

The many species of humanity

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ABSTRACT Naming new human species may seem to be a harmless endeavor, of little interest to all but a few specialists playing out the consequences of different evolutionary explanations of phyletic variation, but it has significant implications in how humanity is viewed because studies of race and human evolution are inexorably linked. When essentialist approaches are used to interpret variation in the past as taxonomic rather than populational, as increasingly has been the case, it serves to underscore a typological view of modern human variation. In terms of how they are treated in analysis, there often seems to be no difference between the species, subspecies, or paleodemes of the past and the populations or races whose interrelationships and demographic history are discussed today. This is not inconsequential because both history and current practice shows that science, especially anthropology, is not isolated from society.

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It seems as though recent progress in paleoanthropology has accelerated. New human species¹ are named each year, reflecting the pace of discovery. This also reflects the increasing propensity to give each new discovery a unique species name, as the idea that speciation is the only mechanism of evolution moves from a debated controversial theory to an underlying assumption, at least in some quar-

ters. Thus, SCHWARTZ [2000] recently reviewed the new hominid fossil discoveries at Dmanisi, Georgia [GABUNIA *et al.* 2000] and suggested as many as 3 human species were there (Figure 1). Comparing the earlier discovered mandible [GABUNIA & VEKUA 1995] with the two new crania he concluded the mandible and each of the two crania may represent different human taxa.

This makes a good number of paleoanthropologists and other biological anthropologists quite uncomfortable, and we would like to explain why, because it goes beyond the simple taxonomic issue of how many human species there are in

¹ Meaning species of the genus *Homo*, not including the habiline species which are more appropriately subsumed in the genus *Australopithecus* [WOLPOFF 1999a; WOOD & COLLARD 1999], and not including the other australopithecine species.



Fig. 1. The two Dmanisi crania, after GABUNIA *et al.* [2000], from a 1.75 million year old site in Georgia. Are these crania of an adult (above) and a crushed juvenile actually two human species?

the three specimens from Dmanisi. This is not the first time that multiple human species have been used to explain the variation at a single site, but we worry Dmanisi and sites like it may be more like present day Nubia than like Plio/Pleistocene Olduvai Gorge. There is more here than meets the eye.

For a good part of the last century, biological anthropology was far from the forefront of progressive thinking about race and human evolution. Some biological anthropologists accepted or actively promoted the notion that human races differed in the extent to which some were more primitive and others more advanced [WOLPOFF & CASPARI 1997]. The writings of the German evolutionist and systematist Ernst HAECKEL [1883, 1905] have echoed through the 20th century,

writings that likened human races to separate species because each (race or species) shared unique characters. Haeckel described separate evolutionary trajectories and varying velocities that left each of them at different evolutionary stages (Figure 2). These related contentions combined in the precept that biology and behavior are linked together at the level of race, and this reverberated through the works of many others.

Carleton COON is perhaps the best remembered of them, with his claim [1962] that independently evolving races had crossed the ‘sapiens threshold’ at different times, and that this delimited their achievements. Aleš HRDLIČKA, founder of the American Association of Physical Anthropologists, accepted the relationship of biology and culture, and wrote [1927: pp. 208-9] “the real problem for the American Negro lies in his brain.”

In a 1926 issue of *Natural History Magazine*, Henry F. OSBORN, president of the American Museum of Natural History, speculated [1926: p. 3] that “if an unbiased zoologist were to descend upon the Earth from Mars and study the races of man with the same impartiality as the races of fishes, birds, and mammals, he would undoubtedly divide the existing races of man into several genera and into a very large number of species and subspecies.” Similar ideas of splitting taxa continue to thrive at the museum, where the current Anthropology Curator reasons that “under current taxonomic practice there is a distinct tendency to underestimate the abundance of species in the primate, and notably the hominid, fossil record” [TATTERSALL 1986: p. 167]. TATTERSALL [1992] rejects the relevance of populational thinking to this issue, and the evidence of



Fig. 2. HAECKEL'S [1883] view of the arboreal primates, conveniently arranged on a tree, reveals the equivalence he held between primate species and human races: "the morphological differences between two generally recognized species – for example sheep and goats – are much less important than those ... between a Hottentot and a man of the Teutonic race" [1883: p. 434]. Each were separate lineages that evolved at different rates, by competition. He wrote, further, that "the lower races – such as the Veddahs or Australian Negroes – are physiologically nearer to the mammals, apes and dogs, than to the civilized European." [1905: p. 390]

genetic polytypism (population structure) known even when he wrote his first essay on the species problem in 1986 (e.g., TEMPLETON [1982]). Tattersall refers to this kind of thinking as "genetic sophistry," and rejects it as well. By doing so, his logic can dictate that any differences between populations must be taxonomic, and the result of isolated gene pools rather than the result of evolutionary forces that create and maintain variation

within them. Given this, it is not surprising that he concludes [TATTERSALL 1986: p. 168] "where distinct morphs can readily be identified it would seem most productive to assume they represent species unless there is compelling reason to believe otherwise."

Human diversity is the quandary. The validity of forensic anthropology rests on the contention that there are distinct morphs for forensic anthropologists to identify, but forensic anthropologists (and all other anthropologists) recognize that human races are not species. For Tattersall, this observation that human races are in a single biological species regardless of their anatomical variations is the "compelling evidence" he speaks of to allow human classification to follow a different set of rules, but can he be sure how others might use his criteria for species identification; can he guarantee how others might apply the ideas he helps keep alive? According to one recent book on race [SHIPMAN 1994], this is not his responsibility.

Then there was Sir Arthur Keith, a key founding figure in British paleoanthropology, who described Hitler as "a naked nationalist, racialist, and evolutionist" [KEITH 1948: p. 388], and wrote "human evolution is carried out by group contending with group ... groups are kept apart and isolated by their mutual antagonisms or aversions. Isolation is a condition that must be preserved if a group is to evolve. It is to the dislike or animosity which separates evolving groups that I attribute the evil feelings which are so apt to arise in Gentile nations towards their guest communities of Jews" [p. 387].

There was a good deal of equivocation in American biological anthropology

during the rise of Nazism, which incorporated many of Haeckel's ideas in what was described at the time as "nothing but applied biology" [LENZ 1931: p. 417]. Earnest Hooton, academic ancestor of almost all American biological anthropologists, was the single American biological anthropologist to rise to the occasion and conduct a campaign against Nazi racism. It came about when Franz Boas, the German-born Jewish founder of the American Anthropological Association, became concerned about the fate of Jews in the Nazi state, soon after Hitler was appointed chancellor. Boas realized that to be effective a Jewish scientist could not make a scientific denouncement of racism, but the scientific community was divided on this issue. He attended the 1934 London meeting of the International Congress of Anthropological and Ethnological Sciences, where J.B.S Haldane, the British evolutionary biologist, spoke out against racism, warning his audience against the abuse of science in support of race theories. Yet Boas was unable to convince the Congress to pass a resolution on the issue. Returning empty-handed to the US, he asked two prominent figures to take public anti-racist positions, Livingston Farrant, president of Cornell University, and Raymond Pearl, editor of *The Quarterly Review of Biology* and *Human Biology*. Both refused. He then turned to Hooton.

As a Harvard professor Hooton held a prominent position and might be listened to. He believed in biological determinism, and his commitment to eugenics reflected how little he thought the environment shaped an individual. Boas, on the other hand, was responsible for the decoupling of the perceived links between biological and cultural change

[STOCKING 1968] that underlies modern anthropological thinking. They truly made an "odd couple" [BARKAN 1988], yet for Boas, Hooton was the only game in town. When faced with the German program of race-hygiene (this was in 1935, at the time when the Nuremberg Laws were being passed), Boas tried to address the problem by proposing that American scientists make a "dispassionate and impartial statement". Hooton wrote the draft of such a statement and sent it to seven leading American biological anthropologists. Only the Bohemian-born Aleš Hrdlička of the United States National Museum would sign it, and a second draft was also unsuccessful. Finally Hooton published his own "*Plain statement about race*" in *Science* [HOOTON 1936]. But the American Association of Physical Anthropologists (AAPA) did not rise to this particular occasion. At their 1939 meeting, a resolution was proposed that disassociated human racial variation from differences in psychology or culture, discredited "Aryan" and "Semitic" racial categories, and denounced racism. It was not passed, but sent to the executive committee of the association, which took no action.

Yet, it could be said that by the 1930's the various 'founding fathers' of anthropology pretty much had it right, even if the AAPA membership did not. Currently, things seem quite different throughout the mainstream of the anthropological profession [ARMELAGOS & GOODMAN 1998; HARRISON 1998]. Biological anthropologists and others vocally and publicly rejected Coon's polygenic theory [DOBZHANSKY 1963; MONTAGU 1963], and the JENSEN [1969] (and later the HERRNSTEIN and MURRAY [1994]) claims of significant biologically

based racial differences in intelligence and learning capacity [BRACE *et al.* 1971; GOULD 1994, 1996]. Biological anthropologists joined the chorus of other anthropologists (e.g. WOLF [1994] and many others) asserting not only that race and behavior (or behavioral capacity) are independent of each other [ARMELAGOS 1995; BRACE 1999; MARKS 1995; WOLF 1994], but that human races were far too similar and intermixed to be described in a way comparable to the races of other animal species (MOORE [1994]; and TEMPLETON [1998], who notes that animal races are usually synonymous with subspecies, distinct lineages within species). Some biological anthropologists [MONTAGU 1964] have long held that human races do not exist, and in the sense of not being comparable to the races (subspecies) of other species, this view has merit. Ironically though, race can now be linked with behavior through the understanding that human racial categories are social constructs [ARMELAGOS 1995; CARTMILL 1998; CASPARI 1997;

MOORE 1994] that, in turn, may effect mate choice and demography.

So one might think that biological anthropology has finally finished off the Haeckelian precepts of separate evolutionary tracks and different evolutionary levels for human races, and with them the biology of racial difference [LITTLEFIELD *et al.* 1982], but not so [ARMELAGOS 1995; BRACE 1982; CARTMILL 1998; GOODMAN & ARMELAGOS 1996; MOORE 1994]. As recently as 1998 the AAPA reviewed a poster on race differences based on independent evolution (Figure 3) by Phillippe RUSHTON [1999] and allowed it to be presented at their national meetings: the association rejected his application for membership the following year. But focus has shifted and population differences are more often the object of study than race differences – whether the populations are defined by geography or by language and culture – and considerable effort is now expended to determine population phylogeny, and thereby origins. Yet, the legacy of racial thinking lingers throughout the human sciences. Populations are often still treated as more or less independently evolving subspecies, in both analyses of their relationships and in theories of their origin, leading to explanations of their evolution that necessitate numerous parallelisms. Parallel evolution does not always produce

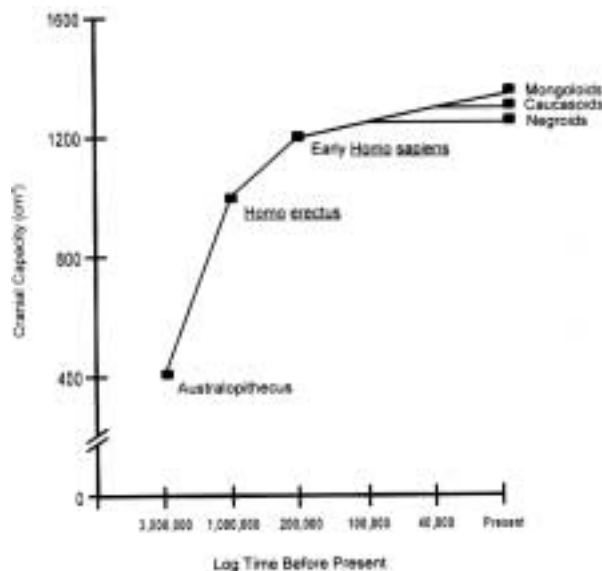


Fig. 3. An example of parallel race evolution is seen in this figure depicting the evolution of cranial capacity in modern human races, from Figure 4 in RUSHTON & ANKNEY [2000]. The three races are shown separating at different points along the curve of increasing cranial capacity in the human line, presumably explaining why their mean capacities differ today, just as Haeckel might have.

exactly the same results in the different evolving lines so the potential for expecting differences, and thereby for inequalities, is created. Least it be thought that this is idle speculation, we remind the reader that while the most recent major academic advocates of racial inequality are not anthropologists, each relies on an evolutionary theory that comes from anthropology – parallel race evolution [RUSHTON 1995; ITZKOFF 2000; RUSHTON & ANKNEY 2000].

Who *else* would analyze populations this way? The answer is surprisingly many, as tree analysis requires the assumption of branching (independent evolution) in order to be valid and tree analysis is the normal way that the genetic relationships of populations (or races) are shown. Trees of relationship continue to be drawn because they are said to *accurately* describe research results; best-fitting trees can always be determined from genetic, anatomical, and even linguistic data [CAVALLI-SFORZA *et al.* 1991, 1994], the question is whether they validly reflect underlying process. Finding trees that accurately fit data does not mean that trees validly reflect the causes of their variation, and the fact is that tree analyses cannot be valid when there is reticulation [HARDING 2000; MOORE 1994, 1995; RELETFORD 1999; SLATKIN 1991]. Moreover, the trees of genetic relationships do not even turn out to be as accurate as generally thought by those who continue to use them. Relationship trees for human populations (Figure 4) fail to meet the criterion of treeness: if trees validly depict relationships, we can expect that all the endpoints on one side of a split (i.e., populations or races) are equally related to all the endpoints on the other side. This is

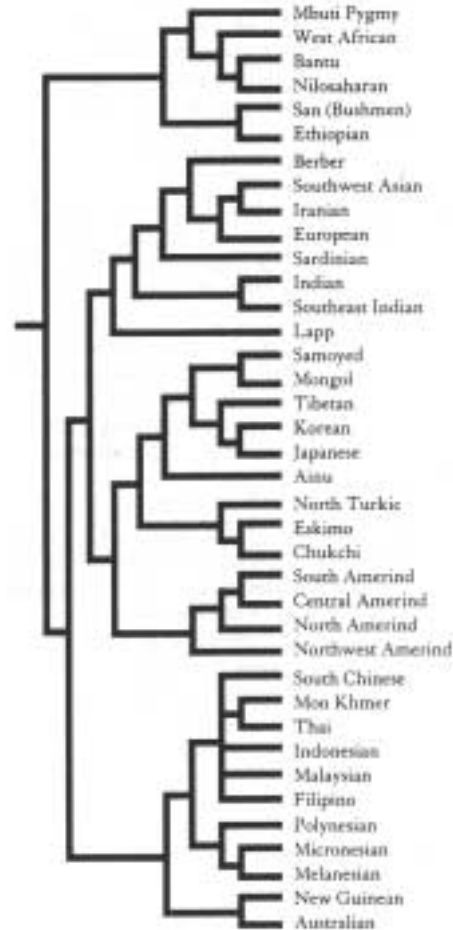


Fig. 4. Tree of genetic relationships among human populations, after CAVALLI-SFORZA *et al.* [1994]. For this tree to have the quality of treeness, all the populations on one side of each split should be equally related to all the endpoints on the other side. For instance, Ethiopians should be equally related to Mbuti Pygmies, West Africans, Bantu, and Nilosaharans.

clearly not the case for human populations [TEMPLETON 1997].

The methodological boundaries of paleoanthropology and studies of modern human variation often blur over just these issues, as the same analytical approaches (and assumptions) are widely used in both. This is an important element of why

some believe that there are 6 or more Pleistocene species of the genus *Homo*; that is, *human* species [TATTERSALL & SCHWARTZ 2000] with multiple species even at single sites such as Dmanisi [SCHWARTZ 2000] and Skhul [TATTERSALL & SCHWARTZ 2000]. To avoid burdensome taxonomic nomenclature, it has been suggested that instead of using species units, human evolution be depicted as the evolution of paleodemes – separate independently evolving human lineages that may or may not be described as different evolutionary subspecies or species [HOWELL 1996]. However, this does not avoid the problems that any branching evolutionary model (including Howell's) raises [WOLPOFF 1999b]. Paleodemes are described as “evolutionary ephemera” with “patchy, even sporadic and impermanent distributions, differentiated by barriers in space and through time.” This makes them just exactly what human populations are *not*, “a succession of ancient populations, morphologically distinct and exhibiting particular spatio-temporal distributions” [HOWELL 1999].

The logical consequences of a branching approach include the return of Haeckel's contention that biology and behavior are linked in humans. Even quite recently there have been phylogenies based on behavior, such as the connection postulated between a modern human species and (what are referred to as) “Mode 3 technologies” [FOLEY & LAHR 1997; LAHR & FOLEY 1998]², or in

the explanation that modern humans were able to replace all indigenous populations because they alone had invented human language [KLEIN 2000]. And this is not all – there are other sources of the assumption of independent population evolution that is implicit in the Eve replacement theory. These are explicated below.

Rapid independent evolution of populations, or racial divergence as evolutionary lineages, is an implicit part of the Eve replacement theory, which TEMPLETON [1998] calls a recent origin Candelabra theory (as depicted in Figure 5), to distinguish it from the older origin Candelabra of Coon's polygenism. This theory, as is well known, posits the recent emergence of modern humans from Africa and the subsequent replacement of local indigenous native peoples across Eurasia by a small group of them. Less often in focus are the implications of this theory for explaining geographic diversification. Over the 100,000 years (or substantially less, according to some interpretations, as discussed below) stipulated for this worldwide process, it is unlikely that anything but the action of selection on nearly isolated genetic lineages descended from the small founder population could account for the pattern and magnitude of worldwide differences that arose. It is true that the amount of genetic variation we are discussing is small; after all, genetic differences between human populations average only 10%-15% of total human genetic diversity that is found in the 0.08% of the human genome that is polymorphic. So short a time frame, and the contrast between the minimal genetic variation and the greater anatomical variation that evolved in it, requires that the population differences

² This is part of an evolutionary model which, according to its authors, does not require that the diverging taxonomic units be different species. LAHR and FOLEY wrote [1998: p. 170] “in reality, whether any of these large-brained late Pleistocene hominids represented a biological species that could not interbreed with the others is questionable.” With the fossils not even necessarily considered species, the parallels with how living populations are often analyzed could not be more explicit.

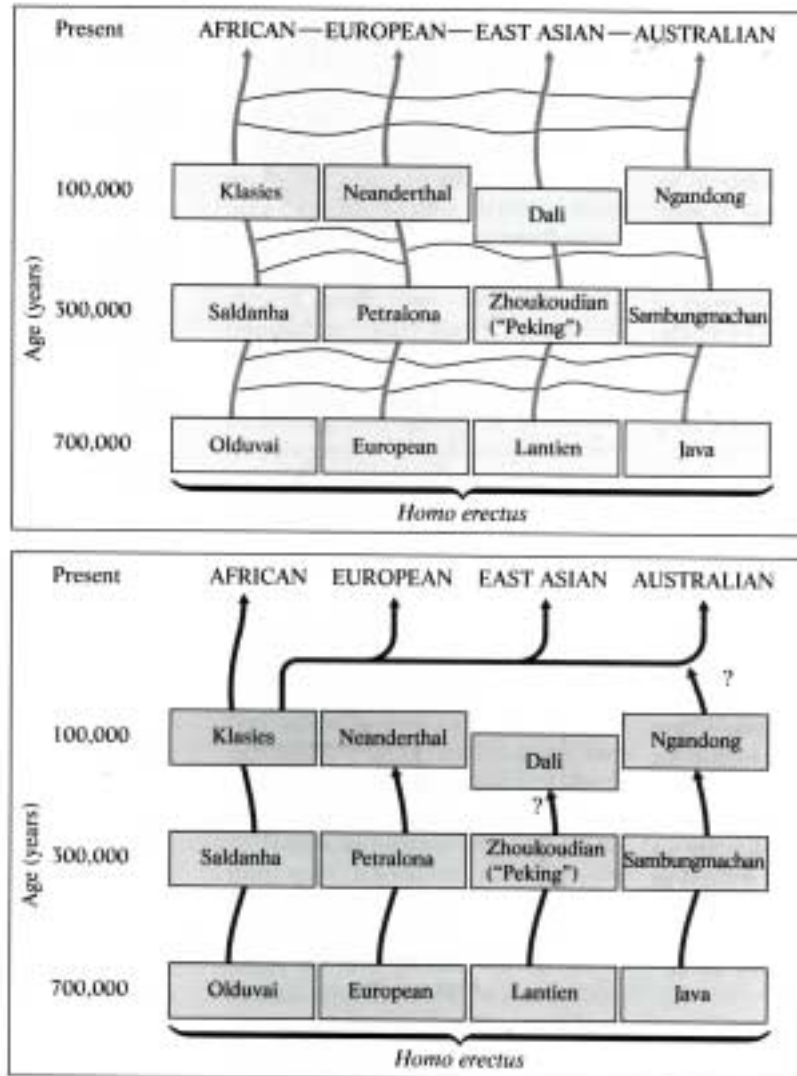


Fig. 5. Comparison of Multiregional evolution (above) and the Eve replacement theory. Note the presence of gene flow in the Multiregional model, shown by the horizontal lines connecting regions, and the absence of gene flow in this depiction of the Eve replacement theory, which was prepared by one of its supporters [LEWIN 1993: p. 81].

are virtually all adaptive [OWENS & KING 1999; HARDING 2000]. The internal tension in this picture is that while the initial population divergence was random with respect to the genome, and associated with reduced variation (the small

founder population requirement), subsequent population diversification had to be selection driven to be possible in the time frame allowed. The shorter the time frame, the more critical a role isolation of the evolving populations had to play.

There are several reasons for this – an important one is the requirement of population expansions from a small founding size to modern size; selection is least effective in expanding populations, and it is unlikely that the present pattern of genetic diversity could have characterized the species during the hypothesized period of expansion and accumulation of adaptive differences from small founding populations.

Presumably, increased admixture in the recent past would account for the low genetic diversity measures within modern humanity today such as F_{st} . Although this scenario seems to be required by the present patterns of genetic variation, it is far from the intent of those who accept a recent origins model, and brings them perilously close to the theories of Madison GRANT [1916], Roland DIXON [1923] and Earnest HOOTON [1931] that there were once-separate races that have only recently hybridized [TERRELL & STEWART 1997].

Separate lineages are required by the Eve replacement theory's explanation of why there is more genetic diversity in Africa than in other regions. The idea that greater genetic diversity in Africa means Africans originated first is well known [although see RELETFORD & HARPENDING 1995; TEMPLETON 1998], but there is a second implication of this theory – the groups colonizing the rest of the world had to be so small that they lost much of their ancestral variability through genetic drift. The necessity of assuming small population size bottlenecks for the founding populations at the origin of these colonists makes the descendant groups into separate evolutionary lineages; at the very least, one lineage division would have

to separate the Africans from the non-Africans.

Finally, *separate lineages are assumed in the branching analyses that provide the main source of support for the Eve replacement theory.* Initially this support came from the recent coalescence times of mtDNA lineages, interpreted to represent time when the last unique common ancestor of human populations lived. Here we discuss three recent examples drawn from studies of Y-chromosome variation. In a recent PNAS paper THOMSON and colleagues [2000] examined three genes on the nonrecombining region of the Y-chromosome, and concluded, “the spread of Y-chromosomes out of Africa was much more recent than was previously thought” [p. 7360]. In the same issue SHEN and colleagues [2000] report a 28,000 year date for the last common male ancestor, from a mismatch analysis of four Y-chromosome genes in the non-recombining region. They identified 98 variants and examined their distribution in samples ranging between 53 and 72 individuals from (what they describe as) the 5 continents. A reconstructed paleodemography provides evidence for exponential growth from what is assumed to be a single source. The authors describe this as being “in accord with the spread of Aurignacian technology and the disappearance of the Neanderthals” [p. 7354]. They are certain they have resolved the Neandertal problem by explaining modern human origins as a recent intrusive, replacement event in Europe, although it does leave one small problem. How did this very small population³ get out of

³ The population had to be very small because the Y-chromosome analysis presumably dates the small population size bottleneck at its origin. One estimate is of a population size of only about 2,000 individuals.

Africa and past the Neandertals in the Levant in order to arrive in Asia, where they developed Aurignacian technology [OLSZEWSKI & DIBBLE 1994; OTTE 1998]? This is a particularly intractable problem because at this time there is no evidence of Aurignacian in the archaeology of North Africa [VAN PEER 1998], no North African influence in the archaeology of the Levant [MARKS 1993], and nobody but Neandertals living in the Levant [BAR-YOSEF 1998].

Perhaps the first emigration of the small group of modern humans out of Africa that the Eve replacement theory must posit was in the eastward direction, toward Asia, and not northward through the eastern Mediterranean where they were blocked by the Neandertal populations. The explanation of how this could be was neatly proposed by CAVALLI-SFORZA [1998: p. 11502], who asserted: “the behaviorally modern humans had three big improvements in culture – language, boats or rafts, and Aurignacian technology.” He reasoned the rafts allowed the moderns to go east from Africa while avoiding the Neandertal-occupied Levant. Of course, this still doesn’t explain why the Aurignacian has not been found anywhere in Africa where the moderns were supposed to have evolved, or how those Aurignacian tools and ideas got back west into Europe without coming up against the same Neandertal problem, as they penetrated the Neandertal-occupied areas.

But it may not matter because there may not have been enough time for this scenario, at least according to conclusions proposed by SEIELSTAD and colleagues [1999]. They date modern male origins to between 17,400 and 5,800 years ago from their analysis of 10

Y-chromosome microsatellite loci. If modernity is monophyletic this interpretation would *also* eliminate the Neandertal *successors* (so-called “Cro Magnons”) from modernity (including the ones posited above to have gone east from Eden), as well as from the ancestry of any living populations, according to the logic applied here (and the authors’ interpretations).

Each of these studies reduces the data to a phylogenetic inference and all of them make the Skhul/Qafzeh remains too old to be modern. These phylogenetic interpretations of the data have implications outside of Europe. They mean that the approximately 67,000 year old skeleton from Liujiang cannot be a Chinese ancestor, no matter how much like Chinese it appears [WU & POIRIER 1995], and that the Mungo 3 skeleton of approximately the same age [THORNE *et al.* 1999] cannot be an Australian ancestor. Once again, this assertion is made no matter what Mungo 3 looks like or the extent of the similarity of this burial to recent local burial practice [BOWLER & THORNE 1976]. If the Y-chromosome data can be validly summarized in terms of phylogeny and coalescence dates (but see TAVARÉ *et al.* [1997], and HARDING [2000]), these particular regional relationships cannot be correct no matter what the morphological comparisons seem to reveal. These studies confuse gene trees with population trees, and yet phylogenetic interpretations in these Y-chromosome publications are taken seriously⁴ since they are published in very prestigious journals, more often than

⁴ The assertion that modern humans originated in Africa and swept across the earth replacing those they encountered is a widely cited fact outside of anthropology whenever the origin of human diversity is discussed, and most often is attributed to anthropology.

not in the Proceedings of the National Academy of Sciences of the USA (PNAS). Are we to conclude, then, that skeletal anatomy can tell us nothing of relationship, or is it that Native Chinese and Australians older than 28,000 years are neither modern humans nor their ancestors?⁵

There are related issues raised by the Human Genome Diversity Project, first envisaged [CAVALLI-SFORZA *et al.* 1991; KIDD *et al.* 1993] as a collage of ideas confusing race, population, and language [TERRELL & STEWART 1997]. It assumes that indigenous peoples are genetically isolated, so tree analyses of phylogenetic relationships between populations or races would be valid and productive [MOORE 1995]. Although Cavalli-Sforza quite explicitly asserts that trees are only a statistical graphics device for representing data [CAVALLI-SFORZA *et al.* 1994], when praising the potential of the diversity project, he attributes a quite different importance to them. Cavalli cites the value of the genes of the !Kung San to potentially illuminate our evolutionary history, as if it were true that the group at the stem of a phylogenetic tree of living races (the San are at or near the root of most of Cavalli's more recent gene trees [CAVALLI-SFORZA *et al.* 1992; CAVALLI-SFORZA 1997; BARBUJANI *et al.* 1997]) could be more plesiomorphic (the phylogenetic term for "primitive") than the others and somehow represent the ancestral condition!⁶ A National Research Council committee chaired by William Schull [SCHULL *et al.* 1998] was set to resolve the vocal, even passionate

controversies that ensued, and concluded that a genome diversity project could go forward, but one that was quite different in scope, intent, and most importantly in its underlying assumptions.

What does all this have to do with human species in the fossil record? We believe the answer is everything, for the studies of race and of human evolution are far more entangled than is generally realized. When dealing with issues of modern human variation, most modern anthropologists and human biologists at least pay lip service to the importance of populational thinking, inspired by the new synthesis⁷. In spite of this, as we note above populations still are methodologically treated like races – as products of essentialist thought. Our interpretations of the past inform our views of modern human variation and vice-versa. When essentialist approaches are used to interpret variation in the past as taxonomic rather than populational, as increasingly has been the case, it serves to underscore the typological view of modern human variation discussed above. In terms of how they are treated in analysis, there often seems to be no difference between the species, subspecies, or paleodemes of the past and the populations or races whose interrelationships and demographic history are discussed today. Science is not isolated from society, as the history of biological anthropology has so sadly shown, and none of us can be sure that the world view we might unconsciously perpetuate is without repercussions.

⁵ This is a solution that actually has been proposed, and not just historically [HARPENDING & ELLER 2000].

⁶ This would be a valid interpretation only if the groups analyzed were different species.

⁷ Although this is not at all universal; some quite explicitly deny the relevance of populational thinking to understanding evolution, and describe the evolutionary synthesis as everything from incomplete to downright misleading and incorrect [TATTERSALL 1992; TATTERSALL & SCHWARTZ 2000].

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Streszczenie

Badania zróżnicowania rasowego człowieka związane są nierozdzielnie z problemem ewolucji naszego gatunku. Jednym z powodów jest fakt, że wykorzystywane w tych badaniach teorie i podejścia metodologiczne, odnoszące się do populacji i do gatunku, stosowane są zamiennie, bez względu na konsekwencje takiego postępowania. Inny powód jest natury historycznej i wynika z kluczowej roli, jaką odegrały w rozwoju antropologii fizycznej poglądy Ernsta Haeckela. Haeckel traktował rasy ludzkie jak odrębne gatunki, ponieważ tak jak one wyróżniały się unikatowymi cechami. Poszczególnym rasom przypisał on odrębne drogi ewolucyjne, charakteryzujące się różnym tempem przemian – w konsekwencji – różnym stadium ewolucji osiągniętym współcześnie. Niewiele różni się to od poglądów niektórych dzisiejszych autorów, sugerujących i „uzasadniających” nierówności rasowe. Jednakże również ci, którzy

nie podzielają takiego poglądu, proponują teorie wyjaśniające przebieg ewolucji człowieka lub podejścia metodologiczne w analizie danych stanowiących podstawę tych teorii, w których zakłada się lub akceptuje niezależny przebieg ewolucji w różnych liniach rozwojowych ludzkości. Najpoważniejszym problemem jest zapewne to, że choć większość współczesnych antropologów i biologów człowieka co najmniej deklaratywnie uznaje konieczność myślenia populacjonistycznego, by pozostać w zgodzie z syntetyczną teorią ewolucji, metodologicznie populacje ciągle traktowane są jak rasy – wytwory myślenia esencjalistycznego. Kiedy, na skutek podejścia esencjalistycznego, zmienność w przeszłości interpretuje się raczej taksonomicznie niż populacyjnie, a tendencja taka się nasila, sprzyja to typologicznemu widzeniu zróżnicowania dzisiejszego człowieka. Sposób traktowania analizowanych materiałów może stwarzać wrażenie, że nie ma różnicy między gatunkami, podgatunkami i paleodemami form kopalnych – z jednej strony, a dzisiejszymi populacjami czy rasami, których wzajemne relacje i historię demograficzną bada się obecnie – z drugiej strony. Nauka jednak nie pozostaje w izolacji od społeczeństwa i jej wyniki mają swoje społeczne konsekwencje.