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G. AULETTA - M. LECLERC - R.A. MARTÍNEZ (eds.)

BIOLOGICAL EVOLUTION: FACTS AND THEORIES

A Critical Appraisal 150 Years After "The Origin of Species"

With an Address of Cardinal Levada

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THE ORIGIN OF MAN: MOLECULAR APPROACH

Olga Rickards and *Gianfranco Biondi*

1. Introduction

Two events about 100 years apart from one another laid the foundation for the scientific study of human beings. In the mid seventeenth century Carl Linnaeus freed mankind from the bonds imposed by a supernatural or metaphysical interpretation of nature, gave humans a name, and assigned them a proper place in the classification of nature. That humans had prehistoric ancestors was an unthinkable notion at that time. Child of the Enlightenment and creationist, Linnaeus based his concept of man on direct observation and knowledge of historical and religious sources. In the first edition of *Systema naturae* (1735) he devised the name *Homo sapiens*, to which he associated the motto, *nosce te ipsum*, and placed humans, along with monkeys and apes, in the same zoological order: Anthropomorpha, which in the 10th edition (1758–1759) was renamed Primates. Classifying man as a primate meant operating a bold shift in the scientific and cultural paradigm of an era that set humans apart from other living beings and far greater than the distance perceived among other animals. This paradigm shift was best described a century later by Thomas Henry Huxley in his *Evidence as to Man's Place in Nature* (1863):

> Thus, whatever system of organs be studied, the comparison of their modifications in the ape series leads to one and the same result — that the structural differences which separate Man from the Gorilla and the Chimpanzee are not so great as those which separate the Gorilla from the lower apes.
>
> But in enunciating this important truth I must guard myself against a form of misunderstanding, which is very prevalent. I find, in fact, that those who endeavour to teach what nature so clearly shows us in this matter, are liable to have their opinions misrepresented and their phraseology garbled, until they seem to say that the structural differences between man and even the highest apes are small and insignificant. Let me take this opportunity then of distinctly asserting, on the contrary, that they are great and significant; that every bone of a Gorilla bears marks by which it might be distinguished from the corre-

> sponding bone of a Man; and that, in the present creation, at any rate, no intermediate link bridges over the gap between *Homo* and *Troglodytes*.
>
> It would be no less wrong than absurd to deny the existence of this chasm; but it is at least equally wrong and absurd to exaggerate its magnitude, and, resting on the admitted fact of its existence, to refuse to inquire whether it is wide or narrow. Remember, if you will, that there is no existing link between Man and the Gorilla, but do not forget that there is a no less sharp line of demarcation, a no less complete absence of any transitional form, between the Gorilla and the Orang, or the Orang and the Gibbon. I say, not less sharp, though it is somewhat narrower. The structural differences between Man and the Man-like apes certainly justify our regarding him as constituting a family apart from them; though, inasmuch as he differs less from them than they do from other families of the same order, there can be no justification for placing him in a distinct order (Huxley 1863, 123–124).

Recent advances in molecular studies have borne out the choice Linnaeus formulated. Humans and gorillas share 97.5% genome identity; and the similarity increases when humans and chimpanzees, and the pigmy chimpanzee or the bonobo in particular, are compared. In view of such close genetic identity, some scientists have proposed enlarging the genus *Homo* to make room beside *Homo sapiens* for the common chimpanzee (*Homo troglodytes*) and for the pigmy chimpanzee (*Homo paniscus*). Others have gone even further to suggest adding one more place for the gorilla (*Homo gorilla*). But looking back, these ideas may not be so farfetched as they appear: even Linnaeus classified under the genus *Homo*, particularly in *Homo nocturnus,* an ape. That said, these taxonomic adjustments should not be misunderstood. Scientists are not disclaiming the enormous difference between apes and us. The point they are making is that in the rest of the animal world that high degree of genetic identity is employed to bring species under the same genus.

Countless years passed while scientific research, working under the constraints of anti-evolutionary prejudice, focused on the features we share with apes and prepared the ground for the now almost indisputable claim that man is just another primate. Today, however, interest has turned to the perplexing question as to how so few genetic differences can determine such wide variation in anatomy, morphology, walking, susceptibility to disease, and in intellectual and behavioral capabilities. This new direction has been boosted by programs that sequence the human genome and that of other primate species, including the chimpanzee.

Earlier, we stated that classifying man among the primates is incontestable, yet many religious circles in Western society, not to mention others, continue to privilege a metaphysical interpretation of nature over scientific evidence to the contrary.

One example of this entrenched opposition to accepting knowledge based on reason and experiment appeared in an editorial published in *La Civiltà Cattolica* in 2003:

> Unquestionably, in the Christian view, there exists a radical difference between humans and animals that is not only a difference by degree (humans are *more* intelligent, *more* able than animals) but also by nature: man is not a superior animal, *more* perfect than other animals; instead, man *is not an animal* at all. Because, although sharing with animals certain anatomic features and brain functions, man alone possesses an immortal soul. Therefore, when one speaks of man, one cannot say, as the animalists do, "man and the *other* animals", as if man were another animal though superior in kind; instead, one should say "man and animals". Man is a "separate being", because created "in God's likeness" (Gen. 1: 26) he is the center and the purpose of creation (Editoriale 2003, 6).

The other founding event dates back to the mid nineteenth century when Charles Robert Darwin challenged creationism with the publication of *On the Origin of Species* (1859) and *The Descent of Man* (1871). Working in the natural sciences, Darwin demonstrated by empirical methods the inconsistencies in the theological reconstruction of life (creationism) with respect to a scientific explanation (evolutionism). He could not dispute the question of the creation insofar as "the creation" refers to a psychological need most of humanity nurtures toward an external and metaphysical power entrusted with our concerns about the present, the future, and inevitable decline and end. Creation may be conceived as a projection of our mind — the same mind that evolution granted us in all its complexity. And, as such, creation's value lies outside the interest of experimental science, as does, indeed, the value of art, for example. In brief, demonstrating the non existence of the creation or a creator is not the task of science. What science does strive to do is prove the extraneousness of any action or principle beyond nature related to the construction, function and explanation of the world, which is self-sufficient and self-responsible.

Darwinian evolutionism could not have been envisaged if our concept of time had not been radically changed from the idea of historical time, as derived from biblical genealogies, to the idea of deep time. In the 150 years since Darwin stretched life's timeline and opened new vistas, evolutionism itself has evolved, going from strength to strength, yet never losing sight of its proponent. The new vistas have been the discovery of genetic laws and the application of mathematics to these laws (the modern synthesis theory), the discovery of a second evolutionary mechanism (molecular neutrality), the abandoning of a linear sequence of evolution (punctuated equilibrium) and the co-existence of several lines of evolution in a group of living organisms (the bush theory).

In 2005 Giuseppe De Rosa corrected the editorial published in *La Civiltà Cattolica* in 2003, placing the problem of man's origin within the context John Paul II had drawn in his *Message to the Pontifical Academy of Sciences* in which evolutionism was attributed the rank of scientific theory, upgrading it from being a serious hypothesis, as Pius XII had admitted in the *Humani generis* encyclical (John Paul II 1996). It is worth noting, however, that at point 6 of his *Message*, John Paul II made a statement incompatible with Darwinian evolutionism, affirming that modern man represented "an ontological leap" (Biondi and Rickards 2008). In his article, De Rosa picked up on John Paul II's line of reasoning, stating that:

> The hominization is to be set within a wider frame of evolution of life on earth, after the creation by God (De Rosa 2005, 3).

and that only when modern man had appeared was the human "threshold" reached:

> But what does reaching the human "threshold" mean for *Homo sapiens sapiens*? It implies both continuity and discontinuity. Continuity in the sense that *Homo sapiens sapiens* is in evolutive continuity with the preceding human forms somatically and culturally; and discontinuity at the spiritual level. (…) This discontinuity at the spiritual level (…) means that in *Homo sapiens sapiens* there is a spiritual principle that can explain the inner presence of activities that transcend a purely material order. This spiritual principle, which unites all human activities, physical, sensory and intellectual, is the spiritual soul. (…) This means that the spiritual soul, as a principle of the spiritual activities of *Homo sapiens sapiens*, represents an ontological "leap", and is therefore qualitative, in the evolutionary process that science can recognize and observe but not explain according to the laws regulating the evolution of living beings (De Rosa 2005, 9–10).[1]

And again, in 2005 Benedict XVI underscored an unbridgeable distance from Darwinian evolutionism, stating that:

> We are not a random, aimless product of evolution. Each of us is the fruit of God's thought (Benedict XVI 2005, 5).

When Darwin postulated his theory of descent by natural selection and the transmission of advantageous variations, which has proved to be a fact, hereditary material was still unknown and traces of our prehistoric past were to be found

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[1] The name *Homo sapiens sapiens* for modern humans is an old nomenclature. Molecular anthropology has proved that we do not belong to the subspecies *Homo sapiens sapiens,* we belong to the species *Homo sapiens*.

only in fossil remains. Today, we know that our past is contained in our DNA and that by analyzing that molecule we can read it.

Molecular analysis touches every corner of biology and medicine. It has also had an impact on research further afield in anthropology and paleoanthropology. And its impact has been practical as well as theoretical. For example, in resolving quandaries that beset classic comparative anatomic classification of fossil remains and living organisms, molecular anthropology has given authoritative answers to four anthropological questions:

1. when did the split occur between early human and African ape lineages?[2]
2. how did our species *Homo sapiens* originate?
3. why is the concept of "biological race" inapplicable to humans?
4. how should primates be classified?

2. The split between early humans and large African apes

In 1967 researchers at the University of California, Berkeley, Vincent Sarich and Allan Wilson, questioned the then almost universally accepted idea that *Ramapithecus*, a primate fossil dated between 15 and 25 million years ago, was the earliest member of the human line (Biondi and Rickards 2004). Morphologic analysis of its dentition and skeletal characteristics seemingly indicated that *Ramapithecus* had appeared on the evolutionary scene after the human clade had diverged from that of the large African apes and that the split must have occurred at some point before 25 million years ago. However, the idea that the two lines had branched away so early met with scepticism in some circles, because results of contemporary genetic studies showed remarkable similarities between man, gorilla and chimpanzee that did not fit the notion that an evolutionary split could have occurred about 30 million years ago (Biondi and Rickards 2004).

In their analysis, Sarich and Wilson calculated the amount of time that had passed since early humans and African apes had diverged by measuring the differences in the amino acid sequences in some of their blood proteins. Since these differences result from copying errors that occur during DNA replication before it is transmitted to the next generation, the errors (mutations) that accumulate from one generation to the next can be used to put a timescale on the divergence between apes and humans. Underlying this phenomenon is the concept of the molecular clock. The same idea lies behind the dating of Medieval manuscripts. With

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[2] Large African apes include two species of chimpanzees: *Pan troglodytes*, or the common chimpanzee, and *Pan paniscus*, or the bonobo or the pygmy chimpanzee, and the gorilla, *Gorilla gorilla*.

each copy, scribes risked miscopying a word: the more the errors, the more times the manuscript was copied, and the more the copies made, the more time had elapsed between older and newer manuscript copies. By counting the number of differences in copies of the same text, the copies can be dated on a timeline.

In the same way, the number of changes between molecules can be taken to count time with the molecular clock and converted into evolutionary time. In brief, the more similar the proteins of different species, the more recent is their divergence from each other. Having determined for specific proteins that the mutations, which are essentially neutral, tend to accumulate at a regular, almost clocklike rate in various different ancestral lineages through time, the number of differences in mutations accumulated between the species will indicate the length of time since they split from a common ancestor.

By applying the molecular clock, Sarich and Wilson estimated that early humans and African apes had probably split approximately 5 million years ago, a finding which ran counter to then prevailing paleoanthropological views. Following the later discovery of more complete *Ramapithecus* remains, the general consensus now rates it as *Sivapithecus*[3] and therefore it represents the ancestor of the orangutan.[4] It wasn't until the 1980s, however, that the scientific community finally accepted the idea of a recent divergence between human and non-human lines. But Sarich and Wilson had left open the question about whether man, gorilla, and chimpanzee had diverged simultaneously or whether the split had occurred at different epochs.

In the early 1980s, two Yale University researchers, Charles Sibley and John Ahlquist, tackled this problem with another technique: DNA hybridization. The two strands of the DNA molecule are held together by bonds that form its complementary base pairs (adenine-thymine and cytosine-guanine). To separate the two strands and obtain single strands, the DNA molecule needs to be heated or treated with chemical agents. After treatment, the DNA molecule returns to its double helix structure. Applying this process to DNA mixtures taken from various different species yields hybrid double helixes with bonds that are stronger the more similar the nucleotide sequences between species, so that more heat is needed to separate the bonds. By measuring the amount of heat needed for separation, the degree of similarity between species can be determined and the evolutionary distance between them (Biondi and Rickards 2004).

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[3] Primate fossils recovered from sites in Turkey and the Indo-Pakistan region, whose most recent remains have been dated to 8 million years ago.

[4] *Pongo pygmaeus*, the large Asiatic ape.

Using this technique Sibley and Ahlquist made the surprising discovery that in contrast with evidence from comparative anatomy, chimpanzees and humans are more genetically similar to each other than either is to the gorilla and that the orangutan is even more distant in evolutionary terms. During their evolutionary course, the first of the four to diverge was the orangutan, then the gorilla, while man and chimpanzee continued to share the same path until they split somewhat later.

The enormous advances in DNA technologies over the past two decades have enabled scientists to date fairly accurately when these lines branched off: the orangutan split away about 14 million years ago; the gorilla lineage diverged about 7 million years ago; the chimpanzee and human lineages were the most recent to diverge from the common ancestor, their split having occurred about 6 million years ago; the bonobo (or pygmy chimpanzee) diverged from the common chimpanzee only 3 million years ago (Biondi and Rickards 2006).

3. The origin of *Homo sapiens*

Thanks to DNA analysis, molecular anthropology has been able to shed light on the question of how *Homo sapiens* originated. But here, too, as in previous controversies about when African apes and hominins went on their separate evolutionary ways,[5] heated scientific debate arose between paleoanthropologists and molecular anthropologists. The controversy was even more complex because the paleoanthropological camp was divided over which of two different scenarios could best explain the emergence of *Homo sapiens* (*Figure 1*). The first, known as the Multiregional or Regional Continuity model, held that modern man had arisen simultaneously from archaic populations inhabiting different regions of the Old World which they had occupied after leaving the African cradle.[6] From its start about 2 million years ago, this gradual evolutionary process was accompanied by a high uninterrupted gene flow between local populations, which would have inhibited the emergence of different species in various regions.

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[5] The zoological subfamily *Homininae* includes the human clade, i.e. humans and their direct and indirect ancestors that appeared on the evolutionary scene after they split from the chimpanzees.

[6] *Homo ergaster* was the first hominin to leave the African continent and then spread to Georgia where he gave rise to *Homo georgicus*, to Asia, where he gave rise to *Homo erectus*, and then to Europe where his descendants were *Homo antecessor*, *Homo cepranensis*, *Homo heidelbergensis* and *Homo neanderthalensis*.

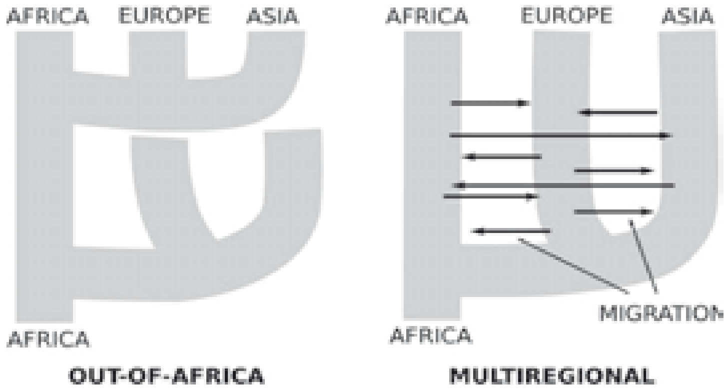

Figure 1. The two evolutionary models proposed on the basis of fossil remains to explain the emergence of Homo sapiens.

The second scenario which other paleoanthropologists embraced was the Out of Africa theory which holds that all mankind has a recent single African origin. In detail, the first modern humans appeared in Africa about 200,000 years ago following a sudden punctuated speciation event, after which they spread throughout the rest of the world, displacing the pre-existing archaic populations and without interbreeding with them. This scenario implies a genetic discontinuity between *Homo sapiens*, the new species, and the pre-existing hominins that belonged to different species. By contrast, the Multiregional model opts for genetic continuity starting about 2 million years ago and allows for a certain degree of hybridization between the various populations that had come into contact (Thorne and Wolpoff 1981; Stringer and Andrews 1988; Biondi *et al.* 2006).

In the attempt to determine which of the two models was more suitable to explain our origins, researchers looked to DNA analysis. In the late 1980s, three researchers at the University of California, Berkeley, Rebecca Cann, Mark Stoneking, and Allan Wilson published their study in *Nature* on the first molecular evidence of a single recent African origin in support of the Out of Africa theory (Cann *et al.* 1987). Studying mitochondrial DNA (mtDNA), a particular type of DNA,[7] they

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[7] mtDNA is contained in the cytoplasmatic organelles called mitochondria where it provides the cell with energy. Its genome is tiny when compared with the nuclear genome (approximately 16,500 base pairs versus 3 billion base pairs). It is a circular, double-stranded DNA molecule which is abundantly found in all cells of an organism (on the order of thousands in somatic cells and hundreds of thousands in germinal cells). These characteristics, together with its location in the cytoplasm, makes mtDNA easy to analyze and to study the DNA in ancient remains. It has a high evolutionary rate, between 10 and 20 times that of portions of the nuclear genome with comparable function.

wanted to see whether in the genetic pool of current human populations there could be ancient genes that had been transmitted by the archaic *Homo* populations, as the Multiregional model assumed, or if ours was a completely modern genome, as predicted by the Out of Africa model.

Mitochondrial DNA is an ideal tool for answering this question. Since it is transmitted exclusively by the maternal line, mothers and daughters share the same mtDNA, without the mutations that may occur in the germinal line of each generation. By contrast, the genes in the nucleus, inherited from both parents, are susceptible to such phenomena as segregation and recombination that reshuffle the genes with each generation, making it more difficult to retrace the gene path back in time.

If, as proposed by the Out of Africa model, mankind had a recent origin, modern human populations would have mtDNA with very few mutations: the mutations would be fairly homogeneous because they would not have had enough time to accumulate. Furthermore, if modern humans had evolved from a single ancestral population living in a geographically restricted environment, the current population inhabiting the area, because older, would show greater genetic variation. If, on the other hand, mankind had evolved from remote and multiregional origins, the various populations would have many mutations and all in equal measure.

When the three Berkeley researchers arranged their results into a phylogenetic tree,[8] it neatly illustrated an African and recent mtDNA origin (the famous Mitochondrial Eve hypothesis). The tree showed two distinct main blocks: one grouped the more diverse types, as shown by the length of the branches proportional to the number of mutations, which resulted solely African, and the other showed all the sequences identified in the rest of the world, plus some African lineages. Since we know that the higher the number of mutations, the greater the length of time to accumulate them, the mtDNA of the African population turned out to be older, and thus represents the most recent common ancestor. The common ancestor's descendents (the African lineages in the non-African clusters) gradually spread across the world, giving rise to various different local populations through time. When the molecular clock was applied to the mutations in the two main blocks, it showed that the common ancestral mtDNA was recent and could be dated to about 200,000 years ago.[9]

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[8] A phylogenetic tree is a graphic representation that permits the comparison between the genomes of various different individuals against the ancestor-descendant scheme.

[9] This clock beats at 2-4 mutations every 100 bases per million years. Another rate of ticking at 12-17 mutations per 100 bases per million years was estimated starting from the D-loop control region of the mtDNA. This region is highly variable and the date set for the origin of our species is between 250,000 and 170,000 years ago.

Additional analysis of the mitochondrial genome gave the same result (Ingram *et al.* 2000). Then in 2002 Alan Templeton, from work on diverse proteins and enzymes, pushed back the origin of *Homo sapiens* to about 600,000 years ago, opening the hypothesis for two migratory waves out of Africa to the rest of the Old World: the first dating soon after the origin and the second at around 100,000 years ago. The conclusions to be drawn from these studies agree with the hypothesis, based on paleoanthropological findings, of a recent single origin of our species.

Of note is that modern humans did not appear 600,000–200,000 years ago;[10] instead, this period marks a genetic divergence which does not necessarily coincide with a population divergence. Because the principles of molecular evolution predict that genetic divergence precedes population divergence, the mtDNA data collected so far are incompatible with the Multiregional model, which holds that the differences that led to the origin of our species began to accumulate about 2 million years ago and that genetic divergence would have been even earlier.

mtDNA holds enormous interest for research into human evolution, yet the molecule accounts for a minute portion of the entire genome (0.0006%). Owing to random or selective phenomena, reconstructing human evolutionary history solely from mtDNA is hazardous, since its pattern of variation may differ substantially from that of other portions of the genome, potentially falsifying the real picture. Accurate reconstruction will take into account an analysis of nuclear gene loci, such as those of Y-specific DNA, which permit retracing the male line of evolution and autosomal inheritance. The wealth of data from studies during the 1990s agree substantially with a recent African origin of modern man (Thomson *et al.* 2000; Underhill *et al.* 2000; Ke *et al.* 2001; Biondi and Rickards 2004, 2006).

Having established that we are a relatively young species and that our ancestors came out of Africa to occupy dry land, the dilemma of our phylogenesis appeared to have been settled. However, some suggested that the experiments on extant DNAs were not robust enough to rule out that *Homo sapiens*, on reaching Europe, had not interbred with the Neanderthals, and that there were two subspecies of the same species: *Homo sapiens neanderthalensis* and *Homo sapiens sapiens*, as proposed by the multiregionalists.

Again, advances in biotechnology helped molecular anthropologists to elucidate the question: the study of ancient DNA (aDNA). The temporal limit of DNA survival, estimated on theoretical calculations to be between 1 and 2 million years,[11]

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[10] The oldest *Homo sapiens* fossils can be dated to about 200,000 years ago.

[11] In the early 1980s, initial studies on aDNA seemingly suggested that DNA extracted from dinosaur bones or insects preserved in amber, tens if not hundreds of millions of years ago,

was perfectly suited for definitively settling the Neanderthal controversy, given that Neanderthal man ranged across Europe, the Near East and western Asia between 300,000 and 27,000 years ago (Jobling *et al.* 2004).

In 1997, just 10 years after the publication of the Mitochondrial Eve hypothesis, a joint team of German and American researchers headed by Svante Pääbo studied the mtDNA of the most famous representative of the Neanderthals, the remains recovered from the Feldhofer Cave in the Neander valley in Germany, which gave the species its name. The team found that Neanderthal mtDNA differs significantly from ours. The comparison between any two sequences of modern mtDNA shows a mean of 8 nucleotide differences, whereas the number of differences between modern and Neanderthal mtDNA sequences is 3.5 times as high. Moreover, to render this value more eloquent, the data were extracted and the Neanderthal sequences were compared against those of current populations from various different continents. Had the Neanderthals contributed to the formation of our species, they would show a closer relationship with individuals currently inhabiting Europe than with those living in other geographic areas of the world. But no trace of a privileged kinship in the mtDNA could be found. The Neanderthal sequences showed 28 differences with respect to those of Europeans and Australians and 27 differences with respect to Asian, African and native American populations. So although the Neanderthals inhabited the same regions as the current European populations, the genetic distances do not support the idea that they are any more closely related to Europeans than to other modern populations. This would appear to further dismantle the theory of regional continuity: that Neanderthal man was a direct ancestor of modern Europeans. But Pääbo went a step further and constructed a phylogenetic tree with the Neanderthal sequences and those of modern man. The answer was even clearer. Neanderthal man located on a side branch of our evolutionary tree; in other words, he may be considered as a cousin of our species. Pääbo's team then applied the molecular clock to put the most recent common ancestor of modern humans and the Neanderthals on a timescale. The estimated period extending from between 690,000 and 555,000 years ago perfectly fit palaeontological and archaeological findings that the two lines had split around 300,000 years ago — set within the perspective that genetic divergence precedes population divergence — thus strengthening the African Eve hypothesis (Krings *et al.* 1997).

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could be analyzed. Today, however, we know that those data were simply laboratory artefacts that resulted from contamination with modern DNA.

But with this came the usual problem of DNA studies: reproducibility demonstrated on other Neanderthal remains. That the Neanderthals were a different species from ours could not be proven with a single sequence. Generally, there is a wide range of genetic variation in primates, and if this were to be the same for the Neanderthals, the sequence Pääbo obtained would have been one of the most divergent. Besides studying diverse Neanderthal fossil remains spatially and temporally distant from the Feldhofer Cave site fossils, whose DNA would necessarily lie outside our interval of variation, scientists subsequently needed to turn their attention to the ancient remains of our species, i.e., those of Cro-Magnon man, whose DNA would be expected to be more similar to ours.

This line of research began in the early years of this century. Comparison of the genetic distance between the 12 Neanderthals studied so far, the 21 samples of ancient *Homo sapiens* recovered from known Palaeolithic sites in Italy, nearly all of which have been analyzed in the laboratories at the University of Rome, Tor Vergata, and samples from thousands of living individuals from different continents showed that the Neanderthals locate completely outside the known variation of our species, whereas no difference was found between ancient and modern *Homo sapiens* (Caramelli *et al.* 2003; Tarsi *et al.* 2006). A recent study estimated that the molecular data currently available for the two species overlap up to a maximum of 120 cross links between us and our Neanderthal cousins in over 12,000 years of co-existence (Currat and Excoffier 2004).

On 12 February 2009 it was announced that a first draft version of the Neanderthal genome had been completed by the Max Planck Institute for Evolutionary Anthropology, in Leipzig, Germany, and the 454 Life Sciences Corporation, in Branford, Connecticut. Obtaining nuclear sequences of the Neanderthals marked a turning point in the reconstruction of the evolutionary timeline of man and his prehistory. Knowing the complete sequence of the Neanderthal genome, it will be possible to compare human and recently obtained chimpanzee genomes and identify the characteristics that can be used to distinguish us from them. For example, we could determine definitively whether *Homo sapiens* and Neanderthals interbred during the period of co-existence, which mtDNA has categorically ruled out, and whether the skin and hair colors of our Neanderthal cousins were dark or fair, as initial studies on the *MC1R* gene regulating melanin has suggested for some (Lalueza-Fox et al., 2007). And we could even resolve the question whether our relatives used speech for communication. Pääbo is currently conducting research in this direction and has seen that the *FOXP2* gene is involved in various aspects of language development.[12] For instance, just a few point mutations is all it takes to seriously impair oral articulation, with subsequent effects on orofacial movement and efficient development of spoken language, including linguistic and grammatical reasoning. The normal form of our gene differs from that of the chimpanzee in two positions on the DNA molecule, which means the substitution of two amino acids in the related proteins. The results of the analysis of the *FOXP2* gene in two Neandertal specimens showed that they displayed a sequence identical to that of our species suggesting that our cousin could have had an advanced type of language like ours (Krause *et al.* 2007).

Therefore, we can state that modern man descended neither from the Neanderthals nor interbred with them: we are two different species, *Homo neanderthalensis* and *Homo sapiens* and we can also state that ancient DNA disproved the Regional Continuity model.

4. Human races: a false concept

In the 1950s, a review of "racial" classification by morphologic features using genetic polymorphisms revealed completely different results (*Figure 2*). Only two decades later did empirical evidence emerge against classifying human biological variation according to a concept of "biological race". Over 85% of genetic variation is encountered among individuals of the same population and only the remaining 15% characterizes different populations. This explains why among populations the distinct morphological differences arising from environmental factors are fleetingly few at the genetic level.

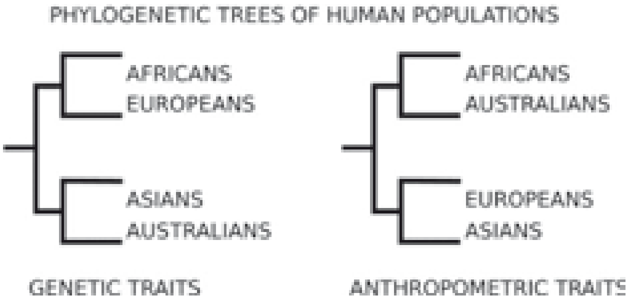

Figure 2. Phylogenetic trees of human populations based on anthropometric and genetic traits.

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[12] The *FOXP2* gene is located on chromosome 7, near the areas associated with autism and other mental disorders.

Moreover, molecular anthropology has shown that we are a young species and therefore cannot be subdivided into "races". Reconstructing the phylogenetic tree of populations based on DNA sequences, specifically mtDNA sequences, resists "racial classification" and shows that no clear distinction can be drawn between "races" in classical anthropology. For example, the populations of the different continents, what were once called "races", are not characterized by a single mitochondrial lineage, so disproving any scientific evidence that races descend from different common ancestors. If, on the other hand, "races" were real taxonomic categories, the populations making them up would share the same line of ascendant (Barbujani 2006; Biondi and Rickards 2002, 2007).

Furthermore, if "race" were a real taxonomic category, it would permit the reconstruction of the phylogenesis of human populations according to an ancestor-descendant scheme. But the concept of "race" fails to do so; it allows only grouping human variation in relation to the environments where our species has lived and still lives. Used in this way, it may be helpful for tracing ecologic history, certainly an important part of biology, but it cannot be scientifically applied to reconstructing phylogenetic history.

5. Classification of the Primates

The fourth and most recent question molecular anthropology has sought to address regards the classification of the Primates. The genetic similarity (from 98.4, when synonymous DNA sites are included, to 99.4%, when non-synonymous sites are taken into account) shared between humans and chimpanzees estimated by Morris Goodman's group in 2003 (Wildman *et al.* 2003) reveals a surprisingly close relationship. This estimate was later confirmed by data published in September 2005 (The Chimpanzee Sequencing and Analysis Consortium) on the complete sequencing of the chimpanzee genome, which indicate that humans and chimpanzees share 97-99% of their genetic material. Given this high degree of affinity, Goodman decided to include in the genus *Homo*, in addition to our species, the common chimpanzee and the bonobo, which would be given the name of *Homo* (subgenus *Pan*) *troglodytes* and *Homo* (subgenus *Pan*) *paniscus*, respectively. This reordering of the Primate classification did not catch the academic community by surprise, since in 1998 Elizabeth Watson (Watson *et al.* 2001), and before her, Jared Diamond in his book, *The Third Chimpanzee: the Evolution and Future of the Human Animal*, had suggested a similar idea. Watson went one step further and included in our genus the gorilla as well: *Homo* (subgenus *Gorilla*) *gorilla*.

What may have appeared a bold new idea was actually anticipated by Carl Linnaeus. In 1747 in a letter to his botanist colleague Johann Gmelin, who had accused Linnaeus of daring to place man with the Primates, he wrote:

> If I had called man a monkey, or vice versa, I would have been scorned by churchmen. Perhaps as a naturalist I could not have done otherwise (Greene 1959).

The implication being that had he not been influenced by authorities, Linnaeus would have gone farther in his classification, given that his observations of nature had suggested a close tie between man and the large apes.

And once the chimpanzees and the gorilla were allowed into our genus, it became easier to give a new identity label to our ancestors who had appeared on the evolutionary scene after the divergence from the large apes. In Goodman's new classification all the familiar genera will be replaced by the single genus *Homo*. The switch from the old to the new taxa will be, respectively: *Sahelanthropus tchadensis* to *Homo* (subgenus *Homo*) *tchadensis*;[13] *Orrorin tugenensis* to *Homo* (*Homo*) *tugenensis*; *Ardipithecus kadabba* and *Ardipithecus ramidus* to *Homo* (*Homo*) *kadabba* and *Homo* (*Homo*) *ramidus; Australopithecus anamensis-afarensis-africanus-bahrelghazali-garhi* to *Homo* (*Homo*) *anamensis-afarensis-africanus-bahrelghazali-garhi*; *Kenyanthropus platyops* to *Homo* (*Homo*) *platyops; Paranthropus aethiopicus-boisei-robustus* to *Homo* (*Homo*) *aethiopicus-boisei-robustus*. Less dramatic will be the task of reclassifying our ancestors already included in the genus *Homo*, to which will be added the subgenus *Homo* (*Homo*) *rudolfensis-habilis-ergaster-georgicus-erectus-floresiensis-antecessor-cepranensis-heidelbergensis-neanderthalensis-sapiens*.

In our opinion, in the near future Goodman's classification although quite revolutionary will force us to rewrite palaeoanthropological textbooks.

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[13] Not all anthropologists are inclined to agree that *Sahelanthropus* is a hominin species since they consider it as an ancestor of the gorilla.

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