Genetic Adaptation of Man

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INTRODUCTION

Today it is known that there exist physiological, morphological and biochemical changes in the human organism during the process of its adaptation to certain extreme environmental factors (e.g. cold and hypoxia). At the same time, the possible existence of some genetic (more precisely genic) changes in the genome of an adapted man or population, that was postulated by a number of investigators, has not as yet been documented by concrete scientific data.

Results of the well-known International Biological Program (IBP) indicate that attempts to reveal certain systematic differences from features of the distribution of genetically polymorphic systems (blood groups, electrophoretic variants of proteins and enzymes, anthropological traits, etc.) between human populations living permanently under different environmental conditions of the terrestrial globe, including extreme ones, were unsuccessful (Baker, 1978). Almost the same results have also been obtained during the realization of "the Multinational Andean Genetic and Health Program" in aboriginals of high – and low-altitude regions of South America (Schull and Rothhammer, 1977; Ferrell et al., 1978). However, the search for specific genes of adaptation, to high-altitude climate in particular, continues (Beall, 2000; Beall et. al., 1994, 1997; Ciminelli et al., 2000; Stroll et al., 2006).

Nevertheless, the very fact of successful adaptation of man to various, different from the tropical climate natural conditions is obvious. The following question arises: was man able to master all the oykumene, remaining at the same time a single tropical biological species without involving his genome?

Let us make a reservation at once the from the genetic point of view adaptation, like evolution, is a unidirectional and irreversible process. All the others (physiological, morphological, biochemical, immunological, etc.) are considered to be reversible, not inheritable, adaptive changes in the organism and are thought to be either acclimation or acclimatization.

Adaptation, like evolution, assumes the participation of three fundamental biological processes: variability, inheritance and natural selection. The most important of them is known to be variability. Without it there is no selection and hence no genetic adaptation and evolution.

As a biological species *Homo sapiens* was shaped in subequatorial Africa and, remaining a single tropical species, was able to master all the oykumene and continues to expand both the zone of permanent residence and to increase his numbers. The question: in what way just man was able to conquer all the dry land – remains unknown.

The species *H. sapiens* always had to and has to adapt himself to climate and its changes, beginning from the time of its appearance under conditions that were complex enough and that, in the long run, gave rise to such profound and perfect physiological flexibility. Therefore, the question only lies in the following: what is the basis of such adaptations.

It is thought that beings undistinguishable from modern man appeared in Africa about 100 000 years ago, 30-40 000 years ago they reached Europe, Asia and Australia, and more than 20 000 years ago – North and South America (Brauer, 1984; Andrews, 1986; Stringer, 1988).

In speaking about modern man - *Homo sapiens sapiens* – three most important features distinguishing him from the other hominoids are usually meant: high physiological flexibility, features of the structure of upper extremities, and aptitude for conceptual thinking. This row also includes such traits as aptitude for bipedal walking, a large neocortex, reduced anterior teeth with dominating molars, a unique sexual and reproductive behaviour, etc. (Harrison et al., 1977). It is clear that this disorderly as to the degree of importance and far from full list characteristic of *H. s. sapiens* can be easily supplemented.

It is obvious that only modern man has adapted himself to high-altitude and northern climate. How our distant ancestors adapted themselves to changing climatic conditions of the middle and late Miocene in Africa, we shall probably never know. But the strategy of adaptation of *H. sapiens*, as we suppose, can still be understood from those changes that occurred in the genome of modern man during the process

of successful adaptation to the extreme natural conditions of high altitude and Far North. This process which lasted several millenniums did not lead serious microevolutionary processes, so that one could speak of the appearance if not of a new species but at least of a subspecies. Therefore, the rule – one species-one ecological niche – known in the animal world, does not apply to man. Even this fact indirectly indicates that the strategy of genetic adaptation of man should nevertheless differ from that in animals. Furthermore, we suppose that the strategy of adaptation of *H. s. sapiens* to high-altitude and northern climate remained the same as in of *H. sapiens* when he adapted himself to changing climatic conditions of the African savannas and beyond them.

GENE OR HETEROCHROMATIN?

The fact that not a single gene or genes of adaptation in man have as yet been found does not actually mean that they do not exist. Examples of genetic adaptation to any of the factors of the natural environment, ecological niches or the whole continent of the animal world have been repeatedly presented. Since man is the most studied and still being studied biological object, we found it appropriate to discuss here all the "pros and cons" of the possibility of the existence of structural genes that have a specific relation to human adaptation to cold and hypoxia.

All those who are searching for a hypothetical "high-altitude" or "northern" genotype are sure or continue to be sure that such specific structural adaptive genes exist (Ciminelli et al., 2000). Some investigators even had time to declare that something similar is possibly present in the genome of highlanders of Tibet, but are absent in Indians of the Andes (Beall, 2000; Beall et al., 1994, 1997; Stroll et al., 2006). We have also searched for genes of adaptation for many years (Ibraimov and Mirrakhimov, 1979; Mirrakhimov and Ibraimov, 1982; Ibraimov et al., 1993). However, no one has as yet been able to find the aforementioned genes, and it is becoming increasingly obvious that this search is possibly vain. Let us at once make a reservation that we do not mean at all that we completely deny the role of inheritance in general in human adaptation. The question is: which part of the human genome is euchromatic or heterochromatic, to be more precise, does the genic or nongenic part participate in the process of adaptation? The necessity for such a reservation is justified by the known circumstance that genetic adaptation usually implies genes, whether they are structural or regulatory.

Since all or almost all the investigators favour the genic component of the genome in human adaptation, I shall briefly outline my "anti[genic]" theses:

1) structural genes that have been located on human chromosomes are only a minor fraction of the total human DNA. Only 3-5% of the DNA in the genome of man are enough to have no less than 100 000 specific structural genes, which enough to ensure functioning of such a complex organism as *H. s. sapiens*. "Each of us has roughly 30, 000 genes, far fewer than the 100, 000 that most researchers had expected. This is somewhat puzzling as some plants have 26, 000 genes; clearly that determines the complexity of an organism" (Buchanan, 2003).
2) not a single protein or enzyme that is completely absent in animals has been found in man;
3) man was and remains the single tropic biological species;
4) during more than a million years of their evolution our ancestors existed in low-altitude tropical Africa and never lived under conditions close to high altitude and the climate of Far North;
5) fully modern humans (*H. s. sapiens)* have emerged from Africa 50 000 years ago, while permanent populations of high-altitude regions and the Far North – still less, maximally severally millenniums ago;
6) almost all the high-altitude populations, with the exception of the Ethiopia upland regions are representatives of Mongoloid or Proto-mongoloid (North and South America) races. This fact assumes that the age of the most ancient populations permanently living at high-altitude populations (e.g. in Tibet) does not exceed 20 000 years, if it is considered that at this time contemporary human races have not yet appeared (Jones et al., 1996);
7) the most recent data show that genetic differences between the presently existing human races are practically small. Strangely, the situation "is not better" between man and our closest kinsman – the chimpanzee. Thus, for example, comparison of the length

of chromosomes of man and the chimpanzee showed that the overall amount of chromosomal material is very similar in these two species: they only differ in the distribution of heterochromatin regions, in pericentric inversions and translocations (Paris Conference, 1971; Supp., 1975; Warburton et al., 1973; Yunis and Prakash, 1982). Experiments on DNA hybridization indicate that at least 98% of the nonrepetitive DNA are identical in man and the chimpanzee – a value that could suggest the possibility of the appearance of a vital hybrid. King and Wilson (1975), summing up numerous studies carried out in various laboratories of the world, have estimated that proteins of man and the chimpanzee are 99% identical. Such a great similarity makes it difficult to give an exact explanation of the large biological differences observed between these closely related biological species;

8) since in his evolutionary past man has never lived under high-altitude conditions and nevertheless was able for last millenniums to master all the high-altitude provinces of the world, the following question inevitably arises: when could the hypothetical high-altitude adaptive genes appear? The problem is also complicated by the question: have these genes (if they actually exist in nature) appeared once, before man began to penetrate into high-altitude provinces (as preadaptation) or every time they appeared again when human populations tried to adapt themselves to the major extreme natural factor of high altitude, i.e., to hypoxia. If we admit the possibility of a repeated appearance of specific adaptive genes in the human genome, then, does this apply to the same genes or these changes occurred in different parts of the human genome? Leaving the question open as to the possible existence of such a mutable gene or genes, let us address another question: how could such favourable mutations spread in the genome of high-altitude populations? These populations are frequently isolated by great geographical distances, frequently in the form of difficult to traverse passes and other obstacles. The problem is also complicated by the fact that aboriginals of high-altitude provinces of Asia and South America never "exchanged genes" in historical times and their ancestors that mastered these mountain regions located on various continents and geographical latitudes in different periods, having a different ethnic composition and ecological experience in the past;

9) the existence of a certain "high-altitude limit" (about 4 500 m above sea-level) for permanent residence of man, and the extremely high infant mortality in high-altitude populations indirectly suggest the absence of effectively functioning specific structural genes in the genome of highlanders (Baker, 1978). For example to estimate reproductive functions in female highlanders we studied pregnancy outcomes in three Kyrghyz populations permanently living at altitudes of 700-900m (I), 2400-2800 m (II), and 3600-4200 m (III) above sea level in Eastern Pamir (Table 1). We questioned women, who had completed their reproductive functions at the time of the study. Indeed, when man has a modern dwelling, clothes, food and a behavioral response, he can exist during a quite long time in the Far North and even under conditions of weightlessness. This is a purely technical, economic and social problem. However, even modern scientific and technical achievements cannot protect man from high-altitude hypoxia;

10) if one is to believe that three qualitative features in man (high physiological flexibility, morphological features of the upper extremities and the aptitude for conceptual thinking) have mainly contributed to his settling on Earth, then, when did he begin to possess such powerful aromorphosis? What were the prerequisites for their formation? Did they arise before or after man to master new natural environments? Can we consider that specific structural genes lie behind these three features of man. If so, then when and why they arose only in man?

11) in the genome of man there are many structural genes and genic complexes with high polymorphism in a population. But they are not inherent only in him and are characteristic of all the animal world. Here apparently the problem is different: a) functions of these genes are too simple and quite ancient and probably not directly related to the complex responses of the human organism to cold or hypoxia; b) since man in his evolutionary past, at least before the

Table 1: The effect of high altitude Pamir on reproductive functions (RF) in female highlanders.

Populations / Pregnancy outcomes	*I*	*II*	*III*
Total number of pregnancies	2964 (100.0%)	2695 (100.0%)	1757(100.0%)
Live births	2724 (91.9%)	2318 (86.0%)	1591 (90.5%)
Stillborns	25 (0.8%)	53 (2.0%)	41 (2.3%)
Spontaneous abortion	173 (5.8%)	324 (12.0%)	115 (6.5%)
Medical abortion	42 (1.4%)	0 (0.0%)	10 (0.6%)
Postnatal mortality	436 {16.0%}	500 {21.6%}	551{34.6%}
Total number of living children	2288 {84.0%}	1818 {78.4%}	1040{65.4%}

(%) of the total number of pregnancies; {%} of the number of live births.

formating of his contemporary appearance, wasn't exposed to cold and hypoxia to the extent of experiencing their selective pressure, it is hard to conceive the existence in his genome of some specific genes or genic complexes of adaptation to cold and hypoxia; c) for an adequate response to the pressure of cold and hypoxia (let alone other known harmful factors of high altitude and the Far North) such a complex organism as that of man could hardly limit itself to responses of one or several structural genes;

12) finally, as to the question: "what does the gene actually do?", one of the leading evolutionists Lima-de-Faria (1988) already pondered deeply over this problem points out: "Genes do not change permanently, as previously assumed, but many genes have been preserved essentially unchanged from bacteria to humans. The many examples include the genes for 28S and 18S ribosomal RNA". "…The gene does not create form and function. The gene products only canalize the reaction in one or other direction". "The creation of the gene introduced several events into the cell: repetition, extra order, speed, fixation of alternatives and increased combination capacity". Speaking about the role of genes in the evolution of man he writes: "Human evolution seems to have depended mainly on changes in regulatory DNAs. The role of structural genes in evolution seems to be a modest one". "…The knowledge of the properties of the regulatory DNA sequences will throw much light not only on human genetic functions but also on human disease and behavior".

Details about the morphology, inheritance, variability and molecular structure of chromosomal Q-heterochromatin regions (Q-HRs) have been given in special reviews (Verma and Dosik, 1980; Ibraimov and Mirrakhimov, 1985; Prokofyeva-Belgovskaya, 1986; Verma, 1988; Bhasin, 2005). Data on the distribution of chromosomal Q-HRs in various natural human populations have been published in a number of articles (Geraedts and Pearson, 1974; Müller et al., 1975; McKenzie and Lubs, 1976; Buckton et al., 1976; Lubs et al., 1977; Yamada and Hasegawa, 1978; Al-Nassar et al., 1981; Ibraimov and Mirrakhimov, 1982 a, b, c; 1985; Stanyon et al., 1988; Kalz et al., 2005; Décsey et al., 2006). Therefore, we shall limit ourselves to brief theses concerning those features of chromosomal Q-HRs which, as we feel, are in favour of their possible selective value in adaptation of man to cold and hypoxia:

1. A fundamental feature of chromosomes of higher eukaryotes, including man, is the presence of two evolutionary consolidated types of genetic material: euchromatin and heterochromatin. Euchromatin – the conservative portion of the genome – contains transcribed structural genes, while heterochromatin – the variable portion of the genome – predominantly consist of nontranscribed repeated DNA sequences. Heterochromatin is universally distributed in the chromosomes of all the higher eukaryotes, amounting to 10%-60% of their genome. About 15%-20% of the human genome are composed of heterochromatin regions (HR) (John, 1988). Chromosomal HRs do not change during ontogenesis and are clearly inherited as discrete features. To-date, two types of heterochromatin are known: C- and Q-heterochromatin. There are several significant differences between them, including the fact that C-heterochromatin is encountered in chromosomes of all higher eukaryotes, while Q-heterochromatin is only present in man, the chimpanzee and gorilla. In man C-heterochromatin is present in all his chromosomes, varying mainly in size, while Q-heterochromatin can only be detected on seven autosomes and the Y-chromosome (Paris Conference, 1971, 1975).

2. despite the fact that chromosomal Q-HRs exist in the genome of three higher primates, their broad quantitative variability is only inherent in human populations (ISCN, 1978; Pearson, 1973, 1977; Seuanez et al., 1976). There are no data on the mean number and the distribution of Q-HRs in natural chimpanzee and gorilla populations. However, the bulk of data in literature suggests that the amount of Q-HRs is greatest in the gorilla and chimpanzee genome and the least amount in man. Let us note that such brilliantly fluorescent chromosome segments are absent in the orang-outang (Seuanez et al., 1976).
3. in terms of genetics Q-HRs are completely inert material, i.e., these chromosomal regions do not contain any structural genes and, therefore, their changes have no consequences for the informative part of the genome and can occur extremely rapidly (Prokofyeva-Belgovskaya, 1986);
4. individuals in a human population differ from each other in the number, location, size and intensity of fluorescence of chromosomal Q-HRs in their genome (Paris Conference, 1971; McKenzie and Lubs, 1975; Müller et al., 1975; Buckton et al., 1976; Yamada and Hasegawa, 1978; Ibraimov and Mirrakhimov, 1985; Kalz et al., 2005);
5. quantitative Q-HR variability in human populations has been studied in sufficient detail (Buckton et al., 1976; Lubs et al., 1977; Yamada and Hasegava, 1978; Al-Nassar et al., 1981; Stanyon et al., 1988). Results of extensive comparative population cytogenetic studied showed that populations of modern man differ significantly (Ibraimov, 1993, 2003). It can be maintained that these differences are mainly related to the natural environment of residence of the human population and not to racial or ethnic features (Ibraimov and Mirrakhimov, 1985). In particular, the amount of Q-HRs is consi-derably lower in the genome of populations living permanently at northern latitudes and high-altitude regions, as well as in newcomers well adapted to extreme natural conditions of high altitudes (mountaineers) and the Far North (drillers), than in populations living in temperate zones of Eurasia (Ibraimov et al., 1990, 1991, 1997). Let us note that both mountaineers and drillers we are dealing with are homogeneous as to racial and ethnic features (Russians) and are natives of low-altitude temperate zones of the former USSR who have migrated to zones with extreme natural conditions because of sporting interests or professional activity;
6. when the mean number of Q-HRs increases, so do, as a rule, the absolute frequencies of Q-HRs on all the seven Q-polymorphic autosomes will increase and vice versa (Ibraimov, 1993). In populations with low mean number of Q-HRs per individual the range of variability in the number of Q-HRs is narrow and vice versa (Ibraimov et al., 1986, 1990, 1991).
7. there are data indicating that Q-HRs located on different Q-polymorphic chromosomes are essence of a similar nature and represent a single structural and functional genetic system. Of primary importance to an individual is the total "dose" and not the location of Q-HRs in any chromosome (Ibraimov et al., 1986, 1990, 1991), and this is in keeping with the well-known concept that "the effect of heterochromatin is additive" (Lima-de-Faria, 1983);
8. the mean number of Q-HRs per individual in a population is greatest in newborns than in older age groups (Buckton et al., 1976; Ibraimov and Karagulova, 2006 a) despite the fact that the number, location and size of Q-HRs do not change in ontogenesis (Phillips, 1977; van Dyke et al., 1977; Robinson et al., 1977; McCracken et al., 1978). This is apparently due to the fact that part of the infants with a greater than average amount of Q-HRs in the genome in a population undergo negative selection in the first years of life (Ibraimov and Karagulova, 2002 a).
9. It was shown that individual with the greatest amount of Q-HRs in the newborn populations have greater probability to die in the first years of life other conditions being equal (Ibraimov and Karagulova, 2006 b)
10. the amount of chromosomal Q-HRs in the genome may be related to the development of certain forms of purely human pathology (Ibraimov and Karagulova, 2002; Ibraimov et al., 2002);

Evidently, in the light of the foregoing, a question inevitably arises: if not genes but Q-heterochromatin, then how can it promote adaptation of the human organism to cold and hypoxia? Let us make a reservation at once that

regardless of whether Q-HR is related or not related to human adaptation, it did not arise during evolution for this purpose, since nothing in nature has a goal. Even if Q-HR does have some selective value, it is not its direct function.

Let us now address the main paradigm of biology: does the part of the genome of man – chromosomal Q-HRs – which as we suppose, are the most suitable for his adaptation genetic material, meet the modern requirements of the theory of evolution?

As Mayr (2000) points out: "evolution involves variation, a struggle for existence and natural selection. Without genetic variation, there can be no evolutionary progress. Natural selection is a two-stage process involving (1) the production of heritable variation; and (2) the winnowing of that variation by environmental demands, with these two stages repeating themselves in each generation".

Data indicating wide quantitative Q-HR variability in human populations, including all the three greatest race groups, have been obtained in dozens of independent studies, including a special scientific program studying chromosomal polymorphism in man in health and pathology in such a multinational and ecologically diverse country as was the former USSR (Prokofyeva-Belgovskaya, 1981).

The fact that chromosomal Q-HR variability is an inheritable and ontogenetically stable part of the genome has already been shown in the first years after the discovery of the phenomenon of chromosomal Q-polymorphism (McKenzie and Lubs, 1975; Robinson et al., 1976; Carnevale et al., 1976).

One of the important components of the evolutionary process – the struggle for existence – as a biological event, has not been studied in the human society for known ethical and other objective reasons.

Natural selection as concerns the modern man does not play a species – forming role but plays a preventive one, and is manifested as morbidity and mortality. Stabilizing selection remains even in the modern economically highly developed countries with a high level of medical service (Jones et al., 1996).

The first evidence as to the possible influence of natural selection on the amount of chromosomal Q-HRs in the genome of man was obtained in 1976 by a group of investigators in Edinburgh, in Scotland (Buckton et al., 1976) when they discovered that individuals in a population with different age groups differ in the mean number of Q-HRs: 4.1, 3.9 and 2.6 in neonates, children aged 7 to 14 years and elderly subjects (65 years and older), respectively. Almost the same results have been obtained by us in Russian and Kyrghyz subjects living in Bishkek (Ibraimov and Karagulova, 2006a). We have analyzed the amount of chromosomal Q-HRs in a genome of neonates deceased first years of life. Mean numbers of Q-HRs per individual in newborn populations were 3, 16 ± 0, 13 in Kyrghyz and 3, 59 ± 0, 23 in Russian, whereas in neonates died 4, 58 ± 0, 23 and 4, 58 ± 0, 37, respectively (Ibraimov and Karagulova, 2006 b). A certain tendency towards decreases in the amount of chromosomal Q-HRs with age was found in two other studies (Nazarenko, 1987; Kurmanova, 1991). We now have data on the possible influence of the amount of chromosomal Q-HRs on the development of certain forms of purely human pathology (Ibraimov and Karagulova, 2002; Ibraimov et al., 2002).

There is no agreement as to the nature of such Q-HRs variability. Earlier we put out a proposal on possible participation of condensed chromatin (CC) in cell thermoregulation; CC being the densest domain in a cell, apparently conducts heat between the cytoplasm and nucleus when there is difference in temperature between them (Ibraimov, 2003). This hypothesis can be checked at the level of cells or organisms. Experimentally we have managed to establish that at the level of organisms there is a broad intra population variability of human body heat conductivity (BHC). It is shown that these individual differences in the BHC are attributed to the amount of chromosomal Q-HRs in their genome (Ibraimov and Tabaldiev, 2007).

It is assumed that, possibly, the biological role of the Q-HRs in the interphase nucleus of the cell is in intensification of the CC compacting thus increasing its heat conductivity (HC). On the HC of CC, correspondently on the amount of Q-HRs in the genome, depends the speed of leveling the difference of temperature between the cytoplasm and nucleus, i.e. the cell thermoregulation. From the HC of the cells the HC of the whole body is made up. This is a physical condition, where the physiological thermoregulation is realized, which is assigned for keeping relative temperature constancy in the inner medium of the organism by leveling the temperature difference in different parts of the body.

Thus, how do we explain age-related differen-

ces in the genome of neonates and elderly subjects? For the sake of convenience let us divide individuals in a population into two extreme groups: with a large and lesser amount of Q-HRs in the karyotype, respectively with high and low BHC (Ibraimov, 1993, 2004) and consider all this using as an example neonates and subjects aged 60 and over.

We suppose that infants with a great amount of Q-HRs in their genome are possibly subject more frequently to over cooling, catarrhal disease, etc. due to high BHC. Whereas, individuals with a low BHC possibly have a certain advantage as concerns their survival in infantile age as compared with those who have a medium and especially great amount of chromosomal Q-HRs in genome.

High morbidity and mortality in infants could be explained, in addition to the known to present day medicine reasons, by a simple physical consideration. As is known, in young children the surface/volume is very high, than that in adults. When one more physical factor, such as high BHC is added, than male neonates, which genome contains more Q-HRs than in girls, become very vulnerable to the factors violating the temperature homeostasis in their immature organism, particularly to common cold and its complications with all subsequent consequences. That is how we explain the "redundancy" of individuals with a lesser amount of chromosomal Q-HRs in genome in the population of elderly subjects (Ibraimov and Karagulova, 2006 b).

Adaptation of man to cold and hypoxia roughly seems to us to approximately represent the following. During the process of evolution man, the chimpanzee and the gorilla have inherited Q-heterochromatin material, among other things from the common ancestors.

However, it was subsequently distributed in their genome unequally, perhaps as a result of population genetic processes that took place in the first stages of diversion of these species. We can hardly hope to learn something about the essence of these processes in the nearest future. However, we know that ancestors of *H. sapiens* got Q-HRs on seven autosomes and the Y chromosome, *P. troglodytes* – only on five, while *G. gorilla* – on eight autosomes and the Y chromosome (Pearson, 1973; Seuanez et al., 1976). Subsequently, each of these species underwent evolution on its own. However, it may be that unusual success attended only *H. sapiens* for the following reasons.

Ecology of the Middle and Late Miocene was far from being smooth, and such climate changes as a fall of temperature, dryness, seasonal and daily fluctuations of temperature became the dominating factors of the environment (Andrews and van Couvering, 1975). Thus, our ancestors, before leaving Africa, could have faced the problem of adaptation to new, more rigorous natural conditions that differed from the climate of the savanna.

According to our model, from the time when in the initial populations of ancestors individuals with different amounts of Q-heterochromatin material began to segregate (as it also happens now), individuals with a relatively low and high BHC appeared (Ibraimov and Tabaldiev, 2007). It was possible just because the number of variable autosomal loci was large enough to ensure the appearance of individuals with different numbers of Q-HRs in a population, and owing to this fact one and the same number of Q-HRs in the genome of different individuals could be secured by very diverse, practically unique combinations of chromosomal Q-HRs. Thus, we are dealing with a complex self-supporting genetic system.

Our ancestors took advantage of this unique feature properly, apparently when climate of the savanna began to change and from the time when they tried to leave it and seek new abodes. This assumption is in keeping with the fact that adaptation in man was not accompanied by formation of species, for, as we suppose, unlike many species of animals and plants, adaptation of man to all the possible places of residence on Earth was not due to changes in the informative (euchromatin) portion of the genome, and it is this that allowed him to remain a single species.

In maintaining homeostasis of the organism the limiting factors were evidently low temperature. Under such conditions, as it frequently happens, preference was given to individuals who were able to perform prolonged and high physical activity. All other things being equal, the most adapted could prove to be individuals with a low BHC.

Individuals with a lesser amount of chromosomal Q-HRs and, accordingly, with a low BHC who had some advantage as concerns survival, could form new populations with a lesser amount of Q-heterochromatin material in the genome, and, although winnowing of individuals with greater amount of Q-HRs continued, the pressure of selection on such populations was on the whole lower than on the initial ones.

It is hard to say why the ancestors of *P. troglodytes* and *G. gorilla* were unable to use the same route. However, the assumption which we feel is likely is the following one: initial Q-HR frequencies on all the variable loci proved to be high enough to produce of individuals with significantly different numbers of chromosomal Q-HRs and, hence, the appearance of individuals with a various BHC who would be able to survive under unfavorable conditions was quite improbable. In other words, the chimpanzee and the gorilla were initially unable to vary the amount of Q-HRs of their genome as much as man could.

The following facts are in favour of this assumption: 1) the range of variability in the number of Q-HRs in the chimpanzee genome is from 5 to 7, whereas in the human population it is from 0 to 10, i.e., considerably wider (Ibraimov and Mirrakhimov, 1985: 2) in the gorilla and the chimpanzee, but not in man, a special type of Q-heterochromatin was found, located on the distal ends of certain chromosomes (7, 11, 20, and 23 in the gorilla; 20, 21, 22, 23 in the chimpanzee), and that itself makes hard to produce of individuals with different amount of Q-HRs in the karyotype less probable. The nature of these bright distal Q-bands that are only present in the chimpanzee and the gorilla is unclear, however, they are stained by quinacrine mustard and show intense fluorescence, suggesting that this is also Q-heterochromatin (Miller et al., 1974).

Let us sum up. The wide quantitative Q-HR variability in our ancestors permitted the appearance of individuals with different BHC, and that was an effective mechanism that allowed individuals with a relatively low BHC to survive under new more rigorous conditions and only then undergo secondary morphofunctional changes. It is possible that the sequence of events was the following one: Q-HRs appear in ancestors of gorilla, chimpanzee and man → Q-HRs are fortuitously and differently distributed on the chromosomes of these three species → in the populations of the direct predecessor of *H. s. sapiens* begin to appear individuals with a different BHC (preadapted, highly flexible) → formation of populations with a relatively low BHC expands their territory → a spectrum of idioadaptive morphological and behavioral changes appears in these populations → experience begins to accumulate → arises the necessity to preserve and transfer it, conceptual thinking and speech develop → 'the subsequent fate of the species is mainly determined by social rather than biological inheritance (Ibraimov, 1993). Let us expressly note that we do not deny the importance of cultural and social adaptation in the formation of *H. s. sapiens*, but we also have no grounds to consider this to be the only way of adaptation of man to environmental conditions.

Thus, we have attempted to establish the conditions that led to the origin of basic features distinguishing man from other animals, i.e. characteristic morphological structure and conceptual thinking, as we feel that formation of such features was due to the considerable physiological flexibility which in turn was due to the wide variation of noncoding part of the genome. Flexibility of man in his adaptation to different climatic conditions allowed him to accumulate the necessary experience and thus has played a decisive role in his evolution, enabling him to change his habitat according to his requirements, purposefully tropicalizing it, and this proved to be of no less importance than bipedality or particular forms of our hands, etc.

We suppose that most probably chromosomal Q-HRs and not specific structural genes were used by man in his genetic adaptation to cold and hypoxia. The chief obstacle on the way to the perception of such a point of view was and remains one very important circumstance: there are no structural genes in chromosomal Q-HRs.

The assumption that natural selection during adaptation could only superficially affect the genotype of various human populations is not new in itself (Harrisson et al., 1977; Baker, 1978). Harrison (1997) noted that much of the optimism during the IBP associated with uncovering natural selection for specific genetic polymorphisms was not justified by research, despite a considerable amount of data that had been accumulated. "Adaptation and adaptability have genetic and evolutionary bases, whether at the molecular level or at the complex physiological, morphological, developmental, and behavioral levels where plasticity is common. Yet there has been limited success in identifying genetic and hence evolutionary evidence for adaptation and adaptability in human population" (Little and Garruto, 2000). Therefore, the statement that adaptation of man to different natural environments did not occur owing to the appearance and selection of specific structural genes or "genotypes" should not be too surprising.

Finally, we would like anyone of our collea-

gues to catch us in delicto flagrante and thus to check the following facts:

1) the amount of chromosomal Q-HRs in the genome of human populations living permanently at northern latitudes and at high altitude is consistently lower than in those living at low altitude under conditions of southern and tropical climate regardless of their racial and ethnic features;
2) the amount and range of Q-HRs in the genome of individuals in various age groups differ, most of all in neonates and least of all in elderly people.

ACKNOWLEDGEMENT

I am grateful to S. Tabaldiev for excellent technical assistance.

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KEYWORDS Chromosomal Q-Heterochromatin. Human Adaptation. Cold and Hypoxia. High Altitude

ABSTRACT It is known that there exist physiological, morphological and biochemical changes in the human organism during the process of its adaptation to certain extreme environmental factors (cold and hypoxia). At the same time , the possible existence of some genetic changes in the genome of an adapted man or population, that was postulated by a number of investigators, has not as yet been documented by concrete dates. We suppose that most probably chromosomal Q-heterochromatin regions and not specific structural genes used by man in his adaptation to cold and hypoxia.

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Anthropologist Special Volume No. **3:** 513-523 (2007)
Anthropology Today: Trends, Scope and Applications
Veena Bhasin & M.K. Bhasin, *Guest Editors*