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CONTENTS:

AFRICA	Page 1
POLYNESIA	Page 10
SIBERIA	Page 13
HISTORICAL ANTHROPOLOGY	Page 18
NORTH AMERICA	Page 24
SOUTH AMERICA	Page 27
LANGUAGE	Page 28
GENETICS	Page 30
SCIENCE and RELIGION	Page 37
PRIMATES	Page 43

AFRICA

Watson, E., Forster, P., Richards, M., and Bandelt, H. **Mitochondrial Footprints of Human Expansions in Africa.** *Am. J. Hum. Genet.* (1997), 61:691-704.

Furthermore, little is known about expansion events within Africa and about their relation to expansions in other parts of the world (compare Di Rienzo and Wilson 1991; Harpending et al. 1993; Sherry et al. 1994; Graven et al. 1995; Eller and Harpending 1996).

Here, we apply a novel intraspecific phylogenetic-network method (Bandelt et al. 1995) in conjunction with new outgroup information (Zischler et al. 1995) and a recent confirmation of the mitochondrial control-region mutation rate (Forster et al. 1996), to 407 published African sequences, in order to investigate these questions. We find that most African mitochondrial sequences appear to be the result of demographic expansions that started ~ 60,000-80,000 years ago, the earliest of which led to the colonization of Eurasia. p. 691

All clusters are starlike, with smooth unimodal pairwise distributions (fig. 2), and are geographically widespread, suggesting both demographic and geographic expansion. The remaining 13% of the sequences, which are not shared between populations and are thus termed "isolated lineages" (L1i), are not clearly starlike or unimodal in the pairwise analysis (fig. 2), although the pairwise distribution is nevertheless approximately bell shaped, possibly suggesting that these lineages are the relics of a less dramatic and more ancient expansion event across

Africa. The network in figure 3 presents the phylogenetic relationships of the isolated African lineages to the four major African expansion clusters. p. 694

The oldest subcluster of this expansion (L3a (fig. 1), consists mainly of eastern-African sequences, suggesting a possible eastern-African origin for the L2/L3 expansion. A lower bound can be set for the arrival of the L3 expansion in western Africa, because of the occurrence of a western African-specific subcluster of L3b, coalescing in a lineage with transitions at np 16124 and 16223 (but not at np 16278), relative to the CRS. Its coalescence time indicates that the expansion of cluster L3 reached western Africa by 30,000 years ago. p. 695

The oldest subcluster within L3a (characterized by transitions at np 16223 and 16311) is eastern African specific, suggesting an eastern-African origin for L3a and thus also for Eurasians. A possible alternative, the Middle East (Stringer 1988; Di Rienzo and Wilson 1991), is less likely to be the origin of L3a, since L2, the sister cluster of L3 (fig. 1), is virtually African specific. p. 696

It has been suggested that a subset of cluster L1a, defined by a 9-bp deletion at np8272-8289 (Vigilant 1990), may represent an expansion of Bantu-speakers (Bandelt et al. 1995; Chen et al. 1995; Soodyall et al. 1996). Another possible marker for Bantu expansions that merits investigation is the sequence motif np 16124-16223-16278 found in southwestern Africa (among the Herero, Nama, and Dama in the data of Vigilant [1990] and Soodyall [1993]. This motif is a subset of L3b, which is widespread in western Africans who mainly speak languages of the Niger-Kordofanian family, of which Bantu is a member. p. 697

This is evident in the example of Watson et al. (1996), in which the population-coalescence times are frequently the result of the fusion of several of the ancient phylogenetic clusters discussed above and therefore, in themselves, are not related to the age of the individual populations—indeed, the individual population phylogenies frequently coalesce on the mitochondrial Eve sequence itself (Bandelt and Forster, in press).

The present work suggests that the starlike phylogenies previously discovered by use of pairwise distributions (Harpending et al. 1993; Sherry et al. 1994) and phylogenetic analysis (Mountain et al. 1995), were generated in eastern Africa 60,000-80,000 years ago by the expansion of a small, closely knit subset of a diverse ancestral mtDNA pool. This implies that the low diversity of modern humans, in comparison with other hominoids (Ruvolo et al. 1994), both within and outside Africa, can be at least partly accounted for by a founder effect that occurred long after the origin of anatomically modern humans. Our sample of isolated lineages is, at present, still too small to allow firm conclusions concerning the period before these major expansions. p. 697

It is curious that only one mitochondrial sequence or, at most, a set of very closely related lineages (the ancestors of L3—and possibly, of L2) should have participated in the earliest major expansion, given that all parts of Africa today harbor diverse, phylogenetically isolated lineages from the earlier period. Since a general environmental change in one area is unlikely to have directly triggered population expansion in only a single mitochondrial lineage, it is possible that a small subpopulation carrying it acquired some advantage, perhaps in response to environmental change, such as the onset of the Last Glacial. p. 697

Alvah's Comments: If Africa was not the source for human expansions but a place where humans expanded into, this paper could be seen to identify Eastern Africa as the original location for the later total colonization of Africa. As an "Out of the Americas via out of Asia" advocate the methods of human dispersals could be seen to mimic that from Australia, being aided by coastal navigation and subsequent migration into the interior. This would help explain the archaeological data from Africa with the earliest sites for Anatomically Modern Homo sapiens near coastal locations including Klaisies River.

Relethford, J. H. **Mitochondrial DNA and Ancient Population Growth.** *American Journal of Physical Anthropology* (1998), 105:1-7.

In recent years, the study of mitochondrial DNA (mtDNA) variation has entered a new phase with an increasing emphasis on interpretations of demographic, rather than phylogenetic, history. Human mtDNA variation fits a "sudden expansion" model, where the human species expanded rapidly in size during the Late Pleistocene. This paper examines the sudden expansion model with the goal of partitioning total mtDNA diversity in contemporary populations into two components—diversity that existed prior to the population expansion and diversity that arose after the expansion. A method is developed for estimating these components. Analysis of mtDNA diversity within selected human populations shows that 64-80% of mtDNA diversity in contemporary populations arose after the expansion, a consequence of a high mutation rate relative to the number of generations since expansion. p. 1

Results suggest that excess sub-Saharan African mtDNA diversity is due to the combined effects of the sub-Saharan African population being larger in size prior to the expansion *and* expanding earlier. p. 1

The issue of excess African diversity also came into question with the demonstration that diversity is not likely to track the age of a population (Rogers and Jorde, 1995), and with analyses showing a larger long-term effective population size in Africa (Relethford and Harpending, 1994; Relethford, 1995). p. 1

The first approach provides a way to partition modern mtDNA sequence diversity into two components—diversity that arose *before* the expansion and diversity that arose *after* the expansion. The second approach is an extension to the comparison between two populations, and addresses contributions to excess mtDNA diversity in sub-Saharan populations. p. 2

The mismatch distribution of most human populations shows a smooth wave-shaped curve. Rogers and Harpending (1992) found that such curves do not resemble the curves expected under a theoretical model that assumes an equilibrium distribution obtained from a constant population size over time. p. 2

While mathematically interesting, simplified models are useful only if their assumptions are valid and they show a good fit to real data. To date, the model has proven remarkably robust to violations of the assumptions including starting from equilibrium q_0 (Rogers, 1992; Rogers et al., 1996). p. 3

The two-parameter model has now been applied to mtDNA data from 25 human samples from around the world. Of these, 23 show an excellent fit to the model of sudden expansion, and the two outliers are cases with known recent population bottlenecks that compromise results (Sherry et al., 1994). p. 3

An alternative interpretation is that Africa had the largest long-term effective population size (Relethford and Harpending, 1994, 1995; Relethford, 1995), an interpretation compatible with both replacement and multiregional models (Wolpoff and Caspari, 1997)

An effective population size is useful mathematically, but can mask a variety of patterns of demographic change. Possible models are limited by the sudden expansion model—rapid growth from a small to a very large population. p. 5

It is clear from equation (10) that if the population sizes of A and B are equal then the excess diversity of A is due entirely to differences in the timing of expansion. Likewise, if populations A and B both expanded at the same time then the excess diversity of A is entirely due to differences in initial population size. p. 5

There are three different ways in which Africa could have a larger long-term effective population size under the sudden expansion model: 1) Africa was larger prior to an expansion which took place across the Old World at the same time; 2) there was no difference in population size among geographic regions across the Old World prior to the expansions, but Africa expanded earlier than other regions; or 3) Africa was larger prior to the expansions, *and* it also expanded earlier. p. 6

The results presented here do not bear directly on the question of multiregional evolution versus replacement, but instead refocus the genetic data on questions of ancient demography. p. 6

Alvah's comment: When the authors address the evidence of Mutational-drift equilibrium found in Native Americans they automatically dismiss the likelihood that they could be the ancestors of modern humans because it is a philosophical given that the "Native" of the Americas originated in Asia. For example "Of these, 23 show an excellent fit to the model of sudden expansion, and the two outliers are cases with known recent population bottlenecks that compromise results (Sherry et al., 1994)." Also, greater Tribal diversity supports a larger base population in the Americas and little if any evidence for bottlenecks as evident in the mtDNA of Native Americans. As an alternative to the Wallace Labs contention of a bottleneck is back-migration at the end of the Pleistocene as Franz Boas identified a hundred years ago.

Amanda B. Spurdle and Trefor Jenkins **The Origins of the "Lamba Jews" of Soth Africa: Evidence from 12F2 and other Y-Chromosome Markers** *Am. J. Hum. Gen.* 1996

The results ability of Y-chromosome polymorphisms to provide a record of male-specific gene flow and human variation has long been recognized, and numerous studies using different Y markers have indicated the value of this approach. p. 1126

The Lemba population of southern Africa Constitutes a group of Bantu-speakers who claim Jewish ancestry. Historically, the Lemba were distinct from their Bantu-speaking Negroid neighbors by their means of livelihood, physical appearance, customs, and rituals (Van Warmelo 1974), and even nowadays the cultural differences between the Lemba and other Bantu-speakers are recognized. p. 1126

More detailed descriptions of Lemba oral history by Professor Mathivha of the Lemba Cultural Association (Mathivha 1992) suggest that the Jewish ancestors of the Lemba, as traders in the 7th century BC, migrated from “the north” to Yemen, where they established both a large community at Sena (Sa’na) and several trading posts along the eastern African coast. The Jewish community of Sena (Sa’na), termed “Basena” was later expanded by exiles escaping the Babylonian destruction of Jerusalem in 586 BC. At some later stage “trouble broke out between the Basena and the Arabs,” resulting in the migration of some Basena to Africa. Here the group split into two, one moving westward to settle in Ethiopia (the “Falashas”), the other (the Lemba) moving southward, finally to establish communities in southern Africa. Dates for the migration from Yemen appear to be inconsistent, and those quoted for settlement en route to southern Africa range from 450 BC to 50 AD (Mathivha 1992). p. 1127

The Lemba exhibit a frequency of .26 for the p12F2/*TaqI* 8-kb allele. Since this allele is absent in Africans and also was not observed in a sample of 60 Polynesians (A.B.S., unpublished data), it would appear to be specific to Caucasoids. The p12F2 data suggest, therefore, that the Lemba gene pool has received contributions from Caucasoid males. p. 1127

The currently available Y-chromosome genetic data do not support a close genetic relationship between the Ethiopian Jews and the Lemba. In conclusion, the historical facts are not incompatible with theories concerning the origin of Lemba, and the Y-specific genetic findings presented here are consistent with Lemba oral history. p. 1132

Alvah’s comment: This paper demonstrates the value of historical myths and cultural identity and genetic collaborations that help verify tribal accounts of the past. With this in mind we should see greater value in testing other models based on Myth from other cultures, including Siberians being descendants of Native Americans as identified by Boas. Alternatives to anthropological “givens”, as to whether present populations in Siberia are/or ARE NOT the ancestors of Native Americans, should be assessed anew.

EUROPE

Hovers, Erella. **The origins of modern human behavior: a Levantine point of view.**
Abstracts for the Paleoanthropology Society Meetings. p. A9

A comparison of several aspects of the archaeological record at Qafzeh and Amud Caves, associated with AMH and Neandertals respectively, suggests that there were no significant differences in the cognitive abilities of the two populations, in their capability for rational organizational strategies, and in their capacities for symbolic behavior. It is also noted that the archaeological manifestations of the Middle-Upper Paleolithic transition in the Levant are not as

spectacular as in Europe. The implications of these observations for tracing the origins of modern behavior and for understanding the conditions which favor its representation in the material record are further discussed. p. A9

Alvah's comment: Again, the "Levant" specimens were behaviorally closer to Neandertals and Homo erectus bringing into question their inclusion into AMH groups despite whatever the limited anatomical support that they were becoming "sapiens" might suggest.

Gauld, S.C. **Allometric Patterns of Cranial Bone Thickness in Fossil Hominids.** *American Journal of Physical Anthropology* (1996), 100:411-426.

Many pre-Holocene populations of the genus *Homo* display mean cranial thickness values that equal or exceed the maximum population averages characterizing recent *H. sapiens* (Brown, 1987). These differences have led researchers to conclude that, relative to anatomically modern humans, the species *H. erectus* and archaic populations of *H. sapiens* exhibit greatly thickened cranial bone (e.g., Jorant, 1938; Twisselman, 1941; Weidenreich, 1943, 1951; Howells 1966, 1980; Trinkaus and Howells, 1979; Murrill, 1981; Wolpoff, 1984; Kennedy, 1991). Because of its differential distribution, cranial thickness is often cited as a relevant trait in cladistic analyses, which rely on the distribution of autapomorphic and synapomorphic character states to establish species' identity and relationships (Delson et al., 1977; Andrews, 1984; Stringer, 1984; Wood, 198; Bilsborough and Wood, 1986; Hublin, 1986; Turner and Chamberlain, 1989). Indeed, some researchers suggest that the thickened cranial and/or postcranial bone found in some early hominids may represent a unique condition among anthropoids (Weidenreich, 1943) or all mammals (Kennedy, 1985). p. 411

Several studies have addressed the significance of differences in cranial bone thickness in modern *H. sapiens*. The strong covariance between extant primate body size and cranial thickness, as well as its positive allometric relationship, are similar to patterns documented for postcranial bone thickness across a broad range of vertebrates, including primates (Biewener, 1982; Ruff, 1987, 1990; Selker and Carter, 1989; Anyonge, 1993; Nelson 1994). In the postcranium this relationship is usually considered a byproduct of the functional interaction between mass and skeletal support. While this may be so, the cranial data demonstrate that the association between mass and thickness is also expressed in non-weight-bearing portions of the skeleton. The strength of the association suggests that, at the interspecific level., measures of bone thickness throughout the skeleton covary primarily in relation to size, with specific biomechanical influences exhibiting secondary, localized influences. It is possible that this covariance is established and maintained through the pleiotropic effects of genetically mediated growth hormone systems that target coordinated growth of the entire organism (Nelson and Gauld, 1994; Shea, 1992). The interaction between mass and cranial thickness, and its effects on intragroup variation, have not been carefully investigated in any primate species. However, a relationship between size and thickness can be found in support for human developmental studies, which show steady, rapid thickness increases during growth (Roche, 1953; Adeloje et al., 1975; Brown et al., 1979). Moreover, in measuring the effects of sex, age, race, height, and weight on cranial thickness in a large cadaver sample, Pensler and McCarthy (1985) demonstrate that only weight covaries consistently, and significantly, with thickness. p. 420

The findings presented here support recent body-weight prediction studies of *H. erectus* in suggesting that Asian, as well as African, members of this species were characterized by substantially large body size (McHenry, 1988; Gault, 1992; in preparation; Ruff and Walker, 1993; Aiello and Wood, 1994). p. 423

Alvah's comments; The quadruped motion of apes leads to the heavier bone mass in Homo erectus while the generalized posture of modern humans could have been predated by a long term stasis from a less quadrapedal/more hominid-like bipedal primate ancestor.

Cole, T.M. **The use of matrix permutation tests for evaluating competing hypotheses of modern human origins.** *Journal of Human Evolution* (1996), 31:477-484.

Perhaps the greatest advantage of matrix permutation tests is their tremendous flexibility (e.g., Hubert & Schultz, 1976; Smouse & Long, 1992), where the specification of different hypotheses seems limited only by imagination of the investigator. p. 482

More than a decade of debate (recently reviewed by Lahr & Foley, 1995) has failed to produce a consensus with respect to the origins of anatomically modern humans. Perhaps the most interesting finding of Waddle's (1994a) study is that the data *are*, in fact, significantly associated with nearly *all* of the models, so that the same data could be used to argue as effectively for one hypothesis as for another. When Waddle's (1994a) results are considered in the context of earlier studies, they suggest that the failure to resolve the issue of modern human origins results from the tremendous complexity of the problem. p. 483

Alvah's comment: By removing Amerindians from the search for Homo Sapiens's wellspring a compatible resolution to Human Origins supporting the Replacement hypothesis remains complex. Every study of Native American origins starts with an "Asian origin" as a given, but what if this is wrong?

Relethford, J.H. **Evolution of Skin Color in Yemenite Jews.** *Current Anthropology* (1998), Vol. 39, No. 1, pp. 150-152.

How long did the evolution of modern human skin color take? Does skin color change rapidly (on the order of a millennium or so), or does it represent evolution over much longer periods of time? On the basis of computer simulation, Livingstone (1969) suggested that modern differences in skin color could have arisen in as few as 800-1,500 generations (roughly 20,000-37,500 years). However, such simulations show us only what *could* happen and not necessarily what actually *did* happen. p. 151

Haldane proposed something along this line when he suggested that, because American Indians near the tropics are not as dark as tropical populations in the Old World, they had not yet fully adapted to their new environment and therefore the evolution of modern human skin color differences took longer than the time since initial habitation of the New World (cited in Livingstone 1969). This paper uses similar logic and extends it to a quantitative analysis of a

specific human population with a known history of movement into a different latitude—the Yemenite Jew. p. 151

The predicted latitude for the Habbani Jews based on their skin color is roughly 32° north latitude, which is the geographic center of Israel. Even though the Habbani Yemenite Jews spent between 1,500 and 2,600 years in a different environment, there has been no change in skin color. It seems that the evolution of human skin color requires greater time depth and is not indicative of a rapid microevolutionary change. Other populations, also with known histories, must be examined to provide further insight into the rate of microevolution in skin color. The basic method here can also be applied to other traits that show a strong geographic relationship. p. 152

Alvah's comment: Archaeological evidence for the initial expansion of humans ~45,000 years ago could, if one looks outside of Africa for the source of this migration, dictate that Old World population variance in skin color, from white in Europe to dark in Africa and India, are primarily climate related.

Comas, D., Calafell, F., Mateu, E., Perez-Lezaun, A., Bosch, E., Martinez-Arias, R., Clarimon, J., Facchini, F., Fiori, G., Luiselli, D., Pettener, D., and Bertranpetit, J. **Trading Genes along the Silk Road: mtDNA Sequences and the Origin of Central Asian Populations.** *Am. J. Hum. Genet.* (1998), 63:1824-1838.

Central Asia, as defined by Soviet scholars, encompasses the territories east of the Caspian Sea to the current boundaries of China along the Pamir, the Hindu Kush and farther to the northeast, and it comprises the republics of Uzbekistan, Tajikistan, Turkmenistan, Kirghizstan, and part of Kazakhstan; in Western literature, Mongolia, Tibet, and Sinkiang (pinyin Xinjiang, western China) sometimes are included. p. 1824

The role of central Asia in early human evolution and history is not well established. According to an old, long-dismissed hypothesis, the nearby Altai region could have been the origin of humankind. It is known that the region was populated during the lower Paleolithic, and there is ample evidence of settlement during the middle Paleolithic, including Teshik-Tash, the easternmost site from which Neanderthal remains have been recovered. It is not clear, however, whether the region was part of a "maturation" phase of anatomically modern humans, a thruway in the colonization of Europe and eastern Asia, or a place where Asian and European groups met after their expansion (Bowles 1977). p. 1825

For a sequence to be assigned either to eastern Asia or to Europe, it had to be identical to, or to differ in no more than two nucleotides from, a sequence found exclusively in Europe or eastern Asia. That approach allowed us to identify 93.7% of central Asian sequences as belonging to an already sequenced eastern Asian or European lineage (table 3). An average of 33.2% of the individuals in our central Asian samples bore a sequence belonging to a European lineage. This fraction became 35.4% when the unassigned sequences were not taken into account. The proportion of eastern Asian, European, and unassigned sequences was not significantly different across central Asian populations ($\chi^2 = 7.67$, 6 df, $P = .264$). p. 1830

Torrioni et al. (1994) did not find, in mtDNA RFLPs in Tibetans, any selective effects attributable to high altitude; we can reach similar conclusions with control-region sequences when comparing lowland and highland central Asian populations. p. 1830

The results of the present study consistently show that the central Asia mtDNA sequences present features that are intermediate between those found in Europe and eastern Asia. This is especially patent in the following: (i) the cline of the frequency of certain nucleotides in specific positions, such as those found at positions 16223 and 16362; (ii) polymorphism at the nucleotide level, as measured by nucleotide diversity—even when the effects of clinal nucleotide positions are discounted; (iii) the average pairwise-difference values, which are intermediate between those of Europe and those of Eastern Asia; and (iv) genetic distances, which locate the central Asian populations between Europe and eastern Asia. Several population history scenarios could have produced the intermediate genetic features of central Asian mtDNA sequences; some hypotheses that could be put forth—such as an Asian colonization of Europe, or vice versa—find no support in archaeological knowledge and would contradict other mtDNA evidence (Ballinger et al. 1992). However, some of the analyses that we performed will allow us to assess the degree to which other, more plausible hypotheses are supported by mtDNA evidence. p. 1830

Alvah's comment: Archaeological support for an Asian origin can be found in looking to dated encounters between Neandertals and H. Sapiens in western Siberia and by looking at the evolution of the earliest progenitors to the Upper Paleolithic in the Russian Steep as Leanova suggests. Also, Johnson et al. 1983 identified Asia as a source for both Europeans and African populations in one of the first mtDNA studies related to anthropology.

Carbonell, E. and Vaquero, M. **Behavioral Complexity and Biocultural Change in Europe Around Forty Thousand Years Ago.** *Journal of Anthropological Research* (1998), Vol. 54, pp. 373-383.

Differences between the [Middle Paleolithic] MP and [Upper Paleolithic] UP are usually assessed by establishing a series of archaeological parameters (technology, spatial organization, symbolic behavior, settlement patterns, etc.) and comparing the documented evidence of each one for both periods (see, e.g., Mellars 1973; White 1982; Kozłowski 1990). p. 374

Two types of factors have had an impact on the scientific community in recent years. On the one hand, empirical and methodological factors have affected the whole range of data published. On the other hand, theoretical and conceptual perspectives underlie the most polemic aspects of the discussion and reflect the multiplicity of paradigms current in the discipline.

In the first place, the contributions made by the field of human paleontology should be mentioned. The theoretical struggle between the multiregional model (e.g., Wolpoff 1989) and the "Out of Africa" theory (e.g. Stringer and Andrews 1988) has highlighted the explanatory weakness of scenarios concerning the transformations which affected hominids and their activities during isotopic stage 3. p. 374

Were the association of the cultural innovations of the UP and [anatomically modern humans] AMH valid, the "Out of Africa" hypothesis would imply an African origin for the UP. However,

with the data available at the moment, it seems that the UP did not appear in Africa before it did in other places (Ambrose and Lorenz 1990; Van Peer and Vermeersch 1990). p. 378

What seems to be obvious is that between 45 and 35 kyr B.P., Europe underwent a period of technical effervescence, with processes of change affecting most of the continent. Both the so-called transitional complexes and the Aurignacian must be understood in this context. p. 379

The idea that transitional industries are the result of acculturation to the Aurignacian contrasts with the differences between the two entities. The Chatelperronian does not appear to be a mere copy of the Aurignacian, but rather a typologically and technologically well defined technocomplex with elements of clear originality. J. Pelegrin (1995) casts doubt on the hypothesis of acculturation, citing the considerable differences between the respective technological systems. Harrold (1989) suggests that the Aurignacian affected the genesis of the Chatelperronian but stresses the typological differences between them. p. 379

Some authors (e.g., Davidson and Noble 1993; Klein 1995; Mellars 1996; White 1989) define a group of cultural features found in the archaeological record which are characteristic of a completely modern type of behavior. Among these new patterns are the appearance of art, the development of bone, ivory, and antler technologies; great synchronic and diachronic variability among lithic artifacts; complex organization of space; and more effective strategies of exploiting the environment. The appearance of completely modern behavior would have been determined by neurological changes which defined the development of a fully human brain. As Binford (1989) has said, one cannot speak of the existence of a fully human culture before the UP. The conception of AMH as a hominid who was more and better organized has been defended by authors who find evidence of more complex social organization and who argue that there was no significant point of contact between [archaic *Homo sapiens*] AHS and AMH. This argument has been expressed in different fields of research, such as symbolic expression (Chase and Dibble 1987), lithic technology (Chauchat 1992; Dibble 1989), burial practices (Gargett 1989), and spatial organization (Pettitt 1997). p. 380

The use of the concepts of mental template and planning as criteria for defining the MP/UP transition involves difficulties which are similar to those related to the concept of style. In these cases, speaking of radical differences between the UP and MP does not seem to be justified. Transporting objects from one place to another and the planning for future needs that this implies have been shown beyond all doubt to exist in the MP and are fundamental factors in determining the variability of archaeological assemblages (Geneste 1985; Kuhn 1995). The ability to mentally develop complex technical processes can be inferred from the operative capacity shown in MP knapping strategies (Van Peer 1991; Boeda, 1994), as well as from the multiplicity of reduction strategies used during the MP (Boeda 1993; Turq 1992; Revillion and Tuffreau 1994). p. 381

One of the most important of these techniques is the excavation of large surface areas which represent the entirety of the space occupied by human groups at particular sites. Only by this means can the relationships among objects in space be plausibly reconstructed and, consequently, the organization aspects of behavior interpreted. Below, we shall discuss the

conclusions that we have drawn from an approach of this type at a site belonging to the end of the MP: the Abric Romani in Capellades (Barcelona Province, Spain). p. 382

The excavation of nine archaeological levels (levels B-J) pertaining to the end of the MP and dated between 50 and 70 kyr B.P. (Bischoff, Julia, and Mora 1988; Bischoff et al. 1994) has given us systematic access to evidence of the occupational variability of the last Neandertals. p. 383

Alvah's comment: Interactions that occurred in the Old World are best divined from the robust evidence from Europe and the accompanying evidence of a Transition from the MP to the UP. The authors point out that this occurred in Europe before Africa. This should cause geneticists to look outside of Africa for the source of Homo sapien expansion, but we seem unwilling to do so.

Since the New World offers little if any evidence of any kind of Paleolithic in pre-Clovis times, we must ascertain what we do have in archaeological support. The best example of human behavior sustaining many pre-Clovis sites is the use of fire. If the indications of fire are simply "geofacts" and not related to Human sapient activities then one might ask why similar evidence of fires associated with hearths are NOT found in or about where Homo erectus lived. If they had a great hoopla would exist, helping archaeologists discern that sapient technologies could be allied with erectus or Neandertals. The evidence of humanly created fires in association with hearths and human fingerprints in pre-Clovis times could help us in determining that they were indeed the product of human behavior. The fact that - fires associated with hearths - are not found in Middle Paleolithic Europe should help scientists in dismissing the fancy that only in the New World do "geofacts" of fires enclosed in hearths, exist.

POLYNESIA

Holdaway, S. **Stone artefact assemblage variability and scales of temporal resolution at Bone Cave, Tasmania, Australia.** *Abstracts for the Paleoanthropolgy Society Meetings.* p. A9

Bone Cave is one of a number of limestone caves in the southwest of Tasmania, Australia that have produced a rich record of Pleistocene human occupation spanning the period from 10,000 to 35,000 BP. This paper reports the results of a technological analysis of 23,000 stone artefacts excavated from Bone Cave. Artefacts found at the site were manufactured from both local and imported stone, and suggest a variety of reduction strategies. Twenty-nine radiocarbon determinations from the site permit a precise chronology to be constructed that indicates the site was abandoned for substantial periods between occupations during the late Pleistocene. Stone artefact assemblages constructed on the basis of the radiocarbon determinations are compared through time to determine the significance of these periods of abandonment. Also considered are the effects of differing temporal scales of resolution on measures of assemblage variability. p. A9

Alvah's comment; Human arrival in Tasmania is consistent with a 35-40 thousand year age. The conservative dates associated with the radiation of Homo sapiens throughout the Old World should rely on this timing by scientifically discriminating the consistency of this modern human boundary for our arrival into the Old World as it continues to be consistently dated as being.

From REVIEWS. Geoffrey Irwin, University of Auckland. Reviewing: Goetzfridt, N.J. **Indigenous Navigation and Voyaging in the Pacific: A Reference Guide.** *Bibliographies and Indexes in Anthropology* No. 6. New York: Greenwood Press, 1992. 294 pp. bib., inds. np. (cloth).

This myth held that, after initial colonisation, many Polynesian islands were so isolated that they could be regarded as laboratories for the study of cultural evolution. However, we now have some predictive modelling for probable prehistoric inter-island contacts, and archaeology, linguistics and biological anthropology are beginning to fill in the facts. p. 415

Evidently there are many observations and arguments in the literature which perhaps have not received the attention and acknowledgment they deserve. Moreover, the annotations themselves, while tersely written, are substantial. Goetzfridt makes no written judgments about the books and articles he summarises but, so far as I am able to tell, what he has to say about them draws out the major and essential points correctly. Altogether, this book comes as a pleasant surprise in being a comprehensive, accurate and therefore most useful, guide to the literature. p. 415

Alvah's comment; Again, the arrival of Oceanic populations ~40,000 years ago did not lead to a further expansion as remote Polynesia was only settled 3,600 years ago. The Americas have been given little serious consideration despite the fact that genetic links to the Americas are clearly not those associated with the earliest radiation's Out of Asia for these earliest Oceanic peoples, as they did not continue into Polynesia.

Betty, D.J., Chin-Atkins, A.N., Croft, L., Sraml, M. and Easta, S.. **Multiple Independent Origins of the COII/tRNA^{Lys} Intergenic 9-bp mtDNA Deletion in Aboriginal Australians.** *Am. J. Hum. Genet.* (1996), 58:428-433.

However, AW222 has C at position 16189; this individual's control region sequence persistently groups with the six Asia-Pacific individuals with the deletion (fig. 1). None of the eight individuals we found with the deletion shares the "Polynesian motif" comprising the C at position 16217, plus G at position 16247 and T at position 16261 (Hagelberg and Clegg 1994; Redd et al., in press). p. 429

It is now clear that there have been multiple deletions and insertions at this site. These findings do not remove the deletion's utility as a mitochondrial population marker. However, these results do mean that a common origin of the 9-bp mtDNA deletion in different individuals or populations must be tested, and not just assumed. p. 431

Alvah's comment; By looking to the Americas admixture can be assessed against the background of the 9bp's distribution (or lack of) in interior populations. If it is found without the Polynesian motif could it represent selection or an ancient linkage to a common haplotype.

Lum, J.K., Cann, R.L., Martinson, J.J., and Jorde, L.B. **Mitochondrial and Nuclear Genetic Relationships among Pacific Island and Asian Populations.** *Am. J. Hum. Genet.* (1998), 63:613-624.

By examining different genetic systems from the same individuals, we have generated patterns consistent with both views. As described above, our mtDNA data are correlated with linguistic data and suggest island Southeast Asia as the origin of Remote Oceanic Islanders. These data are consistent with the express train model. Our STR data, in contrast, are not correlated with linguistic data and highlight affinities between Near Oceanic and Remote Oceanic populations. We have argued that the differences between these patterns result from postcolonization male-biased gene flow. Genetic interactions between populations after initial colonization may have been mediated by a predominately male segment of voyaging societies, engaged in the control of resources. This bias served to preserve pre-existing linguistic differences, lines of status, and hierarchical divisions among matrilineal kinship groups. Thus, we see female settlement as an express train and male gene flow as an entangled bank. p. 622

Alvah's comment; Did the mtDNA express train come from the Americas or is this idea to unscientific to address? Certainly nuclear DNA would indicate admixture with Native Oceanic Peoples who had previously colonized southeast Asia (and beyond) ~40,000 thousand years earlier.

Heathcote, G.M., Stodder, A.L.W., Buckley, H.R., Hanson, D.B., Douglas, M.T., Underwood, J.H., Taisipic, T.F., and Diego, V.P. **On Treponemal Disease in the Western Pacific: Corrections and Critique.** *Current Anthropology* (1998), Vol. 39, No. 3, pp. 359-367.

Their position that climate "would appear not to be the significant determinant of treponemal disease manifestation" (p. 560) is at extreme odds with epidemiological patterning of treponemal infections in the Pacific Islands, where climatic conditions associated with yaws endemicity are tightly circumscribed and include a mean temperature exceeding 18°C throughout the year combined with an average annual rainfall of 1,650 mm, with rainfall exceeding 65 mm for each month (Pirie 1971-72). p. 359

Thus, the treponematoses are conceptualized as discrete diseases outside of an evolutionary ecology framework. This is puzzling, given the claim that "mutation" brought about a replacement of yaws by syphilis in the New World (p. 560). How such a transmutation was operationalized and how it is reconciled with the advocacy of universal differential patterns (yaws versus syphilis) is not discussed.

We do not dispute that the comparative study of treponemal-like lesion distribution in archaeologically recovered skeletal series can be sound and revealing. Bogdan and Weaver (1992) have shown that such an approach can be useful in distinguishing patterns more closely associated (in subcontemporary populations) with nonvenereal than with venereal transmission. pp. 363-364

The Rothschilds' only concession to heterogeneity of expression is the assertion that "the osseous reaction to treponemal infection, although reproducible for each variety, is not uniform among them" (p. 556). "Reproducible" is the key word here, and this leads us to a consideration of the elements chosen and ignored for examination of treponemal changes. p. 364

In view of such a provocative position—that all tibial periostitis may be treponemal in origin—we wonder why no detailed exposition is offered on other (competing) causes of tibial involvement in the Western Pacific. Attention to the differential changes of leprosy (Moller-Christensen 1967, Andersen, Manchester, and Roberts 1994) would have been appropriate, given the claim of pre-Spanish antiquity for leprosy in Guam and the Western Pacific region (Trembly 1995). Tropical ulcers of the shin of nontreponemal origin (Brown and Middlemiss 1956, Ennis, Gueri, and Sergeant 1972) and trauma to the shin with consequent bacterial or fungal infection should likewise have received attention. We are aware of sound criteria regarding differential pathogenesis and skeletal lesions of leprosy, ulcers, and trauma (as well as for their potential for interaction), but in view of the fragmentary and incomplete nature of the Gognga-Gun Beach skeletons a frank discussion of interpretive problems and more detailed discussion on differential regional patterning and appearance of tibial lesions would have been beneficial. p. 364

However, we take issue with elective and unexplained omissions of certain complementary criteria as well as some heterodox claims as to differences in tibial involvement among the treponematoses, including the following:

1. The lack of an explanation why treponemal infection would affect the tibia differently in syphilis versus bejel versus yaws; criteria for differential diagnosis ought to be grounded in underlying biology and patho-physiology.
2. A conspicuous absence of consideration of cranial lesions (e.g., the caries sicca sequence, including stellate scars versus crater lesions) and degree of nasal region destruction (see Hackett 1951, 1976; Steinbock 1976; Ortner and Pustchar 1981).
3. Absence of attention to osseous and dental changes encountered in congenital syphilis such as osteochondritis, periosteal cloaking, foci of osteomyelitis on the medial surfaces of proximal tibiae (Wimberger's sign), mulberry molars, and Hutchinson's incisors (see Bogdan and Weaver, 1992).
4. Failure to recognize several recent contributions toward a differential diagnosis of yaws. Such distinctive osseous involvement is in keeping with clinical observations that juxta-articular nodes (joint effusions) are found in yaws cases but not in venereal syphilis (Kampmeier 1982:586).
5. Failure to consider the skeletal impact of coinfections or secondary infections. Others have found evidence from lesion morphology and distribution that is suggestive of secondary bacterial and/or fungal infections (Hanson 1991, Stodder, Trembly, and Tucker 1992) and coinfection with leprosy (Stodder, Trembly, and Tucker 1992, Trembly 1995) in late prehistoric and early historic Mariana Islanders. p. 364-365

Weisler, M.I. **Hard Evidence for Prehistoric Interaction in Polynesia.** *Current Anthropology* (1998), Vol. 39, No. 4, pp. 521-530.

While some may bemoan the smallness of the sample of three adzes from three sites in two archipelagoes, the great distances involved and the chronological placement of these finds are important for prehistoric Polynesian interaction studies. The voyage to Mangareva from the Marquesas is the longest straight-line distance now documented in the eastern Pacific and attests to the remarkable, purposeful voyages of prehistoric Polynesians. The ties between the Society Islands and the Marquesas, long suspected on the basis of artifact styles (of items such as fishhooks, octopus lures, and adzes), plant distributions (Role 1996: 532), language, and shared human physical characteristics, are clearly demonstrated here by actual artifact transfer. This demonstration has implications for the interpretation of the suspected Fiji ceramic sherds in the Marquesas. Such exotic sherds could represent items brought by colonizing groups which are now in a disturbed, later stratigraphic context (Green 1974:246-47) or the remnants of pots transferred during subsequent interarchipelago interaction. It is unlikely that transfer of Fijian pots was made directly, and the Society Islands may have been part of the conduit of transfer. pp. 528-529

The study results also provide empirical support for Biggs's (1972:149) idea of multiple intra-Polynesian migration and settlement (1972:149; see also Green 1981). This suggestion fits well with Rolett's "interaction and cultural continuity: model, in which two-way voyaging linked distant archipelagoes during early East Polynesian prehistory (1993:47). The radiocarbon dates clearly associated with two Eiao artifacts exported to the Societies and Mangareva and interarchipelago interaction models based on detailed sourcing studies from the Cooks (Walter and Sheppard 1996, Weisler and Kirch 1996) and the Mangareva-Pitcairn interaction sphere (Weisler 1995, 1996, 1997a) clearly demonstrate that long-distance interarchipelago interaction continued long after colonization. Additional sourcing studies of basalt adze material will provide the necessary hard evidence for the scale, frequency, and duration of long-distance interaction, thus providing a firm foundation for understanding the evolution and transformation of Polynesian island societies. pp. 529-530

SIBERIA

Starikovskaya, Y.B., Sukernik, R.I., Schurr, T.G., Kogelnik, A.M., and Wallace, D.C. **mtDNA Diversity in Chukchi and Siberian Eskimos: Implications for the Genetic History of Ancient Beringia and the Peopling of the New World.** *Am. J. Hum. Genet.* (1998), 63:1473-1491.

Our first survey of mtDNA variation in the Chukchi and Siberian Eskimos involved partial haplotype analysis and showed that the "reindeer" Chukchi exhibited three (A, C, and D) of the four mtDNA haplogroups (A-D) observed in Native Americans but lacked the COII/tRNA^{Lys} intergenic 9-bp depletion associated with haplogroup B (Torroni et al. 1993a, 1993b). In contrast, Siberian Eskimos showed mtDNAs from only two of these haplogroups (A and D), and appeared to be the only aboriginal Siberian group lacking "other" haplotypes—that is, mtDNAs that are not within haplogroups A-D (Torroni et al. 1993b; Sukernik et al. 1996). When native Siberian mtDNAs were subjected to high-resolution restriction analysis, most of these "other" haplotypes were shown to be ethnic-, tribal-, or region-specific haplotypes that clustered into

additional haplogroups. This was seen most clearly in the Udegeys of the Sikhote Alin and in the Nivkhs of the lower Amur/Sakhalin Island region (Torroni et al. 1993b). p. 1473-1474

Of these 17 haplotypes, 7 were found to belong to haplogroup A, 6 to haplogroup D, 2 to haplogroup C, and 0 to haplogroup B. In addition, two haplotypes detected in four Chukchi individuals were identified as belonging to haplogroup G, a predominant mtDNA lineage in the Koryaks and Itel'men of Kamchatka (Schurr et al., in press).

Table 2 outlines the distribution of these haplotypes, within and between Chukotkan samples. Haplogroup A haplotypes SIB41 and SIB56 were found to be the most frequent in all Chukchi and Eskimo subdivisions, with the exception of the Naukan, which SIB56 was missing, probably because of the restricted sample size of this group. SIB53, which was observed in two of the three Eskimo subdivisions, did not appear in the Chukchi. The most common haplogroup D haplotype in the Chukchi and the Eskimo was SIB50, with related haplotypes occurring infrequently in either one or the other subdivision(s). p. 1477

All Chukotkan CR sequences specific to haplogroup A exhibited the np 16111 CÆT (16111T) transition, which characterizes both Na-Dene and Amerindian haplogroup A mtDNAs but which was not observed in those from Asian populations (Torroni et al. 1993b; Horai et al. 1996). Aside from the 16111T mutation, either the CÆT transition at np16192 (16192T) or the AÆG transition at np16265 (16265G) further subdivided Siberian haplogroup A mtDNAs and differentiated Chukotkan haplogroup A sequences from related mtDNAs observed in the Koryaks and Itel'men of Kamchatka (Schurr et al., in press). p. 1478

Both sublineages shared the np 16298 TÆC transition (16298C), which defines haplogroup C mtDNAs in both Asia and the New World (Torroni et al. 1993a, 1993b). p. 1477

For haplogroup C, the nodal haplotype is SIB26. It is identical to the Asian haplotype AS65 and to the Native American haplotype AM43 (Schurr et al. 1990; Ballinger et al. 1992; Torroni et al. 1993a). SIB59, which occurred in one Sireniki Eskimo, differed from SIB26 by having two additional mutations not previously seen in other haplogroup C mtDNAs.

For haplogroup D, the nodal haplotype is SIB13. This is identical to AS25 in central and eastern Asia (Ballinger et al. 1992; Torroni et al. 1993a) and to AM88 in the New World (Torroni et al. 1992, 1993a). Interestingly, SIB13 was not observed among the Chukchi and Eskimos, who exhibited a set of haplotypes distinct from those seen in other Siberian populations. Furthermore, the most divergent haplotype in the Chukotkan groups, SIB40 (fig. 3 and table 1), which assumed a terminal position in the cluster, occurred in the Chukchi and Naukan Eskimos, as well as in the Koryaks of northeastern Kamchatka (Schurr et al., in press), suggesting that it belonged to a common gene pool of the latest inhabitants of western Beringia. p. 1481

The haplotypes from haplogroup Y (SIB01-SIB07) and the "other" category (SIB17 and SIB20-SIB25) are also found in Siberia but not in the Americas (Torroni et al. 1993a, 1993b; Schurr et al., in press). p. 1481

Another cluster, encompassing many of the Haida haplogroup A CR sequences and one Bella Coola haplogroup A CR sequence, was defined by the presence of the 16355T mutation in the

absence of the 16331 transition. This mutation differentiates the Haida from other Na-Dene populations and reveals its relatedness to Northwest Coast Amerindians (Torroni et al. 1992, 1993a; Shields et al. 1993) (fig. 5). p. 1483-1484

Finally, the haplogroup A CR sequences that harbored the 16129A mutation delineated a North American Amerindian cluster that encompassed mtDNAs from the Haida, Nuu-Chah-Nulth, and Bella Coola, as well as the Ojibwa. p. 1484

These findings at the phylogenetic level were also reflected in the distribution of shared CR sequences among northern Pacific Rim tribal groups, as summarized in table 6. The putative founding CR sequence for haplogroup A, 07, is identical to CIR11 in the Nuu-Chah-Nulth (Ward et al. 1991). This CR sequence occurs in the Chukchi and Siberian Eskimos, as well as in all of the major linguistic groups of Native Americans residing in the northern Pacific Rim (Ward et al. 1991; Shields et al. 1993; present study). However, the remaining CR sequences from haplogroup A occurred in either the Haida and Northwest Coast Amerindians, the Na-Dene Indians other than Haida, or the Siberian Eskimos and Chukchi. p. 1484

However, recent analyses of CR sequence variation in Native Americans indicate that haplogroup B may be as diverse as haplogroups A, C, and D (Bonatto and Salzano 1997; Stone and Stoneking 1998). p. 1487

Alvah's comment: In a May 1999 gathering of molecular anthropologists Dr. Denise O'Rourke from the U. of Utah reported that Type A mtDNAs was present in ancient Aleutian Island Populations dating to 2000 BC but in frequencies < 10%. Similar reduction in frequencies of Type A in other samples of ancient North American populations could indicate that type A is recently derived being only one mutation beyond mtDNA C and D. Worth noting is the prevalence of C and D in Northeast Asian populations (coupled with the virtual absence of Type A), the eastern perimeter encompassing Boas's "Eskimo wedge." Back migration from the Americas for Siberians, and more recently, the Eskimo, could explain genetic similarities between them and Native Americans yet Boas's conclusions made 100 years ago are rarely, if ever, cited by these authors.

Erlandson, J.M., Tveskov, M.A., and Byram, R.S. **The Development of Maritime Adaptations on the Southern Northwest Coast of North America.** *Arctic Anthropology* (1998), Vol. 35, No. 1, pp. 6-22.

Here, we address three primary issues in the archaeology of the southern Northwest Coast: (1) the antiquity of maritime adaptations; (2) the economic significance of sea mammal hunting; and (3) the nature and importance of fishing and weir technologies. We conclude that the antiquity of widespread maritime adaptations in the area is unknown, that pinniped hunting is best understood as an integrated part of broader subsistence adaptations, that coastal fishing was more diverse and eclectic than previously believed, and that the socioeconomic complexity of some southern Northwest Coast cultures was greater than previous models have suggested. p. 6

Although adapting to the exploitation of sea mammals, fish, shellfish, and birds led to certain parallels in technology, demography, and cultural complexity, significant differences also

evolved due to local variations in marine and terrestrial environments, migration or in situ development of distinctive ethnic groups, interaction with neighboring coastal and interior peoples, and other factors. p. 6

Some of this gap is due to the fact that much of the area is distant from major population centers and large research institutions. Some archaeologists may also have been discouraged from studying an area where "little of historical importance" (Drucker 1939:81) was ever supposed to have happened and relatively little published ethnography was available.

Statements such as Drucker's helped foster the misconception that the southern Northwest Coast was peripheral to the main currents of North Pacific cultural developments. Such views were facilitated by the dearth of detailed published accounts on the early history or ethnography of Native cultures of the area. p. 7

As we define it here, the southern Northwest Coast encompasses most of the eastern margins of Washington, Oregon, and northern California, from just south of Cape Alava on the north to Cape Mendocino on the south (Fig. 1). Like much of the Pacific Rim, this roughly 1000 km stretch of coast is rugged and mountainous, with relatively narrow coastal plains and continental shelves. This juxtaposition of mountains and the sea provided coastal peoples with access to a wide variety of habitats and a diverse suite of marine, estuarine, freshwater, and terrestrial resources. p. 7

Prior to commercial overexploitation, salmon, sturgeon, eels, trout, and other fish were abundant in coastal rivers, some seasonally and others year round. In the early 1900s, annual salmon runs appear to have numbered in the hundreds of thousands in several area rivers and several million in the Columbia River (Cobb 1930).

On land, vegetation communities are comprised primarily of coniferous rain forests, with the coast redwood forest zone dominant in northern California and the Sitka spruce zone to the north (Franklin and Dyrness 1988). The latter is dominated by Sitka spruce (*Picea sitchensis*), western hemlock (*Tsuga heterophylla*), and red cedar (*Thuja plicata*). Compared to more northern areas, plants with edible nuts, seeds, or berries are diverse, with acorns and root plants (e.g., camas and wapato) locally abundant. The most important large game in much of the area were deer and elk, but bears and a variety of medium and small mammals once were abundant. p. 7

Kuzmin, Y.V. and Orlova, L.A. **Radiocarbon Chronology of the Siberian Paleolithic.** *Journal of World Prehistory* (1998), Vol. 12, No. 1, pp. 1-53.

The area under study may be subdivided into two parts: Siberia proper and the Russian Far East. In American geography textbooks they are often described together (e.g., Simmons, 1990). Russian geographers, however, separate these two regions because of significant differences in climate and vegetation (e.g., Suslov, 1961). The territory of Siberia belongs to the Arctic Ocean drainage basin, and the Russian Far East belongs to the Pacific Ocean drainage basin (Fig. 1). p 3

Instead, the Mousterian-Upper Paleolithic transition seems to have occurred gradually in Siberia and the Russian Far East, within the time interval *ca.* 43,000-28,500 BP. p. 31

Hence, we accept this age of *ca.* 23,500 BP as a maximum for Ust-Mil 2 (see also Kuzmin, 1994, p. 368). This interpretation also fits well with the general developmental scheme of microblade industries in Northeast Asia (Yi and Clark, 1985; Abramova, 1989). The anomalous C-14 dates from Ust-Mil 2 [30,000 ± 500 BP (LE-1001), 33,000 ± 500 BP (LE-1000), and 35,400 ± 600 BP (LE-954)] might be explained by the redeposition of "ancient" wood from early Karginian sediments in the lower part of the section into the younger deposits containing the Dyuktai-culture artifacts (cf. Clark, 1988). Similar caveats about the unsuitability of wood as a material for precise C-14 dating of the Dyuktai culture have also been made by Abramova (1979c, 1989) and Yi and Clark (1985). pp. 36-37

It is clear that the Afontovo and Kokorevo cultures coexisted in the Yenisei River basin during the interval from *ca.* 21,000 to *ca.* 11,700 BP. The sequence at Listvenka (Afontovo-like in layers 14-19, Kokorevo in layers 7-13; and Afontovo again in layers 2-6) (Drozdov *et al.*, 1990, pp. 131-147) probably reflects the intrusion, at about 15,000 BP, of a Kokorevo population, northward from the core area some 15,000 BP, of a Kokorevo population, northward from the core area some 150-200 km away. p. 37

During the last 15 years, after larger-scale excavations of the Dyuktai sites, some new dates have been obtained. For Ikhine 2, there are two new dates on bone [presumably submitted after the minor excavations of 1992 (Mochanov and Fedoseeva, 1996, p. 195)]: 20,080 ± 150 BP (SOAN-3185) and 19,695 ± 100 BP (SOAN-3186). These are significantly younger than the previous C-14 dates, which range between 31,200 and 24,300 BP. Ikhine 1 was first dated in the 1980s to 16,660 ± 270 BP (IM-452) (Kashin, 1991). Ezhantsy, for which an age of *ca.* 35,000 BP was originally suggested (Mochanov, 1977), was dated in the 1980s to 17,150 ± 345 BP (IM-459) (Kashin, 1991). Thus, we may accept a preliminary conclusion that the youngest C-14 dates from Ikhine 2, *ca.* 24,600-24,300 BP (Mochanov, 1977), along with newly released dates from Ikhine 1 and Ezhantsy, accord quite well with the general model of the appearance of microblades in Siberia *ca.* 23,000-20,000 BP. pp. 38-39

The distinctive feature of Sartan Glaciation pollen spectra from Yakutia is a very low content of arboreal pollen. We can see the same feature in the Ikhine 1 pollen diagram for the upper part of layer 3 (the overlying layer 2 with artifacts is dated to *ca.* 16,600 BP). A very low arboreal pollen content is characteristic of Ezhantsy, layer 3, containing Dyuktai tools and dated to *ca.* 17,200 BP; and for Ikhine 2, layer 4, dated to *ca.* 31,200-24,300 BP. Based on all the observed data, the radiocarbon age of the Dyuktai culture may be estimated at *ca.* 24,600-10,000 BP.

In the Russian Far East, the earliest C-14 date for microblades is from Ust-Ulma 1, layer 2b, at *ca.* 19,400 BP. Other typical microblade industries from the middle Amur River basin and the Primorye are dated to *ca.* 15,300-10,100 BP, while in Northeaster Siberia, microblade assemblages are dated to *ca.* 13,400-8000 BP. p. 39

The Mesolithic layers have dates of *ca.* 10,500-8200 BP. However, on the basis of the most recent series of C-14 dates, the boundary between the Upper Paleolithic and the Mesolithic at

Eleneva Cave (the contact of the sixteenth and seventeenth cultural layers) dates to *ca.* 9600-9300 BP (Orlova, 1998). In the Angara River basin, Mesolithic sites are dated to *ca.* 9900-7300 BP. On the shore of Lake Baikal, where Mesolithic cultures are well defined (Medvedeve *et al.*, 1990), they are dated to *ca.* 10,300-6500 BP. In the Transbaikal, the Mesolithic as a separate stage (Konstantinov, 1994) is radiocarbon-dated to *ca.* 12,600-6700 BP. p. 40

In Russian archaeology, the most important criterion for defining the Neolithic is the beginning of pottery manufacture (e.g., Krushanov, 1989). The emergence of pottery in East Asia at the end of Pleistocene, *ca.* 14,000-12,000 BP, was one of the most revolutionary innovations in Old World prehistory (Barnes, 1993, pp. 64-72). Thus, the end of the Paleolithic and the beginning of the Neolithic mark a very important chrono-cultural boundary. p. 40

Thus, we now have strong evidence for the existence of the earliest pottery in the Russian Far East occurring at *ca.* 13,300 BP (Kuzmin *et al.*, 1997). In the Amur River basin and the Transbaikal, the Paleolithic-Neolithic transition goes back to *ca.* 13,300-10,400 BP. In other parts of Siberia and the Russian Far East, the transition took place much later: at *ca.* 7900-6700 BP in the Yenisei and Angara River basins and at *ca.* 6000 BP in the Lake Baikal area and Yakutia. p. 41

The archaeology and radiocarbon chronology of the Siberian Paleolithic provide the background for modeling the peopling of the Americas (Morlan, 1987; Powers, 1996). According to West (1996), the initial peopling of extreme northwestern North America (Alaska and adjacent areas) took place *ca.* 11,800-11,700 BP. Thus, the Siberian cultures which may be the "progenitors" of the Paleoindian cultural complexes must be at least 13,000-12,000 C-14 years old. p. 41-42

Some publications on the peopling of the New World (e.g., Dikov, 1979; Morlan, 1987; Laukhin, 1990) show the glaciation in this region as a vast and continuous glacial belt in the mountain ranges, which could have prevented migration toward Alaska. However, the most recent data (Velichko, 1993) show that glaciation was quite limited in most mountain systems, and glaciers were numerous only in the Verkhoyansk Range and the Kamchatkan mountains (Fig. 3). During the Sartan Glacial maximum, the level of the Bering and Chukchi Seas was about 100 m below that of today and the vast landmass known as the Bering Land Bridge connected Siberia and North America. Thus, between 20,000 and 18,000 BP several migration routes to the New World were accessible. Nevertheless, there are no reliable Paleolithic finds of this or comparable age east of the Lena River basin. p. 42

Using the most reliable dates—those on charcoal from primary stratigraphic contexts—we concluded that the age of the Clovis progenitors was at least *ca.* 24,000 BP (Ust-Kova). This suggests that Clovis progenitors could have migrated to North America from southern Siberia before the maximum of the Last Glaciation. However, the complete absence of macroblade sites in Northeastern Siberia (except for the very young sites of Ushki-1 and Kukhtui 3) prevents our tracing the routes of such migrants. This situation constrains all existing models for the peopling of the New World. p. 44-45

The earliest C-14 dates for the Nenana cultural complex in Alaska are *ca.* 11,200 BP and perhaps 11,800 BP (West, 1996). The oldest C-14 age of the Clovis cultural complex in central and

southwestern North America is *ca.* 11,600 BP (Haynes, 1992, 1993; Taylor *et al.*, 1996). The age of Monte Verde in southernmost South America, which is claimed to be the oldest in the Americas, is *ca.* 12,500 BP (Dillehay and Pino, 1997). The fact that Monte Verde is some 500-900 C-14 years older than any other widely-accepted Paleoindian site has resulted in much speculation about the possible timing and routes for the peopling of the Americas. However, the concept of the "practicable accuracy" of archaeological C-14 dates (Krenke and Sulerzhitsky, 1992) makes it difficult to assert that Monte Verde is actually older than the Nenana and Clovis complexes. They are all quite close to each other in age, with differences of <1000 C-14 years, while internal variations in their series of dates are at least 500-800 C-14 years. p. 45

The numerous radiocarbon dates from the Siberian Paleolithic allow us to elucidate the chronology of the most important changes in Siberian prehistoric life and technology. The Middle-Upper Paleolithic boundary may be drawn approximately between 43,000 and 28,500 BP; the Early-Late Upper Paleolithic boundary may be placed at *ca.* 24,000-19,000 BP; and the Paleolithic-Neolithic boundary, between *ca.* 13,000 and 6000 BP. p. 46

Alvah's comment: What is clear from this paper is that the Upper Paleolithic is in it's infancy at 43,000 and that it continued to develop following its derivation, becoming full blown Upper Paleolithic as sapiens migrated into Europe. If the dates are correct the first encounters between Homo sapiens and Homo erectus may have occurred in Western Siberia. Following this encounter the use of lithic tools by H sapiens expanded along with their range. If this trail is traced back into the Americas then the use of "bone before stone" could help in linking pre-Clovis bone tool technologies to Alaska and then into western Siberia. Only in the Americas does an ancestor to Homo sapiens exist that would not require a metamorphous from the separate species that was H erectus.

Park, R.W. **On the Dorset/Thule Analogy for the Middle/Upper Paleolithic Transition.** *Current Anthropology* (1998), Vol. 39, pp. 355-356.

The specific parallels that she postulates (p. 588) between the Thule and the Upper Palaeolithic (and thus distinguishing them from the Dorset and the Middle Palaeolithic respectively) are "population increase, rapid geographic dispersal, permanent human presence, increased sedentism, larger sites, a denser archaeological record, technological innovation, abrupt disappearance of an earlier cultural substratum, and displacement/extinction/absorption of earlier peoples." I would like briefly to address some of these issues for Thule and Dorset. p. 355

HISTORICAL ANTHROPOLOGY

Boas, F. **The Jesup North Pacific Expedition.** *Proceedings of the Thirteenth International Congress of Americanists.* (1905) Easton, PA: Eschenback Printing pp. 91-100.

The diversity of types, languages, customs and beliefs is so great that even a brief sketch of the fundamental features would occupy too much space and time. p. 95

While it is impossible to trace linguistic relationship between the numerous stocks inhabiting the area in question, it has become clear that morphologically the languages of northeastern Asia are not related to the Ural-Altai group of languages. The Chukchee, Koryak and Kamchadal, which are closely related to each other, are polysynthetic, like many of the American languages. They incorporate the noun in the verb, and resemble in all their fundamental traits typical American languages. To a less extent the same may be said of the Yukaghir. In a broad classification of languages, the languages of northeastern Siberia should be classed with the languages of America. p. 95

Owing to the great differentiation of the American race on the Pacific coast, and to the large intermixture of Tungus and Turkish blood in Arctic Siberia, the conditions are so complex that it is difficult to discover relationships without a very detailed study of the anatomical material. p. 95

On the other hand, Mr. Smith discovered that in early times the art of stone-flaking was practised extensively in southern British Columbia, while in later times and in other regions of the coast this art seems to have been almost entirely absent. Furthermore, he found a remarkable change in type between the prehistoric inhabitants of this area and the present race, the former having long and narrow faces and elongated heads, while at present very wide and heavy faces and short round heads prevail. All this goes to show that there must have been a considerable change of population in this region, which in all probability was due to an invasion of tribes from the interior, by which the population of the coast was considerably modified. It is very interesting to know that this conclusion, which is based on archaeological evidence, is borne out by linguistic and ethnological studies. p. 96

Extended migrations must have taken place also in northern British Columbia and in the adjoining parts of Alaska. Here we find the Haida on Queen Charlotte Islands, the Tlingit in southern Alaska, and the Tsimshian on the coast of northern British Columbia. p. 97

While the first two have a type of language somewhat similar, in morphological characteristics, to the Athapaskan, the Tsimshian is quite different. The first two have no reduplication, while Tsimshian abounds in reduplication. The first two have an elaborate verbal system, while the Tsimshian has a very simple method of verb composition. p. 97

The results of the expedition in regard to probable migrations in the Arctic are even more remarkable, and have an important bearing upon the question of the relationship between the tribes of Siberia and those of America. p. 97

This feature is so striking that Mr. Bogoras and Mr. Jochelson have independently reached the conclusion that a close affiliation exists between eastern Siberian folk-lore and that of southern Alaska and British Columbia. Mr. Jochelson finds that the Koryak have many incidents in their tales in common with the Old World and with the North American Indians, and quite a number which are common to the Koryak, the Eskimo and the Indians, but none that belong to the Koryak and to the Eskimo alone. p. 98

This clew once given, we investigated the cultural similarities in this whole area, and found ample evidence that there must have been, at an early period, an intimate relationship between the Indian tribes of the Pacific coast and the peoples of eastern Siberia. p. 98

It seems, therefore, that the expedition has established, on the other hand, a break between the East Siberian tribes and the Eskimo: and, on the other hand, a relationship between the East Siberian tribes and the coast Indians. The investigations of Messrs. Jochelson and Bogoras have also resulted in clearing up the relationship of the Northeast Siberian tribes to the adjoining Asiatics, particularly to the Tungus and Yakut. There is a fundamental break between the types of culture of these Asiatic tribes and of the East Siberian tribes; and comparisons of type, language and culture make it at once evident that the Northeast Siberian people are much more closely akin to the Americans than to other Asiatics.

The data collected by the expedition thus establish the fact that the Chukchee, Koryak, Kamchadal and Yukaghir must be classed with the American race rather than with the Asiatic race. p. 99

Future researchers may somewhat modify our views as to the lines of migrations here discussed, particularly, it seems possible that a more thorough investigation of the Alaskan Eskimo may correct our present conclusions as to the role that this tribe played in communicating Asiatic culture to America, and American culture to Asia, but it may be expected that the question which the expedition tried to solve will be modified by these researchers only in detail. The main fact of the existence of a close relation between the aborigines of Siberia and of America seems to be well established. p. 100

Alvah's comment: Few researchers site this work and/or the conclusions made of a back-migration following the end of the last Glacial. Boas's "Eskimo Wedge theory" encompasses two separate migrations; the Eastern Siberian Populations then the ancestors of the Eskimo. Both of these groups were identified by Boas as coming from North America. Thus, according to Boas, populations often identified as the ancestors of Native Americans, could actually be reflexes of aboriginal Amerindians into the Old World. Since this paper is rarely cited I thought Mother Tongue should at least qualify its existence!

Harkin, M. **Past Presence: Conceptions of History in Northwest Coast Studies.** *Arctic Anthropology* (1996), Vol. 33, No. 2, pp. 1-15.

The question of history, and even more, of temporality, is central to the way anthropologists view their "others," and hence the image that is constructed of them. Johannes Fabian (1983), in his critique of anthropological theory and practice, describes the central issue as a "denial of coevalness." That is, anthropologists (whose opinions are influential in shaping those of other members of their societies) have depicted the "other" in such a way that it is impossible to imagine that he inhabits the same world as we "moderns." These tribal people dwell in historyless worlds that are "cold" in the Levi-Straussian sense. p. 1

I do not believe it is correct to view anthropology as merely reactive to changes happening in the larger world. Rather, anthropology has changed as well due to its own internal institutional and intellectual dynamics. These changes have often themselves had an important effect upon the

larger world. Not only the popularizers, such as Margaret Mead and Ruth Benedict, but the systematizers, such as Claude Levi-Strauss and Leslie White, the originators, such as Franz Boas and E.E. Evans-Pritchard, and the *auteurs*, such as Clifford Geertz and Bronislaw Malinowski, have had a lasting influence on the sensibilities of the educated middle class in North America and western Europe. That is why periodic reexaminations of our professional past are so important. p. 2

But are these phases paradigms? Can we even speak of paradigms in the human sciences? In anthropology at least there have always been multiple voices, multiple churches of orthodoxy. The closest we can come to a paradigm in the Kuhnian sense is probably the central position of Boasian method and theory between 1900 and 1930. (This is the only phase for which I have used the term "paradigm.") This is especially clear in Boas' home field of the Northwest Coast. While Boasians were jousting with their evolutionary-minded British cousins. p. 10

Ethnohistory, in the sense it has developed on the Northwest Coast and elsewhere in recent years, is very much a product of this world. It has numerous advantages, both ethical and theoretical, over previous styles in Northwest Coast research. It highlights, not ignores, the unfair and often barbarous treatment First Nations received at the hands of people of European descent and their institutions, which has occurred in the recent past, and even up to the present day. It views the "native" as an agent, and sees historical processes as dialogic, and not merely local reactions to universal processes (as both acculturation and World Systems theory have it). At the same time, its emphasis on the specificity of culture makes it difficult to view indigenous people as merely bourgeoisie in cedar bark dress (Sahlins 1995:145-189). Finally, it engages current political realities in a way that previous styles of ethnography never could. Legal claims to territory and resources may be strengthened by ethnohistorical research: certainly a sense of historical identity and connectedness with the past may be. It seems that, finally, anthropologists have hit upon the theme that aboriginal people are truly interested in, and which provides a great deal of common ground between the two camps. p. 10

Alvah's comment: Should we examine the Native American contention that they have always been here? As Harkin states "That is why periodic reexaminations of our professional past are so important (p. 2)." Back migration was one of Franz Boas most powerful observations yet it seems unheralded in today's assessments of genetic linkage between Siberians and Native Americans. Harkin asserts; "In anthropology at least there have always been multiple voices, multiple churches of orthodoxy. The closest we can come to a paradigm in the Kuhnian sense is probably the central position of Boasian method and theory between 1900 and 1930. (This is the only phase for which I have used the term "paradigm.") This is especially clear in Boas' home field of the Northwest Coast. While Boasians were jousting with their evolutionary-minded British cousins (p. 10)."

Introductory remarks by Fewkes, J.W., President of the American Anthropological Association. **The Problems of the Unity or Plurality and the Probable Place of origin of the American Aborigines.** *American Anthropologist* (January-March, 1912), Vol. 14, No. 1, pp. 1-59.

At what epoch man came to our continent from a former home; how he made his way hither; and his history since he came, are questions that possess greater and greater attraction as the science

of man becomes broader and deeper. While the majority of anthropologists hold that man's original home was in Eurasia, there are those who advance reasons which in their judgment are equally adequate to prove that he was autochthonous in America, whence he spread to the Old World. Some students have held that America was peopled from the Old World because conditions of life were more complex on that continent than in the New, and because the simians most closely allied anatomically to man are indigenous to the Eastern Hemisphere. As none of the higher apes occur in America, it is reasoned that man, who is regarded as related to these animals, could not have been evolved in America. If we accept the theory that man originated in the Old World, it is evident that his colonization of America is a question of mode of migration, which resolves itself into a geographical or a geological one. p. 2

It can readily be seen that the question becomes a paleontological one, and so far as the determination of the age of the strata in which the anthropologist finds human remains is concerned, a purely geological problem. Unless we are prepared to accept an autochthonous origin of man or his evolution from higher animals in America, the means of primitive migration available, and the conditions of culture implied by a sea voyage, must not be overlooked. It is evident that the situation of islands, the configuration of land, and changes in its contour, are directly connected with all theories of the peopling of America. p. 2

Holmes, W.H. Bearing of Archeological Evidence on the Place of Origin and on the Question of the Unity or Plurality of the American Race.

With regard to this question, the consensus of opinion among students of the subject favors the view that the Old World gave birth to the human kind. Traces of human occupancy are found in the Old World associated with geological formations that may be safely assigned to the close of the Tertiary period, and it is incumbent on those who hold to the theory of American origin to establish occupancy of the New World. Two regions only in America have furnished testimony worthy of serious consideration in this respect—California and Argentina. The testimony in both of these cases is striking and picturesque, giving American man a place in the far Eocene, and is supported with much enthusiasm by a few students who are ready to stake their scientific reputations on the outcome. Recent investigations relating to North American as well as South American early man show that the testimony, if it is to stand, must have much additional support.

In view of these conditions, the theory of an autochthonous origin of the American race may be set aside, and the problem of the arrival in the New World of racial elements originating in the Old World need alone receive consideration. pp. 30-31

Fletcher, A.C. Some Ethnological Aspects of the Problem.

The various kinship groups composing a tribe are apt to be so combined as to express a recognition of the apparently dual natural forces, represented by Day and Night, Summer and Winter, Sky and Earth. This duality concept sometimes takes on an anthropomorphic form and the forces are regarded as male and female, or, they are reflected in social conditions, and represented as War and Peace. The two parts always stand for dissimilar but complementary forces or powers.

Not only in the tribal organization does this duality concept appear, but it is to be found reflected in many of the religious ceremonials of the people. It is to the latter that one must turn for the more direct expression of "religious ideas." It may safely be stated that among the

American race what may be termed "religious ideas" are fundamental to all ceremonials and upon them is built the tribal organization.

These "religious ideas," briefly stated, are founded upon the native conception of the cosmos. In this conception man views all things from his own personality and from this standpoint predicates his relationship to animate and inanimate nature.

Conscious within himself of an ability to move and to bring to pass, he regards motion, whether of body or of mind, as a universal ability and as the simplest and most fundamental manifestation of a mysterious, indwelling power that has brought all things into existence and is the cause of all movement; of the winds, the clouds, the storm, the rivers, the growth of vegetable forms, the activities of animals, and the physical and mental life of man. There is no visible thing within which this mysterious power does not dwell and that is not made active or stable by it. To man, this mysterious power is invisible and only knowable indirectly through its manifestations in nature and living forms. Since all things (for nothing to the Indian is strictly inanimate), including man, derive life and motion from this mysterious power, all things are regarded as in a sense, related to each other, because of the mysterious power that pervades and sustains all natural forms. pp. 37-38

Chamberlain, A.F. **The Problem from the Standpoint of Linguistics.**

It may be said here that the American languages are younger than the American Indians, and that, while the latter may have reached the New World in very remote times via Bering strait, the former show no evidence of either recent or remote Asiatic (still less European) *provenance*. There is thus absolutely no satisfactory evidence, from a linguistic standpoint, of the ultimate Asiatic derivation of the American aborigines; nor is there any of such a character as to argue seriously against such a view, which seems, on the whole, both reasonable and probable. Certain real relationships between the American Indians and the peoples of northeastern Asia, known as "Paleo-Asiatics," have, however, been revealed as a result of the extensive investigations of the Jesup North Pacific Expedition, which have been concerned with the somatology, ethnology, mythology, folk-lore, linguistics, etc., of the peoples on both sides of the Pacific, from Columbia river to Bering Strait and from the Amur to the extreme point of northeastern Asia. The monographs containing the scientific results of the Jesup Expedition are still in course of publication. The ones most significant for American-Asiatic relations are those of Sternberg on the tribes of the Amur, Jochelson on the Koryak and the Yukaghir, and Bogoras on the Chukchee and the Siberian Eskimo. The general conclusion to be drawn from the evidence disclosed by the Jesup Expedition is that so-called "Paleo-Asiatic" peoples of northeastern Asia, *i.e.*, the Chukchee, Koryak, Kamchadale, Gilyak, Yukaghir, etc., really belong physically and culturally with the aborigines of northwestern America; and they probably reached the parts of Asia they now inhabit (or once inhabited, for some of them had formerly a larger area of distribution) from America at a time more recent than the original peopling of the New World from Asia by way of Bering strait. Like the modern Asiatic Eskimo, they represent a reflux from America to Asia and not *vice versa*. In brief, these peoples may be said to be "modified Americans." It is the opinion of good authorities also that the "Paleo-Asiatic" peoples belong linguistically with the American Indians rather than with the other tribes and stocks of northern or southern Asia. Here we have, then, the only real relationship of a linguistic character that has ever been convincingly argued between tongues of the New World and tongues of the Old. The special resemblances of the Gilyak with the American Indian languages, from a morphological point of view, has been treated by Sternberg, in a paper read before the Congress International des Americanistes at

Stuttgart in 1904. In his sketch of the grammar of the Yukaghir, Jochelson points out a number of respects in which that language also resembles the American Indian rather than the Ural-Altaic tongues of the Asiatic continent. And finally, Dr. Franz Boas, in his article on "Ethnological Problems in Canada," makes this statement: "A consideration of the distribution, and the characteristics of languages and human types in America and Asia, have led me to formulate the theory that the so-called Paleo-Asiatic tribes of Siberia must be considered as an offshoot of the American race, which may have migrated back to the Old World after the retreat of the Arctic glaciers." p. 56

Dixon, R.B. **Mythology.**

In its relations to the mythologies of other areas, the most important associations are to be found with northeastern Asia. Here the degree of similarity is most striking, the myths of northeastern Asia and of northwestern America forming practically one great group, the members of which are allied not by form alone, but by actual content of the myths themselves. Except for this area, no clear evidence of relationship has been shown.

This Asiatic relationship must not, however, be regarded as furnishing evidence relating to the origin of the American Indian. It indicates a cultural relationship only, and far from pointing to an Asiatic source for the culture even, the bulk of the evidence would favor the theory that the similarity shown in the mythologies is the result of influences passing from America to Asia, and not in the reverse direction. Such cultural influence, moreover, belongs to a stage in culture far above that which must have been possessed by the ancestors of the present Indian at the time when they first came to America and belongs to a period far more recent than that at which the peopling of the American continent must have taken place. p. 59

Alvah's comment: The preceding concepts helped to one; eliminate the Americas from the search for human origins while the concordance of evidence would seem to qualify the unincorporated theory of a "back-migration" from the Americas into Siberia at the end of the last Ice Age. Funny how we continue to dismiss, without testing further, the idea of human ancestors in the Americas or, even, the fundamental Boasian contention - the unpublished results of the Jesup Expedition - of "back-migration" by Natives Americans into Siberia after the termination of the Last Glacial.

Was this conclusion, and the subsequent rattling of the British-evolutionists cage, to lead Boas to become primarily a data collector. His later reluctance to feed the fire of anthropological debate may stem from the contempt that surfaced when he first identified back-migration for links between Siberians and Native Americans.

Weil, J. **Boasian Anthropology and Identity Politics.** *Current Anthropology* (1998), Vol. 39, No. 3, pp. 391-394.

Each new generation can benefit from a fresh look at the oft-cited passage from Ruth Benedict's obituary of Boas; reiterated in George Stocking's editorial introduction: "he found anthropology a collection of wild guesses and a happy hunting ground for the romantic lover of primitive things; he left it a discipline in which theories could be tested and in which he had delimited possibilities from impossibilities" (pp.3-4). p. 391

NORTH AMERICA

Hall, D.A. **Though Science Sometimes Takes Time, The Consequences Can Be Spectacular.** *Mammoth Trumpet* (1997), Vol. 12, No. 2, pp. 1, 14-17.

These two early Nevada men looked somewhat different from most of the people who are known to have inhabited the area about 5,000 years later. Possibly they represent a population that reached North America before other ancestors of today's Native Americans. Analysis of cranial measurements of skeletons that date to around 9,000 years ago or earlier indicates those people had different morphologies and may have had different roots than later Americans. Forensic anthropologists, expert at determining the physical characteristics of crime and accident victims, say these most-ancient Americans had certain generalized features they see in contemporary Caucasian populations. p. 15

Alvah's comment: Since the European mtDNA markers are found in northern North Americans with little, if any, in South American Indians, then the idea that the First Americans were displaced by later Asian migrants must explain why the European mtDNAs (X Type women lineages) survived only in northern North American populations and/or why, if Europeans were FIRST, European mtDNAs are not represented in South American Populations? The obvious answer is that Europeans were more recent migrants to the Americas. Encounters, at the end of the last Ice Age, between Europeans with Paleolithic technologies, and pre-existing pre-Clovis populations not only fits the genetic data better but, moreover, suggests that intermarriage between these once isolated groups, is an indicator of peaceful assimilation.

Plumet, P. and Lebel, S. **Dorset Tip Fluting: A Second "American" Invention.** *Arctic Anthropology* (1997), Vol. 34, No. 2, pp. 132-162.

Basal fluting of Clovis and Folsom Paleo-Indian points is usually considered as the earliest technical "invention" made by an American population, some 12,000 years ago. The purpose of this paper is to introduce, describe, and analyze another prehistoric American invention—tip fluting of points—which was characteristic of the Early and especially the Middle Dorset cultures in the Late Paleo-Eskimo period (2500-1250 BP). During this period the non-tip-fluted points tended to be unifacial, whereas bifacial points dominated during the Late Dorset (1250-650 BP). This very particular technique has not been observed in any other prehistoric culture in the New or Old World. Only some small North African Neolithic arrow points present an apparently similar feature, but they are much smaller at the very end (Fig. 1a). p. 132

Workman, W.B. and McCartney, A.P. **Coast to Coast: Prehistoric Maritime Cultures in the North Pacific.** *Arctic Anthropology* (1998), Vol. 35, No. 1, pp. 361-370.

Maritime adaptations are earlier in the ice-free North Pacific than farther north, with independent centers of development in Asia and northwest North America. The available evidence from the North Pacific rim suggests that maritime hunting and fishing were Holocene developments that

arose independently of any earlier coastal adaptations during the initial peopling of the Americas. p. 361

Origins and Antiquity of Maritime Culture in the North Pacific

It seems clear that exploitation of marine resources was significantly earlier in more southerly, ice-free seas, both in Asia and North America, than it was farther north. p. 367

The mid-Holocene Hokkaido Jomon people should probably be admitted to the roster of maritime cultures, although farther south full-fledged commitment to maritime subsistence was deflected in part by the richness and diversity of the terrestrial resource base, especially plant food. This situation has parallels on the central and southern Northwest Coast in North America. p. 367

In North America, sea-oriented peoples occupied the Kodiak Archipelago by 6000 years ago (Hausler-Knecht 1993). It seems fully possible that people with a subsistence based on maritime resources had made their way into the eastern Aleutians by or before 8000 years ago. Dated human occupations approaching the Pleistocene/Holocene boundary beyond 10,000 BP are documented for southeastern Alaska and the Queen Charlotte Islands on the Northwest Coast. p. 367

Geographic realities strongly suggest that the early hearths of maritime culture in northeast Asia and northwestern North America developed independently of each other. p. 368

We see nothing in the evidence provided in this volume to make us alter a previously expressed judgment (Workman 1989) that maritime adaptations are mainly a Holocene phenomenon, one of many expensive economic strategies adopted by the ancestors to survive and prosper in a somewhat resource-depleted post-Pleistocene world. p. 368

Stone, A.C., and Stoneking, M. **mtDNA Analysis of a Prehistoric Oneota Population: Implications for the Peopling of the New World.** *Am. J. Hum. Genet.* (1998), 62:1153-1170.

Sequence data indicate a correspondence between each marker and particular hypervariable region I (HVI) mutations (Ginther et al. 1993; Horai et al. 1993; Bailliet et al. 1994; present study). Bailliet et al. (1994) suggested a fifth cluster of lineages that has a unique HVI mutation at nucleotide 16278 and does not possess any of the characteristic markers. p. 1153

A total of 328 bp (nucleotides 16056-16383) of the HVI common to all sequences were used for these analyses. Using the quartet-puzzling method to relate Native American and Mongolian sequences with maximum likelihood resulted in a poorly resolved tree. Of 14,463,090 quartets, 49.3% were unresolved, which indicates that these data are not good for this type of analysis. The g rate heterogeneity parameter a was estimated from the data, giving $a = .30$. p. 1159

Typically, group D lineages are rather dispersed, with very low bootstrap support. This results from the characteristic group D mtDNA HVI mutations that include those at nucleotide 16223 (also found in group A and C lineages) and at nucleotides 16325 and 16362, which fall into the

highly variable class of sites (Hasegawa et al. 1993) found in many other lineage clusters. The Yanomami haplogroups X6 and X7, identified by Easton et al. (1996) as new, independent Native American haplogroups, are generally interspersed among the group D sequences, often sharing the same branch with group D sequences. p. 1160

When only two regions, North America and Haida, were examined, the variation among regions (9.96%) was not significant ($P = .21$), which indicates that mtDNA sequences from the Haida, classified as Na-Dene speakers by Greenberg (1987), are not significantly different from those found in North American Amerind speakers. p. 1163

Thus, according to these data, Mongolians and Native Americans look like members of the same population that began an expansion ~95,000 years before the present (B.P.) (48,000 years under the faster rate). Similar results were obtained when the Mongolian data were subdivided into Dariganga and Khalkha cultural groups and compared to the Norris Farms Oneota. p. 1163

The Norris Farms Oneota possessed a high percentage of single lineages (73.9%) compared to most modern populations. However, this could also reflect Oneota population history. Additional precontact populations should be examined to determine whether a high number of rare lineages is a general feature. p. 1164

Instead, lineage 24 groups with Mongolian sequences that belong to Asian haplogroup F in Kolman et al. (1996). Moreover, as noted by Bailliet et al. (1994) and Forster et al. (1996), Nuu-Chah-Nulth lineages 1-4 probably do not belong to one of the four primary Native American haplogroups. In this research, they cluster with Norris Farms lineage 24 in phylogenetic trees of Native American lineages and with group F Mongolian lineages in phylogenetic trees of Native American and Mongolian lineages (fig. 2). p. 1166

Thus, as noted by Forster et al. (1996), the *HaeIII* site should not be used alone to define any new haplogroup, and it may be questionable to assume that the site is informative about the number of founding lineages. As a result, the conclusion that X6 and X7 represent new founding lineages does not seem warranted, and it seems more likely that they are derived from C and D lineages. p. 1166

The pairwise comparison of sequences from Native Americans and Mongolians sheds some light on the debate over the number and diversity of migrant populations. The data indicate that Mongolian and Native American populations, including the Haida, have not been isolated from one another for a sufficiently long period of time to generate the mutations needed to result in a leading intermatch distribution. These intermatch distributions resemble the distribution generated when two populations diverge and then expand at approximately the same time (Harpending et al. 1993). p. 1167

The AMOVA analysis between the Haida and other North American populations also does not indicate that the Haida are significantly different from other Native Americans. These data thus suggest that the ancestors of the Haida were included in the initial colonization of the Americas and not the product of a later separate migration from Asia. p. 1167

These Native American populations seem to be exceptions to this, since Chibchan populations are agriculturists and the Haida share food procurement strategies as well as geographic location with the Nuu-Chah-Nulth, who have a much smoother mismatch distribution and a high amount of sequence diversity. p. 1167

In their analysis of the Nuu-Chah-Nulth mtDNA data, Ward et al. (1991) suggested that the sequence differences within lineage clusters coalesce ~8,000-15,000 years B.P. and that many of these differences occurred within Amerindian populations. p. 1167

The mtDNA evidence does not support the three-wave hypothesis of migration into the New World. Native American mtDNA lineages are a subset of Asian lineages, and these lineages are typically rare in Asian populations. Consequently, one would not expect to see these same lineages introduced repeatedly into the Americas.

Alvah's Comment: If Types A-D being were "derived Lineages", resulting from pre-Clovis Amerindian isolation during the Wisconsin Glaciation, then Back-migration into Siberia could help explain similarities between the Populations of Northeast Asia that most anthropologists automatically identify as "the ancestors of the first Americans." Boas concluded that this assumption is flawed while his identification of an alternative explanation for the relationship between Northeast Asians and Native Americans has been lost in the 100 year old shuffle of Paradigms lost.

SOUTH AMERICA

Demarchi, D.A., and Macrellino, A.J. **Dermatoglyphic Relationships among South Amerindian Populations.** *Human Biology* (1998), v. 70, no. 3, pp. 579-596.

O'Rourke and Suarez (1985) observed that the synthetic gene frequency maps for South America do not give any evidence of migration or population movement. Instead, they seem to be irregular, derived from isolated populations drifting independently. The fact that blood genetic traits respond readily to microevolutionary processes could be one of the probable causes of such discordances (Froehlich and Giles 1981b).

Of special interest is the close resemblance found between the Andean and the tropical forest groups. This relationship has been described in several studies from different sets of data. Based on morphometrics and material culture, Vellard (1981) proposed that the Quechua's origins may be found in ancient Amazonian populations who displaced the earlier inhabitants of the Andes. Ruffie and colleagues of the Centre d'Hemotypologie du Toulouse observed remarkable genetic resemblances between the Aymara and Quechua and aboriginals from the Amazonian forest, near Guiana (Ruffie and Larrouy 1966; Arnaud et al. 1981). Craniometric and blood genetic studies carried out by Rothhammer and Silva (1989, 1992) also suggest that the origin of Andean populations is probably Central Amazonia. Hoff et al. (1981) also found a close affinity between Andean and Amazonian populations in their dermatoglyphic traits. Based on their own results and those reported by Blaco and Chakraborty (1975) (who worked with 10

serum polymorphic systems), suggested a more recent common origin or substantial gene flow between the populations. Our results are consistent with this conclusion. p. 592

Interpreted in terms of a branching model, our results suggest an earlier separation of the paleo-American-speaking tribes from the original colonizer population of South America and a relatively recent separation of the tropical forest and Andean populations. Although this model overlooks the effect of genetic drift and gene flow on genetic distances (Relethford and Harpending 1994), the pattern of relationship found among the South American tribes seems to be related to shared ancestry rather than to gene flow between geographically proximate populations.

Another possibility is that more than one migration took place into South America. Although several studies based on mtDNA founding haplotypes suggest a single wave of migration into South America (Merriwether et al. 1995), morphological evidence from fossil remains (Neves and Pucciarelli 1991; Munford et al. 1995) and morphological and mtDNA analyses from dental remains carried out on recent Fuegian-Patagonian samples (Lahr 1995; Fox 1996) indicate that the biological diversity in South America might be the result of at least two migration waves. The highly significant separation between the paleo-Americans and the Andean and tropical forest cluster found in this study supports this hypothesis. p. 593

Ribeiro-Dos-Santos, A.K.C., Santos, S.E.B., Machado, A.L., Guapindaia, V. and Zago, M.A. **Heterogeneity of Mitochondrial DNA Haplotypes in Pre-Columbian Natives of the Amazon Region.** *American Journal of Physical Anthropology* (1996), 101:29-37.

Thus, although only haplotypes shared by Asian populations were detected, a wide haplotype variability was observed. If our sample is representative of Pre-Columbian South America, the percentage of haplotypes (39%) not belonging to the four haplogroups described by Horai is much greater than in contemporary indigenous populations. This permits us to suggest that, in addition to the postulated bottleneck effect during the migration from Asia to the Americas, the depopulation effect started by European colonization in the 16th century contributed to the reduction of genetic variability of Amerindians. p. 29

There is no agreement about data interpretation, and even the possibility of a restricted number of ancestral lineages has been questioned. p. 30

The reduced number of mitochondrial lineages detected among contemporary Amerindians may be the product of a bottleneck effect during migration from Asia to the Americas (Wallace and Torroni, 1992), or the consequence of the drastic reduction in the number of individuals after contact with Europeans (Uebelaker, 1992; Cunha, 1992), or both. In any case, the idea of a reduced number of founding lineages is not consensual (Ward et al., 1991; Horai et al., 1993; Balliet et al., 1994). p. 30

Despite the fact that this was a relatively small sample, a wide haplotype variability was demonstrable: in addition to the four haplogroups described by Horai et al. (1993) corresponding to 61% of the sample, there were eight samples that did not belong to any of these haplogroups, which we have tentatively assembled into groups V and VI. p. 35

The two mutations are shared by different ethnic groups, indicating that they precede by a long time the entry of the first inhabitants into the Americas. The (C Æ T) transition in nt 16,233 is detected at low frequency among Blacks, Caucasians, and Mongoloids of the Asia-I group, and at high frequency among Mongoloids of the Asia-II group (Horai and Hayasaka, 1990). p. 35

If our sample is representative of Pre-Columbian America, the proportion of haplotypes not belonging to the four haplogroups of Horai et al. (1993) is much greater than in contemporary indigenous populations. This finding, however, is also supported by our results obtained in contemporary Amerindian populations from the Amazon, showing that 7% of the haplotypes obtained concomitantly by RFLP and sequencing lack one of the characteristic markers of the four haplogroups (S.E.B. Santos, A.K.C. Ribeiro-dos-Santos, D. Meyer, and M.A. Zago, unpublished). This permits us to suggest that the reduction in genetic variability observed in present-day Amerindian populations could also be attributed to the depopulation effect that started in the 16th century, which decreased the population size by more than 95% (Dobyns, 1966), in addition to the bottleneck effect during migration from Asia to the Americas, as proposed earlier. p. 36

Alvah's comment: If pre-Clovis populations inhabited the Americas behind the veil of Glacial barriers, and if migration(s) went both into and back out of the Americas at the end of the Last Ice Age, then the effects of encounters between once isolated populations must be re-assessed. Could the evidence of Type X - E mtDNAs in Northern Amerindians indicate admixture from Europe? Would this encounter have been a vector to later genetic variability?

LANGUAGE

Ganger, J., and Stromswold, K. **Innateness, Evolution, and Genetics of Language.** *Human Biology* (1997), 70: 2, pp. 199-213.

Given that the rules of syntax are too complex for a general-purpose learner to deduce without training and that children do not require training, children cannot be general-purpose learners when it comes to language. They must come equipped with special-purpose learning algorithms that allow them to learn language in a rapid and error-free manner.

Observational and experimental studies provide additional evidence for the innateness of language. p. 200

The order in which children acquire grammatical morphemes of English is also relatively uniform across children (Brown 1973; de Villiers and de Villiers 1973), as is the order in which children acquire complex constructions such as questions, negatives, datives, and passives (Stromswold 1988, 1989, 1990, 1995; Snyder and Stromswold 1997). As we will see in the final section of this paper, although some children are faster than other children at acquiring language, the fact that most children acquire the components of language in essentially the same order suggests that language development is largely the result of innate processes. p. 201

For example, the creolized language of second-generation pidgin speakers includes embedded and relative clauses, aspectual distinctions, and consistent word order, despite the absence of such features in the input language (Bickerton 1981). Thus children who are given a pidgin as their language input go beyond their input and "invent" a language that is more complex and includes the grammatical necessities of natural language. Studies of creolization thus provide compelling evidence that human children are programmed to develop a specific kind of language even with minimal input. p. 201

Evolution of Language

In evaluating evolutionary theories of language, it is useful to think of them as divided along two dimensions. The first major dividing line is the means of evolution. At one extreme is adaptation, according to which language evolved by Darwinian natural selection for some purpose, such as communication. Opposing adaptation is nonadaptation, which can be realized as exaptation (the appropriation of previously developed structures for new functions), serendipity (the opportune birth of a structure or function as a by-product of other structures), or various other possibilities. p. 202

Several researchers have argued that syntax serves as a link between mental representation and speech or motor control and that syntactic properties are due to trade-offs between these functions. The linguist Frederick Newmeyer provides a representative example of this type of theory. According to Newmeyer (1991), our ancestors already had a system of conceptual representation and a system of vocalization in place when selection occurred for syntax (a system linking the two). thus syntax was not selected for *directly* because of its communicative and representational functions but because it served as a link between preexisting systems. p. 204

Lieberman (1984) pointed out that the physiological and anatomical adaptations in jaw shape and the tongue and larynx placement required for speech are disadvantageous for breathing and swallowing. He argued persuasively that such a detrimental situation could not have evolved unless it caused improvements in syntax or some other aspect of language. Therefore speech and syntax must have evolved in concert, not in succession. p. 205

Bickerton (1990) made specific claims about when and how this representational ability evolved. He argued that the jump from proto-language to syntax was made all at once in one species. According to Bickerton, the diversity of tools and artifacts one might expect from a linguistic society was not present in pre-*sapiens* species, so ours must have been the first to use language. p. 205

A second problem with Bickerton's theory is that, just because children make a leap in their second year of life from a proto-language to full-fledged syntax, this does not imply the same leap could have been made in a single mutation. As we saw earlier, syntax is not much use without highly developed systems of communication and representation. Despite what is certainly a narrowly constrained *Bauplane* of the human brain, syntax probably did not develop all at once without some form of these other abilities in place, nor is it likely that these other abilities developed without syntax. Given that these abilities must have coevolved, Bickerton's jump is more likely to be an extended period of coadaptation, as Lieberman proposed. p. 206

The physiological and functional proximity of language to tool use may account for how language evolved, but not why. To answer this second question, Greenfield proposed that language evolved as a way to pass on knowledge of tools to others. If an individual can benefit from the inventions of previous generations, he does not have to reinvent the wheel, so to speak, with each problem. p. 206

To sum up, it is difficult to advance the study of evolution of language if we do not know the purpose for which language was adapted. Language may have been adapted for a specific communicative purpose, such as tool use or hunting, or for communication in general. It may have been adapted for better representation of the world, which in turn allowed for more abstract thought and reasoning—or perhaps just for better hunting. But, as Chomsky warns, language may merely be a spandrel of the brain's complexity and hence may not have been adapted at all. Researchers must realize that when they propose that language was adapted for a particular function, no matter how innocent and intuitively obvious that purpose seems (e.g., communication), is not uncontentious. Researchers need to put more effort into justifying the function of language that they advocate. Such argumentation must be an integral part of a good theory. pp. 207-208.

Although all adults eventually arrive at essentially the same basic level of linguistic competence in their native language, the rate at which they acquire language varies. As discussed earlier, one of the most striking qualities of language acquisition is its robustness and uniformity. p. 209

Alvah's comment: How long language has been used is directly related to how long Homo sapiens have been sapient. Old World forms of Homo including erectus may have expressed some ideas through language but their physical anatomy, specifically the area of the larynx, made it difficult to articulate certain sounds. Language, and the copacity to express ideas through it offer another exaple seperateing sapiens from erectus.

GENETICS

Bandelt, H., and Forster, P. **The Myth of Bumpy Hunter-Gatherer Mismatch Distributions.** *Am. J. Hum. Genet.* (1997), 61:980-983.

This cluster, described by Bandelt et al. (1995), includes the major African 9-bp deletion subcluster (Soodyall et al. 1996) and is widespread in Africa. It is even found as single outliers in Sardinia, the Middle East (Di Rienzo and Wilson 1991), and Turkey (Calafell et al. 1996). According to Horai and Hayasaka (1990) as well as Tamura and Nei (1993), this cluster constitutes the deepest rooting lineage of their mtDNA trees, and in other analyses it would also branch off very deeply. Therefore, all these populations, including ≥ 9 of the 13 populations used by Watson et al. (1996), such as the Senegalese Mandenka, coalesce close to mtEve. The coalescence time of 9,000-21,000 years for the Mandenka and thus for mtEve, as calculated by Watson et al. (1996) in their table 3, compares unfavorably with current estimates of 140,000-160,000 years for mtEve (Horai et al. 1995; Tamura and Nei 1993). The other populations in their table 3 fare little better. p. 981

Recent admixture of a group of very distant lineages (such as the 9-bp cluster) into two or more populations inflates genetic distances, and a tree analysis of these distances (their fig. 3) can misinterpret this recent admixture as an ancient population split. p. 981

It is interesting to note that a few of these sequences were found in non-Khosian populations, and these sequences presumably represent recent admixture. The reduced median network (fig. 2) for this data reveals that the !Kung lineages are inseparable by all but six private mutations from other southern African populations. In particular, 8 of 18 Nama (Khoi) lineages are interspersed in the !Kung (San) cluster. Even the outlier sequence in the !Kung (outside the network) is close to other Khoisan sequences: it differs from a Sekele sequence at only one position. The !Kung hence seem to represent only a splinter of a former widespread Khoisan population, and their differentiation from other Khoisan populations may have occurred quite recently relative to the !Kung coalescence time. p. 982

Alvah's comment: Does this paper suggest that admixture could be the cause for the widespread distribution of the 9bp deletion in Africa? Given that the highest frequencies of the 9bp marker in Africa is in Madagascar, a recently populated adjacent-region of Africa, the origins of the Phoenicians of the Mediterranean could also be, possibly, traced to southeast Asia. Outliers of this marker in Europe; "It is even found as single outliers in Sardinia, the Middle East (Di Rienzo and Wilson 1991), and Turkey (Calafell et al. 1996)." could mimic the evidence in Africa, as that resulting from recent admixture.

Macaulay, V.A., Richards, M.B., Forster, P., Bendall, K.E., Watson, E., Sykes, B., and Bandelt, H. **mtDNA Mutation Rates—No Need to Panic.** *Am. J. Hum. Genet.* (1997), 61:983-986.

It has been argued (Paabo 1996; von Haeseler et al. 1996) that fast sites such as these will predominate among recent coalescences and be underestimated in more ancient ones, so that the faster rate (which they call the "pedigree" rate) may be more appropriate to a timescale of hundreds or thousands of years, whereas the slower rate (which they call the "phylogenetic" rate) may be suitable for a timescale of hundreds of thousand or millions of years. With respect to the phylogenetic rate, a timescale of millions of years is unrealistic, since many positions in the control region would have been saturated with transitions over this timescale—which is the reason why transversional, rather than transitional, divergence is used to estimate the phylogenetic rate (Ward et al. 1991). A timescale of roughly the past 150,000 years would seem to be reasonable for the application of this rate, since this was the range in which it was calibrated (by use of the transition-transversion ratio in modern human populations). p. 94

In order to test empirically whether the pedigree rate is more appropriate at evolutionarily recent time depths, we can compare the performance of the pedigree rate against the conventional phylogenetic rate in the case of the settlement of the Cook Islands in central Polynesia. The settlement of Polynesia is a special case of population expansion, since it is very recent (occurring ~1,000-3,000 years ago) and well-dated archaeologically. Furthermore, it is characterized by the spread of a particular mtDNA lineage group defined by a 9-bp deletion and a distinctive control-region-sequence motif. This lineage group must have arisen prior to the settlement of Polynesia, since it is ubiquitous throughout the region, and indeed phylogeographic

analysis of lineages from Southeast Asia confirm this (Melton et al. 1995; Redd et al. 1995; Sykes et al. 1995). Applying the conventional mutation rate to data from the Cook Islands (Sykes et al. 1995) yields a coalescence time of $1,100 \pm 800$ years ago—in agreement with the archaeological dates of 900-1,300 years ago for the first settlements (Bellwood 1978). Applying Howell et al.'s pedigree rates to the same data yields a coalescence time <150 years ago. Such a date could be explained only by very recent population bottlenecks, which would be very difficult to reconcile with the observed uniformity of lineages across Polynesia. This observation strongly suggests that the phylogenetic rate is appropriate to vents at least as recent as 1,000 years ago. p. 984-985

Howell, N., and Mackey, D. **Reply to Macauley et al.** *Am. J. Hum. Genet.* (1997), 61:986-990.

However, there is no gold-standard clock for the rate of mtDNA divergence, particularly within the D-loop. Standard phylogenetic estimates of the rate of human mtDNA divergence vary widely, and they are associated with high degrees of statistical uncertainty (e.g., see Adachi and Hasegawa 1996; Howell et al. 1996; Parsons et al. 1997), in part because of the different models of mtDNA evolution that have been used by different investigators. p. 987

Furthermore, Tajima (1993, table 7) showed that the molecular-clock hypothesis was *not* supported among all subsets of hominoid mtDNA sequences that were analyzed with his statistical tests. p. 987

Overall, these results do not support a simple explanation for the high pedigree divergence rate in which HVR2 hypermutational hot spots "swamp out" a slower overall rate of D-loop divergence. On the other hand, failure to correct for site heterogeneity of mtDNA mutation rates confounds *phylogenetic* analysis and produces serious biases in estimates of the overall mutation rate, the time of the last common ancestor, the transition-transversion ratio, population genetic parameters, and Tajima's D statistic for neutrality (e.g., see Hasegawa et al. 1993; Wakeley 1993; Bertorelle and Slatkin 1995; Aris-Brosou and Excoffier 1996; Yang 1996; Wakeley and Hey 1997). p. 987

Those observations support a high pedigree divergence rate. Overall, one could conclude that the results of Bendall et al. (1996) support our suggestion (Howell et al. 1996) that it is the phylogenetic-divergence-rate estimates that are biased, possibly because they fail to adequately incorporate the effects of site variability in mutation rates. p. 988

Furthermore, it is not yet clear at what level selection acts (replication, segregation, or phenotypic expression) or to what extent random drift predominates over selection, particularly during oogenesis (e.g., see Jenuth et al. 1996).

We suggested that the high pedigree D-loop divergence rate, relative to phylogenetic rates, may reflect the failure of a substantial proportion of new D-loop mutations to become fixed at the population level (Howell et al. 1996). Although definitive data are not available, it seems safe to posit that the fixation probability is <1 (unless one makes the unlikely assumption that all new mutations will become fixed). It then follows that the pedigree divergence rate must exceed

the phylogenetic rate, because of the different time scales (see the further discussion below). p. 988

One must be cautious, even skeptical, pending further analysis, but selection may explain the observation, by Parsons et al. (1997), that some newly arisen D-loop mutations occur at sites with below-average levels of polymorphism within the population. p. 989

Pedigree analysis may be more heavily dominated by random drift, whereas phylogenetic analyses may be more influenced by selection, because of the greater time spans inherent to phylogenetic analysis. p. 989

As Macaulay et al. (1997) mention, one expects that there should be a decline in divergence rates as the time depth increases, presumably as a failure of newly arisen mutations to become fixed, but there is not yet sufficient information for us to expect the monotonic decline that they suggest. It is premature to make, as they do, these comparisons between phylogenetic analyses and pedigree studies. p. 989

Bower, B. **DNA's Evolutionary Dilemma.** Science News (1999), Vol. 155:88-90.

Mitochondrial DNA shows a great deal of individual variability, which as buttressed assertions that it can help to trace the evolutionary history of human females. Researchers have largely believed that mitochondrial DNA changes occur randomly and accumulate at a constant rate in isolated populations, making them suitable for dating ancient population splits.

But mitochondrial DNA may not be so predictable, according to some researchers. Sections of its sequence of nucleotides undergo surprisingly rapid changes, even within one or a few generations, argues Neil Howell of the University of Texas Medical Branch in Galveston. Mitochondrial DNA alterations may not tick away like hands on a reasonably accurate evolutionary clock, Howell maintains.

Some of these genetic-sequence variations have spread through populations with a speed suggesting that they somehow aid the survival of their bearers, he adds. If natural selection has reshaped the mitochondrial landscape over relatively short spans of time, it raises serious doubts about the accuracy of estimated ages for evolutionary trees and sizes of ancient populations. p. 89

"Far too often, anthropological geneticists draw conclusions about human evolutionary history without testing hypotheses or exploring alternate models," Mountain remarks. "In some cases, this is because data are insufficient. In other cases, the immediate impression generated by the data blinds us to alternatives."

Hammer, who remains undecided on how modern humans evolved, suspects that investigators will increasingly experiment with statistical formulas for weighing the contributions of natural selection and other factors to DNA diversity. p. 90

Alvah's comment: In its own way population genetics is confounded by similar modes of change as found in Linguistics. Genetic adaptation could be seen to mirror - language isolation; admixture - language borrowing and; genetic affinity - population or language survival.

Deciphering the amount of influence each has on the other should help researchers in unmasking new data as it come in.

Fregeau, C.J., Tan-Siew, W.F., Yap, K.H., Carmody, G.R., Chow, S.T., and Fourney, R.M. **Population Genetic Characteristics of the STR Loci D21S11 and FGA in Eight Diverse Human Populations.** *Human Biology* (1998), v. 70, no. 5, pp. 813-844.

A highly polymorphic multiplex short tandem repeat (STR) system composed of D21S11, FGA, and the sex-typing system amelogenin (AMG) has been used to investigate allele frequency distributions in two Canadian Caucasian samples (British Columbia and Alberta), three Canadian aboriginal populations (Coastal Salishans from British Columbia, Ojibwa from northern Ontario, and Cree from Saskatchewan), and three ethnic groups from Singapore (Chinese, Malays, and Asian Indians. p. 813

Results from the 2 X N contingency table exact tests for population differentiation demonstrated that the Canadian samples from two different provinces were not distinguishable from one another at either STR locus and therefore could be combined to form one Caucasian group. Likewise, Chinese and Malays from Singapore did not show significant differences at either STR locus. In contrast, all other examined populations exhibited differences deemed statistically significant. As a complement to our study, we compared D21S11 allele frequency distributions in 21 worldwide populations and FGA allele frequency distributions in 14 populations. Many alleles never previously reported in worldwide populations were identified in Canadian aboriginal and Asian samples from this study. Twenty-four D21S11 and 29 FGA alleles were distinguished in worldwide groups. Interesting similarities in allele frequency distribution patterns across populations suggest that the STR polymorphism at these loci predates the geographic dispersal of ancestral human populations. p. 813-814

Interestingly, the Canadian aboriginal frequency pattern resembled other populations but demonstrated a bias for both small (<262 bases) and large (>290 bases) FGA alleles. p. 826

An overall look at the D21S11 allele frequency distributions revealed striking similarities in the distribution patterns across populations, despite large variations in allele frequencies (see Table 8 and Figure 1A). Two D21S11 alleles exhibited high and similar incidence in all surveyed populations irrespective of their ethnic or geographic origin. Allele 222 was detected with frequencies of 18-29%, and allele 226 had incidences of 15-28% with the highest occurrence in the Cree from Saskatchewan (35%). Interestingly, these alleles were two of the three most common alleles across worldwide samples. This suggests that alleles 222 and 226 have been in existence since before the geographic dispersal of humans and that they represent two ancestral alleles from which all other D21S11 variants have evolved. p. 833

Previous studies have indicated that populations belonging to one major group [European (Caucasian), Asian, Amerindian, African, or Pacific Islander] show a greater degree of similarity in the extent of genetic variation (Deka et al. 1995; Holgersson et al. 1994; Jorde et al. 1997). Our results from the population differentiation test are in agreement with these reports. Populations of European descent showed overall no statistical differences in D21S11 allele

distribution (data not shown). Populations of Asian descent (i.e., Chinese and Malays) showed greater similarities to one another than to populations of European descent or any other group examined. Interestingly, for D21S11 Canadian aboriginals were as different from one another as they were from the Caucasians or other groups reviewed for this study. p. 834-835

All groups followed the same distribution pattern, with the exception of the Canadian aboriginals, which showed a few distinct features. The incidence of allele 262 observed for this major group (11-20%) was the highest seen in all populations reported to date. Others showed frequencies of 0.5-7%. Allele 274 was less frequent in Canadian aboriginals (4-10%) than in any other sample (13-34%). Larger variants (≥ 290 bases) were more abundant in Canadian aboriginals, Africans, and Hispanics than in any other population so far analyzed (Table 9). Conservation of allelic modes together with a universally high degree of polymorphism among the geographically and ethnically dispersed populations suggests that polymorphism at the FGA locus predates the geographic dispersal of present-day human populations. p. 837-838

In addition, Canadian Caucasians did not show any significant differences at either STR locus when compared to Caucasians from around the world. In contrast, aboriginals from three different locations in Canada showed significant differences in D21S11 and FGA allele frequency distributions, although the Ojibwa from northern Ontario and the Cree from Saskatchewan displayed more similarities to one another than to Coastal Salishans from British Columbia. Chinese and Malays from Singapore were similar at both D21S11 and FGA STR loci and showed more similarities in allele patterns to one another than to Asian Indians from Singapore.

The high degree of polymorphism at both the D21S11 and FGA loci was universal, regardless of the geographic locations of worldwide populations, suggesting that the polymorphism probably predates the divergence of human populations.

Both D21S11 and FGA STR systems were easily resolved on a model 373A DNA sequencer. Combined with the sex determination system amelogenin (AMG), both STR systems could be used in confidence in widely differing ethnic groups as a screening DNA typing multiplex system or in combination with other STR multiplexes to increase discrimination for human identity testing. Alternatively, D21S11 and FGA could be used along with other polymorphic STR markers to further investigate microsatellite microvariation in closely related populations. p. 839

Alvah's comment: This paper (as well as others including Chakraborty and Weiss 1992; Ward et al. 1993, and Johnson et al. 1983) describes ancient genetic connections to the Americas that would seem to point to an inclusion of the Native Americans for Homo sapien origins.

Malaspina, P., Cruciani, F., Ciminelli, B.M., Terrenato, L., Santolamazza, P., Alonso, A., Banyko, J., Brdicka, R., Garcia, O., Gaudiano, C., Guanti, G., Kidd, K.K., Lavinha, J., Avila, M., Mandich, P., Moral, P., Qamar, R., Mehdi, S.Q., Ragusa, A., Stefanescu, G., Caraghin, M., Tyler-Smith, C., Scozzari, R., Novelletto, A. **Network Analyses of Y-Chromosomal Types in Europe, Northern Africa, and Western Asia Reveal Specific Patterns of Geographic Distribution.** *Am. J. Hum. Genet.* (1998), 63:847-860.

Markers of the genetic diversity of the human Y chromosome currently are considered to have the potential to provide information on male-specific patterns of migration in the past. The desirable characteristics of markers of this kind are a high level of polymorphism in the population and the lowest possible incidence of recurrent mutations. p. 847

Our results strengthen the idea that the phenetic similarity among haplotypes, represented as a network, is, to a large extent, the result of common descent from one or a few ancestral states and the subsequent molecular-radiation process. p. 848

We used equation (2) of Goldstein et al. (1996) to evaluate the space of possible values of t (the time, in generations, for the coalescence of haplotypes within each network) for a range of mutation rates μ and effective population sizes (N_e) (fig. 4). For $\mu = 5.6 \times 10^{-4}$ (Weber and Wong 1993), the large $(CA)_n$ variance for network 1.1 resulted in an estimate of $t > 3,000$ generations, or 60,000-75,000 years. The two largest networks with derived characteristics—that is, networks 2.1 and 3.1—both showed much lower values, $t = 1,000$ -3,000 generations. Finally, the three smaller networks—1.2, 1.3 and 1.4—gave estimates of $t = \sim 300$, ~ 200 , and ~ 450 generations, respectively. These latter estimates are fairly insensitive to different values of N_e). p. 855

Emphasis should be put on the caution with which the maps must be interpreted. A specific frequency pattern is the result of both the migration and admixture of people, possibly associated with demic expansions, and of local expansions of types, because of drift and/or founder effects. The aforementioned factors could, in principle, be discriminated against when a large collection of autosomal data is used (Cavalli-Sforza et al. 1994), whereas such discrimination is not always possible in the case of nonrecombining Y-linked markers. Indeed, an enhanced effect of drift has been postulated and demonstrated for this chromosome world-wide (Torroni et al. 1990; Sprudle et al. 1994; Jobling and Tyler-Smith 1995; Scozzari et al. 1997; Underhill et al. 1997). The confinement and high frequency of network 2.1 haplotype 21-19-23-19 in Morocco (see above) suggests a strong drift that is able to affect markedly the shaping of the corresponding map (fig. 1e). p. 856

The map shows a clear southeast-to-northwest gradient all over Europe, a main feature of maps obtained with autosomal, Y-chromosomal, and mtDNA data (Cavalli-Sforza and Minch 1997, fig. 1b-d). The poor coverage of areas east of the Mediterranean gives less support to such a gradient over western Asia, in our map. p. 857

Barbujani et al. (1998) and Richards and Sykes (1998) warned against use of the age of molecules to infer the dating of splitting of the populations that carry them. In our data, too, the events that have led to the attainment of the observed frequencies of networks with derived characteristics may have occurred much more recently than the origin of the different types. p. 857

Our data also reveal the contribution of recent lineages (networks 1.2, 1.3 and 1.4) that emerged from an ancient background. In particular, network 1.2 haplotypes might represent a novel characteristic of chromosomes involved in the neolithic gene flow into mainland Europe from the southeast. p. 857

In fact, it is likely that migrants' and preexisting populations' gene pools were not completely differentiated. Such an event leaves space for a wide range of values for the proportion of chromosomes that reached the present frequency by virtue of neolithic (or more recent) phenomena. The main conclusions of the present study can be summarized as follows: (1) there is a low level of homoplasy among dinucleotide microsatellite haplotypes; (2) there is high structuring of populations, with regard to Y-chromosomal network frequencies; and (3) networks are optimal markers for population studies addressing the radiation and dispersal processes associated with the preneolithic/neolithic transition. p. 857

Vieland, V.J., and Hodge, S.E. **Book Review of Statistical Evidence: A Likelihood Paradigm**, by Richard Royall. *Am. J. Hum. Genet.* (1998), 63:283-289.

Most of current statistical practice is based on frequentist principles—notably, on the Neyman-Pearson paradigm for hypothesis testing or on Fisher's conception of significance testing. Evidentialism is undoubtedly the least familiar school of statistical thought, both within the field of statistics itself and, certainly, among consumers of the statistical literature. This remains true, at least in part, because journal editors and peer reviewers almost invariably ask that statistical results be reported in familiar frequentist terms. But our predilection for the familiar notwithstanding, *evidentialism is, arguably, the only body of statistical theory that is fully consistent with the practice of science.*

To justify this extravagant claim, we need to consider the *purpose* of statistical analysis in scientific contexts. Evidentialism views the purpose of statistical inference as the *measurement of the strength of evidence* conferred by a given set of data in favor of one hypothesis over another. This may seem a wholly natural objective for scientific data analysis, and we will take it as a given that this is the objective that we are pursuing. But, in fact, much of standard statistical practice is based on a quite different conception of statistical inference—namely, as a set tools for *decision making* in the face of uncertainty. This latter objective need not in any way involve the concept of evidence. p. 284

We then select the "best" testing procedure, one that minimizes the probability that we will fail to reject the null hypothesis when it is in fact false (the type II error rate) for the selected significance level. p. 284

Similarly, once we have data in hand, we are no longer satisfied with reporting the probability that a certain erroneous outcome might occur when we perform a test of this sort. Rather, we would like to have some way to determine whether we have been misled in this instance. The predetermined significance level of a Neyman-Pearson test does not give us this information. p. 284

But can the *P* value be made to do double duty, both as the predictive type I-error probability and as a measure of the strength of evidence? What is the relationship between the question of statistical evidence and the frequentist's interest in error rates? Are these really just two ways of naming the same statistical quantities, or are these fundamentally different kinds of quantities? And, if the *P* value is not the appropriate measure of the strength of evidence, then what is? Although these questions might seem too philosophical to require the attention of genetics

researchers, the methods that we choose for analysis of genetic data ought perhaps to depend on the answers that we give. The evidentialist's answers begin with the recognition that the familiar frequentist methods cannot be made to satisfy our interest in the measurement of evidence. p. 284

Some statisticians might prefer to talk about testing a "null" hypothesis without reference to an alternative hypothesis. As we have already seen, however, the law of likelihood expressly applies to comparisons between two hypotheses: evidence counts against one hypothesis only insofar as it favors the other. This insistence that any proper measure of evidence must involve two hypotheses rather than one is a cornerstone of evidentialist theory. p. 284-285

The current debate over the relative merits of "parametric" (LOD) versus model-free linkage methods has tended to gloss over this fundamental distinction between the two approaches: the LOD score (defined broadly, as above) is not simply one among the many available test statistics; it may be the *only* one of them that is suitable to address the question, What is the strength of the evidence for linkage?

Failure to make a clear distinction between frequentist hypothesis testing and evidentialist measurement of evidence has given rise to a body of literature in human genetics in which frequentist methods are freely mixed with evidentialist objectives—a body of literature in which the *P* value is treated as a valid answer to the evidentialist's question and in which the LOD score is used to address the frequentist's concerns. The result is that we now enjoy a canon of statistical practices for linkage studies that draw simultaneously from logically incompatible first principles. The appearance of *Statistical Evidence* on the scene at this time is therefore especially timely for the field of human genetics. p. 287

In a similar vein, we would have been interested in greater discussion of the assessment of the strength of evidence in multivariate contexts, or in the presence of additional "degrees of freedom." It is well known that, all other things being equal, the more parameters that we estimate from the data, the larger our resulting likelihood will be. Therefore, the magnitude of the LR is affected by the difference in the number of parameters estimated in the numerator and denominator.

Alvah's comment: These examples of genetic factors could be applied to language study, when the shoe finds the right foot or Cinderella (the fairest hypothesis in the land) is invited to the ball.

SCIENCE AND RELIGION

Gould, S.J. **Lyell's Pillars of Wisdom.** *Natural History* (1999), Vol. 108, No. 3:28-34, 87-89.

Apparently grandiose or catastrophic events really occur by a summation of small changes through the immensity of geological time—the deep canyon carved grain by grain, the high mountain raised in numerous increments of earthquake and eruption over millions of years.

Second, the claim for a nondirectional or steady-state earth: Standard geological causes (erosion, deposition, uplift, and so on) show no trend either to increase or decrease in general intensity through time. Moreover, even the physical state of the earth (relative temperatures,

positions of climatic belts, percentages of land and sea) tends to remain roughly the same or to cycle around and around through time. p. 32

When a scientist proposes such a comprehensive system, we often gain our best insights into the sources and rationale for his reforms by explicating the alternative worldview of his opponents. New theories rarely enter a previous conceptual void; rather, they arise as putative improvements or replacements for previous conventionalities. p. 32

Incidentally, this account of catastrophism as a genuine and interesting scientific alternative to Lyellian uniformity disproves the conventional canard, originally floated as a rhetorical device by Lyell and his partisans but then incorporated uncritically as the conventional wisdom of the profession. In this Manichaeian account, catastrophism represented the last stronghold for the enemies of modern science: the struggle of theologically tainted dogmatists to preserve both the literal time scale of Genesis and the miraculous hand of God as history's prime mover by invoking the doctrine of global paroxysm to compress the grand panoply of geological change into a mere few thousand years. In fact, by the 1830s all scientists—catastrophists and uniformitarians alike—had accepted the immensity of geological time as a central and proven fact of their emerging profession. p. 34

But on an Earth in steady-state, built entirely by modern causes acting at current intensities, the present becomes, in an old pedagogical cliché, "the key to the past," and Earth's entire history opens to scientific study. Thus, in a famous statement of advocacy, Lyell condemns catastrophism as a doctrine for despair, while labeling his uniformitarian reform as the path to scientific salvation:

Never was there a dogma more calculated to foster indolence, and to blunt the keen edge of curiosity, than this assumption of the discordance between the former and the existing causes of change. It produced a state of mind unfavourable in the highest conceivable degree to the candid reception of the evidence of those minute, but incessant mutations, which every part of the earth's surface is undergoing . . . The student instead of being encouraged with the hope of interpreting the enigmas presented to him in the earth's structure—instead of being prompted to undertake laborious inquiries into. . . causes now in operation, was taught to despond from the first. Geology, it was affirmed, could never rise to the rank of an exact science—the greater number of phenomena must forever remain inexplicable. . .

In our attempt to unravel these difficult questions, we shall adopt a different course, restricting ourselves to the known or possible operations of existing causes. . . We shall adhere to this plan. . . because. . . history informs us that this method has always put geologists on the road that leads to truth—suggesting views which, although imperfect at first, have been found capable of improvement, until at last adopted by universal consent. (Principles of Geology, vol. 3, chap. 1, 1833).

Large intellectual struggles cannot be won by success in easy and simple skirmishes. Adversaries must also be outflanked on their home ground, where superior knowledge and forces

should have rendered them invincible. A new theory must meet and encompass the hardest and most apparently contradictory cases head on. p. 87

At most, Vesuvius teaches us that the increments of gradualism can be large at human scale—the lava field versus the eroded sand grain—while still small by global standards. In 1830, at the end of a long chapter entitled "History of the volcanic eruptions in the district around Naple," Lyell wrote:

The vast scale and violence of the volcanic operations in Campania [the region of Italy surrounding Naples] in the olden time, has been a theme of declamation. . . . Instead of inferring from analogy that. . . each cone rose in succession—and that many years and often centuries of repose intervened between each eruption—geologists seem to have conjectured that the whole group sprung up from the ground at once, like soldiers of Cadmus when he sowed the dragon's teeth.

Moreover—continued Lyell, in closing the first volume of his tenth edition (1867)—even by purely local standards, natural catastrophes usually impose only a fleeting influence upon history. p. 87

Alvah's comment: Gould offers us again, a heaping plate of evolution and theory building through examples drawn from the past and the study of it science attempts to unmask.

Gould, S.J. **Second-Guessing the Future.** *Natural History* (1998), Vol. 107, No. 7, pp. 20-29, 64-66.

In my parish, the dubious (and admittedly somewhat contradictory) status of most famous second-place finisher goes without contest to Alfred Russel Wallace, who, in 1858, during a malarial fit on the Indonesian island of Ternate, devised virtually the same theory of natural selection that Darwin had developed (but hadn't published) in 1838. In a familiar story, Wallace sent his short paper to Darwin, a naturalist he greatly admired and who, as Wallace knew, had a strong interest in "the species question" (although Wallace had no inkling of Darwin's particular, and nearly identical, theory and probably didn't even realize that Darwin had a theory at all). Darwin, in understandable panic, turned to his best friends, Charles Lyell and Joseph Hooker, for advice. In a resolution known to later history as the "delicate arrangement," Darwin's friends made a joint presentation to the Linnean Society of London in July 1858: they read both Wallace's paper and some unpublished letters and manuscripts by Darwin, establishing his earlier authorship of the same idea. p. 20

Because Wallace lived a long time (1823-1913), wrote copiously both for his bread and from his convictions, and held a variety of passionate and quirky views, he left us a vast legacy of varied content and quality. He campaigned ardently for the right and the just, according to his idiosyncratic standards, and he fought valiantly for a set of causes usually deemed "cranky" both in his own time and today—including phrenology and spiritualism (where he nearly came to blows with skeptics like Darwin and Huxley)—and against vaccination, which he called "one of the foulest blots on the civilization of the nineteenth century." p. 21

Wallace presents a simple thesis as the foundation for his epitome of the nineteenth century—a standard view about the relation of science to society, stated in the context of a particular time. Science, Wallace argues, has made unprecedented gains, largely expressed as technological advance (at least in terms of impacts upon everyday life), but this progress has been blunted, if not perverted, by our failure to make any moral improvements, especially as expressed in the alleviation of social inequities. Thus, and ironically, the progress of science, however bursting with potential for social improvement, has actually operated to increase the sum total of human misery. p. 22-23

In order to estimate its [the nineteenth century's] full importance and grandeur—more especially as regards man's increased power over nature, and the application of that power to the needs of his life today, with unlimited possibilities in the future—we must compare it, not with any preceding century, or even with the last millennium, but with the whole historical period—perhaps even with the whole period that has elapsed since the stone age. p. 23

We of the 19th century were morally and socially unfit to possess and use the enormous powers for good or evil which the rapid advance of scientific discovery had given us. Our boasted civilization was in many respects a mere surface veneer; and our methods of government were not in accordance with either Christianity or civilization. This view is enforced by the consideration that all the European wars of the century have been due to dynastic squabbles or to obtain national aggrandizement, and were never waged in order to free the slave or protect the oppressed without any ulterior selfish ends.

Wallace then turns to domestic affairs, with the damning charge that our capitalist system has taken the wealth accrued from technological progress and distributed the bounty to a few owners of the means of production while actually increasing both the absolute and relative poverty of ordinary working people. In short, the rich get richer and the poor get poorer:

One of the most prominent features of our century has been the enormous and continuous growth of wealth, without any corresponding increase in the well-being of the whole people; while there is ample evidence to show that the number of the very poor—of those existing with a minimum of the bare necessities of life—has enormously increased, and many indications that they constitute a larger proportion of the whole population than in the first half of the century, or in any earlier period of our history. p. 25-26

Alvah's comment: One of my favorite scientists from the past has to be A.R. Wallace. The evolution of anthropology into an applied science continues to wane, a warning he left in his writings.

Haley, B.D., and Wilcoxon, L.R. **Anthropology and the Making of Chumash Tradition.** *Current Anthropology* (1997), Vol. 38, No. 5, pp. 761-793.

As Powell indicates, "there appears to have been no appellation in use among them to designate themselves as a whole people" (Powell 1891:67). We assume that Powell's action reflects the popularity of the "ethnographic principle" of defining nations by linguistic or racial criteria (Renan 1990 [1882]). These were the criteria used by European and American intellectuals from 1880 to 1914 to distinguish "nations" (Hobsbawm 1992:95-102). From the start, then, the boundaries of a Chumash identity bear the stamp of an arbitrary and historically contingent outside ideology. p. 767

The people who spoke them—from Morro Bay to Malibu and inland at least to Tejon Pass—were never unified into a single or even a few overarching polities prior to their complete incorporation into the Spanish mission system by 1804. There were, in fact, a number of named group identities among Chumashan-speakers corresponding to village, language, or region (Heizer 1952, 1955), and significant regional cultural differences and episodic warfare between villages existed in pre-mission times (Kroeber 1910, 1953 [1925]; Blackburn 1975:8-15; Glassow and Wilcoxon 1988; Johnson 1988; personal communication, 1995). p. 767-768

He further assumes that material remains on the northeastern boundary were associated with Chumash-speakers (Kroeber had felt that they might have been Salinan), and he treats the southern Channel Islands occupants as non-Chumash (Kroeber had lumped them with Chumash materially but with Shoshoneans linguistically) (cf. Hudson and Blackburn 1982:17-38). King adopts the position that Chumash society has developed in place for more than 7,000 years (King 1990:200; cf. Arnold and O'Shea 1993), and Gibson (1991:14) places the beginnings of Chumash culture "about 10,000 years ago." p. 768

The widened meaning of the term "Chumash" provides ideological fodder for Chumash Traditionalism. King et al. (1985:97-105) participate in this by employing Edward Spicer's (1971) idea of persistence to authenticate Traditionalist claims of a continuous link between the Chumash past and present. The persistence argument rests upon an unsupported assumption that what is tradition and who is indigenous are fairly continuous and bounded from past to present, maintained through "organized *resistance* to change, and persistence of traditional values, custom, and cosmologies beneath a veneer of assimilation" (King et al. 1985:97). However, their own research documents a "new religion . . . [derived from] spiritual leaders from other tribal groups . . . [and] academic works" (pp. 102-3). The new religion is "conceptually *distinct* from other aboriginal pattern . . . [and] heavily infused with pan-Indian elements" (pp. 103-4). King et al. report that a person becomes a Traditionalist through "an awakening of his or her Indian identity" and that the movement's "ethnic boundaries and group solidarity are enhanced by self-imposed isolation from the non-Indian community and by the performance of rituals . . . [in] communities . . . [and] ceremonial encampments . . . [where] revivalistic doctrines developed and were elaborated" (pp. 103-4). They overlook these findings when they appeal to an imagined persistence with unsubstantiated rhetoric: "Cultural traditions, as such, span the generations, and therefore transcend the lives and experience of individual group members" (p. 102).

Similarly, Diana Wilson (1994), exploring "indigenous" reactions to the portrayal of American Indian cultures in Los Angeles museums, argues that her consultants, some of them Chumash, are "authentically indigenous" (p. 37)—that they possess an "American Indian way of knowing" wielded strategically against a "Western academic knowing," a relationship which is

"grounded in the historical facts of colonization" (p. 42). Despite their sometimes coming from families whose previous identities were "Mexican," her consultants' "subjective awareness of being indigenous . . . apparently survived" (p. 365). p. 768-769

Alvah's comment: This article is an affront to Chumash Reality, a step in the wrong direction that was aimed at deterring any influence and or historical stewardship for the Point Conception. It is more about Vandenberg and U. S. claims to it. The following statement is the same kind of ethnocide, informative if in only identifying that the messengers in anthropology are serving their own agenda, a new cavalry aimed at undermining examples of cultural identity and the continuation of a Past.

Clark, G.A. **NAGPRA, the Conflict between Science and Religion, and the Political Consequences.** *Society for American Archaeology* (1998), Vol. 16, No. 5., pp. 22-25.

Laws like NAGPRA strike at the heart of a scientific archaeology because they elevate the cultural traditions and religious beliefs of Indians to the level of science as a paradigm for describing or explaining reality. Political considerations thus take precedence over disinterested evaluation of knowledge claims, with tragic and irreversible results [G.A. Clark, 1996, NAGPRA and the Demon-Haunted World SAA Bulletin (14(5):3, 15(2):4] p. 22

Science can be defined as a collection of methods for evaluating the credibility of knowledge claims about the experimental world. Science does not pretend to certainty; it only seeks better and better approximations of it. Scientific conclusions are continuously subjected to critical scrutiny. Science is, therefore, self-correcting. No topic or question is "off-limits" to science. The only thing that is antithetical to the scientific worldview is dogma. Dogma is the stuff of religious belief. From the standpoint of science, the illusion of absolute, unchanging truth is the most pernicious of vanities. p. 22

From this perspective, humans are only animals (albeit highly intelligent, technologically sophisticated, socially complex ones). Religious views of humans and their place in nature, dependent as they are on concepts that have no reality outside the mind, are epiphenomena (and—for a materialist—absurd). In other words, one cannot simultaneously understand and accept evolution and sustain a believe in the nonmaterial. From the standpoint of science, religious beliefs are curious survivals of earlier cognitive evolution. What probably happened is that, as our cognitive capacities expanded slowly over the Pleistocene millennia, we came to imagine more and more complex realities, and populated them with the gods, demons, and spirits that are the stuff of conventional religious belief. The question science would put to religious is: Why do humans have religious beliefs at all, since there is absolutely no empirical support for them? p. 22

Science is not "about" religion, however. It is not about moral truth, although it can sometimes help us in our struggle to reach appropriate moral decisions. Clearly, humans did not evolve in this hemisphere. Indians haven't always been here, regardless of what their origin myths might say. p. 24

The worldview of Western science is under serious and sustained assault, and there is a danger that "science-like" views of reality will perish in the face of a multipronged attack in which mysticism, religious fundamentalism, creationism, and the believers in the paranormal combine with postmodernist academics to attack the critical realism and mitigated objectivity which are the central epistemological biases of the scientific worldview. p. 25

Alvah's comment: The Science of anthropology has its roots in European "Dogma" statements like Clark's "Clearly, humans did not evolve in this hemisphere. Indians haven't always been here, regardless of what their origin myths might say. (p. 24)" should be more cautiously addressed for the origins of Modern humans remains unsolved as does the quest to resolve the timing and or theoretical acceptance of a pre-Clovis presence. Are the two, as scientists call them, "holy grails" of anthropology perhaps related? Since only 11% of the data generated from the two prevailing theories of human origins are compatible with each other, perhaps it is time to look to the Americas for a source for the "Replacement" of Homo erectus. What the Native Americans believe is that WE have been modern longer then Modern Humans have been in the Old World while people like Clark remain stagnated by unproven theories that find us tracing human origins back to uncultured beings.

Watkins, J. **Native Americans, Western Science, and NAGPRA.** *Society for American Archaeology* (1998), Vol. 16, No. 5., pp. 22-25.

As with most scientific writings aimed at the rather specialized population of scientists studying Native American human remains, one of the paper's [Clark's] fundamental flaws is its failure to deal with the differing perceptions of the scientific and Native American communities. While it is extremely difficult to offer a single "Native American perspective" on anything, I will proceed to offer a generalization as if it were possible to do so. p. 23

Maybe American Indians and scientists are doomed to operate on opposite ends of the emotional spectrum—passion versus dispassion. Where scientists feel drawn to cold facts, American Indians feel drawn to those things outside of the demonstrable world (Clark's "epiphenomena"). Perhaps scientists should stop being so dispassionate, stop trying to step outside humanity, and join the rest of the world. I don't trust a person who has no passion! p. 23

I believe science and religion are remarkably intertwined, a double helix spiraling across time and space. Neither should exist without the other, for each one gives us different information and different perceptions on the human condition. I argue, unlike my materialist colleague, that is the very fact that we are aware of such things (rather than blindly accepting of them) that places us at the top of the intellectual pyramid. p. 23

Like the philosophical tree in the forest, if "a precontact aboriginal culture of the New World vanishes without a trace," and there is no "Western observer there to record information about them," do they make a sound? p. 25

We, as anthropologists, are standing on the edge of a forest with an almost impenetrable growth in front of us. We can try to bulldoze our way through it, but we will destroy all that might be

ahead of us; we can try to circumvent the forest, and run the risk of losing our collective lives in the resultant uncharted wilderness; or we can look for the path between the trees, moving carefully, taking the journey one step (and roadblock) at a time. An army does not pass through a forest as a single body, but rather as an allied group of individuals. We must be an army on a common campaign—an army of individuals working to reach a common goal. p. 25

PRIMATES

Ross, C., Williams, B., and Kay, R.F. **Phylogenetic analysis of anthropoid relationships.** *Journal of Human Evolution* (1998), 35, 221-306.

Anthropoidea—the group that includes monkeys, apes and humans—has long been recognized as a "natural" group among primates, united by a suite of features of the skull, dentition and postcranium. Anthropoidea is also generally—although not universally (Cachel, 1979)—thought to be monophyletic, descended from a common ancestor not shared with any other primates.

However, the relationships of anthropoids to other primates are not yet resolved. Advocates of several competing hypotheses continue to debate the merits of their respective models. This lack of consensus reflects a broader uncertainty of the relationships among primate higher taxa and the fossil groups thought to have given origin to them. Why does this debate persist? Is it because key fossils are yet to be discovered? It is well established that fossils are vital for deciphering relationships among living taxa because they contain novel combinations of primitive and derived characters and because they preserve morphologies more closely approximating ancestral conditions (Gauthier et al., 1988; Huelsenbeck, 1991; Novacek, 1992). In the case of anthropoid origins however, most workers agree on the relationships between living taxa (tarsiers and anthropoids are more closely related to each other than to strepsirrhines); it is the relationships of certain fossil taxa to the living groups that are debated. p. 221-222

Questions surrounding anthropoid origins

Debates concerning the origins and early diversification of the Anthropoidea have centered around several related questions:

- (1) Is Anthropoidea a monophyletic group, and if so what are its synapomorphic features?
- (2) To which group of fossil or extant primates is Anthropoidea most closely related?
- (3) How do Eocene and Oligocene anthropoids of Africa (Parapithecoidea, Propliopithecidae, Oligopithecidae) relate to the Platyrrhini and Catarrhini?

With respect to anthropoid monophyly, older views such as those of W.K. Gregory (1922) that catarrhines and platyrrhines evolved from separate and not very closely related Eocene "tarsioids" have been largely abandoned. p. 222

Several workers at the 1992 Anthropoid Origins Conference and Workshop at Duke University (Fleagle & Kay, 1994) voiced the possibility of a nonadapid, nonomyid, and nontarsier origin for anthropoids (Culotta, 1992). p. 224

This suggested that the anthropoid clade might be as old, or older, than the earliest omomyids and adapids and that a fundamental dichotomy might exist between omomyids and adapids of the Northern continents and Anthroidea of Africa and South America. p. 224

There is wide agreement among paleoprimatologists that tarsiers are more closely related to anthropoids than to strepsirrhines (Purvis, 1995). The evidence comes from molecular data (Koop et al., 1989a,b; Porter et al., 1997) and soft tissues (Hubrecht, 1897; Luckett, 1975, 1976; Shoshani et al., 1996). The complete data set presented here provides definitive support for this hypothesis: tarsiers and anthropoids are found to be more closely related to each other than to strepsirrhines. p. 245

Strength of various hypotheses

Adapid-anthropoid hypothesis. This hypothesis receives support from the dental evidence but is not supported by the cranial or postcranial evidence, or the evidence overall. Rather, the majority of the evidence better supports the hypothesis of an adapid-strepsirrhine clade exclusive of anthropoids and tarsiers. Indeed, of the three hypotheses evaluated here, the adapid-anthropoid hypothesis was by far the least well supported. p. 246

Our preferred tree is illustrated in Figure 14. We believe the tarsier-anthropoid hypothesis is the best hypothesis of anthropoid relationships at present, for three reasons. First, the tarsier-anthropoid hypothesis is the best-supported by the data presented here. p. 256

Second, the tarsier-anthropoid hypothesis (and the associated [omomyid(tarsier-anthropoid)] hypothesis) is corroborated by functional analysis of character transformation series (Ross, 1996). Third, this hypothesis provides the most parsimonious reconstruction of features that are unique to tarsiers and anthropoids; the post-orbital septum and the anterior accessory cavity of the middle ear. p. 256

To evaluate the phylogenetic position of Anthroidea, morphological data on 291 dental, cranial and postcranial morphological characters were collected for 57 taxa of living and fossil primates and analyzed using PAUP and MacClade. The dental evidence provides some support for the notion of an adapid origin for anthropoids, the cranial evidence supports the tarsier-anthropoid hypothesis, and the postcranial evidence supports monophyly of Prosimii and Anthroidea. Combining these data into a single data set demonstrates Anthroidea to be monophyletic and the traditional anthropoid synapomorphies to have evolved mosaically. p. 257

Overall, the available data do not allow definitive statements regarding the interrelationships of the haplorhines: *Tarsius*, Omomyidae and Anthroidea. Many key fossil taxa (e.g., *Eosimias*, *Afrotarsius*) are still poorly known and we lack critical fossils sampling the divergence of the higher taxonomic levels of primates. Clearly, many more fossils are required before we can determine the precise phyletic relationships of tarsiers, omomyids, and anthropoids. p. 258

Alvah's comment: Just a sampling of the current status of early primate ancestors and the fact that the fossil record is often not complete enough to make absolute the choices for the pre-primate form that led to higher primates.

August 3, 1999

Dear John,

Thanks for your last e-mail and the distinction between reporting and OPINION. I agree with your analysis of my "comments" and offer them only to identify new insights to "traditional" guidelines. If you want to use the "articles" without my opinions/comments feel more than free to do so. My comments are rather incomplete thoughts, in the first place, while I could better "report" on specific papers if I knew the ones you plan to use in the next issue of MT. Please let me know what articles you plan to identify/use so that I might be able to properly editorialize/report what the authors are stating.

I trust that you will continue to offer your own insights to the articles, as you did the last issue, even if you omit mine. You are the Editor and I am more than pleased to be able to even participate. Moreover, if you find any of my comments polemic please rephrase them for me or leave them out entirely.

I realize that you are planning to complete the next issue shortly and I promise to respond quickly once you let me know what articles you want me to report on. I am also finalizing a short addition concerning my opinions of "Who were the FIRST Americans?"

Best regards,
Alvah

Editorial

There have been several developments in the last 6 months concerning who were the “FIRST People” to inhabit the Americas. The alternative, promoted by a few publicity-minded researchers, would have the “FIRST” Americans coming from Europe across the Bering Strait before a later group of proto-Amerinds arrived and replaced them. Some form of genocide of these FIRST European People - by later Amerinds - has even been proposed. Unfortunately, this analysis is being used to question basic aboriginal rights including the validity of Native American stewardship of their ancestor’s remains, a Native Heritage as defined by NAGPRA.

The basis of the “who was first” argument started with the earliest evidence of an American Paleolithic stage, commonly known as Paleoindian Traditions (). Since “Fluted” Points are unique to the Americas, with no other evidence of similar Paleolithic tools previous to Clovis, it has long been a contention that people from Europe with tools similar to Upper Paleolithic Industries were the First Americans (“Clovis First” theory)(). Today we know that there were INDEED pre-Clovis Populations, with little, if any, technologies associated with Old World Upper or Late Paleolithic Industries(). The question I would like to pose is, could UP equipped People migrating from Northeast Asia into North America, at the end of the Last Ice Age, have influenced pre-Clovis Amerindians leading to the development of Paleoindian Traditions? If so, is there any genetic correlates to support this hypothesis? The answer could be a resounding ALVERMATIVE!

Since it is now archaeologically sanctioned, that earlier pre-Clovis Populations were living in the Americas during the Pleistocene, a new formula must emerge in order to properly interpret cranial, genetic, and archaeological data. Since European mtDNA lineages are found exclusively in northern North American Amerind speakers, but not in Aboriginal Groups further south (or, in Central or Southern America), it could be postulated that Europeans were assimilated into the northern-most Amerindians following a post-Ice Age migration from Northeast Asia. European mtDNA Lineages (Haplogroup X) are retained by North American Tribal Groups, primarily Ojibwa and Algonquian speakers, (). The dawn of the New World’s first Paleolithic coincides with the timing of the removal of Glacial Barriers. Could these ‘Earliest Europeans to the Americas’ have introduced Old World technologies previously unknown to pre-Clovis Amerindians? The genetic data would seem to indicate that Type X mtDNAs represent an isolated migration unrelated to earlier pre-Clovis Amerindian Populations that must have been here before the assimilation of Europeans since the European marker is found where assimilation between pre-existing Amerindians and later arriving Europeans would have first encountered People already inhabiting the Americas.

Moreover, if the FIRST Americans were “Europeans”, then one would expect Haplogroup X mtDNAs to have survived in Central and South America, where they (X type mtDNAs) are virtually absent (). Europeans, accordingly, could not have been the FIRST Native People of the Americas. Rather, the identification of some European mtDNA ancestry in pre-Columbian Amerindian cemeteries (Stoneking et al. 1998) hints of a peaceful assimilation into, principally, the northernmost Amerindians who genetically retain evidence of the point of contact between once isolated New and Old World Populations. The development of Paleoindian Traditions (Clovis) could be directly attributed to this “European” migration, with diffusion of Old World UP know-how into pre-existing pre-Clovis Populations (). Since, little, if any, lithic components of a similar nature are found at Monte Verde, it could be assumed that an outside influence may have contributed to Paleoindian Traditions and the increased production of archaeological signatures associated with lithic tools.

We must remember that J. H. Greenberg (1987) was cautious when he dated “Amerind”, and its 11 language stocks found in North and South America, basing the first of the three languages on a chronological generation that conformed to the archaeological consensus of the time (i.e. Clovis First being < 12,000 ybp).

"It may plausibly be connected with the Paleo-Indian (Clovis) culture, which dates back at least 11,000 to 12,000 years. Although we have presented linguistic criteria to establish a relative chronology of the three migrations, we have considered only archaeological correlations as a source for an absolute chronology."

Skepticism surrounding acceptance of a pre-Clovis occupation of the Americas has long confounded the development of new theories. The significance of a pre-Clovis occupation of the Americas is a greater time depth, affording a suitable interpretation befitting the detection of extensive genetic and linguistic diversity (). This reality must now incorporate the prospects of post-Ice Age assimilation of once isolated (Old World) populations into earlier pre-Clovis Amerindian People. Migration scenarios could identify both European expansion into (Stoneking et al. 1998), and Amerindian back out of, the Americas (Boas 1905, 1910; Hicks 1998), after the last Ice Age. The recognition of a substantial pre-Clovis Amerindian population celebrates, as part of the equation, the peaceful assimilation of European/Asian People (Haplogroup X) with Upper/Late Paleolithic Industries at the end of the Last Ice Age.

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