Bryan Sykes, *The Seven Daughters of Eve*, Bantam Press (2001).
(A chapter-wise summary.)

1. The author is a professor of genetics at the Institute of Molecular Medicine in Oxford. Till 1986, his work was on the genetical causes of *brittle bone disease*, which is due to defective collagen -- the protein in the bones -- of the new-born baby. In that year, Robert Hedges, the head of the carbon dating laboratory in Oxford, posed to him the question whether it might not be possible to get some thing more, viz., some genetic information, from the calcium of old bones ? The two submitted a research proposal to determine the amino-acid sequence of the extant collagen in old bones, and thus indirectly, via the genetic code, work out the sequence of the collagen gene.

This proposal never took off, which was a blessing in disguise, because it was about then that Kary Mullis made a revolutionary breakthrough (for which he later got a Nobel in 1993). Using his Polymerase Chain Reaction (PCR) it was now possible to exponentially amplify even very small amounts of DNA rather quickly, using a copying mechanism in which ~~the~~ the DNA strands were simultaneously copied from both ends.

Thus it made sense now to search directly for some molecules of DNA, howsoever few, in the old bones, and then PCR them. In 1988 the author, with Erika Hagelberg, examined three human thigh bones just excavated from an archeological site at Abingdon. Their hope was to find some intact DNA in their hypdroxyapatite, a mineral found in bones, because it was commonly used in labs to absorb DNA.

The process was laborious. After freezing in liquid nitrogen, bone was powdered, then its calcium extracted chemically, leaving a sludge whose proteins were rinsed away using an enzyme much as done by some detergents, and then fat removed by using chloroform. Using PCR they were able to very faintly detect some molecules of DNA in the remaining bone extract. Fear of being scooped made them rush their findings promptly to *Nature*, where they appeared in the issue of December 1989.

The Mullis reaction involved a soup containing, besides the bone extract and the raw materials for making new DNA copies, that is, the nucleotide bases, the catalysing polymerase enzymes and some magnesium, and also, a couple of short DNA fragments to focus on a specific gene which alone was to be amplified. The mitochondrial gene was chosen simply because it is a hundred times more abundant than any other, and so seemed the best bet. To fire the reaction, this soup needed to be pushed through about 20 thermal cycles — boiling, cooling, warming, boiling, ... — in three hours, which is drudgery if done manually (nowadays automatic machines do it) but Sykes found an easier way using his *Genesmaid*, that is, his electrical tea kettle, suitably rigged with some thermostats.

A media frenzy followed, possibly ignited by Sykes himself who had been a TV reporter for three months under a science/media scholarship some time back. Anyway, he obviously is media savvy. For example, when the *Observer* wanted to know possible future applications, he mentioned the well-known problem of deciding whether the Neanderthal Man had really become extinct, but then, tongue-in-cheek, also that maybe now we can clear up *whether Ramses II was actually a woman* !

To rule out possible contamination of bone extract by modern human DNA in the lab, they had run a control experiment involving amplification of DNA found on some old, but well-preserved pig ribs, found from the wreck of *Mary Rose*, a galleon sunk by the French in 1545 off Portsmouth harbour, which had been lying there in mud under 14 metres of water, till 1982, when it had been raised up. The *Independent* reported this part of their research work thus : "*Pig brings home the bacon*".

In 1991, a prehistoric human body, the *Iceman*, was discovered in the Italian Alps by a mountaineering couple. Hundreds of such finds had been made before in the high and dry Andes, but never before in the not so high, nor so dry, Alps. Radiocarbon dating fixed the age of *Iceman* at about 5000 years old, also a prehistoric iceaxe and a bag made of birch bark were found near it. Sykes and a Munich team, independently, detected the same DNA in these remains. This particular sequence was unmistakably European, thus ruling out — he recalls that the Piltdown man "discovery" of 1912 had fooled everybody till 1953, when carbon dating revealed that it was a fraud — an elaborate hoax involving somebody actually using one of the Andean corpses in the Alps!

Sykes says that a question from the *Sunday Times* reporter prompted him to give the name of a living European having the Iceman's DNA sequence. It turned out a close friend of his, Marie Moseley, fitted the bill, so Sykes had the pleasure of making her into an instant celebrity: "*Iceman's relative found in Dorset*" was how this particular newspaper was entitled ! Here, Sykes adds that his work of the next 10 years was inspired by the "sense of connection" which he now began to observe in Marie, who actually started feeling close to her "relative" from long long ago. He mused that "perhaps we only need to look around us, at people alive today, to unravel the mysteries of the past".

2. Genetics too goes way back, at least to Aristotle, who, around 300 B.C., opined that the father supplied the pattern, the mother nurture, and that the baby would be an exact copy of pop unless "interfered with" in the womb. This led to the idea of a pre-formed *homunculus*, which even the pioneer of microscopy, Van Leewenhock, imagined he could see curled up in the heads of sperms. [Though chauvinistic, this theory still seems nearer the truth than the next: there is clear assymetry between the assigned rôles of the famale ovum and the male sperm.]

His near-contemporary, Hippocrates, thought however that both pop and mom produced seminal fluids, and their percentages decided the baby's characteristics. This *blending* theory seems reasonable, and as Sykes stresses, is adequate to explain most commonplace observations. However, Darwin's theory of evolution by natural selection contradicts it. New, but favourable, small changes would have been quickly diluted away and lost in such a continuous blending process.

Mendel, from his sweet-pea experiments of 1860s, was the first to get a true inkling : whatever it was (now called genes) that finally decided the various characteristics of the off-spring, must be transmitted equally, and in discrete portions, by both parents.

This turned out to be largely (that is, except for mitochondrial genes and sex chromosomes) true. However Mendel's forgotten and virtually unread work played no rôle in this. It was rather two practical

advances : much better-ground microscope lenses, and superior chemical dyes. Thanks to these, researchers could now actually see cells, the fertilization of the ovum, and the mitosis process. During these, they infallibly saw the snake-like unweaving and weaving of thread-like coloured (because of the dye) strands, which they promptly dubbed *chromosomes*, and by 1903, the conviction was widespread that these ~~chromosomes~~ contained the secrets of heredity.

How exactly ? This took a long time to work out. ~~Originally,~~ the focus had shifted ~~was on the~~ to *proteins*, crumpled strings of twenty *amino-acids*, for these alone seemed to be complex enough chemically to explain the intricate biology. The much simpler *deoxyribonucleic acid* or DNA, made from just four *nucleotide bases*, was largely ignored, till in 1953, Crick and Watson worked out the beautiful geometry of this molecule: it consisted of two strands of these four bases, seemingly juxtaposed like two intertwining spiral staircases, and — this, not the alleged double helix, is the crucial thing! — with invariably the pairing

A ⟷ T C ⟷ G

between the bases (A for adenine, T for thymine, C for cytosine, G for guanine) of the two strands. This pairing is the key thing used by nature for the hi-fi copying mechanism occuring in cell mitosis.

The DNA is confined to, and never ventures out of, the chromosomes (which, but for mitochondrial genes, are all in the cell nucleus) and is pure information only, just like a computer tape. The actual "hard-hitters" are indeed the proteins — enzymes, hormones, antibodies, collagen, keratin. haemoglobin, etc. — each of which is made, as per the *genetic code*, under the aegis of a specific DNA string: triples of bases in this instruct the cell to manufacture a corresponding amino-acid, and the sequence in which these twenty roll out one after another characterises the protein in question. These amino-acid strings are in appearance usually very far from linear, in fact their foldings play a major role in each protein's function.

A decisive and important discovery was that nature uses exactly the same genetic code — that is, a triplet of bases makes one and only one amino-acid — in all living organisms, from the meanest plant bacteria to a complicated mammal. This universal nature of the genetic code strongly suggests a common origin for all life on this planet.

3. Within the genes for keratin, the protein of *hair*, there are small differences which are responsible for their differing colours and textures. The classification of these differences, and the rules governing their transmission, have yet to be worked out completely.

The genetics of a more basic but invisible distinguishing feature, our *blood group*, is however completely known. This knowledge was gained slowly and painfully. Though there is evidence that the ancient Incas had successfully practiced blood transfusion (they all had blood group O) the consequences were often terrible when these were attempted in the 1600s in Italy, so much so, that they were banned for a long time in many Europe countries. They were resumed, with more caution, in the 1800s, but with similar results. By 1875, Lalois had observed that mixing blood from differing species resulted in clumps of blood cells

which often burst out. Finally, in 1900, Karl Landsteiner identified the four basic ABO groups : A, B, AB and O; their genetical rules resemble those of Mendel's sweet peas and were worked out by Herschfeld and others. The Rh positive and negative blood subtypes — named thus because Rhesus monkey blood was used in the identification — were found in 1940, but again (!) by the very same Lansteiner, with Weiner. Their genetical rules are more complicated, and were worked out by the great British geneticist and statistician, R. A. Fisher.

During the Great War, Herschfeld and his wife identified, while working in the laboratory of the Royal Serbian Army, the blood groups of a large number of soldiers of diverse nationalities fighting with the Allies. In a 1918 paper, which was re-published after translation into English in the *Lancet* of 1919, they drew rather sweeping conclusions from this data. As Sykes engagingly puts it, "*geneticists, then as now, are never shy of grandiose speculation*" ! The Herschfelds decided that humans were made up from two different "biochemical races", Race A and race B, and, since the percentage of blood group B was highest in the soldiers from India, that "we should look to India as the cradle of one part of humanity", but they were unsure as to the origins of race A, though in general Europeans had the highest percentage of blood group A.

Such sweeping conclusions cannot be drawn from data about just one genetic system, blood groups, e.g., the Herschfeld data also implied that Russia and Madagascar be deemed racially similar! The liberal American physician Boyd stressed this fact while continuing to collect more blood group data. The baton then passed on to Mourant, who owed the Cambridge job, which enabled him to seduluously devote his entire life to collecting blood groups, to R. A. Fisher. This because the emotionally unhappy 34 year-old medical student Mourant (who wanted to become a psychoanalyst after a failed attempt to become a geologist) had located for Fisher a family of twelve siblings whose blood groups gave the first practical proof of the genetical rules which R. A. Fisher had proposed for the transmission of Rh factor.

If an Rh negative mother bears the children of an Rh positive father there is no problem with the first baby. But this child is usually Rh positive and some of its blood goes into the mother's blood stream during delivery. The mother's immune system recognises this antigen as foreign and begins to develop antibodies. This lead to a very severe problem, commonly called the "blue baby syndrome", during the subsequent pregnancies. These days the mother is injected antibodies against Rhesus positive blood cells right in the beginning, thus obviating the need for her immune system to respond to these. The curious fact that in Europe both Rh types occured with almost equal frequencies (the rest of the world is predominantly Rh positive) indicated to Mourant that it must be a rather recent mixture, otherwise, natural selection should have eliminated one or other of the Rhesus types.

The Basques, have always stood out from the other Europeans. For example, their language, Euskara, is totally different from any other. They have been the subjects of many scientific and pseudo-scientific studies, e.g., Vallois believed their skeletons were more like the fossils of 20,000 years ago, than those of other Europeans. Naturally, they drew the attention also of Mourant. He found that the Basques were almost all Rhesus negative, whereas in the other Europeans he found both

types. He concluded that the Basques were descendants from the original inhabitants of Europe, while the remaining were mixtures of these and more recent arrivals, probably the first farmers from the Near East.

By now an immense amount of data pertaining to many genetic systems (blood groups being just one) had been amassed. Cavalli-Sforza and Edwards made an in-depth statistical study of all this data using the early computers. An article by Edwards in the *New Scientist* of 1965 explains the basic idea. Imagine a tribe whose totem pole carries 100 discs, some black, other white, arranged in some order. When a tribe splits in two each group takes with it a copy of this pole. Also every year there occurs one random colour change in the disks of a pole. The *genetic distance* between two different tribes is defined to be the number of colour differences in the disks of their totem poles. This is a very good measure of the time elapsed since the two tribe had a common ancestor. This basic idea remains unchanged: only nowadays *genetic drift* is observed directly in the DNA strands (instead of some statistical or metaphorical totems) of individuals, which, unlike tribes, are obviously perfectly well-defined genetical entities.

The above work, since it used many genetical systems, avoided the pitfalls into which the Herschfelds had fallen, but continued to suffer from the fact that a genetically ill-defined term, tribe or population, remained central. Its *population trees*, in which the nodes and branch points stood for instances of this ill-defined term, were first drawn with admirable and modest intention, but were soon over-interpreted by zealous and incautious followers. The way out was shown in the following landmark paper, which in fact has continued to serve as the template for all further work in this field till today.

Allan Wilson, Rebecca Cann and Mark Stoneking, "*Mitochondrial DNA and human evolution*", Nature, January 1987.

The 134 end points of the tree depicted in this paper are individuals, and so are the nodes of this tree, each representing the last common ancestor of the two people who branch off from it. The shortest length connecting any two of these people is a measure of the genetic distance between them measured using differences in one special gene, the mitochondrial, whose properties we shall go into presently. This tree shows many genetically close individuals in "populations" previously assumed to be quite far from each other, thus confirming that this concept was genetically ill-defined. Next, the mutation rate of this gene being very steady, it was actually possible to accurately estimate in years the time till the last common ancestor for any two of the individuals. *When the time till the root of the tree, that is, the common ancestor of all the 134 people, who were chosen at random from all nationalities, was worked out, it turned out to be only 150,000 years ago.* The conclusion was inescapable: all of us on this globe alive now, had a single common ancestor who lived about this long ago.

This settled a long-simmering debate between anthropologists. Everybody agrees, because of the antiquity of the human fossil record from east Africa, that the genus *Homo* originated only in that continent about two million years ago, and then, over the next million, spread slowly to cover all but the most inaccessible parts of the earth. For all these years the extant species was *erectus*. Fossil record also makes it all

but certain that *Homo sapiens* also appeared in Africa much before the other continents. There was controversy however as to whether there was a more recent emigration "*Out of Africa*" of this species too, to all the other continents, or whether — this is what the "multi-regionalists" believed — our species had evolved separately on each continent out of the local *erectus*. Had this second school of thought been correct, the first common ancestor of all of us alive now, must have lived at least a million years ago. The much smaller value, which Wilson and his two students got, showed that the "Out of Africa" school of anthropologists had got it right: there was an emigration out of Africa, this time of our very own species, which began about 150,000 years ago only !

4. Mitochondria are within the cell, but outside its nucleus, floating in the cytoplasm. They help the cells use oxygen to produce energy, so more vigorous the cell, more mitochondria it contains, e.g., those of muscles, nerves and brain contain upto a thousand each. Each mitochondrion is enclosed within a membrane which contains the enzymes required for the aerobic metabolism; as these consume the fuel we obtain from food, using oxygen, they heat up, and partly this is the heat which keeps us warm; more importantly this produces the high energy molecule ATP, which is used by the body to run virtually everything. Buried in the middle of the mitochondrion is a mini-chromosome, only 16,500 bases long (the nuclear ones add up to 3,000,000,000 bases!), which hold the code for the oxygen-capturing enzymes. However, curiously, many other genes governing the workings of the mitochondria are situated in the nuclear chromosomes. Curious too is the fact, that like bacterial DNA, the mitochondrial DNA strands are closed circles. In fact it is believed that they were once free-living bacteria who sought to make a living by invading more advanced cells. The relationship became symbiotic, since cells also got a great boost by being able to use oxygen, and to ensure that these welcome guests don't leave, some of the essential DNA for their working got transferred to the nucleus !

Unlike the nuclear genes, which are inherited from both parents, the mitochondrial ones are inherited only from the mother. The cytoplasm of her egg cell is stuffed with upto 250,000 mitochondria. In contrast, the sperm has vanishingly few, just enough for it to swim up the uterus, and these too are jettisoned with the sperm tail, as soon as the successful sperm head enters the egg. The fertilized egg, and so its various duplicates which ensue, as it develops first into an embryo, then a foetus, finally the new-born baby, and eventually an adult, all contain copies only of the mitochondria originally in the mother's egg. Some mutations occur spontaneously now and then in this subdivision process, and those which occur in germ-line cells, as against the somatic ones, do get transmitted to the next generation. Most of these are quite neutral in character, only a very few are disabling, so most go unchecked, and this genetic drift is simply measuring the time elapsed, forming thus a "molecular clock". The mutation rate in the mitochondrial gene is about twenty times that in the nuclear ones, making the rate of this clock just right for studying human evolution.

Unlike Wilson and his two students, who had considered mutations all around the mitochondrial DNA circle, Sykes decided to focus on only a short stretch, called the *control region*, which is only 500 bases long. This stretch does not carry codes for anything in particular, so its mutations are bound to be very neutral indeed, in fact its only function

seems to be sort of geometrical, it just has to be there so that mitochondria can sub-divide properly. The only problem could be that it was mutating too rapidly, which wouldn't do, because in evolutionary work, one needed to look at upto 6000 human generations, so some short-term stability is essential.

What was needed was a check on the mitochondrial control region DNA of a known sufficiently large matriarchal family. At this point Sykes recalled having read as a boy in some encyclopedia that all the golden *hamsters* in the world are descendants of just one female! Together with an undergradate assistant Tomkins he started looking into this. Soon they were in contact with Roy Robinson, a self-taught amateur scientist of great distinction, who was the world's leading authority on hamsters. He confirmed what Sykes had read. Apparently in 1930 some zoologists had captured in Aleppo, Syria, four unusual golden hamsters, of which only one was female. Back in Hebrew University, Jerusalem, they started to breed prolifically. Soon they were getting distributed all over the world. Besides lab use they turned out to popular pets. What contributed to this craze was that they soon started developing many attractive fur coat varieties: piebald in 1947, then cream, cinnamon, satin, tortoiseshell, and many more. It wasn't difficult to mate selectively to develop these strains further. Very lucky for Sykes was the fact that Robinson had an example of each and every one of these coat varieties. In fact, so eminent was he in this field that, any time a new coat variety appeared anywhere in the world, a sample of the fur was sent to him. Unfortunately one needed quite a few hair to obtain enough DNA for the lab test. It was unreasonable to ask the owners to part with so many of their pets' hair. However, another assistant, Richards, then had the brainwave that it might be possible to get the required DNA from the hamster droppings ! "It worked a treat". And obviously, there was no problem inducing the owners to part with these! Eventually, the mitochondrial control region of 35 hamsters was sequenced. It turned out to be absolutely identical in each and every case, showing thereby, that it had remained stable for the approximately 250 hamster generations since that original female was found in Aleppo. Of course, there was a chance that human DNA might not be as stable, but considering the basic nature of mitochondria, this appeared remote, so Sykes decided from here on to use the control region only.

5. The last of the Romanovs, namely, the Tsar Nicholas II, his wife, and their five children, were all killed (some believe one or two of the children survived) in 1918, but the bodies had never been found. In 1991, remains of nine bodies were dug out of a shallow grave in the Urals near Ekaterinburg. Since a family doctor and three servants had also been shot, this was two less than there should have been, but this tied with accounts that before their hasty burial (the White army was closing in on the Red holding the town) an attempt had been made to burn them, but only the two smallest bodies had been so disposed.

Skeletal reconstruction and conventional forensic genetic fingerprinting showed independently that five of the remains were of a family, parents and three daughters, and the others were unrelated. Mitochondrial gene sequencing confirmed this. Moreover, it showed that the female parent had an unbroken maternal connection with Prince Philip, as indeed the late Tsarina had. Likewise, it was known that the late Tsar had an unbroken maternal connection with a Count Trubetskoy now living a life

of comfortable retirement in Côte d'Azur. The Count's control region sequence read 126, 169, 294, 296. This means that, of the five hundred bases in the sequence, only four differ from those of a reference sequence (the first one sequenced in 1981) and these are situated at the 126th, 169th, 294th and 296th places. On the other hand, the sequence from the male parental remains read 126, 294, 296 !

The original trace from the sequencing machine showed, for the Count's sequence, a clear red (for T) peak at position 169, while the presumptive Tsar's showed a blue (for C, same as in reference sequence) peak. A closer look showed however a small red blip under the blue peak. So, was this a mixture of two different sequences ? The only way to confirm this was to try to separate the two by making *clones*. That is, some bacteria are induced to accept this DNA. Only a very few do, but then only these are kept, and allowed to multiply, after which DNA is recovered from the ensuing bacterial colony. In this way, 28 clone DNAs were prepared. It was found that 21 of these had the main sequence 126, 294, 296, but the remaining 7 also had the Count's extra mutation at position 169. The researchers had stumbled by chance on an instance of *heteroplasmy*, a rare state where a new mutation, in this case at position 169, is part way to becoming established.

There has been many an *Anastasia* (the fourth daughter) since 1918, the most well-known being Anna Anderson (played by Ingrid Bergmann in the movie). As Sykes puts it she "died before the cold eye of genetics could be turned on the case", for, just a few years after her death, mitochondrial DNA was recovered from a stored biopsy, taken when Anna was in hospital in 1979: it was nothing like the Tsarina's ! Likewise, there have been many claiming to be Alexei (the youngest child, the crown prince), however it is almost certain that the Romanovs were terminated that day in 1918. Sykes naughtily mentions that (ignoring heteroplasmy) his very own mitichondrial DNA sequence is exactly that of the dead Tsar's, so it follows that he (and many others, because it is a common sequence) shares with the Tsar a common maternal ancestor within the last ten thousand years: "Not close enough for me to make a realistic claim to the Romanov fortunes, I think."

The above estimate, viz., *one difference in control region between two people having a common ancestor 10,000 years ago*, is in fact crucial in Syke's work, and is discussed further later on. We note here that (assuming all life is related: universality of the genetic code strongly suggests this is the case) any two people clearly must have had a common maternal (for that matter, also a paternal) ancestor, the DNA serves only to put a time estimate on when they had the most recent one.

6. Sprinkled across the vastness of the Pacific are thousands of tiny and remote islands. The Polynesians had reached these long ago. *Where did these intrepid voyagers come from and how did they get here?* Sykes says he was drawn to this enduring puzzle in 1990 literally by accident: vacationing in Rarotonga, one of the Cook Islands, he fractured his shoulder, so had to prolong his stay, and started thinking about this. He persuaded the hospital to give him remnants of 35 blood-sugar tests (diabetes is common there); of these, only 20 were intact when he arrived back in Oxford. When he sequenced their control regions, he found that, excepting one sample, all were in the same *cluster*: sixteen had 189, 217, 247, 261 and three 189, 217, 261. He assumed that the

very different twentieth — 144, 148, 223, 241, 293, 362 — was from a "tourist" who had, like him, needed some medical care.

The evidence of archaeology and language, and the types of Polynesian domesticated animals and plants, all point to an origin in south-east Asia. However the winds and currents in the south Pacific move from east to west, from Americas to Asia. In fact the the first Europens to explore the Pacific, the Spaniards, traversed it in this direction only, and then would use the great circle route, past Japan and Alaska, and south down the coast of North America, to return to their bases in Central America. Some condescending westerners thought this was proof enough: the natives must have drifted down with the current from America. The celebrated voyage of Heyerdahl on a small balsa raft, *Kon-Tiki*, from South America to the Tuamotu Islands showed how it can be done. However so compelling was the physical evidence of an Asian origin, that mainstream anthropology saw this only as a gimmick.

As long ago as 1923 an attempt had been made to solve this puzzle of the Pacific via blood groups, but this data with only three totem discs, A, B and O, yielded no definitive conclusion. With *tissue types* (the bread and butter of cellular immunologists, with whom Sykes' institute is seemingly crammed full!) one has far greater diversity, and the verdict was in favour of south-east Asia; however a rare tissue type, HLA-Bw48, is found only in some native Americans and Polynesians. The shortcoming of using tissue type for such work, as against mitochondrial gene, is that it is hard to ascertain the genetic distance between two types, for example, between HLA-Bw48 and other Polynesian tissue types.

Comparing his Rarotonga cluster with data of native Americans that had begun to circulate, Sykes noticed that one of the four American clusters was close: it read 189, 217. Also, both shared a peculiarity: opposite the control region there were eight *missing bases* in the mitochondrial circle. "Things were looking up for Heyerdahl." On his second trip back to Rarotonga, Sykes stopped over in Hawaii to meet Wilson's ex-student Cann, who was working there with her student, Lum. Even though this is 3000 miles to the north of Rorotonga, they too had the same main cluster, but what floored Sykes was that the "tourist" DNA had occured in a native Hawaiian too! Clearly, this was in fact a secondary Polynesian cluster, unlike any from the Americas. From Rarotonga, he brought back 500 more blood samples. It seemed that sequencing them, and comparing with other data, would solve the puzzle.

7. Curiously, this denouement was hastened along by the pioneering work, on the inherited diseases of the blood, done before by Sykes' boss, David Weatherall! The main diseases, *sickle cell anaemia* and *thalassaemia* are both caused by tiny changes in the haemoglobin genes. In the former, the usually circular red blood cells visibly change shape and can no longer slide past each other in the very narrow blood vessels. In the latter, the haemoglobin forms clumps inside these cells, which are then destroyed in the spleen. Repeated blood transfusion is the only effective remedy, and is quite beyond the public health budgets in most of the affected regions.

These are (or were till recently) the malarial regions of the world. The carriers of these haemoglobin gene mutations become resistant to the malaria parasite, so natural selection had encouraged these mutations.

However off-spring of two carrier parents get a double dose of this mutation and develop these potentially fatal anaemias. *It was field work in the islands of south-east Asia and Oceania that had finally proved the connection between thalassaemia and malaria:* so the freezers of the Institute were chock-full of DNA samples from these islands!

In 1992, Sykes sequenced over 1200 mitochondrial DNAs. The 8 base deletion (of 19 of the original 20 Rarotonga samples) being the easiest to spot, he first looked at it: it was very common in Samoa, less common as one went westward to Vanuatu or New Guinea, lesser still in Borneo and Phillipines which are still further to the west. This trend suggested an Asian origin, the similar deletion in some native Americans being due to the fact that another branch of the same people had crossed over into that continent via the Bering land bridge of long ago. The westwards trend of the Rarotonga cluster was telling: its main component 189, 217, 247, 261 waned, while the minor component 189, 217, 261 waxed progressively, but as one neared Asia, both faded out to be replaced by just 189, 217 or its new and different offshoots. Sykes says, "I rang as many people as I could think of", but nobody had seen the difference at the 247th spot (the defining mutation of the Polynesians) in any native American: clearly *"Heyerdahl was wrong"*.

So, the ancestors of the Rarotonga main cluster had originated around Taiwan (because that's where maximum variants of 189, 217 are seen now). As they went island-hopping eastwards, some of their "totem poles" (either 189, 217 or 189, 217, 261) picked up the mutation at 247 just east of Borneo, with this dominating as they progressed all the way till Easter Island. From Borneo on, this coincides with archeological conclusions drawn before by dating the various findings of *Lapita pottery*, a distinctive style these mariners favoured. Similar genetic trails, leading north-east to Hawaii, and southwards to New Zealand (the Maoris have the same DNA type as Polynesians), intersect this eastward one in the Moluccas, just east of Borneo, and indeed near Moluccas is where one finds maximum variants of 247 now.

The secondary "tourist" cluster was found all over Polynesia but was everywhere far from common. And, there was one found in Vanuatu, two more in Papua, but it was in the mountainous interior of New Guinea that it is found in abundance. These people were there even 40,000 years ago, about the same time when the first Australians had entered that vast continent. About 5000 years ago, at least one female from them, a direct maternal ancestor of our "tourist", must have joined a Lapita canoe heading east into the unknown.

These canoes were double-hulled, often reaching enormous sizes (the first Europeans in Polynesia saw some 30 metres long) with a prow at each end, so could be tacked across the wind and reversed without turning around. The necessary navigational skills must have developed with experience. To begin, the islands were close, it was only a question of reaching a visible target (this is true till the Solomon Islands, and these indeed were all settled well before Lapita pottery). Also, sailing against the wind is not altogether a bad idea, it means a relatively easier journey back, in case the need arises. Travelling along a fixed latitude, keeping a setting or rising star in the same position relative to the canoe is not hard at least in theory, but these people also travelled northeast to Hawaii, and most awesome: way, way,

south to discover New Zealand! This implies amazing skills!! Maybe they knew about the special colours taken by clouds over land masses, or maybe they followed sea birds homing back, or did they perhaps, as some sailors undoutedly can, detect far-off land (even a hundred miles away) by dipping their feet in water to feel the interference pattern made by the underlying swell and its reflection from land ? And *why*, at all, did these amazing people make these perilous journeys ?

Genetics rules out Heyerdahl's explanation that *kumara*, the Andean sweet potato came alongwith the Polynesians from America. It was the other way round: these people travelled even to that continent, and brought this crop back. But, perhaps because these expeditions were mostly male, they have left no mitochondrial trace in South America. However, two sequences from Tahiti did match sequences found in Chile, these are perhaps traces of women who joined them on the return trip.

8. In 1993, just when its funding was about to lapse, an amateur archeologist, Roger Pedersen, volunteering at the dig in Boxgrove, England, found a very old human shin bone. Promptly christened the *Boxgrave Man*, it joined a handful of previous finds — the skeleton of the *Neanderthal Man* near Düsseldorf, Germany, in 1856, being the most famous — about which there was uncertainty if it belonged to our species, or to an earlier human species, now extinct. In Europe, the oldest finds which are unmistakenly those of our own species, are of the *Cro-Magnons*, cavemen who lived about 45,000 years ago in southern France and northern Spain. They had much more finely crafted tools, and most surprisingly, *have left behind, in over two hundred caves, strangely beautiful and vigorous wall paintings of wild animals!* Similar finds of both types (but never, for the second, similar art work!) have been made in other continents, those of Africa being much, much older.

Despite the paper of Wilson et al., "multi-regionalists" of Europe still stubbornly insisted that their Cro-Magnon ancestors were descendants of the Neanderthals; not, as the opposing "replacement school" maintained, emigrés from Africa or elsewhere. It seemed some more genetical evidence and arguments, about this question of ancestry, were needed, and the next chapter deals with this work.

9. Just as Polynesia's two (interbreeding) clusters, the main and the 4% touristy, showed two kinds of ancestors, Sykes claims that, were present-day Europe a mix of Cro-Magnons and Neanderthals, it must also have two distant clusters.

[*Sykes's reasoning is wrong: n distant clusters only indicate n or more kinds of ancestors!* For example, after sufficiently more time, clearly only one of the present females of Polynesia will be an ancestor of that future population, which will then have only one cluster. Also, the *genetic diameter*, i.e., the maximimum number of mutations between two members, of this future and probably bigger population, will be more, because of genetic drift, than of the corresponding present cluster, but might be much smaller than the present genetic diameter.]

In 1992 his team sequenced 500 samples from schools in Wales, probably the oldest population in Great Britian, and found a *genetic diameter of only 8 mutations*, so it had a common maternal ancestor about 80,000 years ago. It seemed, from data coming in, that the figure is about the

same for all Europeans; so they are either all Neanderthal, else all Cro-Magnon, definitely not a mix of the two. To rule out the first, Sykes then mentions that ***the maximum number of mitochondrial control region mutations separating two people on earth has been found to be 14*** (e.g., between a fisherman in Cook Islands and a cook in Wales).

[This only indicates some physical contact between present European and the remaining world populations about 140,000 years ago; there were then other, possibly even distant, clusters, which in all this time have died out mitochondrially, but may have left other genetic traits?]

So (says Sykes) ***Europe is descended exclusively from the Cro-Magnon*** [?], not only that, it seems Sykes thinks that these arguments imply that ***the Neanderthals and Cro-Magnons either could not interbreed, or at best could produce only hybrid infertile offsprings.*** Fossil evidence shows that in Europe they did overlap for some tens of thousands of years, so definitely had ample opportunity for interbreeding.

More interesting than his flawed logic are some facts mentioned in this chapter, notably that, ***in 1997 control region DNA was sequenced from the original 1856 Neanderthal skeleton, and it was found to be 26 mutations away from today's average.***

[Lets see if this clinches the issue ? Assume that this skeleton is about 80,000 years old — the carbon dating of skeleton must have been done, but is not mentioned in this book. The last common maternal ancestor of Europe, who lived then, can reasonably be supposed to have today's average. But, as the note above on Polynesia explains, it is ***not*** reasonable to suppose, simply because the older population was smaller, that its genetic diameter was at most that of today's, i.e., 8 mutations. In fact such an assumption would be begging the question: genetic diameter falls suddenly when a cluster disappears.]

Of course, if this 1856 skeleton itself is very old — Sykes mentions that ***some Neanderthal remains recently found in Spain are only 26,000 years old***, but doesn't say if their DNA has been tested — than some of these 26 mutations could be due to its antiquity.

In 1998 the partial skeleton of a child seemingly intermediate between Neanderthal and Cro-Magnon was found in Portugal, its DNA has yet to be tested. It is after mentioning this, that Sykes jumps to talking about a possible infertile hybrid offspring of Neanderthals and Cro-Magnon.

[That this is a jump is clear if one notes that of all the, very much fertile, females of Polynesia only one will win the genetic sweepstakes, i.e., end up as the maternal ancestor of the future Polynesia.]

He speculates that the Neanderthals might have had two more chromosomes than the Cro-Magnon, i.e., 2 more than our 46 chromosomes — great apes, the primates nearest to us today, do have 48 — so their offspring would have the odd number 47 which would explain its infertility, much like that of mule, which has 63 chromosomes, intermediate between its father, ass, which has 62, and its mother, mare, which has 64. ***So maybe a chromosome test, which Sykes thinks within the realm of possibility, on one of these Neanderthal remains will finally settle the issue ?*** [Of course for Sykes himself there is no doubt even now.]

10. The *Palaeolithic* or Old Stone Age covers the time from the appearance of the first stone tools, 2 million year ago, till the end of the last Ice Age, 15,000 years ago. The *Lower Paleolithic* coincides with time when only *Homo erectus* was around, the *Middle Paleolithic* that of the Neanderthals, and the *Upper Paleolithic* is deemed to start with the advent of *Homo sapiens*, so in Europe with the Cro-Magnons about 45,000 years ago: the delicately worked flint tools of this age are worlds apart from the crude hand-axes of the Lower Paleolithic. The *Mesolithic* or Middle Stone Age takes us from the end of the old Ice Age, to about 10,000 years ago, that is, the beginnings of *agriculture, the techical revolution which eclipses any other in the history of man.* It is only at this end of this age, from which the *Neolithic* or New Stone Age commences, that one starts seeing a whole new set of tools — sickles, grindstones, the first evidences of pottery, etc.

The Cro-Magonons were Europe's *hunter-gatherers*; amazingly, by 10,000 years ago, similar people were all over the earth, everywhere except Polynesia, Madagascar, Iceland and Greenland. At this time agriculture, i.e., *human enslavement of wild plants and animals, started in at least nine different parts of the world.* The Fertile Crescent (of Syria, Iraq, Turkey and Iran) of the Near East being the first. Here, the hunt had come to the hunters, trails of antelopes criss-crossed the grassland, and the seeds of wild grasses they gathered were plentiful. This relative immobility helped them notice that some seeds they had accidentally spilled would germinate and start growing the next year. To avoid the bother of going out to gather them, they started doing this deliberately. Over time, since the heavier grain was chosen more often by them for the next crop, this encouraged the mutations producing better grain. The domestication of some wild animals, for example, of goats in the Near East, cattle in India, yaks in Central Asia, llamas in the Andes, also dates from this time. This enslavement of other species signalled that *homo sapiens* was now dominant, and helped this species to increase its dominance at a much faster rate.

One hunter-gatherer had needed the resources of 10 square kilometres to survive. Now, by growing crops and rearing animals, the same land could support upto 50 humans. So their numbers mushroomed, and they started living in close proximity. Also some of them had much more time in hand, so there developed craftsmen, mystics, artists, etc. However it was not all good news. The denser population and its proximity to carrier animals often led to epidemic diseases like smallpox. Slowly resistance was developed but when these pathogens encountered a new human population, they would explode again with their initial fury, e.g., *the Europen settlement of North America was facilitated by the accidental, and sometimes deliberate* (biological warfare?) *infection of native Americans by epidemic diseases like smallpox.*

Was there a replacement of the Cro-Magnons by the farmers from the Near East (just as they themselves had relaced the Neanderthals) or was it the *idea* of agriculture, rather than the farmers themselves, which spread into Europe? This was the question which Sykes decided to attack now. By 1995 his team had sequenced an enormous amount of mitrochondria in Europe. In fact by that time a number of papers, using computer analysis of such data had started appearing. However nothing striking was

revealed. In fact genetically Europe seemed to be rather boring compared with say Africa. The trouble, it turned out, was these computer programmes. They were designed to make trees reflecting the observed genetic differences. But there could be an enormous number of trees fitting the same data. For example, did the mutation at 189, 311 come after one at 189, or after the one at 311 spot ? Sykes, with the mathematical help of Bandelt, saw the way around it was simple: put these mutational ambiguities in the branches of the trees, alternatively allow parallel paths. It is genetic distance that alone defines clusters, one shouldn't worry too much about the exact relational fine structure of the sequences within the cluster. This rather pragmatic approach helped them see that *mitochondrially all of Europe splits off into seven rather distinct clusters* (actually in the beginning they had settled on six, later noting that the biggest should really be two). This clustering was already a big improvement on the previous papers.

It turned out that the *genetic age*, i.e., the time till the last common maternal ancestor, *of six of the seven clusters was much more than 10,000 years*, going often way back into the time when only the hunter-gathers, the Cro-Magnons, were around. This was against the ~~established~~ prevalent dogma that agriculturists from the Near East had over-run Europe. Sykes says that he was in doubt about these findings till they looked again at those very special people of Europe: *in the Basques were seen examples of all these six clusters, but never any of the seventh.* This last was a much younger cluster, only 10,000 years old at the most. Checking the frequencies of this cluster on the map of Europe they got added substantiation. *The seventh cluster had spread into Europe from the Near East along exactly the two routes which had been uncovered before by means of archeological findings.* More precisely, the route marked by findings of *Linear pottery*, which heads up the Balkan, across Hungary towards the Baltic, and that of *Impressed Ware* which stays close to the Mediterranean, winding around Spain and Portugal into western Britain. Finally they found that such DNA and its modern variants abound from where this migration had started, viz., amongst the Bedouins of the Near East. Conclusion: *most of modern Europe has genetic history extending directly into the Upper Paleolithic, only about 20% of Europeans belonging to the seventh cluster coming from the Near East. There had been no wholesale replacement of hunter-gatherers by farmers in Europe, instead it was mostly the idea of agriculture which had spread.*

11. Before Ammerman and Cavalli-Sforza had put forward their now widely accepted ideas in the 1970's, the contemporary taste had been similar: mostly indigenous development, gradual adoption of agricultural methods, but without a large scale movement of people. A huge amount of data regarding blood and many other genetic tests had been contoured on the map of Europe, and the *gradient lines of gene frequencies*, which mainly went south-east to north-west interpreted by Cavalli-Sforza as a *demic diffusion* of these people from the Near East into Europe. He had used some differential equations of R. A. Fisher, who had referred to their solution as *wave of advance.* Curiously, as these new ideas became accepted, it was Fisher's terminlogy which came to be preferred, and perhaps its dramatic sound led to an over-interpretation of what Ammerman and Cavalli-Sforza had suggested.

When Sykes announced his findings at a Barcelona conference in 1995, most archeolgists believed that such a tsunami of farmers had indundated

the original hunter-gatherers of Europe. The linguist Colin Renfrew used it even to explain how European languages (barring Euskara and the Uralic) stemmed out from the root language, *Indo-European*, which was once spoken in Turkey. The link of this extinct root with Sanskrit was worked out as long ago as 1786 by William Jones, a judge of the British Raj. [Perhaps Renfrew also postulated a similar eastward wave to explain how this other linguistic branch grew from the root ?]

Sykes feels his introduction as speaker in this 1995 conference, by Bodmer, a collaborator of Cavalli- Sforza, was less than gracious: *"And the next speaker is Bryan Sykes who is talking about Mitochondria. I don't believe in mitochondria"*. But is happy to recall that "I could almost see the steam coming out of his ears" by the time he finished his talk. Finally the findings of the Sykes team did get published as *"Paleolithic and Neolithic lineages in the European mitochondrial gene pool"* in the July 1996 issue of the American Journal of Human Genetics.

A few issues later this Journal published a letter by Cavalli-Sforza, and reply to the same by Sykes. The former pointed out that the contribution of the farmers, as per his demic diffusion, was about 26 % which was good news for Sykes being not too far from his 20 % but then he launched a serious attack on the mitochondrial methodology used. Firstly, the control region was unreliable being riddled with mutations. To counter this *Sykes' team swapped samples with Antonio Torroni, who had been doing similar work using another segment of the circle, and each re-tested using their own segments. Again the same seven clusters were seen.* Incidentally, Sykes at this point adopted *Torrini's notation* using letters for these clusters, and the fanciful female names he dreamed up later start with these letters: *U for Ursula, etc.*

Secondly, Cavalli-Sforza felt the mutation rate being used was way off. This objection is much harder to meet, also crucial, e.g., if Sykes was off by a factor of 10 they had shown nothing.

One way of calculating mutation rate had been to find genetic distance between chimps and man and use 5 million years ago as the time when they had a last common ancestor. This gave rule-of-thumb "one mutational difference = common ancestor 10000 years ago". *Same figure was calculated using accepted fact that America had been settled about 12000 years ago from the DNA data of Native americans.* Being off by as much as a factor of 10 seemed crazy anyway, it was ruled out even by his previous work on Polynesians: then they would have arrived there only 300 years ago, after the Europeans ! There was need however for a direct measurement, *the mutation must occur during one of the twenty-four cell divisions in the female germline between one generation and the next. They found 1.5 % of people do indeed have a mixture of two mitochondrial DNAs (like the Tsar) and it takes an average of six generations to establish.* This independent approximate laboratory estimate also matched the figure above mentioned.

Only one objection was left unanswered by Sykes: *mitochondrial gene was only one gene, subject to all sorts of statistical fluctuations, was it justified to deduce so much, so to speak, from just one kind of totem pole, when the body actually carries so many ?*

The single strand of a nuclear chromosome, which goes into a sperm or

egg cell, is made after some *recombination*, or switching of some parental and maternal chromosomes, in the previously double stranded DNA. *It is this scrambling which advances evolution*, but also makes tracing a nuclear gene through the generations very hard. In the March 1999 issue of the *Proceedings of the Royal Society* there appeared a theoretical paper by John Maynard Smith* which argued forcefully that such a mechanism must be going on even in mitochondrial DNA because other factors could not explain its high mutation rate. Also there was another experimental paper in the same issue, by friend turned enemy, Erika Halgeberg, saying she had actually observed something which could be only recombination in mitochondrial DNA from a tiny island in Polynesia, viz., a systematic mutation at the 76 th position was cropping up in fully half the tested samples.

The theoretical paper was found to be based on wrong published data by Sykes mathematical coworker, Vincent Macaulay, and Maynard Smith gracefully accepted the error. The experimental one seemed unsound: the upto 8 identical DNA circles in a mitochondrion could recombine as much as they wanted but would produce nothing new, for that there had to be a different DNA circle, but such a one could only come from the sperm, but that seemed impossible. So probably there had been a systematic error made in the testing. Sykes resequenced twenty of his own samples from the same island with nothing going on at number 76. But obstinate Erika had dug in her heels, and refused to either share her data with Sykes, or to retract the paper. In the meantime mitochondria was losing credibility: in the 1999 Oxford exams it was mentioned by many students as unreliable. Finally there was a showdown between Erika and Bryan at a Cambridge conference. But, it was only well into the year 2000 that the mistake was finally conceded in print. Erika's machine had "played up" and had shown position 86 as 76 half the time, the assumed mutation at 76 was in fact the normal base at 86, there was no such mutation ! *"Mitochondria had survived the recombination scare."*

12. The *Cheddar Man*, a 9000 year old (3000 years before farming began in Britian) skeleton found in 1903 from Gough's Cave interested Sykes greatly. For, in a limestone cave, the calcium of the bones is unlikely to have leached away, so the hard hydroxyapatite was likely to be still guarding some in tact DNA within it. (As against this, no bones, and thus no DNA, are found in the *peat-bog bodies*, but the dilute acid of bogs inhibits bacterial and fungal decay, so a lot of their protein survives.) This precious skeleton is now in the National History Museum in London. The curator, Stringer, allowed Sykes to first have an equally old deer bone, from the same cave. Plenty of DNA was found in this. So he was then allowed to make his test on the big toe of Cheddar Man, however the 17.8 mg of powder carefully drilled out from this yielded no DNA. After this, during a conversation with the curator, Sykes observed that the Cheddar Man's teeth looked in better shape than his own! At this, Stringer showed him *the lower jaw of a young man, "with teeth as good as in a toothpaste ad", found in the same cave, which had been carbon-dated to 12,000 years ago!* With the help of his dentist, Sykes taught himself how to extract a little dentine from a tooth embedded in a jaw, by drilling a tiny hole which could then be hidden by a colour-matching cement. After this, the curator allowed him to test on this jaw: *DNA was found in it and lay smack in the middle of the largest of the six clusters!* Sykes' findings had now been vindicated by a direct DNA test on a sufficiently old skeleton.

*"The doyen of evolutionary biologists": he introduced the concept ESS (evolutionarily stable strategies) independently of John Nash but later it is practically same, a Nash Equilibrium.

Actually, as part of a TV science series, he was allowed later to test also one of the teeth of the Cheddar Man himself: DNA was found and belonged to one of the six clusters. The TV series, which also dealt with the excavation of a Saxon palace, was shot in the grounds of a school where this archeological find was made. Twenty *DNA samples, taken now by gently rubbing a small brush against the inner cheek,* from this school were tested. Two were a perfect match with the Cheddar Man, a third very close. The first two being teenagers, their names were with-held to avoid media intrusion into their young lives. A wise precaution, for soon the pulp press was propositioning the third, Targett, the history teacher, to pose almost in the nude with a replica of his ancient relative for £ 10,000 ! "Being a sensible man, conscious of his standing as a teacher, he declined." Sykes also recalls visiting Lord Bath, the *Loins of Longleat*, so-called because he maintains a number of "wifelets" on this estate besides his legal wife, also a number of African lions which tourists pay to see. Gough's Cave is a part of this huge estate. A DNA test, on the Lord himself, revealed no close relationship to the Cheddar man, but it turned out that his butler, Cuthbert, was another perfect match !

13. Cavalli-Sforza answered the last of his criticisms partly by himself. The paper, *"The genetic legacy of Paleolithic* Homo sapiens *in extant Europeans: a Y-chromosome perspective,"* which appeared in *Science* of November 2000, of which he is one of the many authors, has shown that European prehistory, as revealed by a totally different gene, matches closely that revealed by the mitrochondrial gene.

The Y-chromosome is the smallest in the nucleus, still its 60 million bases make it extremely long in comparison with the 16.5 thousand of the mitochondrial. However it is found only in men, this being due to the fact that the single gene on it which matters, SRY, is the one which turned the embryo away from becoming a girl, towards becoming a boy. Half of the father's sperm have this chromosome, the other half the X-chromosome; had one one of the latter entered the mother's egg, the baby would have been a girl. Since most of this long linear molecule is junk DNA, it was expected that it would have enough and steady mutations, and thus could serve as another molecular clock, and could be used to develop a parallel paternal genetic history. Yes, the two ends of it are subject to some recombinations with the X-chromosomes, and so only the remaining 90% should be so used. But in the beginning it was disappointingly found that it was too stable. In one study a 14,000 base long segment taken from this middle was found to have only one mutation for the 12 men tested, in another a 700 base segment was found ~~to~~ identical in 38 samples. Despair set in, and fantastical suggestions by some that long ago perhaps societies had just one important man acting as a stud, and that was why there was so little variety in it. A hard slog however revealed that there were lots of mutations, but spread all over the length of the chromosomes. Later it was found that *many of these mutations take the form of doubling of some segments*, and since such doublings are easy to spot, this suddenly made DNA fingerprinting of this chromosome a practical reality. These we have in fact met before: *the "missing nine bases" in the mitochondrial gene of some Polynesians, wasn't so much a deletion, as a duplication of a nine base segment in the rest of us.* It seems this work has benefited and been vitiated by big business: many labs are doing parallel work, building

their own evolutionary networks, and not readily sharing the fingerprinting information with each other.

The above paper interprets Y-chromosome data from 1,007 males from 25 European and Middle East locations. They found for Europe now ten Y-chromosome clusters, so, one can say, imitating Sykes imaginative phraseology, *ten sons of Adam !* This new Y-clock then placed most of these last paternal ancestors in the Upper Paleolithic Age, before the advent of farming in Europe, ended up *supporting the conclusion, reached before by Sykes and his team, that the ancestry of the present European gene pool was 80% Paleolithic and 20% Neolithic.*

14. *Each clan mother obviously needed to have at least two daughters who have extant descendants, and she perhaps lived where the original sequence has had time to gather the maximum variations*, this being tempered by other factors, e.g., Scotland won't do because it was uninhabitable then. It is mentioned that 95% of Europens belong to one or other of these seven clans. Drawing on established archeological and climatic records Sykes writes in next 7 chapters the possible life stories of these seven women. Sticking to the science only, there is little here.

15. *U for Ursala.* The oldest cluster, going back to 45,000 years ago, 11% of Europe belongs to it, he situates this "daughter of Eve" in Greece. The Neanderthals were very much around then. Evolutionary adaption had ensured that ovulation did not occur in a mother until her child was old enough to walk comfortably with his nomadic group, and since life span of even 35 was very exceptional then, population was exceedingly small. The Cheddar Man belonged to U.

16. *X for Xenia.* The next oldest, 25,000 years ago, so it was even colder now. This cluster is 6% of Europe, the mother is sited between the Black Sea (then of course a lake) and the Caspian.

17. *H for Helena.* The next oldest cluster goes back to 20,000 years ago when the Ice Age was almost at its peak. This is by far the biggest cluster, fully 47% of Europe belongs to it (so that young man who left us his jaw in Gough's cave was H) and the clan mother is sited in southern France, this time with lots of direct evidence: that's where all those Cro-Magnons caves with the wonderful artwork are!

18. *V for Velda.* Lived 17,000 years ago in northern Spain, still colder then, her descendants account for 5% of Europeans.

19. *T for Tara.* Living 17,000 years ago in north coastal Italy was Sykes very own clan mother, reason maybe she is depicted as the most ingenious? She discovered how to boat ! Hers come to 9 % of Europe.

20. *K for Katrine.* Her clan is 6% of Europe, she lived 15,000 years near Venice, of course not much flooding then, sea was still a hundred miles away.

21. *J for Jasmine.* Compared to the others she had a much easier time, being amongst the much more advanced farmers of what is now Syria. Her descendants who emigrated there come to just under 17% of Europe. All these percentages add up to 101% but previously was mentioned only 95% of Europe belongs to the seven clusters, so maybe there is significant

overlapping between some clusters ? That is, some of them have very indistinct boundaries between them ?]

22. Using mitochondrial gene, *world population splits roughly into 33 clusters.* Of these 13 are in Africa, amongst these all the oldest, as shown in Figure 7, which shows their ancestry upto the *Mitochondrial Eve* of Wilson et al., 150,000 years ago, when total human population was about 2,000! Only one of the old African clans, Lara, accounts for the future history of extant humans outside Africa, it is highly unlikely but theoretically possible just one female of this clan came "Out of Africa". The route must have been across Egypt, the straits of Gibraltar is a very deep channel, which has never been a land bridge, though only 15 km across.

There are signs in Israel of *Homo sapiens* there 100,000 years ago. Perhaps they remained in the Middle East for another 50,000 before venturing out. The four genetic clans of Mongolia or therabouts are closely linked to Native Americans. This crossing probably occured 12,000 years ago, though a minority opinion, largely based on just two isolated older sites in Brazil and Chile whose dating is contoversial and where no human remains have been found, opts for a much older crossing about 50,000 years ago. These people were trapped within two huge ice sheets for thousands of years in Alaska, till a narrow harsh corridor opened into the Great Plains of North America. The subsequent settlement was very swift. About 1% of Native Americans belong to a fifth *Y-h* clan like that of Polynesia which might indicate a parallel oceanic infiltration of humans into that continent via people going up the Asian coast, then down the Pacific coast till central America.

Out of the Near East there might also have been a different emigration towards India along the coast, but the rising sea waters have erased archaelogical signs of this route. This easier route may also explain the amazing recent finding that *Homo sapiens were there in Australia 60,000 years ago*, that is, before Europe and Central Asia! This riddle will take some time to solve: right now, Native Australians are very wary of DNA tests conducted by erstwhile oppressors, so there is hardly any genetical data available concerning them.

There is also a hunter-farmer type of problem regarding the genetic pool of modern day Japanese. Those in the very north and south seem descended mostly from people who reached there 12,000 years ago, the others mostly from those coming from Korea much later. Seems genetics will have something of value to say about all such questions.

23. In this moving last chapter Sykes emphasises that *"The whole of early human pre-history is based on the decisions of individuals or, at the very most, small bands"*, so very different from the present world of governments, corporations and invasions. *"A boat sinks. A Polynesian island is not discovered for another hundred years."*

We the living, each hold a thread going out from the brightly-lit stage of life into an ever-increasing darkness containing tiers of all the previous generations which preceded us. *"I pull on the thread and one woman's face in every generation, feeling the tug, looks up at me."* This connection is umbilical. *"A thousand rows back stands Tara herself, the ancestral mother of my clan. She pulls on the cord. In*

the great throng a million ancestors sense the tug in lines that radiate out from her source. I feel the pull in my own stomach." He is happy that his work has corrected partly the stupidity of thinking in terms of patriarchal trees only, and suggests usage of a *matriname* which will facilitate construction of matriarchal trees in the future.

He gives many examples. A Jamaican in Bristol, happy beyond measure at knowing the exact African DNA cluster she belonged to. Of a Korean DNA sequence which keeps cropping-up in both Norway and Scotland. Of a Somerset dairy farmer with an African sequence, a legacy perhaps of a Roman slave. Of two fishermen, living on the same island off Scotland, the genetic history of one going westwards via Portugal into South America and then Asia, and that of the other, eastward via Finland back into the same Central Asian region! *"These stories and others like them make nonsense of any biological basis for racial classifiation."*

Sykes writes, *"At a recent confrence I sat aghast in the audience as patent lawyers and biotechnologists debated the pros and cons of patenting genes"*, one view being that DNA which can now be synthesized is patentable like any other chemical: *in fact patents are being filed every day claiming ownership of various parts of our genes!* There he was looking at people to whom the human genome was like ticker-tape of a stock market, while to him DNA was what connects us to the mysteries of the past and enhances, not diminishes, our sense of self.

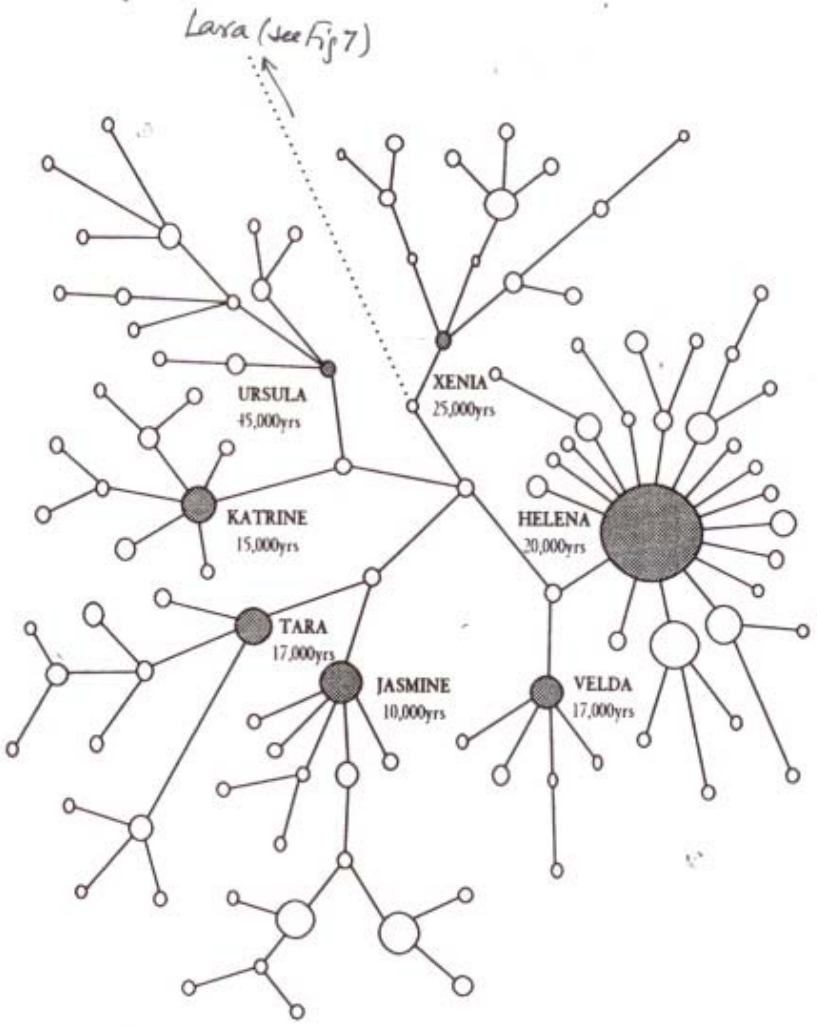
Lara (see Fig 7)
URSULA
45,000yrs
XENIA
25,000yrs
KATRINE
15,000yrs
HELENA
20,000yrs
TARA
17,000yrs
JASMINE
10,000yrs
VELDA
17,000yrs

Figure 6

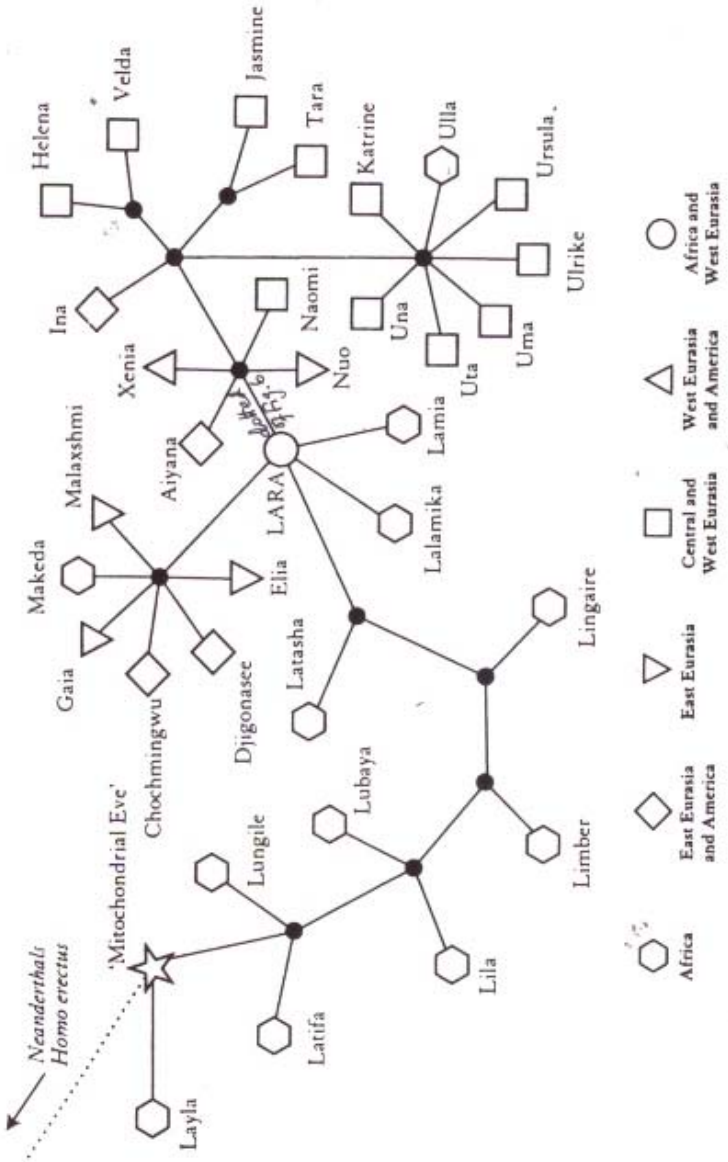

Figure 7
WORLD CLANS AND WHERE THEY ARE FOUND