SYNCHRONISING PALAEONTOLOGICAL AND GENETIC EVIDENCE TO PROVE THE OUT-OUT-AFRICA THEORY

by

Elisabeth Hamel, Ebersberg

Summary

Ever since the birth of modern anthropology, two theories explaining the more recent origin of mankind have evolved: the former multi-regional-evolution model and the later out-of-Africa theory. Latest skeletal findings move researchers to state that the origin of Neandertal man and *Homo sapiens sapiens* is situated in Africa and nowhere else. But sceptical scientists continued levelling criticism, until data obtained from newest genetic experiments led scientists to formulate the dazzling out-of-Africa theory and to elucidate this topic quite clearly. Results from DNA-analyses on mitochondrial DNA together with new statistical methods seem to deliver accurate proof that all *Homo sapiens* may look back to a common origin, even stating when the separation took place. The following article aims to contribute to a deeper appreciation of archaeological findings and recent genetic analyses by describing and comparing steps which have been taken in both fields of science on the way down the evolutionary ladder and are subject to review in the light of evidence.

AFTER TWO WORKERS accidentally found the first skeleton of a Neandertal man in a quarry outside Düsseldorf, Germany, in 1867, extensive research and discourses on the more recent origin of mankind arose. Charles Darwin's theory of evolution (Darwin, 1899) shattered the traditional notion of life, and — since its inhabitants and culture were looked upon as quaint and curious by the first colonists — no one even dared suspect man's origin to be located in Africa. In the later part of his life, Darwin refuted the view he had helped establish, that the cradle of mankind was situated in Africa, as no bones older than those found in Asia had been excavated anywhere else until the late 20th century.

In 1939-43 Franz Weidenreich (Weidenreich, 1939-43) proposed a polycentric theory of modern human origins. This approach was further developed in the 1980s by scientists like Milford Wolpoff, Wu Xinzhi and Alan Thorne (see Lahr, 1996 for more literature). They

introduced the multi-regional-evolution model. Weidenreich's multiregional theory had lacked a theoretical mechanism for the maintenance of world wide parallelisms for the regional evolution of humans from archaic ancestors and was based on a handful of fossils. It was revised to become a model of clinal evolution in which gene flow homogenized differences and prevented speciation. (Wolpoff, 1989, 1996) The scientists claimed that human beings had first emigrated from Africa to other continents 1,000,000 years ago, all the while sustaining a link through genetic interchanges between regions, and with regional evolution that gave rise to "distinct racial traits". Different species evolved after a long separation had taken place during the last ice age which began about 73 000 years ago. Accordingly, the Neandertal and modern man were thought of as mixed. Due to continued interaction between our ancestors from Neandertal in the upper

Palaeolithic area, a genetic mixture has given rise to the only human species inhabiting the earth until now, the *Homo sapiens sapiens*.

The idea that modern humans have a recent origin in Africa was put forward in 1903 and 1905 by Julien Kollmann (1834-1918) who argued that the human "races" were derived from African Pygmies being the first modern humans. In addition he considered Neandertals to be more divergent than any of the "races" derived from the Africans, and, therefore, as having a different origin. (Kollmann, 1903, 1905)

More recent discoveries support those scientists who adhere to the out-of-Africa theory. Scientists state that even if modern and Neandertal man had mixed or hybridised, both must have originated in Africa and certainly did interact at a later time. Some researchers claim that the two species never mated and that the Neandertals died out completely, without leaving any genetic trace behind.
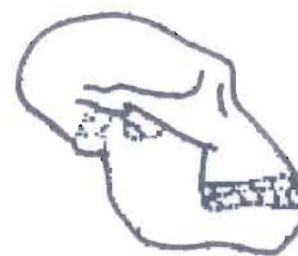
Palaeontological Records

A DECISIVE FACTOR in the specific process of human evolution was the climatic and morphological change that took place in East Africa. It is recorded that global temperature cooled down approximately 10,000,000 years ago. Seasons in Africa became more radical: months of heavy rain were now followed by dry periods. The morphological change occurred because the African tectonic plate divided, thus causing trees to diminish and the savannah to expand. In response to the impact on the body, early primates had to adopt to a life in a dry climate that only produced woody and thorny food.
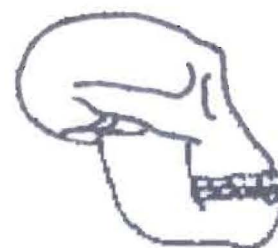
Between the years 8,000,000 BC and now, a 6000 km rift stretching from Jordan to the Zambezi, was formed by the separation of the tectonic plate which is responsible for an even more significant climate change in East Africa. Several dislocations along this rift account for a radical weather barrier: clouds sweeping over

from the Atlantic Ocean brought enough humidity to the western side of the rift, whereas it only rained seasonally on the other side. Animals living on the eastern side developed sturdier teeth as they had to chew the hard shrubs at their disposal and their feet adapted to the scorched ground they had to walk on. Gradually, this boundary was responsible for the hominoids evolving differently on both sides: chimpanzees emerged in the west, while hominids entered their "East-Side Story" (Ives Coppens, 1994).

This severe temperature change dramatically affected the subsequent evolution of the hominids. The only available record of this transition is found in Omo; excavations made there in 1992 show that Ardipithecus ramidus began walking on his feet and had developed a larger brain. Palaeontological data discovered in Kanapoi in 1994 and 1995 prove that this creature was succeeded by Australopithecus anamensis, who lived in the Turkana Basin in Kenia, approximately 4,000,000 years ago. His skeleton already resembled that of a human.
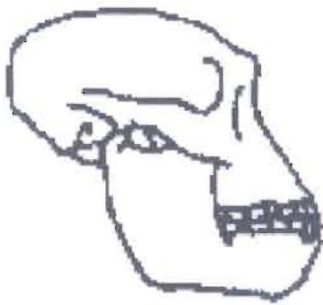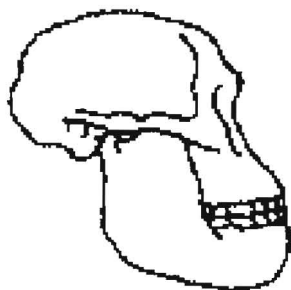

Figure 1: Ardipithecus ramidus

Figure 2: Autralopithecus anamensis

THE NEXT SPECIES in the chain of evolution is represented by the 3,000,000 year old Australopithecus afarensis; a well-preserved skeleton was found in Hadar, Ethiopia, and has been nicknamed "Lucy". (Johanson, 1981) According to footprints in Laetoli, Lucy and her kin had no difficulties walking on two feet, although their feet were still equipped with all climbing abilities. A skull of this species was found in 1991 and brought a brain with the size of a present-day chimpanzee to light.
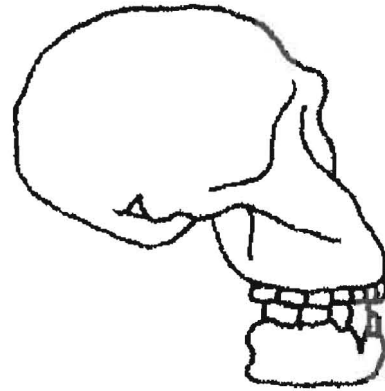

Figure 3: Australopithecus afarensis

About 2,800,000 years ago the climate became even more dry and brought about diversification – the Australopitecus boisei and Australopitecus robustus, who had stronger jaw bones and sturdier molar teeth. A more fragile variation, known as Australopithecus africanus, was found in Taung, South Africa (Dart, 1925); he lived between 2,100,000 and 1,500,000 years ago. Scientists also discovered that stone tools and implements were first used then and there. (Dart, 1925)

Figure 4: Australopithecus africanus

Figure 5: Homo rudolfensis

THE MISSING LINK in the study of human evolution was found in Koobi Fora: the *Homo rudolfensis*, who lived between 2,100,000 and 1,800,000 years ago. (Wood, 1992) This unexpected discovery of 1991 – made in a layer of sediment which was unusual and rare for that period – brought fragments of teeth to light and points to *Homo rudolfensis*, the linkage between the *Homo ergaster* inhabiting Africa and the *Homo erectus* living abroad.
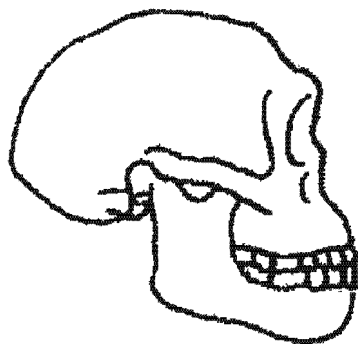

Figure 6: Homo erectus

Homo rudolfensis seems to have lived prior to *Homo habilis* or *Homo erectus*. His skeleton already resembles that of an *Homo sapiens*. He had a smaller jaw than his predecessors and was able to use more stone tools to prepare his meals. Further missing

links up the ladder to *Homo erectus* have not yet been found. The *Homo habilis* seems to have moved south, and this migration turned out to be a "cul de sac" for his future development. (Schrenk, 1997)

Figure 7: Homo sapiens
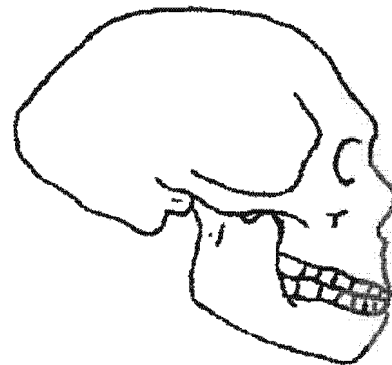

Figure 8: Homo habilis

The *Homo rudolfensis* remained in the east and evolved into the *Homo ergaster*, the African species of *Homo erectus* who populated Europe as *Homo heidelbergensis*. His brain had reached full size and he possessed all marks of a qualitative change in his brain sections. His maturation into *Homo erectus* could have taken place in Europe as well as in Asia. By the time *Homo erectus* had become *Homo neanderthalensis* in Europe, *Homo*

erectus in Africa had undergone a transformation into *Homo sapiens sapiens*.

Figure 10: Homo sapiens sapiens

In the 1970s, scientists identified a remarkable find – which had already been made in 1953 in Saldanha, South Africa – as a 400,000 year old skull and jaw fragment of an intermediate form of *Homo erectus* and *Homo sapiens sapiens*. A later variant, aged 200,000 years, was discovered in 1936 in South Laetoli; still younger variants were found in Lake Ndutu, the West Olduvai Gorge, and in Ethiopia during the 1990s. This species received the name *Homo sapiens sapiens* and was dubbed "our direct ancestor". Fragments found in Skhul, Haifa, seemed to prove that he first left Africa 100,000 years ago.

Figure 9: Homo neanderthalensis

But the real dispersal did not occur until the Upper Palaeolithic, about 45,000 years ago (Klein, 1999). Most recent well-dated evidence is presented by Robert Walter et al. stating that modern humans were living along the Red Sea coast of Eritrea during the last interglacial around 125,000 years ago, exploiting near-shore marine food resources in that region (Walter et al, 2000). So modern humans might have spread from Africa along the shorelines of Arabia and into southern Asia. They could have progressed all the way to Indonesia at times of low sea level 65,000 years ago (Stringer, 2000). Palaeoceanographic data indicate that the Persian Gulf became very shallow with internal circulation of water, during the last glacial maximum. But the corridor did not remain open for a long time as arid conditions settled across the Sahara with the onset of glaciation (Reiss, 1980).

THE APPEARANCE of the *Homo sapiens sapiens* in Europe ended the stay of the *Homo neanderthalensis* on the face of the earth, who gradually vanished, never to show up again (Krause, 1999). In Spain modern humans arrived later than everywhere else. Here and in Croatia Neandertals are recorded to have survived there until 27,000 and 28,000 years ago respectively. In Spain, the Zafarraya cave evidence demonstrates a relatively long coexistence of Aurignacien-maker populations, very likely anatomically modern humans, and Neandertal Mousterian-maker populations that show a certain acculturation process. (Hublin, 1995)

Modern humans seem to have been more skilled than Neandertal populations in coping with extreme cold climates. Climates, during the Last Glacial, were more severe for example in Eastern Europe than in other parts of Europe and Neandertal occupations on the East European Plain were particularly scarce after the beginning of the Last Glacial (73,000 years BP). In contrast to the Neanderthals, modern humans successfully colonized the central East European Plain under full glacial conditions. (Hoffecker, 1999)

AS NEANTERTALS and modern-day man may have shared a neighbourly life in specific regions during identical periods of time, there should be some evidence that they have mixed. A skull was found in Israel, which hints at shared characteristics of the Neandertal and modern humans, but experts have not been able to agree on this point. (Klein, 1996) Another skeleton of a 4-year-old boy was found in Portugal. The prominent chin, characteristic of early modern humans, and the stocky trunk and short limbs, characteristic of Neandertals, may reflect an interbreeding 24,500 years ago between early humans and Neandertals. (Reuters, 1999) But little is known about ancient child skeletons either from Neandertals or from modern humans. Even though the two species mixed, it is not certain that those hybrids were able to produce further descendants. This case may be comparable with the hybrids with donkey and horse which in general remain sterile because of their great genetic distance. So Neandertal man may nevertheless have been marginalised and consequently died out, never having procreated fertile offsprings with modern humans before disappearing forever. In general neither earlier nor later modern European crania show any of the facial and occipital specialistions obeserved in the Neandertal group. (Lahr, 1996)

In conclusion, a wide acceptance of the view of a single, recent and African origin is supported by the modern human's morphological homogeneity, the discontinuities in the fossil record outside Africa, the chronological contrast between the first appearance of modern humans in Africa and in the rest of the world, the tropical body proportions of the earliest modern Europeans in contrast to those of Neandertals, and the uniformity of the modern human morphology. (Lahr, 1998)

Figure 11

Today

Homo sapiens sapiens

Homo sapiens
neanderthalensis

archaic
Homo sapiens

Homo
erectus

Austsralopithecus
robustus

Homo
habilis

Austsralopithecus
boisei

Homo
rudolfensis

Australopithecus
africanus

Australopithecus
aethiopicus

Australopithecus
afrensis

Australopithecus
anamensis

Ardipethcus
ramidus

0,5
1,0
1,5
2,0
2,5
3,0
3,5
4,0
4,5
5,0
5,5

also out of Africa
eastern Africa
southern Africa

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Figure 11 a

Homo sapiens sapiens

Homo nanderthalensis

Homo sapiens

Homo erectus

Homo habilis

Homo rudolfensis

Australopithecus africanus

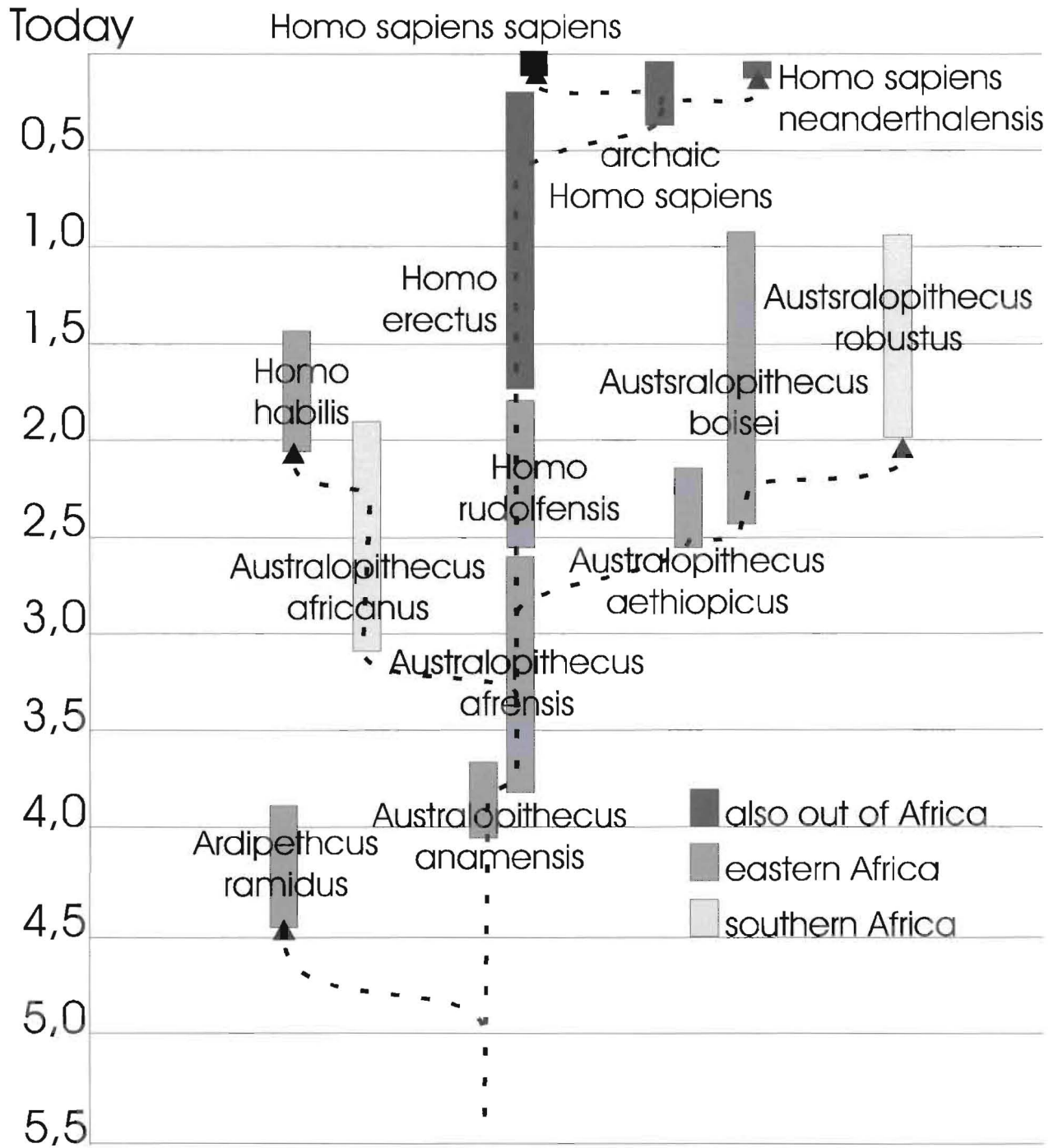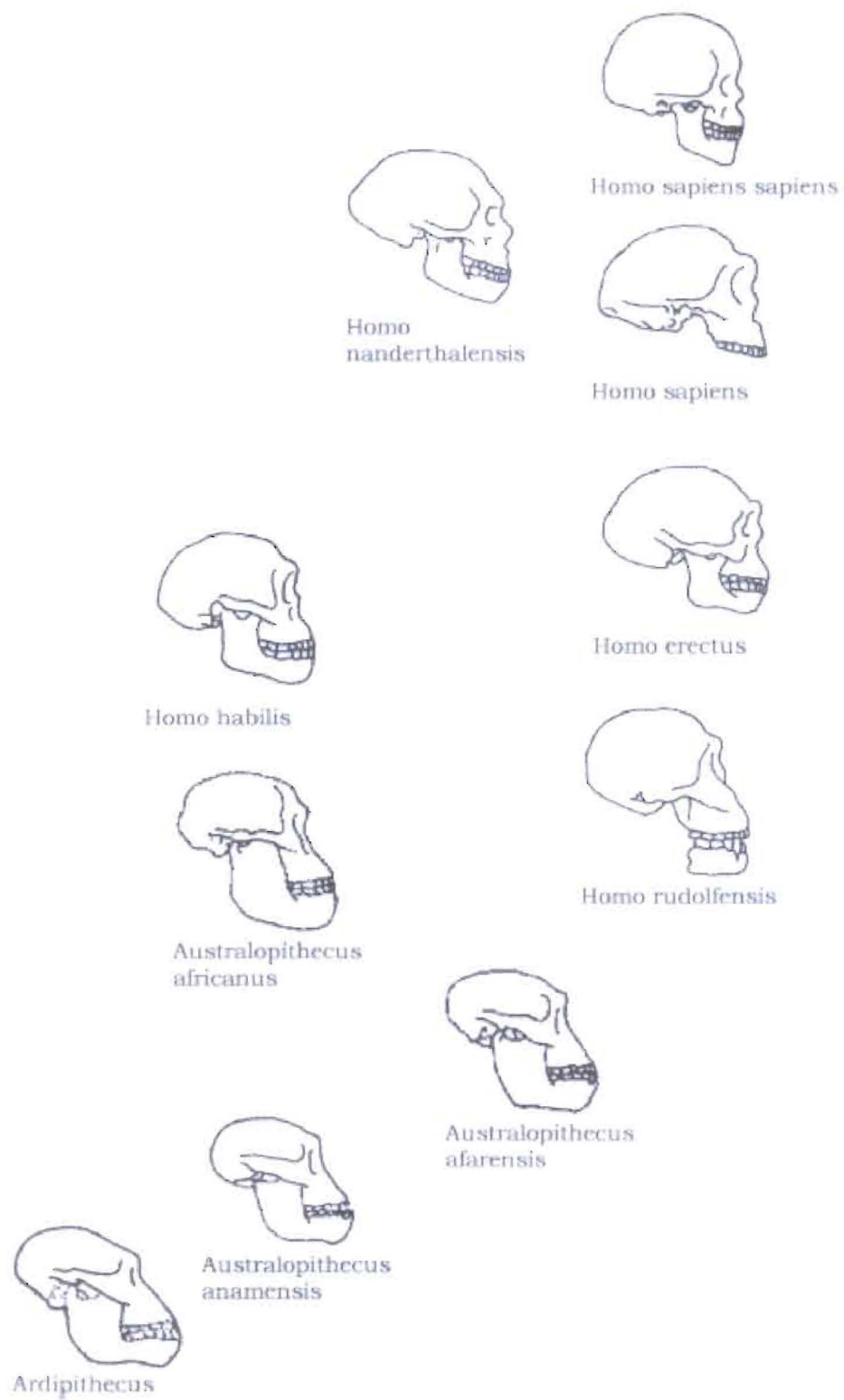Australopithecus afarensis

Australopithecus anamensis

Ardipithecus

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Genetic Analysis and Evidence

NEXT TO ARCHAEOLOGICAL DATA, human genetics promises to be the second best foot to stand on when reconstructing the past. Yet, the genetic approach is very unique. In contrast to bones and artefacts, genes cannot be seen nor touched. Only advanced technologies and technical finesse enable qualified researchers to investigate and identify genes.

Mutations alter the sequence of base pairs that are linked together by bands between pairs of bases comparable with the rungs of a ladder. The bases differ from rung to rung, and the sequence of these differences is the genetic code. Four bases, Adenine, Cytosine, Guanine or Thymine, carry the inherited information just like the limited number of letters in an alphabet.

S.A. Tishkoff et el. observed STR alleles (Short tandem repeat marker, which means a stretch of DNA consisting of a set of 10 to 50 nucleotides (=rungs of the ladder) repeated hundreds or thousands of times) of many more different sizes in sub-Saharan African populations than in non-African populations. Furthermore, they found that the so-called ALU-chromosomes (defined by presence or absence of a 285-basepair fragment) of sub-Saharan African populations are observed in combination with a large number of STR alleles. In contrast, ALU-chromosomes in non-African populations are observed almost exclusively in combination with a single STR allele. Based on this pattern, the authors conclude that the common origin of non-African populations is much more recent. (Tishkoff, 1996) This may suggest the out-of-Africa theory.

MOST GENETIC CHANGES are simple base substitutions. Astounding and persuasive data can be obtained with mitochondrial sequences. Mitochondrial DNA (mtDNA) appear in great numbers and are well preserved under favourable conditions for thousands of years, thus allowing the inquisitive explorer to look back into remotest times more efficiently and

effectively than with nuclear DNA (harboured by our chromosomes). When mutations occur, the message changes, but as only a small number of mtDNA-sequences are functional, neutral mutations can accumulate unaffected by natural selection and are preserved from generation to generation. Each of those random mutations is like the ticking of a clock; it advances the hands one notch – the so-called "molecular clock" makes time estimation possible. (Kimura, 1979) The history of those mutations reflects the history of our species. So we are living testimony of our oldest ancestors and carry all evidence needed to reliably find our heritage as well as the extension and position of our brothers and sisters from the long-forgotten past within us.

IN 1987, the publication of phylogenetic analysis of human mtDNA sequences was among the first attempts to use molecular genetics to explore human origins. (Cann, 1987) The surprising claim was that human populations today are descended from a small ancestral population living in Africa, numbering approximately 40,000 individuals. (Sherry, 1997) Estimates of the size of the effective ancestral population to all humans suggest that at the moment of the bottleneck phase it was composed of not much more than 10,000 individuals. Palaeodemographic models have also shown that the hominid population was never large enough to sustain the gene flow necessary to maintain the long-term global homogeneity required by the multiregional model. (Manderscheid, 1996) In addition, in terms of mtDNA, lineages of African populations are significantly more diverse than those outside Africa and all lineages coalesced between 200,000 and 150,000 years BP. (see Lahr, 1998 for more literature).

A study carried out by Antonio Torroni et al. in 1993 (Torroni, 1994) aimed to examine several mtDNA sequences of Caucasians to detect their origin. European genes turned out to be characterized by specific mutations having occured within the time span of

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13,000 to 56,500 years ago, this means after the separation of their Asian and African ancestors. As *Homo neanderthalensis* seems to be a direct descendant of the *Homo erectus* who colonized Europe about 700,000 years ago the estimated ages of Caucasian mutations indicate that none of them have originated in Neandertal populations. So at least the results of those tested samples of modern humans support the hypothesis that *Homo sapiens sapiens* arose independently and replaced Neandertals. The authors recognized the value of mtDNA for molecular anthropology, since mtDNA can be extracted from preserved bones and tissues and they suggested that further studies from recovered fossils at European and Middle Eastern archaeological sites may permit increasingly reliable correlations to be made between recent fossil evidence and molecular anthropological data.

This idea was realized in 1997 and 1998 by Matthias Krings et al. (Krings, 1997; Krings, 1999) A fossil fragment was genetically analysed and compared with genes of present-day humans. The sample of this tested fossil was taken from the famous Neandertal man found in 1856 near Düsseldorf. Having extracted two mtDNA-sequences of 379 340 nucleotides respectively, the team compared them with the corresponding sequences of 2,051 humans and 59 chimpanzees and found that Neandertal man was genetically too far apart from modern humans to be definitely called an ancestor. The average number of mtDNA sequence differences between modern humans and the Neandertal was found to be about three times that among humans, but about half of that between modern humans and modern chimpanzees. According to time estimates humans and chimpanzees had branched off 4 to 5 million years ago, while Neandertal and modern man may have done so between 317,000 and 741,000 years ago. In other words, the age of the common ancestor of the Neandertal and modern human mtDNAs is estimated to be four times greater than that of the common ancestor of human mtDNAs. A second team under Igor V. Owtschinnikow has isolated a short sequence from another Neandertal mtDNA in march 2000 (Wong,

2000). Even though the fossil was found in a completely different region, and even though it was much younger than the first sample, the analysis has brought the same results.

So, Neandertal man is probably not our ancestor – but he may be our cousin. As long as no further experiments of other fossils are carried out, critical voices will still be heard and the above data will not suffice to prove that *Homo sapiens sapiens* is an early offspring of *Homo erectus* (the ancestor of Neandertal man). In order to find a single genetic Neandertal trace among modern humans, thousands of modern human samples would have to be examined and compared with all available analysed samples of Neandertals found up to now, which has not yet been done. A great number of European individuals, viz. 821, have already been analysed (Richards,1996) and turned out not to stem from the Neandertal lineage.

IRRESPECTIVE OF WHETHER we are descendants of the Neandertal or not, recent studies seem to prove our single recent African origin. In 1985, Allan Wilson, who invested much time and energy in mtDNA-analyses, realised that mtDNA would someday offer precise information about the past (Wilson et al., 1985), although we are looking back to ancient times from the present point of view. Since mtDNA can only be maternally inherited among humans and are (contrary to nuclear DNA) non-recombining, they do present the possibility of tracing back an early female lineage.

Following Allan Wilson's idea, in 1987 J. Avise et al. devised a special method, which has become known as "phylogeography" (Avise et al. 1987). They realized that mtDNA was "not "just another" molecular marker". But mtDNA are an important means for studying the process of human evolution and migration as well as founder effects.

Illustrating example of a phylogenetic tree

The procedure of creating a phylogenetic tree is illustrated by the following example. In reality sequences harbour hundreds or thousands of nucleotide positions, and there are back-mutations and parallelisms which is called homoplasy.

Sequence of nucleotide positions (bases consisting of Adenine, Cytosine, Guanine or Thymine alternatively) remaining unchanged are marked by "-"

```
reference sequence  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
sample no. 1        - - - - - - - - X- - - - - - - - - - - -Y - - - - - - - - - - - - -
sample no. 2        - - - - - - - - - - - - - - - - - - - - -Y - - - - - - - - - - - - - -
sample no. 3        - - - - -D - - X- - - - - - - - - - - -Y - - - - - - - - - - - - - -
sample no. 4        - - - - - - - - - - - - - - - - - - - -Y - - - - -E - - - - - - -
sample no. 5        - - - - -D - - X - - - - - - - - - - -Y - - - - - - - -U - - - -
```

Letters like D, E, U, X or Y are defined by mutations (transition from one of the four bases to another) having occurred on a certain nucleotide position.

IT CAN BE SEEN at one glance that the mutation indicated by Y is present in each of the samples. So Y can be considered as the oldest mutation and marks the deepest node. A still rather common mutation is represented by X and must reflect a later branching. The mutation D is shown twice and gives rise to a further/later branch within the tree Y, X. E must have branched off before X and D occurred. U must have taken place after the D mutation as it is absent from sample no. 3. When the mutations are put into a chronologic order with exclusion of all nucleotide positions that are common in each sample, we receive a parsimonious indirected tree. (*Parsimonious* means that as few mutations as possible are used to create a tree).

	mutations	tree	(number of samples with common mutations)
	chronologic order		
sample no 2	Y		
sample no 1	YX		
sample no 3	YXD		
sample no 5	YXDU	5Y — 3X — 2D	
sample no 5	YE	1E	1U

Samples with the mutations E, D, U, X, Y may be found in each region with a different percentage giving a hint where the mutations occurred and where they had been carried. Especially when samples situated at the deepest node are found in region A and derivatives in region B, we can deduce a migration event from region A to region B. So the geographic distribution and variation of mtDNAs can be highly informative in defining potential range expansions and migration routes in the distant past. In conclusion, mtDNA analyses allow us to illucidate three dimensions, i.e. genealogic lineages (defined by mutations on a nucleotide position), time depth (estimation according to mutation rate) and localization (geographic region where the samples are to be found). This is called "phylogeography" and has produced promising results. The more sequences are analysed the more detailed connections between population groups can be established. A tree is rooted with an outgroup and all analysed samples cluster in lineages which can ideally (when sufficient sequences are analysed) be traced to one common root for all human beings living on the earth today and even back to a common ancestor of all primates.

A team consisting of Elizabeth Watson, Peter Forster, Martin Richards, and Hans-Jürgen Bandelt published a study in 1997 (Watson, 1997), in which they described different lineages in Africa and showed that only one of them migrated into Europe, Asia, and America. The phylogenetic analysis was performed by using the median algorithm of Hans-Jürgen Bandelt et al. (1995), in which parallelism and back-mutations can be detected. Samples of individuals belonging to nine African population groups, which were introduced in other studies, provided the data. The groups listed below were selected in reliance on Joseph Greenberg's "Language Phylum of the African Languages".

Number	Population	Language
19	!Kung	Koisan
13	Mbuti	Nilo-Saharan
17	Biaka	Niger-Kordofanian
110	Mandenka	Niger-Kordofanian
10	Songhai	Niger-Saharan
23	Tuareg	Afro-Asiatic
21	Yoruba	Niger-Kordofanian
20	Hausa	Afro-Asiatic
60	Fulbe	Niger-Kordofanian
14	Kanuri	Nilo-Saharan
27	Turkana	Nilo-Saharan
4	Kikuyu	Niger-Kordofanian
27	Somali	Afro-Asiatic

Four main groups crystallized: L1a, L1b, L2, and L3. The remaining 13% were categorised into group L1i, now called L1-other (see figure 12). The analysed Neandertal sequence (described above) shares with the proposed root seven nucleotides at characteristic positions and matches cluster L1a at two base positions (shown by asterisks), so that one !Kung together with one Turkana sequence might be an outlier of the branch connecting L1a.

Based upon time-estimate, most of the lineages expanded within Africa between 80,000 to 60,000 years ago. With an age of 100,000 years, L1-others is the oldest one and represents 100% of !Kung and 77% of Biaka. So Kollmann (see above) was not quite so wrong in supposing that modern humans stem from Pygmies. We now can say that !Kung and Biaka by living in great isolation from other populations arising from the same lineages in the course of time, may have kept the original characteristics which the pionineers of modern humans were carrying when they populated the African continent. A very recent study (Chen, 2000) confirms that Biaka Pygmies and !Kung seem to represent one of the most ancient African populations. Marta M. Lahr considers the Khoisan speaking populations (Hadza, San and Khoi) as relics which were superimposed by the expansion of agriculturalists. With exception of the various Pygmy populations in West Africa who are believed to have lost their original language and borrowed the farmers'

language (Lahr, 1996), the language of these populations is not only very unique in words and grammar but also the sounds especially in consonants. Reproductive isolation turns out to be the only criterion for diversification between living species.

Group L2 may be close to L3, and both are well represented in Africa (except for !Kung of Botswana), but the exciting thing is that L3a, which is a subgroup of L3 and originated 60,000 years ago, constitutes nearly the only group found in areas outside Africa. (According to a study made in 1998 (Rando, 1998) and the recent study of Yyu-Sheng Chen (Chen, 2000) new genetic markers have given rise to a new grouping of L3. As the data do not comprise all population groups described here and as in Chen et al. not the same statistical method has been used the results are not taken into account in this paper.)

See Figure 13: Frequencies of Clusters in African Populations

In the columns on the map of Africa in the above figure, the older groups are depicted in the lighter, the younger groups in the darker dotted shades. It is evident that the older groups inhabit East Africa and the younger ones West Africa. Even though younger mtDNA lineages found in the major part of West Africa have not been verified as having emerged there (a westward migration may have taken place later), the east-west-gradient should not be ignored.

Even though several groups populated the earth at the same time when modern humans left Africa, only those belonging to the clusters classified in group L3a were dominant in the rest of the world; they are supposed to have been more skilled at hunting, cooking, and protecting themselves from intense heat and cold than members of the other groups – but perhaps they just appeared at the right moment at the right place. Humans first appeared on the eastern

Figure 12

Network of isolated African lineages L1-others and L1a, L1b, L2, L3
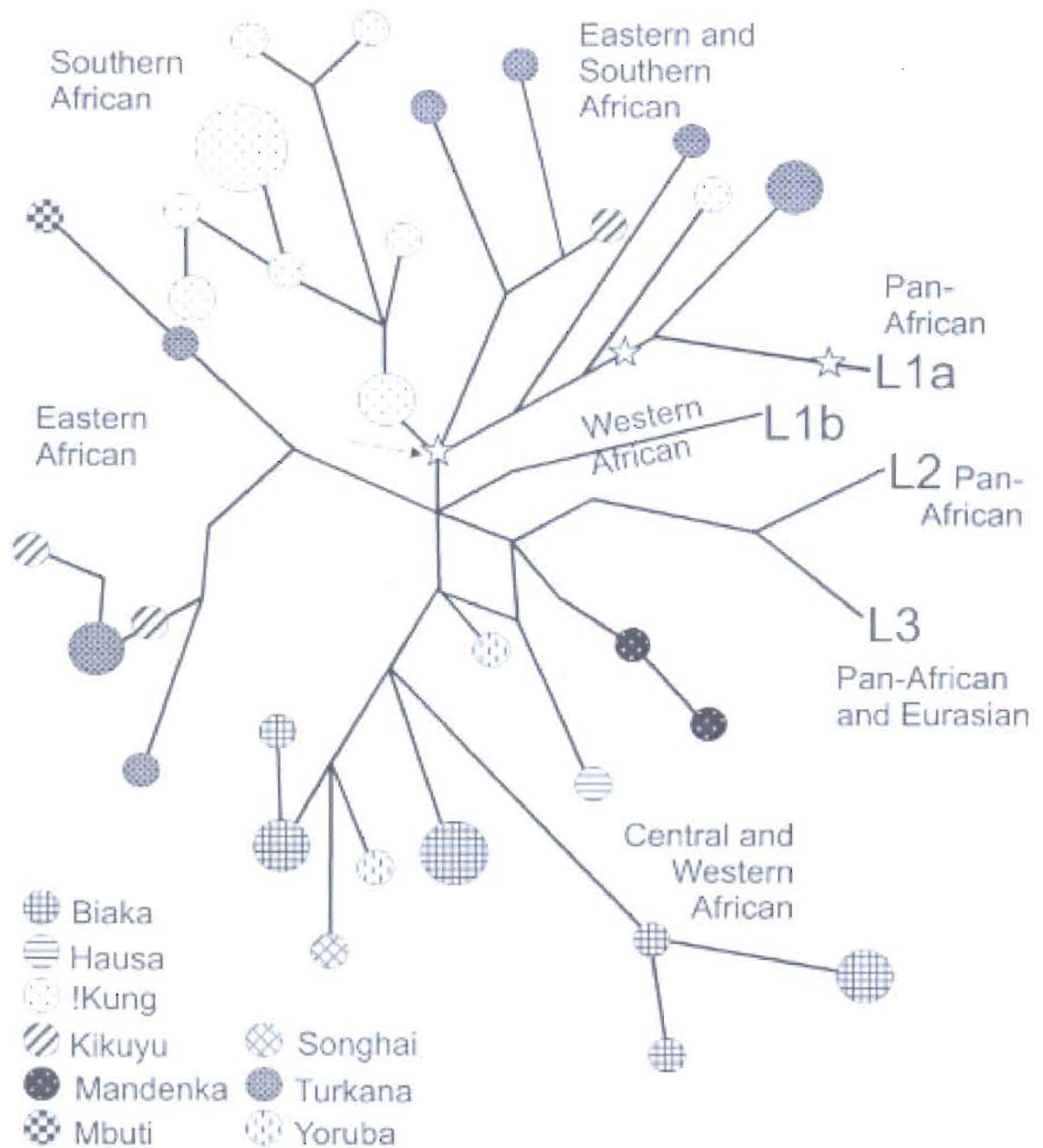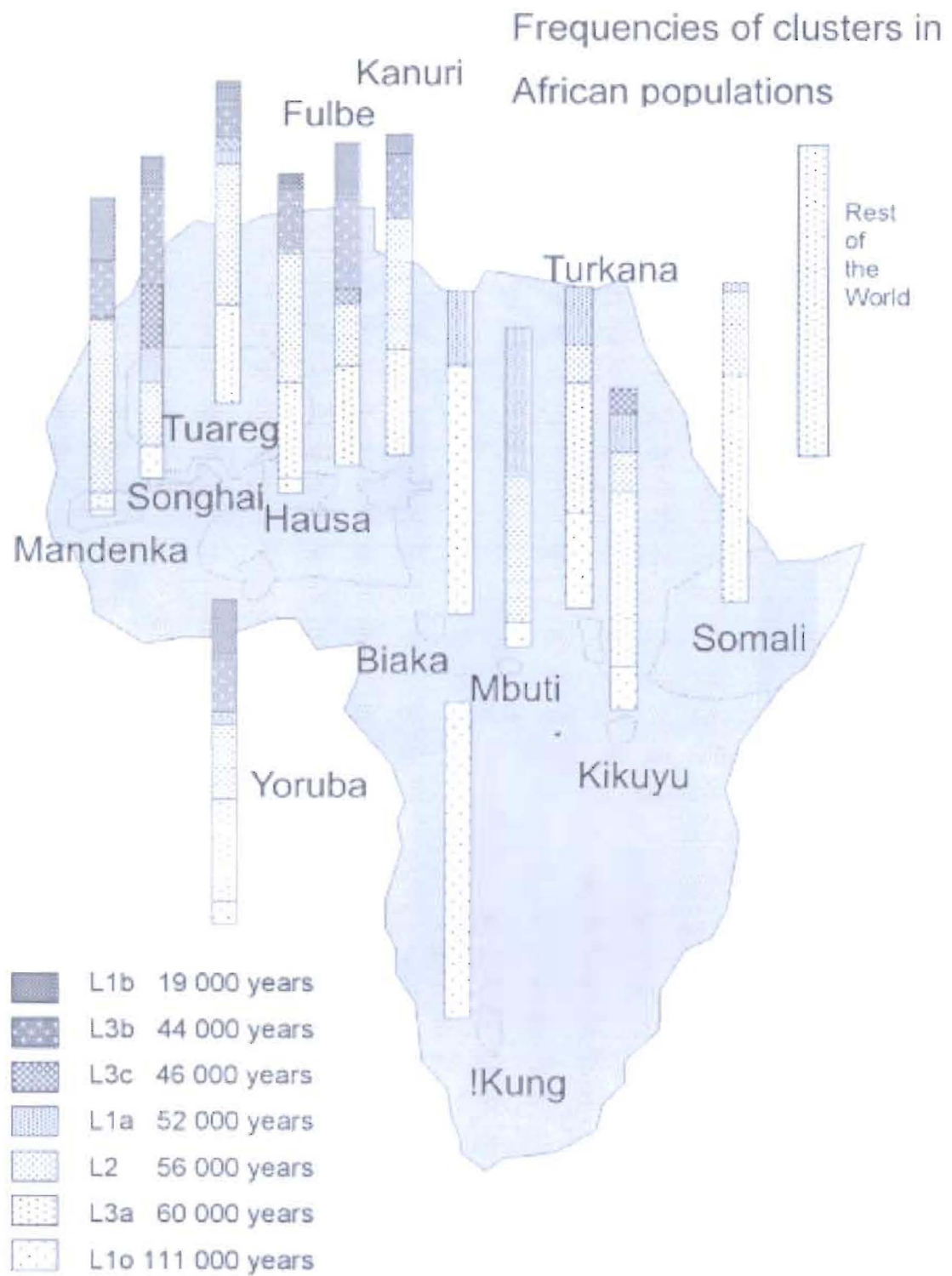(the putative root is indicated by a flash)

Southern African

Eastern and Southern African

Pan-African

L1a

Eastern African

Western African

L1b

L2 Pan-African

L3

Pan-African and Eurasian

Central and Western African

Biaka
Hausa
!Kung
Kikuyu   Songhai
Mandenka   Turkana
Mbuti   Yoruba

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Figure 13

Frequencies of clusters in African populations

Kanuri
Fulbe
Turkana
Rest of the World
Tuareg
Songhai
Hausa
Mandenka
Biaka
Mbuti
Somali
Yoruba
Kikuyu
!Kung

L1b 19 000 years
L3b 44 000 years
L3c 46 000 years
L1a 52 000 years
L2   56 000 years
L3a 60 000 years
L1o 111 000 years

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half of the African continent (this is in accordance with palaeolontology) and later spread to the south and the west.

Group L1a is found on the Island of Sardinia, maybe because of later trade and commerce with seafaring peoples. Except for younger mtDNA subgroups outside the African continent, so far all lineages are found to have originated in Africa, thus confirming the archaeological/palaeontological records.

When nuclear DNA data (Cavalli-Sforza, 1994) and mtDNA data are brought in relation to each other there seems to arise an inconsistency (Mountain, 1998). While mtDNA data shows more diversity in Africa than in the rest of the world, nuclear DNA data indicate more homogeneity in African populations than elsewhere. This can be explained by the fact that all African mtDNA lineages have mixed more and more over time, giving rise to a relatively homogenous nuclear (recombining) DNA. On the other hand those small groups who left Africa stemmed from one sole lineage but underlay drift and a considerable bottleneck-effect with dispersal, contraction and isolation, and thus gave rise to great differences in nuclear DNA such as blood groups, proteins, enzyme and immunological polymorphisms.

A subgroup of L3, called M has long been regarded as an ancient marker of East-Asian origin. Recent studies (Quitana-Murci, 1999) show that the origin of M is in Africa, having arisen approx. 60,000 years ago. As it is absent in the Levant and present in high frequency in the South Arabian peninsula it renders the first genetic indicator for the only successful early dispersal event of modern humans out of Africa. In addition it might be the first genetic indicator of the migration route of *Homo sapiens sapiens* through eastern Africa along the coast toward Southeast Asia, Australia and the Pacific Island – a confirmation of palaentological records mentioned above (see Stringer, 2000). The separation of Asian M from eastern-African M took place more than 50,000 years ago.

All M groups in eastern Africa, Asia and sporadic Mediterranean have another marker, i.e. C on position 10873, which is also found in L1, L2 and most L3. Conversely all non-M groups which originated outside Africa carry T on position 10873. The ancestral state is C and is present in primates (like common and pygmy chimps, gorilla and orangutan) so it may indicate a real marker leading back to a common ancestor of primates.

Conclusion

While palaeontology and genetics have only delivered snapshots of a continuing discourse on evolution, both inspire us to acknowledge that the cradle of mankind stood in East Africa which "is the richest region in the world, a region ecologically unstable and thus promoting differentiation through a spatial and temporal mosaic of ecological barriers" (Lahr, 1996). From there modern humans spread to the south and the west, dynamically taking over the entire world about 50,000 years ago. In contrast to former times modern humans are now the only surviving species of *homo* living on earth today.

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Zusammenfassung

Für den Ursprung des modernen Menschen waren seit Darwins Evolutionstheorie mehrere Evolutionsmodelle in der Diskussion. Eine multiregionale Evolution wird aufgrund neuester Funde von der out-of-Africa Theorie verdrängt, welche die Wiege der Menschheit vor 200 000 Jahren in Ostafrika ansetzt und eine getrennte Entwicklung zum Neandertaler postuliert. Palaeontologische wie auch genetische Daten liefern dieser neuen Sichtweise gleichermaßen Bestätigung. Die verschiedenen molekulargenetischen Ansätze beleuchten diese Sachverhalte jeweils von einem anderen Blickwinkel aus. Dabei gibt es im Moment keinen Anhaltspunkt dafür, daß heute lebende Menschen genetische Komponenten aus einer eventuellen Verbindung mit dem Neandertaler-Mensch tragen.

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A short note about the author

Elisabeth Hamel was born in Obertraubling, Germany, in 1952. After having completed High School, she received the French diploma for translation and interpretation, specialising in natural sciences. In 1998 she began writing a book on the topics which have captivated her attention ever since: anthropology, biology and languages. In the projected book, she discusses genes and European languages, elucidating world-wide modern human migrations. She regularly visits lectures on these subjects offered at the University of Munich in order to intensify scientific knowledge.

Correspondence address:

Elisabeth Hamel
Eggerfeld 3c
D-85560 Ebersberg
Phone/Fax: ++49(0)8092-24361
E-mail: elisabeth.hamel@ebe-online.de
Homepage: http://ebe-online.de/home/emamel