A variety of other decorative techniques were in fact also used and most of the pottery which is found is plain.

The pivotal place that the Lapita culture has in interpretations of Southwest Pacific prehistory has been recognized for a little over 20 years. Jack Golson's early insights concerning the significance of Lapita distribution were followed up by Roger Green. It is in large part because of Green's continuing empirical research and theoretical formulations that our research horizons now extend beyond comparison of pottery types to consideration of settlement pattern, long distance exchange, social and economic organization and even the linguistic affiliation of Lapita pottery-using groups.¹ With the ever-increasing flood of data on Lapita it is now perhaps an appropriate time to review the developments of the last 20 years and suggest possible reformulations and new directions in research which are worth considering.

By the late 1970s a widely accepted, perhaps even 'orthodox', view had developed to explain the Lapita phenomenon, albeit in several slightly different versions.² In this view the origins of Lapita and its bearers can be traced fairly directly to eastern Indonesia and the Philippines in terms of language, genetics, food plants, canoe technology, and pottery manufacture and decora-

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tion. Southern Mongoloid Austronesian speakers bearing this culture had established themselves in the already inhabited Bismarck Archipelago by 4,000 years ago, then soon afterwards set off across Island Melanesia to colonize Polynesia and eastern Micronesia. In Island Melanesia (excluding Fiji) Melanesian populations were already established by this time, either speaking Non-Austronesian (Papuan) languages or Oceanic Austronesian languages. The Lapita populations did not make extensive genetic or cultural contact with the Melanesians and were generally restricted to settling on small offshore islands. The view that they were a group of endogamous traders is not as widely accepted as other aspects of the theory. When they reached Fiji, Polynesia and eastern Micronesia, however, they entered empty lands and in these areas Lapita represents the culture of the initial inhabitants. Polynesians and the inhabitants of eastern Micronesia are thus closest genetically to the Island Southeast Asian ancestors of the Lapita people. In Melanesia, the Lapita populations were overwhelmed or absorbed by their Melanesian neighbours by about 2,000 years ago, and perhaps a thousand years later the basically Polynesian Fijians were affected by a migration of Melanesians from the west so that today Fiji has a transitional 'mixed' population.³

There are four components of this view of Lapita which can be challenged, partly on the basis of new evidence and partly on reinterpretation of the old.⁴ These concern origins of Lapita, distribution of Lapita sites, contemporary cultural complexes and successors to Lapita. As already shown, the view requires a fairly direct transfer of culture, genes and language from Island Southeast Asia, allowing only a short pause in northwest Melanesia before the colonization of Polynesia and eastern Micronesia by Lapita-using Southern Mongoloids. An alternative hypothesis is being pursued by those (from various countries and institutions) involved in the Australian National University Lapita Homeland Project, who see some Southeast Asian input but consider that the Lapita culture is in large part an indigenous development in northwest Melanesia derivative from the earlier cultures of the region.

Closely linked to the orthodox view of origins is the necessary existence of other (indeed earlier) cultures throughout Island Melanesia, excluding Fiji. Lapita is thus only one of several contemporary cultural complexes in the area. In so far as this view relates to areas south of the Bismarcks-Bougainville region, it can similarly be challenged, and an argument made for Lapita as the founding culture in much of Island Melanesia, as it is in Polynesia.

It has often been noted that Lapita sites in Melanesia are generally found on small offshore islands, thus supporting the view that other populations were already established on the major islands. But this apparent settlement pattern could be an artifact of sampling factors resulting from the differential effects of post-depositional landscape change. A previously inhabited Melanesia is also necessary to explain the disappearance of the Lapita culture in this region. In previously uninhabited Polynesia the bearers of the Lapita culture became the ancestors of the present Polynesians and so cultural continuity is argued. In Melanesia, however, Lapita populations in the orthodox view were absorbed or conquered by those already there. The alternative hypothesis which needs to be considered is that there is cultural continuity between Lapita and the cultures which followed in Island Melanesia as well. These four points will be considered in turn.

THE CLEAREST link between northwest Melanesia and Island Southeast Asia is in language. The Oceanic Austronesian languages of the area are ultimately descended from Proto-Austronesian, a language perhaps spoken in the Taiwan-northern Philippines area. The immediate ancestor of the Oceanic languages was Proto Eastern Malayo-Polynesian (PEMP) which broke up after a group of its speakers moved into northwest Melanesia (the north New Guinea coast and the Bismarck Archipelago). There was a period of perhaps several centuries after the PEMP break during which the innovations which define the Oceanic subgroup developed. Pawley calls this period 'Pre-Oceanic', to distinguish it from Proto-Oceanic (POC), the later stage when the language began to break up into two or more separate languages.⁵ The break up is attributed to the spread of Oceanic speakers from the Bismarcks into southern Melanesia and east to Fiji and Polynesia, a spread which can be associated with the dispersal of the Lapita complex to these areas (further discussed below).

Two questions appear crucial: What was the impact of this PEMP migration on the cultures of northwest Melanesia? And how long was the period of Pre-Oceanic development? The island of New Guinea, the Bismarcks and probably Bougainville were already inhabited by Non-Austronesian (NAN) speakers at this time.⁶ On current archaeological evidence it is difficult to assess the impact on these previous inhabitants of incoming populations who may have entered the area as early as 5000 B.P.⁷ We do however have some archaeological evidence concerning the cultures already there which is suggestive.

Pleistocene occupation in the Bismarck Archipelago has recently been established.⁸ Some 11,400 years ago, the inhabitants of Misisil Cave in west New Britain were importing obsidian from sources in the Talasea area on the Willaumez Peninsula about 80 km to the north. Specht has suggested that sea transport of this obsidian is likely, despite the much longer journey, because of the rugged mountainous terrain between Misisil and the north coast.⁹ Occupation of another rock shelter (Alanglong) on the south coast of west New Britain by 6,500 to 8,500 years ago has been suggested on the basis of deposition rates but has yet to be confirmed.¹⁰

On New Ireland the earliest evidence of human occupation comes from Balof shelter on the east coast, the lowest layers of which have been dated to 6800 ± 410 B.P. Associated with the date is Talasea obsidian from New Britain, 600 km away following the coasts. Other stone material from early layers of Balof comes from the central plateau of New Ireland, and the west and south coasts, giving further evidence of long distance movement of resources at this early date.¹¹

Whether these populations had an agricultural base is unclear. Some NAN speakers on the mainland of New Guinea were certainly agricultural by 9000 B.P. The pig had been introduced to New Guinea by 6000 B.P. and possibly considerably earlier.¹² Evidence is now accumulating that the natural distribution of many food plants, previously assumed to be solely of Southeast Asian origin, may have included the New Guinea area and so independent domestication of various crops such as taro is a distinct possibility.¹³

Thus PEMP speakers moving into the area encountered a population engaged in long distance movement of stone and presumably other resources by sea, a population probably already engaged in agriculture utilizing crops which would have been familiar to the newcomers. Pottery may well have been introduced by the new arrivals, occurring somewhat earlier in Southeast Asia than it does to the east. The Lapita style itself appears to be a Melanesian innovation, bearing no convincing close relationship to Southeast Asian pottery styles of the period despite assertions to the contrary.¹⁴ It would therefore seem quite possible for northwest Melanesia to be where the basic elements of the Lapita culture came together, a mixture of old and new which may have coalesced over a considerable time. The ocean-going double canoe which is primarily distributed in eastern Melanesia and Polynesia may well be an innovation of this region.¹⁵ The view of a basically ready-made culture arriving in the Bismarcks and staying briefly before heading on to Polynesia no longer seems so persuasive. What time scale are we thinking about?

The earliest sites in northwest Melanesia which can probably be assigned to Austronesian-speaking populations have been located in the Admiralty Islands where an inland site on Manus island has produced a date of 4160 ± 90 B.P. and a coastal site on Los Negros island off the east tip of Manus has given dates of 4290 ± 100 B.P. and 3910 ± 70 B.P.¹⁶ The excavator, while admitting the potential sampling errors of small testpit excavations, has tentatively identified these sites as aceramic but points out that pottery was probably manufactured at this time in nearby areas. The colonization of the Admiralties, involving an open ocean crossing of some 240 km, appears to have occurred several hundred years prior to the Lapita dispersal.

From Elouae in the St Matthias Group, north of New Ireland, come two dates from a single hearth feature associated with Lapita materials. The older date is 3900 ± 260 B.P. while the younger is 3030 ± 180 B.P. The Elouae site contained obsidian both from the Admiralties 300 km to the east, and Talasea 430 km to the south.¹⁷ Anson favours the earlier date for Elouae on the basis of his own analysis of Lapita decoration from several sites, in which Elouae clustered with Talasea and Ambitle Island (southeast of New Ireland), suggesting a chronological separation of several centuries between these and other Lapita sites outside the Bismarcks region. His analysis considerably strengthens the case for the development of the Lapita culture within the Bismarck Archipelago and its subsequent dispersal thoughout Island Melanesia.¹⁸ The earliest reliable dates for Lapita outside the Bismarcks all occur later than 3500 B.P.¹⁹

A period of perhaps up to a thousand years for the Pre-Oceanic stage seems possible, with the settlement of the Admiralties perhaps in the mid-fifth millennium B.P. and the Lapita dispersal in the mid-fourth millennium. It may be wrong however to associate the Lapita dispersal solely with Proto-Oceanic speakers. There is no reason to believe that the NAN speakers of the Solomon Islands south of Bougainville and extending to Santa Cruz have been in this region any longer than the Oceanic Austronesian speakers.²⁰ Green has argued that the NAN speakers migrated to the Reef-Santa Cruz Islands in the post-Lapita period, in order to associate the Lapita sites of the area with Oceanic Austronesians.²¹ Apart from loss of pottery making about 2,000 years ago, however, there appears to be cultural continuity in the area with no evidence of an intrusive population.²² It certainly seems possible that the initial Lapita expansion from the Bismarcks involved both Oceanic and NAN speakers.

GREEN has identified five cultural assemblages south of the Bismarcks which are potentially contemporary or earlier than Lapita in Island Melanesia. They are represented in the basal layers of Fotoruma or Poha Cave on Guadalcanal, assemblages associated with pottery on Anuta and Santa Ana in the southeast Solomons, the Mangaasi pottery sites of central Vanuatu, the aceramic southern Vanuatu sites excavated by Shutler, the paddle-impressed sites of New Caledonia, and the notorious tumuli of the same region.²³ Since this survey new evidence has become available allowing us to place the southeast Solomons pottery complexes convincingly within the Lapita tradition,²⁴ and pottery has now been recovered from Erromango in southern Vanuatu with both Lapita and Mangaasi affiliations.²⁵ A date from Aneityum in southern Vanuatu suggests initial occupation only at about 2900 B.P., well within the period of the Lapita complex.²⁶

No pottery was found in the Fotoruma cave but otherwise the artifact assemblage would fit easily with what we might expect to find at a Lapita site, and at 2920 ± 110 B.P. within the Lapita time range.²⁷ In such cave sites, perhaps only representing transitory or occasional use, we may not find a representative range of the material culture of the time. Aceramic occupation of Guadalcanal contemporary with Lapita cannot be established with certainty on the basis of this one site. The case remains open.

While Green suggests that the earliest Mangaasi sites in central Vanuatu remain to be found and that Mangaasi is likely to be the founding culture there with Lapita as intrusive,²⁸ the case is by no means convincing. The earliest acceptable Mangaasi dates go back no further than 2595 ± 95 B.P.²⁹ We may well

still be missing up to a thousand years of prehistory from this area, suggested by the presence of a few decorated Lapita sherds at Erueti on Efate insecurely dated to 2300 ± 95 B.P. and associated with possible plain Lapita ware and Mangaasi pottery. While the Lapita is often seen here as an intrusive tradition, it should be noted that the Erueti date overlaps with the earliest Mangaasi date at two standard deviations and so could well be contemporary. The nonpottery artifacts from the Erueti site and the early levels at the Mangaasi type site are closely comparable in shell and stone adze forms and Tridacna rings which are not found in later central Vanuatu sites.³⁰ The earlier part of the central Vanuatu sequence which we have yet to find may well consist of sites transitional between Lapita and Mangaasi (see below).

A similar situation is suggested for southern Vanuatu but with pottery making probably abandoned by about 2,000 years ago. A single date from a rockshelter on Tanna of 2370 ± 90 B.P. was the basis for suggesting a fully aceramic sequence for this area. The next earliest date obtained from the site was from a burial dated 1650 ± 100 B.P. and the nature of early occupation is thus unclear.³¹ Similar doubts to those on the significance of the Fotoruma cave evidence should be entertained. From the neighbouring island of Erromango a ceramic occupation at Ifo village is bracketed between two dates: 2310 ± 70 B.P. and 2220 ± 70 B.P. Ceramic decoration is a local variant of Mangaasi, although a classic dentate-stamped Lapita sherd in secondary deposition and an incised Lapita sherd in the site suggest that an earlier Lapita occupation is present in the vicinity.³² A pollen sequence from Aneityum spanning the period from 5500 B.P. shows major changes and evidence for burning of the vegetation associated with a date of 2940 ± 80 B.P. This is interpreted as showing initial human impact on a previously pristine environment. No habitation sites of comparable age have yet been located on the island.³³

The New Caledonian sequence has recently been clarified by Green and Mitchell. These authors consider in detail the question of the tumuli, noting that a range of different phenomena have been lumped together under this term, some clearly natural, some (containing burials) clearly of human construction, and some of uncertain origin.³⁴ By a skilful manipulation of the several confusing radiocarbon dates for certain tumuli, none of which are associated with any artifactual material, Green and Mitchell present a case for aceramic pre-Lapita occupation by Oceanic-speaking Austronesians about 4,000-5,000 years ago. They reject on the other hand Shutler's hypothesis of an association for the tumuli with a 'non-Austronesian, aceramic, pre-neolithic'³⁵ occupation of New Caledonia and the rest of Island Melanesia dating to 10 000 B.P. Other researchers have not found 'concrete' mound cores with associated 'postholes' to be the convincing evidence of human construction that Green and Mitchell do.

Part of their argument for pre-Lapita occupation is based on linguistic data, the diversity of New Caledonian languages supposedly reflecting a greater time

depth than a Lapita occupation allows.³⁶ Dating language dispersal is a tricky business, and a subtle shift has occurred over the last 20 years away from lexicostatistics as an independent dating technique for the dispersal of Oceanic languages to putative associations between dated archaeological remains and language stages. In a recent consideration of linguistic differentiation, Pawley notes that time is only one of the controlling factors in a very complex situation of economic and social change subsequent to settlement of particular island groups which can lead to continuing unity or substantial language differentiation.³⁷ Green and Mitchell's argument also relies on other evidence of early widespread aceramic occupation in Island Melanesia, citing both Fotoruma Cave and southern Vanuatu as examples.³⁸ As we have seen, neither provides a firm basis for such an interpretation.

Paddle-impressed pottery is found in New Caledonia at sites contemporary with the earliest Lapita occupation of the island. Frimagacci hypothesized at one time that this pottery was not a separate tradition from Lapita but solely an innovation in construction technique which later became the mark of particular groups. In a later publication he saw the paddle-impressed technique as either having been introduced by the Lapita immigrants or having been borrowed by them from other populations already there or who arrived contemporaneosly.³⁹ Green and Mitchell, labelling the paddle-impressed pottery as the 'Podtanean' style after one of the sites where it is found, build a tentative case for it representing a cultural complex separate from Lapita but in contact with it. They do not speculate as to where this complex or its bearers originated.⁴⁰ Frimagacci's initial interpretation seems the most likely. Lapita pottery was often finished using a paddle and anvil technique, before decoration. The only difference in construction of the Podtanean style is that the paddle used was carved and therefore further decoration was unnecessary. In other aspects of material culture (for which the evidence is admittedly scanty) there is no difference between Lapita and Podtanean sites, such as we would expect if separate cultural complexes were present.⁴¹ There is also nothing in these early pottery sites indicative of contact with a prior aceramic group or groupings.

In conclusion, strong archaeological or linguistic evidence is lacking for cultural complexes contemporary with or earlier than Lapita in Island Melanesia south of the Bismarcks-Bougainville area. It would seem a more parsimonious explanation to suggest Lapita as the founding culture for the area with cultural differentiation occurring later.

THE CONCENTRATION of Lapita sites in Island Melanesia on small offshore islands has been interpreted as evidence that the larger islands were already inhabited by other people, either an earlier migration of Oceanic speakers or populations of NAN speakers.⁴² This pattern, however, is open to another interpretation, the clue to which is given by the association of Lapita sites with natural events such as changes in land elevation relative to sea level, dune for-

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mation subsequent to Lapita occupation, and changes in coastlines accompanied by the flooding of sites via stream and sea action.⁴³ Post-depositional geomorphic changes have tended to reduce Lapita and other early site visibility on larger high volcanic and continental islands, in comparison with site visibility on smaller, generally coralline islands. In stable environments on high islands or where recent uplift has occurred unaccompanied by extensive alluviation, site visibility is good and early sites have been located. We might also expect early evidence of settlement to be forthcoming in deeply stratified cave deposits, although due to sporadic use these may not provide representative samples of cultural material.

The high density of Lapita sites on Tongatapu, Uvea (Wallis), the Reef Islands, Malo and Niuatoputapu reflects this difference in site visibility and is not necessarily culturally significant. These areas are all either uplifted coralline islands, or small volcanic islands with no substantial sources of alluvial or colluvial material to bury the cultural deposits. In addition, since Lapita occupation former shorelines have become tectonically uplifted removing the sites from any danger of marine erosion.⁴⁴ Other Lapita sites have been found in similar locations.⁴⁵ Caves and deeply stratified rockshelters have also not surprisingly yielded Lapita materials.⁴⁶ In the Admiralty Islands, apart from at the Kohin cave, only one decorated Lapita sherd has been located, this from a hilltop.⁴⁷ The two earlier (probably) aceramic sites in the Admiralties are an inland rockshelter and an open site revealed by a surface scatter of artifacts from a later phase of occupation.⁴⁸ Most Admiralty Islands sites so far located date to within the last 2,000 years. Earlier sites on Lou Island come from exposures of a soil mantled by up to 3 m of ash and pumice deposited about 2000 B.P.⁴⁹

The earliest coastal New Guinea sites are either where uplift of marine terraces has occurred, sometimes found because of stream erosion of soils which developed subsequently (the Huon Gulf, Aitape), or in stratified rockshelters (Kukuba, Rupo and Ouloubomoto in southern Papua).⁵⁰ Nowhere else in the New Guinea lowlands have archaeological sites older than 2000 B.P. been found. This pattern contrasts strongly with the extensive evidence for Pleistocene and Early Holocene occupation in the Highlands. Burial of early sites by alluvial deposition and extensive coastal progradation would seem best to explain this surprising settlement pattern. The general lack of early sites on the main islands of the Solomons and Vanuatu could be similarly explained, coupled with a general lack of intensive archaeological survey. On Erromango in southern Vanuatu pottery sites were only located in areas of Holocene uplifted coral terraces which had not subsequently been covered by alluvial deposition.⁵¹ On Aneityum evidence was obtained of extensive shoreline progradation and alluvial build up within the last 2,000 years. In the river valleys tested no land surfaces older than 2,000 years were located in stratigraphic sections sometimes over 4 m in depth.⁵² Earlier sites are presumably buried under many metres of alluvium a considerable distance from the shore and will be extremely difficult to locate.

The New Caledonian Lapita sites occur on the coast on raised marine terraces and dunes which have not been subsequently deeply buried. Some of these sites were exposed by coastal erosion, one as a result of a sand mining operation.⁵³ That other early sites also exist deeply buried under alluvium in some of the larger river valleys has long been established, although the significance of these sites has only recently been recognized.⁵⁴ In 1945 a well was dug in the middle of the extensive alluvial plain of Moindou. The stratigraphy consisted of 9 m of alluvium on top of *in situ* decomposed friable red schists. Fragments of pottery of Oundjo style (post 2000 B.P.) were found in the top 3 m of the deposit, and further pottery, most closely linked to the Podtanean style which is earlier than 2000 B.P.,⁵⁵ was located at 6.5 m depth. In 1889 similarly early pottery was recovered at 6 m below the surface on the plain of Niza.⁵⁶ These findings suggest that settlement pattern interpretations based on the presently known distribution of Lapita and other early sites in New Caledonia may be distorted.

Finally, we should recall the pattern of Lapitoid sites on Futuna and Alofi (Horne Islands).⁵⁷ Four pottery bearing sites are known, three on volcanic Futuna and one on the raised limestone island of Alofi. The Alofi site was a surface scatter of pottery on an inland plateau, while two of the Futuna sites (both in recently uplifted areas) were revealed by land disturbance: airfield construction and the digging of irrigated pondfield gardens. The final site was revealed by a stream cutting down over 2 m through colluvial-alluvial deposits to erode a Lapitoid site dating to 2120 ± 80 B.P. Eroded sherds were found washing out on to the beach some 300 m away. Two thousand years ago the site would have been on the beachfront. In addition to the site being covered by erosional deposits, there is evidence that the coastline has been tectonically uplifted since the Lapita occupation.⁵⁸

We are finding Lapita sites where they are easily visible because of postdepositional geomorphological factors and this is giving a false picture of their distribution. We should expect them to be as numerous on high volcanic islands as they are on small, offshore coralline ones. Where we have a reasonably representative sample of sites the picture is one of quite dense coastal settlement.⁵⁹ If this pattern is equally applicable to the larger islands, and there seems no reason why it should not be, then clearly many Lapita sites remain to be found. Either the situation represents 'an initially small population with the capacity to reproduce fast enough to supply its own recruits',⁶⁰ or movement of large numbers of people out of an already densely settled Bismarcks-Bougainville area. The first interpretation is generally favoured but the second also needs serious consideration.

LATE Lapita pottery sequences throughout much of the area of its distribution show remarkably similar changes. The tendency is for reduction in design elaboration over time with ultimate loss of any decoration except notched rims in some areas. A plain ware element is present in all Lapita sites but becomes more dominant over time. The complex vessel forms of earlier Lapita sites become reduced to an assemblage comprising only simple jars and bowls.⁶¹ This transition is best defined in the Lapitoid series of western Polynesia and Fiji, with Early Eastern Lapita (generally prior to 1000 B.C.) characterized by classic dentate-stamped decoration and complex vessel forms, through Late Eastern Lapita up to 500 B.C. where dentate stamping declines in importance, to the Polynesian plain ware of the latest sites.⁶² It was this plain ware which was transferred to the Marquesas and is found in the earliest sites there dating to about 2000 B.P.⁶³ Pottery disappears from sites throughout western Polynesia soon after this time. The generally parallel ceramic sequences from the Fiji-Tonga-Samoa area are taken to represent groups in a continuing communication network. These Lapita populations are considered ancestral to the present Polynesians.⁶⁴

More recently the parallel nature of developments at western Lapita sites has also been recognized with the definition of Lapitoid plain ware assemblages dating from 2900 to 2000 B.P. from Santa Cruz, the Reef Islands, Anuta, Tikopia, Taumako, Santa Ana and Bellona, with related assemblages from Buka and the Banks Islands.⁶⁵ In Santa Cruz the plain ware sites partially overlap in time with other sites using decorated Lapita pottery.⁶⁶ Plain pottery has also been found in eastern Micronesia in Truk dating to about 2000 B.P., and at several locations on Ponape where one site was dated to 400 A.D.⁶⁷ Some of the Ponape material displays notched rims reminiscent of the Melanesian late Lapitoid material.⁶⁸ It seems highly unlikely that the earliest eastern Micronesian sites have yet been found.⁶⁹

About 2,000 years ago throughout the southeast Solomons pottery production ceased, although pottery was then imported to Tikopia and Vanikoro from Vanuatu to the south.⁷⁰ Indeed by this time production of identifiable Lapita pottery had ceased everywhere except perhaps New Caledonia. This island appears to have remained somewhat isolated from trends occurring in the rest of the Lapita area but Lapita pottery production ceased here as well about 1800-1700 B.P.⁷¹

Contemporary with the final phases of Lapita and continuing long afterwards in some areas we find the incised and relief pottery or Mangaasi style widespread in Melanesia. Pottery construction techniques are similar to Lapita although in some cases a harder paste is produced. Vessel forms are generally similar to late Lapitoid forms i.e. simple bowls and jars. Incision and applied relief do occur in some earlier Lapita assemblages but detailed comparisons have not yet been made although Mangaasi designs appear to be distinct from Lapita.⁷²

Mangaasi-like pottery is found from Wuvulu and the Admiralties in the north to southern Vanuatu and New Caledonia in the south. In Wuvulu it

dates to 1500 B.P. and in the Admiralties we have an associated date of 2070 ± 120 B.P.⁷³ In Watom this style is found with Lapita pottery made from similar fabric and dating to 2420 ± 110 B.P.⁷⁴ At Lesu in New Ireland a related pottery style dates to 2460 ± 120 B.P. A single dentate-stamped sherd there suggests the presence of an earlier Lapita site somewhere in the vicinity.75 Generally plain Lapitoid pottery occurs with Mangaasi-related ceramics in the Buka-north Bougainville area dating to 2480 ± 140 B.P. From about 2000 B.P. onwards, only pottery of Mangaasi type appears to be in use.⁷⁶ Imported Mangaasi ceramics are found on Tikopia at 1990 ± 100 B.P. and on Vanikoro dating from at least 1750 ± 85 B.P.⁷⁷ From Pakea in the Banks Islands an assemblage containing ceramic elements linked both to Lapitoid plain ware and Mangaasi dates to 2240 ± 70 B.P.78 As already mentioned, the earliest Mangaasi sites in central Vanuatu go back to 2595 ± 95 B.P., while the Mangaasi-related pottery from Erromango in southern Vanuatu dates to 2310 ± 70 B.P.⁷⁹ The Oundjo style in New Caledonia is also interpreted as a Mangaasi variant. It is sometimes found in late Lapita sites there but generally dates to after 1800 B.P.⁸⁰ In Fiji about 2000 B.P. there is a change from Lapitoid plain ware to paddle-impressed ceramics of the Navatu phase. There is some question as to whether paddle-impressed sherds are present in earlier Fijian Lapita assemblages as well. A few paddle-impressed sherds are also known from plain ware assemblages in Tonga.⁸¹ In other aspects of material culture such as adze forms there is continuity in the Fijian sequence.82

It has been noted that several of the above assemblages contain both Late Lapitoid and Mangaasi elements, suggesting that they are transitional between the two. Previously the occurrence of both styles together has been interpreted as evidence of mixed deposits.⁸³ The alternative possibility of cultural continuity has not been given the consideration it deserves. Kennedy argued that although new decorative elements (Mangaasi) appear about 2000 B.P. in the Admiralties sequence there was basic cultural continuity with no intrusions or sharp breaks. A recent reanalysis of the Watom ceramics by Anson suggests that the incised and relief style develops from Lapita rather than being intrusive. Both styles were technologically and compositionally similar and probably locally made.⁸⁴ Specht interpreted his north Bougainville-Buka evidence as showing a break between the Lapitoid Buka style and the Sohano style linked to Mangaasi. Stratigraphically, however, the two styles could not be clearly separated and continuity is found in pottery temper and probably in importation of obsidian and in non-ceramic artifacts.⁸⁵

In Tikopia Kirch and Yen noted a definite cultural break between the Kiki Phase with locally manufactured Lapitoid ware and the subsequent Sinapupu Phase when Mangaasi pottery was imported. New artifact forms occur and some drop out but Kirch and Yen are careful not to rule out a basic cultural continuity, noting that many identical artifact forms occur in both phases.⁸⁶ Kirch points out that Ward's Pakea site contains pottery typical both of the late

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Lapitoid wares and of Mangaasi. He suggests on the basis of the Tikopia sequence that the Pakea site may be mixed. An alternative interpretation, however, is that Pakea is another transitional site where ceramics related to both traditions were being produced.⁸⁷ Erueti on Efate appears to be another transitional site although its stratigraphic integrity is not certain.⁸⁸

The Ifo site on Erromango is clearly not mixed in its lower levels where good organic preservation, well-defined midden concentrations and stratified ash lenses established stratigraphic integrity. Decorated ceramics, with one or two exceptions, represent a variant of Mangaasi with punctate designs dominant and incising rare. Only 12% of the sherds show any decoration (at the Mangaasi type site the figure was 38-46%),⁸⁹ the plain pottery consisting of a range of temper types including calcareous as well as mineral tempers. One sherd appears to be a New Caledonian import while the rest were probably produced locally. Artifact types include a hinge region Tridacna adze and a grooved sea urchin spine, both of which would be at home in a Lapita site.⁹⁰

Frimagacci has claimed that at the Boirra site in New Caledonia, Lapita and Oundjo (Mangaasi) tradition pottery were in use contemporaneously. Green and Mitchell suggest that this deposit is mixed but the basis for this contention seems to be solely that both kinds of pottery occur together. Cultural continuity seems as likely an explanation, and a degree of continuity between Podtanean and Oundjo styles is indeed recognized by Green and Mitchell.⁹¹

There are thus several candidates for sites transitional between Lapita and Mangaasi assemblages: Watom, Buka, Pakea, Erueti, Erromango (the Ifo site) and Boirra in New Caledonia. On the basis of his analysis of the Yanuca site, Hunt argues for continuity in western Fiji between Lapita and the subsequent Navatu phase.92 The argument for a widespread and generally similar sequence of ceramic change within the western Lapita tradition including forms transitional from Lapita to Mangaasi requires a continuing communication network throughout the region. Many of the islands in the western Lapita area are intervisible and there is evidence from the period 2500-2000 B.P. of continued communication across the wider ocean gaps. Thus we know of connexions between New Caledonia and the Loyalty Islands and New Caledonia and Erromango in southern Vanuatu.93 The sea gap between Tikopia and the Banks Islands was clearly being crossed at this period as shown by the movement of Banks Islands volcanic glass north to Tikopia as well as Vanuatu Mangaasi pottery to Tikopia and Vanikoro. At this period Tikopia also has links to the main Solomons chain through the import of Ulawa chert.⁹⁴ At the other end of the Solomons chain, the Buka area links to the main Bismarcks region by the presence of Admiralty Islands obsidian.95 This admittedly attenuated chain of connexion supports the evidence of parallel ceramic changes for some form of continued communication allowing us to suggest cultural continuity from the Lapita period.

A superficial analysis of non-ceramic artifacts from the area also suggests

basic continuity between Lapita and later sites. The samples are hardly adequate but as Terrell stated, when confronted by a similar lack of representative samples in examining Bougainville pottery,

While the . . . traits were not selected at random from a large, well-defined set of traits and it is doubtful that all the traits presented ought to carry the same weight, an attempt to quantify similarities and differences has the merit of objectifying what might otherwise be solely impressionistic claims.⁹⁶

Table 1 gives the list of artifact types considered and their distribution, while Table 2 gives coefficients of similarity, computed by dividing the pairwise matches by the sum of the pairwise matches and mismatches.⁹⁷ The results are at least suggestive of basic overall continuity between a range of Lapitoid, putatively 'transitional' and Mangaasi-related sites. Fotoruma Cave was included to test the suggestion made earlier of its basic similarity to Lapita assemblages. Early Oposisi and Nebira 4 combined were included because of the suggested relationship of these early south Papuan coast sites to Lapitoid assemblages. These sites are thought to represent the settlement of pottery-using Oceanic speakers at points along the south coast at about 2000 B.P. This analysis only very weakly supports the Lapitoid affinities suggested by study of the pottery.⁹⁸

In his discussion of Lapita non-ceramic artifacts, Green states:

The Lapita cultural complex exhibits a full range of portable artifacts typical of many Oceanic assemblages. What is distinctive is that many items in the Lapita sites of a particular area are not present in other cultural complexes either contemporary with it or later, often because they had to be imported.⁹⁹

He then goes on to list the general inventory of Lapita associated artifacts, most of which are included in Table 1. While there is clearly some regional variation within Lapita sites,¹⁰⁰ the majority of the artifacts listed are widespread both in time and space contrary to Green's assertion.

A case worth considering, then, can be made for continuity between Lapita and successor traditions throughout the area of its distribution. The case for cultural continuity in western Polynesia has rarely been questioned, but for Fiji and the rest of Island Melanesia such a view has not been popular. This seems surprising as linguistic continuity, except on the Polynesian Outliers and one or two other special cases, has been generally accepted. It is usually explained, however, either by Lapita colonists learning the languages of the inhabitants already present as they moved through the area, or by these populations learning the language of the Lapita people they subsequently absorbed culturally.¹⁰¹ If cultural continuity is argued there seems little need for such complex explanations.

Behind the orthodox interpretation of Lapita as a separate cultural tradition is the idea of the Lapita colonists as an endogamous group of Polynesian physical type moving out of Southeast Asia through an area already inhabited by people of Melanesian physical type and then into previously uninhabited

	Watom	Lesu	Buka	Fotoruma	SZ-33	SZ-47	Tikopia-Kiki	Early Anuta	Tikopia-Sinapupu	Banks (Pakea)	Erueti	Mangaasi	Erromango	New Caledonia	Oposisi/Nebira 4	Tonga/Samoa
Bone point	_	х	х	_	_	х	_	_	х	_	_	_	_	_	_	х
Bone spatula	х	х	х	_	_	_	_	_	_	_	_	_	_	_	х	_
Shell Microadze (KT*1)	_	_	_	nd	х	х	х	-	-	х	_	_	_		-	
Shell adze (KT3)	х	-	х	nd	х	-	х	х	х	х	-	х	-		-	_
Shell adze (KT4)	х	х	х	nd	х	х	х	х	х	х	-	х	-	-	-	-
Shell hinge-region adze (KT6-8)	-	-	-	nd	х	х	х	х	х	?	Х	х	х	-	-	х
Cassis lip adze (KT9)	-	-	Х	-	-	Х	-	Х	Х	-	-	-	-	_ `	-	-
Shell one-piece fishhook	-	-	-	-	Х	Χ.	Х	х	Х	-	-	-	-	-	-	х
Shell trolling lure	х	-	Х	-	Х	-	х	-		-	 .	-	-	-	_	-
Grooved sea urchin spine	-	-	-	-	-	-	х	-	-	-	-	-	Х	-	-	х
Cypraea net weight	-	-	-	-	-	-	-	-	Х	-	-	-	-	х		-
Flat shell bracelet segment	-	-	-	-	х	-	х	-	-	-	-	-	-	-	-	х
Small shell bead	-	-	Х	Х	-	-	Х	х	Х	х	?	Х	х	-	х	х
Trochus armband	х	х	х	х	х	х	х	х	х	х	-	Х	-	х	х	х
Conus ring or bracelet	-	х	х	х	х	х	х	-	х	х	х	х	х	х	х	х
Cypraea peeler or lure	-	-	-	-	-	х	х	х	х	х	-	-	-	х	-	х
Coral abrader	-	-	-	-	-	х	х	х	х	-	-	-	-	-	-	Х
Sea urchin spine abrader	-	-	х	х	-	х	х	х	х	-	-	-	-	-	-	х
Drilled marine tooth	-	-	х	-	-	-	-	-	-	-	-	-	-	-	х	
Spondylus pendant	-	-	-	-	-	-	х	х	-	-	-	-	-	-	-	-
Tridacna ring	х	-	х	_	х	?	х	х	х	-	х	х	-	_	-	х
Oval/Plano-convex stone adze	х	-	х	х	х	-	х	х	-	-	х	х	-	х	-	х
Arca shell netsinker	-	х	х	-	-	-	-	-	-	х	-	-	-	х	-	-
Coral or basalt slingstone	-	х	-	-	-	х	-	-	-	-	-	-	-	-	-	-
Human cranial bone tablet	-	х	-	-	-	-	-	_	-	_	-	-	-	-	х	-
Strombus or Conus pendant	-	-	-	-	-	-	-	х	-	х	-	-	-	-	-	-
AVT VILT																

TABLE 1-Non Ceramic Artifact Type Distribution in S.W. Pacific Sites.

• KT-Kirch Type

Polynesia and eastern Micronesia. This supposedly explains the physical differences between Melanesians and Polynesians, the Fijians being a 'mixed' group who are basically Polynesians but have been affected by later Melanesian migrations.¹⁰² Recent physical anthropological research disputes Howells's conclusions concerning the Fijians, showing that they are not generally a mixed population but are basically Melanesian.¹⁰³ Most physical anthropologists do not think it possible to derive the Polynesian physical type from any Melanesian populations by processes of founder effect and adaptation.¹⁰⁴ This would of course be the easiest way to explain the archaeological and linguistic evidence, and at present the physical anthropological explanations seem distinctly out of step. It must be remembered that we have virtually no Lapita skeletal material and the available data on physical anthropology are largely from recent populations after over 3,000 years of genetic change.¹⁰⁵ Possibly the human biology of small populations and the processes of founder effect and adaptation in the Pacific are not understood well enough yet for any firm conclusions to be made on the basis of comparison of recent or modern populations. The problem may be as much with the current models as with the available data.

IT SOMETIMES seems as though archaeologists are undervaluing their own data, either in comparison with linguistics or physical anthropology. Thus Bellwood speaks eloquently of the 'populations of archaeological evidence . . . hideously ravaged by time and the tropical climate'.¹⁰⁶ Under such circumstances, archaeology is seen only as a 'witness' to the 'linguistic version of Austronesian origins' and in particular its counterpart, 'the viewpoint of biological anthropology'. In Bellwood's writings we see reproduced the contemporary Polynesian myth of an origin unconnected with the supposedly 'primitive' Melanesians, an origin more closely linked to the 'high civilizations' of Asia or of other lighter skinned peoples.¹⁰⁷ In so doing a large part of the archaeological data from Melanesia is ignored. Although the myth stems in part

TABLE 1-Legend and sources.

X, present; ?, possibly present; -, absent; n.d., no details available. Sources of information and site dates (unrecalibrated) are: Watom (c. 2400 B.P.) – Specht, 'Preliminary report . . .'; Lesu (c. 2450 B.P.) – White and Downie, 'Excavations . . .; Buka (2500-1450 B.P.) – Specht, 'Prehistoric and modern pottery . . .'; Fotoruma (Occupation A and B, 2900-1600 B.P.) – Black and Green, Radiocarbon Dates . . .; Santa Cruz-33 (Decorated Lapita, and plain ware) (c. 2700 B.P.), Santa-Cruz-47 (plain ware 3200-2050 B.P.) – McCoy and Cleghorn, 'Summary report . . .', Pat McCoy, pers. comm.; Tikopia Kiki Phase (2700-2100 B.P.), Tikopia Sinapupu Phase (2100-800 B.P.) – Kirch and Yen, Tikopia . . .; Anuta (2800 BP-before 2000 B.P.) – P. V. Kirch, 'A Revision of the Anuta Sequence', Journal of the Polynesian Society, XCI (1982), 245-54; Banks Islands, Pakea – (2250-1900 B.P.) – Ward, 'Prehistoric settlement . . .'; Erueti (c. 2300 B.P.), Mangaasi (2600-1st millennium A.D.) – Garanger, Archéologie . . ., Erromango (c. 2300-2200 B.P.) – author's data; New Caledonia (3000-1800 B.P.) – Green and Mitchell, 'New Caledonian culture history . . .'; Oposisi (c. 2000 B.P.) – Vanderwal 'Exchange . . .'; Nebira 4 (c. 2000 B.P.) – J. Allen, 'Nebira 4, an early Austronesian site in central Papua', Archaeology and Physical Anthropology in Oceania, VII (1972), 92-124; Tonga and Samoa (3000-2200 B.P.) – Jennings et al., Excavations on Upolu . . ., J. Jennings and R. N. Holmer, Archaeological Excavations in Western Samoa, Pacific Anthropological Records 32 (1980), J. Poulsen, 'Archaeological excavations on Tongatapu', in I. Yawata and Y. Sinoto (eds), Prehistoric Culture in Oceania (Honolulu 1968), 85-92.

	Watom	Lesu	Buka	Fotoruma	SZ-33	SZ-47	Tikopia-Kiki	Early Anuta	Tikopia-Sinapupu	Banks (Pakea)	Erueti	Mangaasi	Erromango	New Caledonia	Oposisi/Nebira 4	Tonga/Samoa
Watom	_	0.25	0.44	0.25	0.50	0.18	0.33	0.31	0.24	0.21	0.20	0.50	0.00	0.18	0.18	0.17
Lesu	0.25	_	0.38	0.20	0.19	0.31	0.14	0.10	0.22	0.29	0.08	0.23	0.09	0.27	<i>0.40</i>	0.17
Buka	<i>0.44</i>	0.38	_	<i>0.42</i>	0.39	0.35	<i>0.41</i>	0. 4 0	0.47	0.33	0.27	0.47	0.13	0.25	0.33	0.35
Fotoruma	0.25	0.20	<i>0.42</i>	-	0.33	0.23	0.38	0.33	0.33	0.38	0.50	0.67	0.33	0.33	0.38	0. 42
SZ-33	0.50	0.19	0.39	0.33	-	<i>0.41</i>	0.65	0.39	0.39	0. 4 0	0.33	0.58	0.15	0.21	0.13	<i>0.41</i>
SZ-47	0.18	0.31	0.35	0.23	<i>0.41</i>	-	0.50	0.50	0.69	0.35	0.20	0.31	0.13	0.19	0.12	<i>0.53</i>
Tikopia-Kiki	0.33	0.14	0.41	0.38	0.65	0.50	-	0.63	0.55	<i>0.42</i>	0.29	0.47	0.24	0.21	0.15	0.67
Early Anuta	0.31	0.10	0. 4 0	0.33	0.39	0.50	0.63	-	0.65	<i>0.41</i>	0.27	0.47	0.13	0.18	0.11	0.50
Tikopia-Sinapupu	0.24	0.22	0.47	0.33	0.39	0.69	0.55	0.65	-	<i>0.41</i>	0.27	<i>0.47</i>	0.20	0.25	0.18	<i>0.59</i>
Banks (Pakea)	0.21	0.29	0.33	0.38	0. 4 0	0.35	<i>0.42</i>	<i>0.41</i>	<i>0.41</i>	-	0.25	0.50	0.27	0.33	0.23	0.28
Erueti	0.20	0.08	0.27	0.50	0.33	0.20	0.29	0.27	0.27	0.25	-	0.63	0.50	0.22	0.22	0.38
Mangaasi	0.50	0.23	0.47	0.67	0.58	0.31	0.47	<i>0.47</i>	<i>0.47</i>	0.50	0.63	-	0.33	0.27	0.27	0. 4 0
Erromango	0.00	0.09	0.13	0.33	0.15	0.13	0.24	0.13	0.20	0.27	0.50	0.33	-	0.11	0.25	0.31
New Caledonia	0.18	0.27	0.25	0.33	0.21	0.19	0.21	0.18	0.25	0.33	0.22	0.27	0.11	-	0.20	0.27
Oposisi/Nebira 4	0.18	0. 4 0	0.33	0.38	0.13	0.12	0.15	0.11	0.18	0.23	0.22	0.27	0.25	0.20	-	0.19
Tonga/Samoa	0.17	0.17	0.35	<i>0.42</i>	0.41	0.53	0.67	0.50	0.59	0.28	0.38	<i>0.40</i>	0.31	0.27	0.19	-

from Captain Cook, its particular Polynesian cast was given by the Maori Scholar Te Rangi Hiroa (Peter Buck) with his view of the 'Vikings of the Sunrise'.¹⁰⁸ As a growing Pan-Pacific nationalism links the varied peoples of the region, a Melanesian origin for the Polynesians is likely to be seen as more acceptable, even politically useful. Perhaps then we shall see a shift away from the biological viewpoint which Bellwood favours.

The intent of this paper has been to raise questions about various aspects of the orthodox explanations regarding Lapita culture. While none of the alternative positions put forward here are cast in stone, they do seem to have some empirical support given our present state of knowledge. Far from Lapita being a basically intrusive Southeast Asian cultural complex, its form and much of its content may have developed in the northwest Melanesian area. Over much of Island Melanesia Lapita could well be the founding cultural complex, as it is in Fiji and western Polynesia. Our present picture of Lapita settlement pattern and site density may be severely skewed because of post-depositional landscape change on the larger islands. Subsequent cultural traditions, aceramic in the southeast Solomons and linked with Mangaasi-style ceramics in much of the rest of Island Melanesia, could have developed out of Lapita and therefore not be intrusive. Thus an argument for cultural continuity can be made in Island Melanesia as it is for western Polynesia. This provides us with a simpler framework of Southwest Pacific prehistory, but I would claim a no less interesting one.

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2 Authors of the works here cited do not necessarily hold to all aspects of the model and some have changed their view since the publication referred to. See P.Bellwood, Man's Conquest of the Pacific (Auckland 1978); idem, The Polynesians (London 1978); idem, 'The Great Pacific Migration' in Yearbook of Science and the future for 1984 (Chicago 1983), 80-93; Green, op. cit.; R.C.Green, 'Models for the Lapita cultural complex: an evaluation of some current proposals', New Zealand Journal of Archaeology 4:7-19 (1982); R.Shutler and J.C.Marck, 'On the dispersal of the Austronesian

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4 In preparing this review I have been influenced by the work of many scholars, only some of whose ideas have yet been published, in particular Jim Allen, Dmitri Anson, Jack Golson, Roger Green, Phil Hughes, Jean Kennedy, Pat Kirch, Pat McCoy, Jim Specht, Peter White and Douglas Yen. Important refs include D.Anson, 'Lapita pottery of the Bismark Archipelago and its affinities', PhD thesis, University of Sydney (Sydney 1983); J.Kennedy, 'Archaeology in the Admiralty Islands: some excursions' *Bulletin of the Indo-Pacific Prehistory Association* 3:22-35 (1982); idem, 'On the prehistory of western Melanesia: the significance of new data from the Admiralties', *Australian Archaeology* 16:115-22 (1983); J.P.White and J.Allen, 'Melanesian prehistory: some recent advances', *Science* 107:728-34 (1980).

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Roger Green was most helpful during the preparation of this paper by sending me several references which were otherwise unavailable. The paper was typed by Irene Takata. Comments on an earlier draft were received from George Grace, Bion Griffin, Pat Kirch and Pat McCoy.

12 The Polynesian Outliers

Continuity, change, and replacement

Patrick V.Kirch

ALONG THE FRINGES OF MELANESIA, AND ESPECIALLY ON THE SMALLER HIGH islands and atolls lying to the east of the main island arcs, are some 18 societies known collectively as the Polynesian Outliers (Fig. 1). Unknown archaeologically until very recently, these outliers have nonetheless stimulated theories and arguments about Polynesian origins for three quarters of a century. William Churchill, in his 1911 monograph *The Polynesian Wanderings*, argued that the Outliers were relict settlements that marked the trail of the Polynesian migrations from west to east, a viewpoint sustained more recently by the linguist A. Cappel.¹ Thilenius on the other hand maintained that these Polynesian enclaves in a Melanesian sea represented east-to-west back migrations and drift voyages, and suggested that the settlement histories of these islands might be quite complex.² This view was upheld by Sir Peter Buck,³ who saw in it support for his thesis that the Polynesians had migrated through Micronesia.

In the last two decades, linguistic studies have done much to clarify the relationships between the Outlier languages and those of Triangle Polynesia, and have lent credence to Thilenius's arguments. Bayard used the lexical data available in 1965 to attempt a lexicostatistical classification of Outlier languages.⁴ The major advance in Outlier linguistics, however, came with Pawley's analysis of shared innovations in phonology, lexicon, and morphology,⁵ which demonstrated that all known Outlier languages are attributable to the Nuclear Polynesian subgroup of Polynesian. Pawley defined a

Samoic-Outlier subgroup of Nuclear Polynesian, in which the Outlier languages were classed with Samoan, East Futunan, the Tuvalu dialects of Vaitupu and Nanumea, Tokelauan, and Pukapukan. This subgrouping model clearly supported the view that the Outlier populations derived from Triangle Polynesia (the 'blowback' argument). He also suggested that the Outlier languages might themselves be further subgrouped, with certain northern outliers in particular forming a relatively clear-cut subgroup. Such subgrouping might be anticipated, given multiple origins for Outlier populations, from differing sources within Triangle Polynesia.

Biggs clarified the position of Anutan,6 one of the southeast Solomons Outlier languages, offering a parsimonious hypothesis to account for the putative Tongan loan words identified by Green.⁷ Biggs suggests that these Tongan lexemes were already a part of the East Uvean (Wallis Island) language brought to Anuta by drift voyagers sometime in the mid-second millenium A.D. Ross Clark,⁸ dealing with the evidence from three Vanuatu Outlier languages, agreed with Pawley that these belonged to Nuclear Polynesian. He reiterated the complexities of the linguistic situation, however, in noting that the membership of Samoic-Outlier 'and its characteristic innovations, have yet to be precisely defined'.9 While Mele-Fila and Futuna-Aniwa in Vanuatu appear to form a low-order subgroup, these could not be clearly grouped with any specific Samoic-Outlier languages. Most recently, Howard has examined the northern atoll Outlier languages (Nukuoro, Kapingamarangi, Takuu, Luangiua, Sikaiana, Nukumanu, and Nukuria), and concludes that these constitute a valid subgroup that Howard terms 'Equatorial Outlier'.¹⁰ He further suggests that these languages group with Ellicean (Tuvalu).

While linguistic analyses have shown that the Outlier languages fall unquestionably within the high-order Nuclear Polynesian subgroup, and are thus linked with certain languages of western Polynesia (especially Samoan, East Futunan, East Uvean, and Tuvalu), the internal relationships and further subgrouping of the Outlier languages remain obscure. A northern subgroup of Equatorial Outliers seems well supported, Anutuan and Tikopian are clearly linked, and Mele-Fila and Futuna-Aniwa also form a distinct subgroup. Beyond this, the linguistic picture remains hazy, and awaits further detailed research.

An important theoretical contribution to Outlier settlement history was the computer simulation of drift voyaging by Ward, Webb and Levison.¹¹ A large number of simulated voyages originating in the west Polynesian region made successful landfalls on Outlier islands, particularly Ontong Java, Taumako, Nukumanu, Tikopia, and Anuta, but on others as well. East Uvea, East Futuna, Rotuma, and Tuvalu were identified as highly probable source areas. These results thus corroborate the conclusions of Thilenius, Bayard and others that the settlement of the Outliers was probably due (at least in large part) to

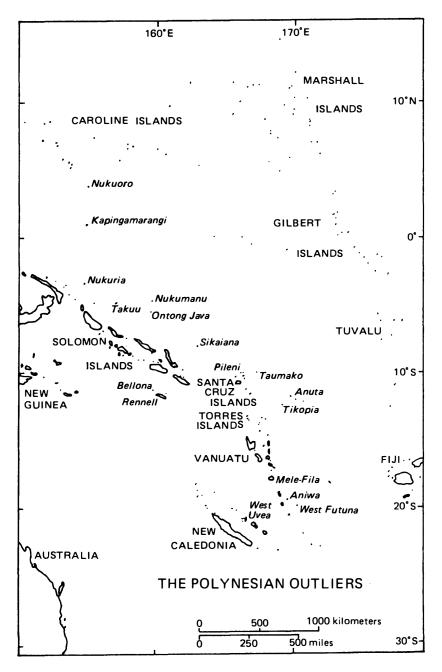


FIGURE 1: The Polynesian Outliers (indicated by the names in italics).

difficult to assess the evidence from Nukuoro and Kapingamarangi. In the latter cases, relatively late settlement (probably from different source areas) and a continuity of occupation, with the likelihood of secondary settlements or contacts (e.g. with other Micronesian islands), appear to have been the case. Certainly, there is nothing in the archaeological records of either island that would suggest cultural replacement. Thus, Nukuoro and Kapingamarangi may well exemplify the east-to-west drift voyage model of Outlier settlement, with relatively shallow time depth.

Southeast Solomons Outliers

Whereas the northern atolls exhibit relatively shallow time depth and continuity of occupation, the situation among the Outliers of the southeastern Solomon Islands is far more complex, with cultural sequences extending back nearly three millennia. To date, the islands of Anuta and Tikopia have been most intensively investigated, and their complex sequences will be reviewed in some detail, although evidence from Taumako, Rennell, and Bellona will also be considered.

Anuta. Among the smallest yet most densely populated islands of the Pacific, Anuta lies 137 km northeast of Tikopia (Fig. 1), and these two Outlier societies maintained close social and economic ties. Anutan oral traditions speak of two periods of settlement, with an autochthonous population (the earth-sprung *apukere*) having been supplanted some 12 generations ago by immigrants from Uea, presumably Uvea. The first linguistic study of Anutan, by Green, indicated that the language was derived from Nuclear Polynesian, although a period of Tongan borrowing was suggested.¹⁸ More recently, Biggs has outlined a hypothesis for the inclusion of these Tongan loan words, suggesting that Anuta was colonized by Uveans not long after Uvea itself had been conquered by Tongans (in about the 16th century A.D.).¹⁹ Thus the Tongan loan words were introduced into Anutan speech via Uvea, and not as a result of a Tongan intrusion in Anuta.

The archaeological investigation of Anuta, by Kirch and Rosendahl in 1971,²⁰ revealed a complex stratigraphic situation in the main settlement site underlying the present village, with radiocarbon dates indicating initial settlement of the island about 950 B.C. With such time depth, it is clear that both the Anutan oral traditions and the linguistic evidence are relevant only to the latest phase of this lengthy prehistoric sequence.

To summarize briefly the Anutan sequence as recently revised,²¹ the island was colonized around 950 B.C. by a population making Lapitoid plain ware ceramics. The origins of this initial population are unknown, although the presence of a chert nodule of possible Futunan origin, and the ceramics themselves, point to Futuna Island in west Polynesia as a likely homeland. If so, the first settlement of Anuta represents a very early 'outlier' situation, at a time when 'Polynesian culture' and language were only just beginning to be differentiated from Fijian and other east Melanesian languages and cultures. After a period of unknown duration, but presumably still in the first millennium B.C., the island was hit by a particularly severe cyclone, resulting in the deposition of a substantial dune deposit, capping the initial settlement site. The island was subsequently abandoned, quite probably due to the inability of the population to recover from the storm devastation (the island is only 0.4 km² in area).

The duration of the putative occupation hiatus is not known, but by A.D. 580 the island had been recolonized, this time by a population lacking the use of ceramics. Indeed, the artifact array from this resettlement phase is quite skimpy, consisting only of *Cassis* and *Tridacna* shell adzes, coral and sea-urchin spine abraders, shell scrapers, and stone-outlined house foundations. Thus, it is impossible to state if these settlers were Polynesian drift voyagers, or groups from one of the closer Melanesian islands. Later in the stratigraphic sequence, however, several new portable artifact types appear, which may mark the intrusion of a new population, quite likely the Polynesian-speaking ancestors of the present lineages. Whether this intrusion was peaceful or violent, a complete replacement or simply a phase of heavy cultural and linguistic influence, cannot be assessed on the archaeological evidence.

What is clear is that Anuta has been the recipient of at least three distinct phases of settlement and cultural intrusion, with a major hiatus separating the first and second of these. There is no evidence, however, that long-distance relationships ever existed between these Anutan populations and any of the societies on surrounding islands, except with Tikopia during the few centuries immediately prior to European contact. When we turn to nearby Tikopia, however, a rather different picture emerges.

Tikopia. Though he lacked the benefit of archaeological data, Sir Raymond Firth's comments on the origins and development of Tikopia culture proved prescient: 'One thing seems clear, that whether or not there was any ancient stratum of Polynesian population on Tikopia, the modern Tikopia society is the result of a fusion of a number of elements from a variety of islands – mainly Polynesian but probably some Melanesian also. Hence Tikopia culture, and presumably language, are complex products.'²² Indeed, it is likely that purposeful colonization, drift voyages from numerous islands, and formalized long-distance trade or exchange relationships all played a role in building the society so well documented by Firth.

The Tikopia sequence has been treated in detail in the recent monograph by Kirch and Yen.²³ Three major prehistoric phases were defined on the basis of artifactual and faunal data, with several subphases. Unlike Anuta, there is no hiatus in the occupation sequence, and certain traits exhibit continuity over several millennia. Other traits, such as the presence of distinctive ceramic wares and particular foods, allow us to clearly define periods within the sequence. The island was colonized early in the first millennium B.C., by makers of a Lapitoid plain ware, as in the Anutan case. A number of exotic materials, however, raise the question of external contacts. These include metavolcanic adzes, volcanic glass from at least two sources, and several kinds of chert (Fig. 3). Some of these materials may have been brought by members of an initial settlement voyage; others may reflect continued contacts with Lapita settlements on neighbouring islands, such as Nendö.

At around 100 B.C., a fairly radical change occurs in the sequence, marked by the sudden replacement of the Lapitoid plain ware by imported ceramics, decorated in the Mangaasi style, and almost certainly deriving from northern Vanuatu. (Mangaasi-style pottery, named after a site on Efate Island, was widely distributed throughout Vanuatu in the first and early second millenia A.D. The pottery is characterized by incised and appliqué decoration.) Other artifact changes are recorded as well, and turtle, shark, and rays drop from the faunal record. This middle, or Sinapupu Phase, continued until about A.D. 1200, when the Mangaasi style ceramics ceased to be imported, apparently as a result of the cessation of Mangaasi pottery manufacture throughout Vanuatu. However, contacts between Vanuatu (especially the Banks Islands) and Tikopia did not cease and may even have increased, for volcanic glass continued to be imported from the Banks Islands in greater quantities than previously.

The final phase of the Tikopia sequence, from A.D. 1200 to European contact, is one marked by an absence of ceramics, and the appearance of several new traits, including exotic adzes of oceanic basalt, probably imported from west Polynesia. At some point in this phase exchange relationships were also established between Tikopia and Vanikoro, relationships that continued into the time of European contact. Turtles and elasmobranchs reappear in the faunal sequence, perhaps reflecting Polynesian concepts concerning the edibility of these species.

Far from being an isolated microcosm, Tikopia has been a node in several networks of cultural (and presumably linguistic and physical) interrelationships. While there is no evidence of a cultural *replacement* of the sort proposed by Davidson²⁴ for some other Outliers, there is abundant evidence for major change in local technology, food consumption, production, and settlement patterns. In the middle phase, these changes may well reflect the influence of social groups in Vanuatu, with whom the Tikopia of that time appear to have been in regular contact. Most recently, arrivals from various west Polynesian islands have become culturally dominant, yet various 'Melanesian' traits persist even in modern Tikopia, such as the ceremonial use of betel nut, cycads, and crotons. Often assumed to be recent borrowings from nearby Melanesian islands, these may as well reflect the persistence of tradition from earlier phases in Tikopia itself.

Taumako. The small high islands of the Duff Group lie about 330 km northwest

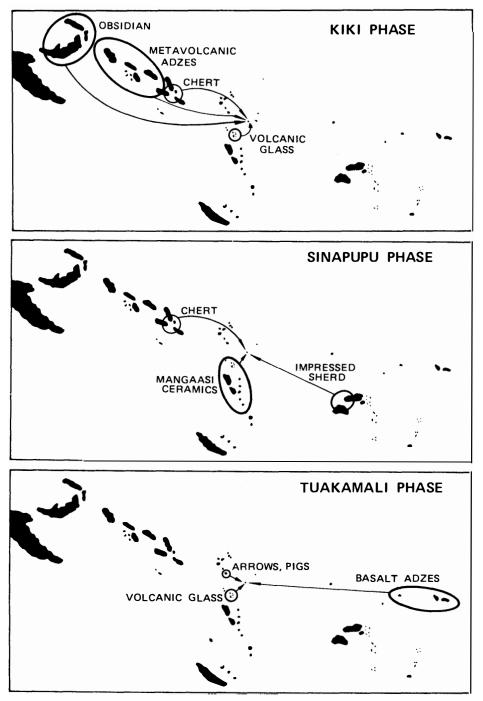


FIGURE 3: Origins of exotic materials in Tikopia (after Kirch and Yen, Tikopia).

of Tikopia, and are within a night's sail of the Reef Islands, where early Lapita settlements were established by 1600 B.C.²⁵ Excavations by B. F. Leach and J. Davidson at several major sites in Taumako in 1978 defined a cultural sequence beginning in the mid-ninth century B.C. and continuing until the present.²⁶ Initial colonization parallels the situation in Anuta and Tikopia, with a locally manufactured Lapitoid pottery, Tridacna adzes, Trochus arm bands, and other material culture traits typical of the early phases of Anuta and Tikopia. Though continuous, the Taumako sequence is not without significant cultural changes, particularly in the first millennium A.D., with the cessation of local pottery manufacture, and the introduction of several new material cultural traits. The arrival of a group of Polynesian speakers in about the mid-second millennium A.D. may be indicated by the presence of exotic basalt adzes, as in Tikopia and Anuta. A definitive treatment of the Taumako sequence must await the full publication of excavation and analytical results. For the present, however, it can be safely stated that the Taumako sequence, like that of Anuta and of Tikopia, does not fit a simple pattern of initial colonization and development in isolation. Rather, a series of influences and contacts with other islands and societies to the west, south, and east is clearly indicated.

Rennell and Bellona. The large upraised makatea-type islands of Rennell and Bellona lie to the southwest of the main Solomon Islands chain, and are likely to have received drift voyagers from Outliers to the east as well as from western Polynesia. Some archaeological investigation has been carried out on both islands, although their respective sequences are as yet incompletely defined. Chikamori²⁷ determined that Rennell had been settled by 2090 ± 105 B.P., although it is unclear if this represents initial colonization. Pottery was not discovered, but one-piece fishhooks from this horizon are remarkably similar to those from early phases of Anuta and Tikopia. Poulsen's work on Bellona²⁸ at the Sikumango site yielded Lapitoid plain ware comparable to that from Anuta, Tikopia, and Taumako, dated to 2070 ± 80 B.P. Earth and stone mounds appear later in the Bellona sequence, about A.D. 1000. These are associated in Bellonese oral tradition with the hiti, an autochthonous population said to have pre-dated the ancestors of the present population. As Poulsen and Davidson have both noted,29 however, the issues of possible cultural replacement or of secondary colonization cannot be resolved on the present incomplete archaeological evidence.

Vanuatu Outliers

Two of the southern outliers, West Futuna and Mele-Fila, have received limited archaeological scrutiny. Shutler³⁰ excavated several sites on West Futuna, and one rockshelter (Site FuRS12) yielded a stratified sequence that has been dated by the ¹⁴C method. Unfortunately, there are inconsistencies in the radiocarbon results, with three early dates on intrusive burials (all by Gakushuin Laboratory) being out of sequence with dates (by University of California at Los Angeles and Washington State University) on the early rockshelter midden.³¹ The burials, with grave goods similar to those in Tuakamali Phase burials on Tikopia, are certainly as old as the 11th century A.D. and the possibility remains open that the island could have been occupied as early as A.D. 300. No ceramics have been recovered from the island, which may be a sign of relatively late settlement by Polynesian speakers.

In the Mele area of Efate, however, the situation is more complex, with a relatively late (c. 16th to 17th century A.D.) settlement of the small offshore island of Mele, presumably by the ancestors of the present day Polynesian-speaking population.³² On the nearby mainland, however, Mangaasi-style pottery is extensively distributed over the landscape, indicative of a much longer settlement sequence of the area. Further excavations in the Mele area will be necessary to clarify the details of what may prove to be a long and complex cultural sequence, with possible Polynesian replacement in the second millennium A.D.

The Shutlers also conducted excavations in an extensive midden on Fila Island off the coast of Efate. They reported a number of shell ornaments (some associated with burials), shell adzes, and potsherds, the latter evidently decorated in 'Mangaasi' style. Radiocarbon age determinations indicate settlement as early as A.D. 860, but the occupation sequence—including the timing of the cessation of pottery production—remains to be clarified. As in Mele, a possible replacement of an earlier population by Polynesians may be indicated.

OUR current knowledge concerning the cultural sequences and time depth for the nine Outliers reviewed above is summarized in Figure 2. Although there are major gaps in the picture (such as the dearth of information from the equatorial atolls fringing the Solomons), there can no longer be any doubt as to the complexities of Outlier settlement history.

The early and lengthy sequences of the southeast Solomons Outliers (especially Anuta, Tikopia, and Taumako) should not be surprising, for several reasons. First, as Ward *et al.* noted, ³³ these islands have the highest probabilities as drift-voyage 'targets' among all Outliers, and may have received drifting cances from the east even early in the first millennium B.C. (the Fiji and west Polynesian region having been settled by at least 1500 B.C.). Second-ly, these smaller, high islands (well suited to colonization) are within one or two days' sail from the larger islands of the Santa Cruz group, and were probably discovered not long after the settlement of the latter by Lapita people in the mid-second millennium B.C. Once colonized, all of the southeast Solomons Outliers except Anuta were continuously occupied, yet their sequences are characterized by repeated immigration and contact with people from other islands and societies. Thus the various oral traditions that, for example, attribute the origins of the present Anutan and Tikopian lineages to arrivals from Uvea, Rotuma, Fiji, or Tonga in the latter second millennium A.D.

represent only the latest phase in a lengthy sequence of primary and secondary settlement.

The northern Outliers of Nukuoro and Kapingamarangi both appear to have been settled relatively late, and fit more closely the 'blowback' theory originally proposed by Thilenius. The late colonization of these islands may be accounted for not only by their isolation (and lesser probability of receiving drift voyagers from the east), but by the geomorphic consideration that these atolls may not have offered stable islets suitable for human settlement until well into the Christian era. In parts of the western Pacific, atolls only began emerging above present sea level about 4,000 to 3,000 years B.P., and in many cases the lag between coral growth and sea level rise may have resulted in geomorphologically unstable islets until well into the Christian era. In any event, the first colonists on both Nukuoro and Kapingamarangi appear to have already been adapted to atoll conditions, suggesting that we look to the other equatorial Outlier atolls and to the Tuvalu group for the immediate sources of the Nukuoro and Kapingamarangi populations.

The culture histories of the southern Outliers are still hazy, although the evidence from Futuna and Mele-Fila suggests a relatively late Polynesian settlement, either directly from west Polynesia, or from one of the southeast Solomons Outliers. In the case of Mele-Fila, such a late Polynesian settlement would appear to have replaced people who produced Mangaasi pottery.

THE prehistoric sequences of the archaeologically investigated Outliers have revealed these small islands to have varied and complex settlement histories. The Outliers are not simply vestiges of an early Polynesian migration, as Churchill would have had it. Nor, however, are they isolated enclaves of Polynesian drift voyagers who arrived well after the settlement of Triangle Polynesia, although it is clear that wind-blown canoes from the east have made successive impacts on Outlier archaeology and prehistory. First, it is clear that Outlier culture histories are often as complex as those of the major southwest Pacific archipelagoes, and that no single framework or theory can account for Outlier settlement as a whole. Each Outlier must be investigated on its own terms. Second, the very term 'outlier' (while too ingrained to abandon) is misleading, a misnomer. Though they are outlying with respect to Triangle Polynesia, these islands are central to the prehistory of the entire southwestern Pacific, and their sequences mirror major cultural currents that have created distinctive patterns of ethnic diversity in eastern Melanesia.

Among the major cultural episodes reflected in Outlier culture histories, we may briefly consider four. The first and earliest of these, witnessed in the southeast Solomons Outliers, is the apparent expansion of a Lapitoid plain ware horizon in the first millenium B.C. The colonization of Tikopia, Anuta, and Taumako occurred almost simultaneously in archaeological time, and the material cultural assemblages of these early settlements are extremely similar (there are hints that Rennell and Bellona will also prove to have comparable early first millennium B.C. settlements). Further, these early Outlier components correspond with similar Lapitoid plain ware assemblages in the Reef Islands and on Nendö. The significance of this Lapitoid expansion in the first millennium B.C. has yet to be carefully considered, but it is evident that the Outliers will provide critical evidence for interpreting this major cultural episode.

A second major trend reflected in the Outlier sequences is the sudden and widespread cessation of Lapitoid plain ware manufacture throughout eastern Melanesia (and indeed, in western Polynesia as well). That such pottery ceased to be produced at virtually the same time on so many widely dispersed islands would hint that an explanation for this phenomenon must be sought from a regional perspective, and not in terms of local developmental sequences. Possibly, this cessation of Lapitoid plain ware production may prove to be correlated with the third major cultural trend mirrored in the Outlier sequences, the expansion of a Mangaasi-style ceramic horizon. At present, this is well documented only for Tikopia, although there are hints of southern cultural contacts in the Taumako sequence as well.

The fourth major cultural episode mirrored in the sequences of every Outlier is, of course, the onset of Polynesian immigrants, particularly later in the second millennium A.D. Although drift canoes from the east probably were a factor in Outlier settlement histories for three millennia (as suggested, for example, by the probable East Futunan chert in the early Anutan assemblage), the frequency of east-to-west voyages appears to have greatly increased after A.D. 1000. One interesting aspect of Outlier oral traditions is the frequent reference to Tongan wars, invasions, and conflicts.³⁴ These are particularly clear, for example, in the traditions of both Tikopia and Anuta. It is doubtful, however, that Tongan war parties actually invaded all of the Outliers where Tonga stories have been recorded. More plausible, perhaps, is that immigrants from west Polynesia brought with them stories and traditions relating to the great Tongan expansion of the 16th to 17th centuries, including the conquest of such islands as Uvea, Niuatoputapu, Niuafo'ou, and Rotuma.³⁵ Thus the Outlier traditions may be an echo of political currents that swept the west Polynesian region in the final centuries before European contact.

Finally, the recent advances in Outlier prehistory give cause to question the long held notion of Oceanic islands as cultural and anthropological 'laboratories'. This concept, which has been espoused by various Oceanic scholars for at least three decades, may be more valid in the remote outposts of eastern Polynesia, e.g. Easter Island and Hawaii, where single colonizations and subsequent developments in isolation appear to have been the case. In the southwestern Pacific, however, the idea of island isolates is inadequate. Islands are physically bounded ecosystems, but island societies had no discrete barriers to the potential for interaction with others beyond their shores. Simple models of cultural development, whether invoking vestiges of an era of west-to-east Polynesian migrations, or more recent drift voyages from western Polynesia, are out of place in the complex world of the southwestern Pacific.

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