JIŘÍ A. MEJSNAR

THE EVOLUTION MYTH

OR THE GENES CRY OUT THEIR URGENT SONG, MISTER DARWIN GOT IT WRONG

KAROLINUM

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PREFACE

Humankind celebrated the year 2000 as the advent of a new century and a new millennium. The impressive millennial fireworks set off above the famous trio of pyramids on the Giza Plateau marked 5,000 years of the history of Mediterranean civilization, the basis of Euro-American culture. Photographs of the fireworks on the night sky above the pyramids, symbolizing today's connection to the painful but also bright moments of the human past and future opportunity, travelled as a message round the world.

The year 2000 also witnessed another peculiar event. For the first time in human history, Man entered a new century, knowing his own genome, with all the consequences of this revolutionary achievement. In 1988, the US Congress approved the Human Genome Project, which was to take fifteen years. An international undertaking, it formally began in October 1990, and was completed five years ahead of schedule. It is perhaps humankind's most ambitious scientific undertaking ever. Surprisingly quickly, thanks mainly to the efficiency of the private sector, the US President, Bill Clinton, and the British Prime Minister, Tony Blair, declared the first survey of the entire human genome complete in June 2000. This great historical success alone, however, does not bring us nearer to elucidations of the origin of life, the origin of species, and the origin of Man. Nonetheless, the successful charting out of the human genome is based upon decisive discoveries that molecular biologists and geneticists made during the second half of the twentieth century. The experimental data behind these discoveries must be taken into consideration when considering the three main problems in explaining the origin of life.

It may well be asked, does one need yet another book on the topic, when so many works, on the origins of life, species, and Man have already been published during the past two hundred years? One does indeed, and the chief reason is that during those two centuries the authors of these publications have based themselves upon a great many hypothetical considerations, without adequate scientific means to address such problems. Scientific advances made in cosmology, molecular biology, and genetics offer more reliable data, allowing us to calculate, for example, the age of the Universe, the period in which the biblical Eve lived, and, with good justification, to reject the possibility of the Neanderthals and primates being our ancestors. These data have to be presented to readers of all professions and occupations who are interested in these questions.

Another reason for such a publication is related to biological evolution and how it may have taken place. It is astounding how many people, including professionals, at the start of the new millennium, still believe in the mechanism of 'natural selection'.

Amongst experts, evolutionary biology has been contributing to this belief. In the previous century, this discipline has developed into a wide field in which authors have published their findings and intellectual constructs, most of which they are quick to call 'theories'. This book is against evolution, which means that it intentionally refuses to get involved in countless evolutionary conjectures. The reason is simple. No evolutionary biologist has so far put forth even one experimentally verifiable hypothesis formulating the emergence of a new biological species or at least a new organ by means of evolution. For example, it is easy to proclaim: 'Terrestrial vertebrates evolved from fish'. A hypothesis that would, upon verification, support such a claim should somehow sound as follows: The following ten genes [...] participate in the embryonal development of gills and ten completely different genes [...] in the embryonal development of lungs. The DNA that constitutes the ten genes for the lungs of the assumed descendents differs from the DNA of the ten genes for the gills of the assumed ancestors in twenty per cent of the bases, that is, a total exchange of *x* million chemically defined bases. This change in DNA took place in evolution on Earth in the period [...] by such [...] molecular mechanisms, randomly operating in such a [...] sequence, resulting in such [...] transitional forms of respiratory organs gradually less like gills and more like lungs during natural selection.

Amongst the general public, the evolutionary orientation is supported by the mass media and various public activities such as the

HMS Beagle Project (rebuilding the ship that took Darwin on his distant voyages), a 24-carat gold coin, issued in Tristan da Cunha to mark the 200th anniversary of Darwin's birth and celebrating 'one of the greatest scientists ever', or the launch of a new American journal, *Evolution, Education and Outreach*, 'to aid in the teaching of evolutionary theory'. Such activities have little in common with science.

During the last six decades, molecular biology has, besides surveying the entire human genome, collected experimental results indicating the great stability of the gene. This stability is definitely not for the benefit of random variations of the gene. The research has provided the given number of known complicated techniques that allow molecular manipulation with DNA, and lead to intentional change, that is, variation in the gene. The complicatedness of these techniques make them inaccessible to Nature. This book also aims to present these basic results. They are difficult to reconcile with the hypothesis of continuous biological evolution based on the natural selection of random variations, and consequently indicate that 'the origin of species by means of natural selection' is not an ingenious theory, but a poor hypothesis.

The book is intended for the general public. The explanation of some facts cannot avoid including some technical terms. They are printed here *in italics*. Despite the intention to avoid terminology unfamiliar even to the inquisitive non-specialist, some terms, particularly those used in molecular biology and genetics, are printed, when first occurring in a chapter, *in underlined italics*. This indicates that they also appear as glossary entries. Some complicated facts or arguments are explained in greater detail in four appendices.

CHAPTER I. MAN IN NATURAL CLASSIFICATION

in which it will be discussed how the scientific classification of species, including Man, is merely tentative empiricism, having nothing to do with the objectively existing regularity discovered in Nature.

Wandering through nature, we have to marvel at the variety of life, with its many animal and plant forms. Even when looking through a microscope, we are amazed, for example, at the bizarre, complicated structure of the snail's 'love arrow' or the multiplicity of microorganisms. It is therefore understandable that the millions of different organisms we observe around us must somehow be sorted and organized into groups and then into groups of groups, each comprising a set of smaller groups, to aid our orientation amongst them and our study of them.

As an analogy, consider the problem librarians face in classifying books and other publications. In their place, we would immediately feel pressure to select a set of criteria according to which we could arrange our collection of books. The results of our activity might, for example, be shelves containing history books, shelves for science books, shelves for art books, and so on.

To solve the sorting and organization problem of the multitude of life forms requires the careful observation of the characteristic features that can help us to put organisms into practical groups of a manageable size. Like the librarian's, this sorting activity is called *classification*. The current classification system has its origins in the eighteenth century and has become absolutely essential for scientists all over the world to facilitate their search for information about a given organism, and to help them to exchange new data about it.

The classification system helps the general public to understand this information and to find its bearings in it. For scientists, it is indispensable. Only in this sense, however, can we talk about 'scientific' classification. It has nothing to do with any scientific achievement involving the discovery of an objective regularity in Nature, as, for example, in the system expressed by the periodic table of the chemical elements. There, the elements are listed in order of increasing atomic number (roughly reflecting increasing atomic mass) thus yielding *periods* (the rows of the table), and showing the periodic repetition of the same properties collected in *groups* (the columns of the table). Coming back to biological *scientific classification*, it is not, for the time being, important to us whether by the regularities in Nature we mean Natural Laws, that is, mathematically inviolable logical structures confirmed by our experiments, or mean collections of observable forms, features repeatedly emerging and accepted as generally valid facts. It follows from this that the organisms themselves do not really fall into the group that one has selected and named according to their characteristic features. The groups do not exist independently of the convenience they offer in sorting them.

If one has sorted the characteristic features well, one's sorting and the resulting system of grouping will be widely accepted because the classification is useful for present purposes. Nevertheless, if someone else is more successful in choosing characteristic features, then his or her classification may prove to be more useful for biological studies, even if the final classification system and resulting groups are distinctly different from the former ones. Returning to our library analogy and the problem of organizing books in a new system, we may find that the 'history' shelf has disappeared, because books about the history of discoveries are now on the shelves related to discoveries, and books on the history of kings, emperors, and their wars are now on shelves related to politics. When making such a basically arbitrary rearrangement, one has to be aware of the possible discomfort it will cause to others who formerly knew their way around that library. Though the new system could be more functional in future, those who are unaccustomed to it will still be completely confused.

Coming back to *natural classification*, you may recall that every organism is given a scientific name in Latin, which consists of two parts. The first name indicates the *genus*, the second the *species*; in terms of group size, the *species* is the smallest group and the *genus* is the next smallest in the classification system. For example, the scientific name for Man, as is commonly known, is thus *Homo sapiens*.

We must now deal with one fundamentally important consideration at this level. Take a biologist who wants to find some logical way to bring Man into the natural classification system, that is, to select the human characteristics that are most suitable for differentiating humans from other organisms. The human skeleton has a skull, a backbone, and four extremities. Crocodiles, birds, foxes, and pigs, and some fish have these features, yet all look very different from humans. The biologist therefore needs to find additional characteristics to distinguish them from humans. Newborn human beings suckle milk from their mothers. This characteristic works well for sorting organisms into the *class* Mammalia. It turns out to be a useful feature and allows the biologist to exclude all fish, amphibians, reptiles, and birds. Within the *class* Mammalia, the biologist still needs to introduce additional characteristics in order to exclude organisms such as foxes and pigs from the *genus* of Man. While foxes and pigs look very different from man, monkeys, especially tailless apes such as gorillas, chimpanzees, orang-utans, and gibbons, bear more than a passing resemblance to him. This enables one to put them into a common group. This decision emphasizes that mammals have the most complicated central nervous system enabling more complicated patterns of behaviour, their eye-sockets are oriented frontally in the skull, their wombs have particular characteristics, and the first of their five-finger (pentadactyl) forelimbs can be put in opposition to the remaining four. In this way, foxes and pigs are logically excluded, and the *order* Primates, the common group containing both man and monkey, is introduced. Such a process requires precise work and a deep knowledge of the classified organisms; it yields a logical natural classification system which is meaningful and offers general orientation and a means of communication among zoologists.

On the other hand, having the same selected characteristic features for the groups under discussion, but nothing more than these arbitrary selected data, the biologist could use them in different ways. Before doing that, one must be aware of the meaning of 'characteristic features'. They involve not only structural similarities obtained by comparative anatomy, but also functional similarities revealed by the methods of comparative physiology, biochemistry, comparative immunology, and other disciplines. To ensure a clear general understanding, let us restrict our discussion to structural data as an example of characteristic features. For the moment, it is not important whether the structural data, considered descriptively, just as a matter of form, are collected as the characteristic features at the distinguishing level of comparative anatomy or at the molecular level investigated by molecular biologists. Mammals have four limbs, as do crocodiles, and both groups, mammals and crocodiles, have four-chambered hearts (unlike the three-chambered heart common to most other reptiles). These and other data could be used to formulate the hypothesis that mammals have a common four-legged ancestor that was not at the same time an ancestor of the crocodile. But the mammalian ancestor and the crocodile ancestor both have their imaginary common four-legged ancestor with other characteristics convenient to the hypothesis in some imaginary time in the past. Using the same logic and going forward, one can correctly state that wine yeasts have no limbs, and are single cells containing a discrete nucleus just like mammals, crocodiles, and other multicellular organisms. Continuing in this line of thinking, one can consider hypothetical ancestors of unicellular and multicellular organisms, both of which have a nucleus. Using this method of speculation, one arrives at a common ancestor for wine yeasts, crocodiles, and mammals. If bacteria (cells with no nucleus) are included in this deduction, then one ultimately finds the common ancestor of all organisms.

In general, once they have the data collected during the observation of similar organisms, biologists can use the data in two ways, placing them into well-arranged systematic groups. In the first, like the precise work of a librarian, they can use *taxonomic classification*. The second way utilizes the same arbitrary selected features plus the introduction of imaginary time. They can then argue that organisms sorted into a given group acquired their similarities from a hypothetical ancestor living in an earlier time. The ancestor initiated a set of gradual changes under unclear circumstances, which took place from one generation to the next and created characteristics that ultimately led to the organism's being classified in a different taxonomic group. This mode of consideration is called *biological evolution*. Evolution is thus understood as a continual process by which new species arise as a result of small incremental changes to a pre-existing species over a certain period.

After this part of our discussion, it should come as no surprise that systematic zoologists have, during the last fifty years, substantially re-arranged the *natural classification* system, including the *phyla*, the highest classification rank. Biologists other than systematic zoologists, who fifty years ago possessed a sound knowledge of *natural classification*, are now in the position of people who have come back to the re-arranged library; they have to abandon the notion that they know their way around it. The large rearrangement of the *natural classification* system is mentioned here because it can help one understand the essence of the taxonomic scaffolding into which Man has been bound, especially when the scaffolding is used to support the notion of evolution. Moreover, we should not overlook the strange iteration underlying the evolutionary hypothesis, in which arbitrarily selected features or characteristics of a given taxonomic group provide the evidence for evolution; and as evolutionists learn more and more about evolution, they find new features that help them to rearrange organisms into rearranged taxonomic groups.

CHAPTER II. THE AGE OF MAN

in which you will read that Man appeared on Earth between 150,000 and 200,000 years ago. Man has therefore inhabited our planet for the relatively short period of between only 6,000 and 8,000 generations.

Man, who at the onset of the twenty-first century numbered more than six billion, today, at the time of publication, numbers more than seven billion, has inhabited our beautiful planet Earth for between 150,000 and 200,000 years. In genetics, one generation is 25 years. If we calculate the number of generations based on this length of time, it comes to the relatively small number of between 6,000 and 8,000 generations. How do we know this and how can we measure a quantity like the age of mankind?

Nowadays, we have this basic result at our disposal thanks to a great deal of painstaking work in molecular and cell biology, genetics, palaeoanthropology, archaeology, and palaeontology. The estimation of the age of Man has resulted from a selection of complimentary data from all those disciplines and putting them into their proper place to complete our jigsaw puzzle.

Mitochondrial DNA (mtDNA), from the circular *chromosome* of *mitochondria*, has proven itself to be very useful in this particular field of study. Recall that bacteria are the smallest cellular organisms without a cellular nucleus. Structurally more complex organisms (beginning with nucleated algae and fungi), all plants and animals are composed of cells equipped with a cellular nucleus, that is, eukaryotic cells. Mitochondria are organelles of the eukaryotic cells with a decisive role in cellular energetics. For that role, they contain in their fluid interior (the *mitochondrial matrix*) the enzymes of the *citric acid cycle* (also called the Krebs cycle). This is a cyclic pathway of chemical reactions, in which the metabolites from our food liberate electrons. This interior compartment is enclosed by an inner membrane. Within this inner membrane lies a complex *respiratory chain* together with a protein complex for so-called *oxidative phosphorylation*. (The respiratory chain utilizes the energy of the delivered electrons; these electrons pass through the cascading steps of the respiratory chain, and their energy is utilized for the translocation of protons outside the inner membrane. Oxidative phosphorylation is the process that – on account of the energy delivered by the translocated protons – yields molecules of ATP, as the universal energy-storage molecule in living cells.) Detailed current knowledge of mitochondrial energetics can be found in any modern biochemistry or physiology textbook.

The simplest unicellular eukaryotic organisms have a single large mitochondrion. Generally, with the increasing complexity of organisms the number of mitochondria increases in their cells. Returning to our estimation of the age of mankind, all human cells have hundreds of mitochondria, each containing a circular double-stranded mtDNA molecule, forming the mitochondrial chromosome. The mtDNA molecule (see **APPENDIX 1**) represents the human mitochondrial *genome*. It consists of 16,569 base pairs and contains 37 *genes.***(1)**

Molecular biology, focused on the mitochondrial chromosome, is a key source of quantitative information about the age of mankind. The mtDNA molecule offers several advantages for this study. Perhaps the main advantage is that, unlike nuclear genes (on chromosomes in the cell nucleus), which are inherited from both parents and therefore mix in every generation, mtDNA is inherited only maternally. Women, consequently, behave as *haploids*, which means that a pair of breeding individuals can transmit only the woman's mtDNA (contrary to four parental haploid sets of transmissible nuclear genes, among which are combined those that are randomly transmitted to *diploid* offspring). The woman's mtDNA can only be changed at some points by *mutations*.

It may be beneficial for non-biologists to review the main steps of a classic article published in the prestigious journal *Nature*. The authors isolated mtDNA molecules from representatives of seven geographic regions: Africans, Asians, Caucasians, aboriginal Australians, aboriginal New Guineans, one African American, and one aboriginal South African; all together, 147 individuals were included in the study. The mtDNA from each individual was purified and cut into 370 small fragments. (The 'scissors' are enzymes called *restriction endonucleases*.) Each fragment was analyzed for differences in mtDNA sequences between individuals, due to point mutations. (Point mutations are discussed in **APPENDIX 3**.) Then, divergences were evaluated within and between the respective populations. The timescale of the mutations was found,

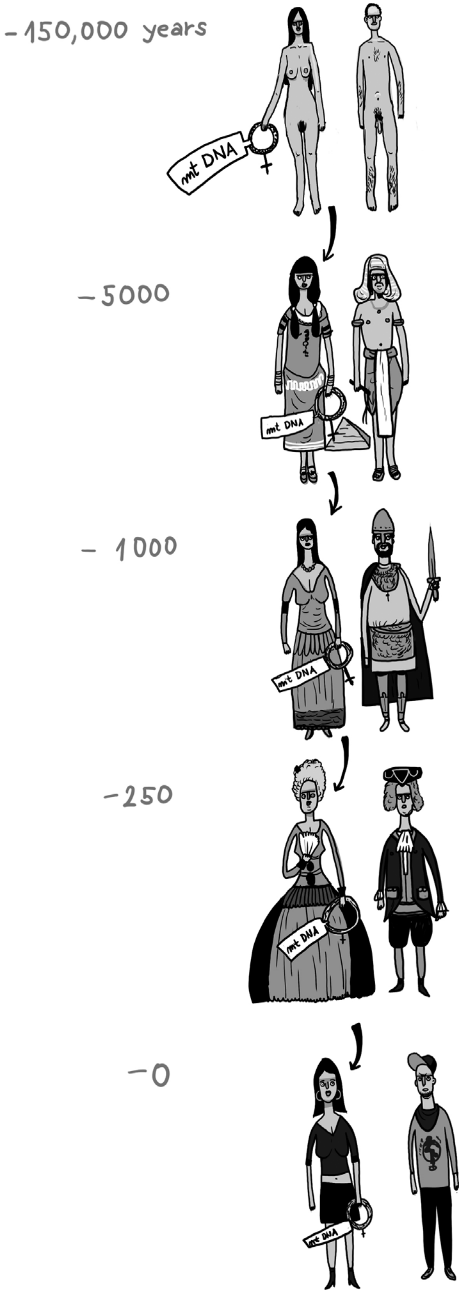

Fig. 1 mtDNA transmission only maternally.

on the assumption that mtDNA sequence divergence accumulates at a constant rate in humans, which lies between two and four per cent per million years. The results imply that all surviving mtDNA types are derived from a common woman ancestor who existed between 140,000 and 290,000 years ago.**(2)**

The conclusion achieved in this way immediately leads to an obvious question: What is the validity of the mtDNA method used? From this follows another question: How decisive is a statement based on a comparison of individual human mitochondrial genomes? The underlying data on molecular biology and genetics are among the brilliant achievements of the twentieth century. Anyone who has a more intimate knowledge of the process (a discussion of which is beyond the scope of this book) has to accept the high-resolution mapping of mtDNA. A calibration of the rate of revealed mtDNA *variations* has to be provided in human populations that colonized a specific region at a defined time and remained in relative isolation after colonization. The method of calculating the divergence rate is described in detail for New Guinean, Australian, and American aboriginal mtDNAs elsewhere.**(3)** Extensive research is of course currently underway to obtain a more exact calibration of the timescale. Additionally, like any method for quantitative measurement, mtDNA timing has some attendant problems, both general (for example, in relation to nuclear DNA studies and in relation to the younger age of certain fossil sites) and technical (the 370 fragments per individual cover only 9 per cent of his or her mtDNA genome). More exact time calibration and the future solution of particular problems, however, do not substantially change the conclusion relative to the presented age of humans.

Combining this mtDNA chronology with archaeological and demographic data, most studies date the disconnection of Man's mtDNA from all pre-existing Eurasian *Homo erectus* or *Homo neanderthalensis* mtDNA to 500,000 years ago at the earliest.**(4)** The mtDNA age of Man matches well for humans who arose in Africa, probably followed by migration out of Africa by a small part of their population, which has been dated by the Genographic Project to 200,000 years ago.**(5)** Why is this determination of the age of Man so important for us in this book? It allows us to accept as a fact the existence of humankind during this period. Then, all efforts to connect humans with the *genealogy* of those hominids living before the period of Man have failed and all assertions to the contrary remain, at present, hypotheses, contradicting the presented data.

CHAPTER III. CRO-MAGNONS AND NEANDERTHALS

in which it is written that within the period beginning with mitochondrial Eve Man has remained biologically unchanged. The only distinct human type that preceded this period and at first shared the territory was the Neanderthal. The only evolution of Man has been in the development of the human way of life, culture, and technology.

Man is no older than about 200,000 years. This fundamentally important fact is the result of solving the puzzle, as presented in Chapter II. In other words, the previous chapter presents molecular biology and genetics, clearly showing that all people now on Earth share their origin in the maternal line from mitochondrial Eve, or biblical Eve, if you like, who lived some 200,000 years ago.

The period 200,000 years ago is projected in the geological timescale at the *Pleistocene*, to the *Upper Palaeolithic* period dating from 1,800,000 to 11,000 years ago. According to anthropologists and archaeologists, there are two Palaeolithic (Old Stone Age) representatives currently classified as the species *Homo sapiens* and generally known as Cro-Magnons (archaeologists today call them European Early Modern Humans) and Neanderthals.

Cro-Magnon man is named after the first finding of remains of his five skeletons in the Cro-Magnon rock shelter near Les Eyzies-de-Tayac-Sireuil in the Dordogne department in 1868. If you would like to find the place and mainly to experience this beautiful region of southwest France, bordering on the Bordeaux region of elegant wines, you have to be inspired with the courage and boldness of the Cadets de Gascogne (Captains of Gascony), you have to be touched by the hidden profound sensuality of Cyrano de Bergerac, and be impressed by the paintings of Henri de Toulouse-Lautrec.

During the next century and a half, the discovery of the original place near Les Eyzies has been followed by the discovery of other sites all over Europe, from Spain, with its famous Altamira Cave, to the fossil sites at Předmostí and Mladeč in Moravia (the Czech Republic), to the Ural Mountains. Since the 1970s, the name Cro-Magnon can generally be used for early humans all over the world – in North Africa, the

Middle East, Central Asia, and even for Palaeo-Indians in North and South America.

What is the age of the oldest Cro-Magnon remains? The data are inferred mainly using the radiocarbon method, the principle of which is elucidated in **APPENDIX 2**. The type specimen from the Cro-Magnon discovery at Les Eyzies is dated to about 28,000 years ago.**(6)** Perhaps the oldest remains from Europe were found in Peștera cu Oase, Romania, dated by radiocarbon ^{14}C spectrometry to between 34,000 and 36,000 ^{14}C years, equivalent to about 45,000 calendar years ago.**(7)** In addition, we have to bear in mind data concerning the migration of the Cro-Magnons. Their exodus from Africa to Eurasia began about 100,000 years ago and continued over the Arabian Peninsula to Central Asia and back into Europe, probably along the Danubian corridor towards the sites presented above.**(5)** The origin of the Cro-Magnons therefore has to be older than 100,000 years. To sum up, that means that the results documenting the age of Man have been achieved in three ways. Therefore, just as various means of transport (for example, bicycle, car, plane) enable one to achieve different speeds of travel, so various methods used to determine the age of Man yield various ages. The surviving fossils are not older than 50,000 years. Migration studies demonstrate that the Cro-Magnons originated more than 100,000 years ago. These conclusions correspond well with the mitochondrial DNA data described in the previous chapter.

Cro-Magnon people anatomically more or less resembled us, because their *genotype* is identical to that of the present population. Contrary to their appearance, which did not fundamentally change, their way of life was continuously changing, faster and faster, the closer they (we) came to the twenty-first century. Cro-Magnons living at Palaeolithic fossil sites were primarily hunters. Their tribes however, lived as a community, using a developed division of labour. As the Czech actor-writer George Voskovec said: 'The man who was courageous hunted the mammoth, the one who was reliable tended the fire, and the one who was neither courageous nor reliable held the post of chief or magician.' No doubt, they had knowledge of rituals; it is fair to say that Man, since his origin, has been affected by 'ideology'. Coming to what are now the archaeological sites of Europe, they hunted with spears, axes, and clubs, and made sophisticated tools of chipped flint. (Archaeologists divide the Stone Age into three periods mainly according to the type of tools used.) People