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Review Article

From Whom and How Did Modern Humans Originate?

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Abstract

When, where, from whom, and how modern humans came into being our questions that will always intrigue us. Significant progress has been made in this regard, although we are still far from obtaining complete answers to these questions. The first question has been answered: about 200,000-300,000 years ago, there were already beings indistinguishable from modern humans. Encouraging results have also been obtained regarding the place of origin: it is East Africa, although disputes about the multi-regional or African ("Out of Africa Model") origin of humans are still ongoing. The question of our ancestors remains a subject of heated debate: who were they and why did they vanish? However, the most difficult question is: how and why did creatures with 46 chromosomes instead of 48, characteristic of all higher primates, arise, what lies behind this and why were they able to colonize the entire landmass of the Earth? Our own data indicate that modern humans are direct descendants of individuals with 46 chromosomes who emerged during a period of profound climate change in East Africa. It was they who managed to adapt to all the climatic and geographical conditions of the Earth, form a new biological species, survive, and shape modern human races.

Kew Words: origin of modern humans; cell thermoregulation; human adaptation; human body heat conductivity; chromosomal Q-heterochromatin regions

Introduction

The question of when modern humans first appeared, despite its importance, is not particularly topical, and the answer will be found eventually. After all, the very fact that modern humans exist suggests that they must have a history. It would be interesting to establish the exact place of origin of *Homo sapiens*, although this no longer has any fundamental scientific significance, because during this time the Earth's climate has changed many times and will continue to change under the influence of humans themselves. The question of the direct ancestors of modern humans (*H. s. sapiens*) is more relevant, if only because we are more interested in our own evolutionary future. In this sense, the emergence of humans as a single tropical biological species with a unique karyotype, not characteristic of other higher primates, seems to be the most important. Our task is not to analyze existing literature on the historical time, place of origin, and possible ancestors of humans. We will be mainly interested in the question of how and why individuals with 46 chromosomes could have emerged from populations that had a karyotype with 48 chromosomes, and what lies behind this? It is obvious that it is not a matter of quantity, since both animals and plants exist with this number of chromosomes. We have already discussed the possible role of genes in human adaptation and origin [1-3].

Based on our nearly half-century of research into the polymorphism of chromosomal Q-heterochromatin regions (Q-HRs) in human populations living in a wide variety of climatic and geographical conditions in Eurasia and Africa, both normal and pathological, we have come to the conclusion that, probably, modern humans (*H. s. sapiens*) originated from a single population consisting of individuals with 46 chromosomes in their karyotype. Before presenting our data, we considered it necessary to provide brief information about the polymorphism of chromosomal heterochromatin regions (HRs) in human populations. A fundamental feature of chromosomes of higher eukaryotes is the presence of two 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 consists of non-coding DNA sequences. By now, enormous data have been accumulated on chromosomes of human and higher primates. A comparative analysis demonstrated that the differences between them are largely confined to the pericentric inversions and the amount of heterochromatin [4-6]. 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 is composed of heterochromatin [7]. To date, two types of chromosomal heterochromatin regions (HRs) are known: C- and Q-HRs. There are several significant differences between them: l) C-HRs is found in the chromosomes of all the higher eukaryotes, while Q-HRs - only in man (*Homo sapiens*), the chimpanzee (*Pan troglodytes*) and gorilla (*Gorilla gorilla*); 2) C-HRs are known to be invariably present in all the chromosomes of man, varying mainly in size and location (inversion); 3) Q-HRs variability can be found in man on only seven autosomes (3, 4, 13, 14, 15, 21 and 22), as well as on chromosome Y; 4) human populations do not differ from each other by the amount of chromosomal C-HRs [8-15]. Chromosomal Q-HRs polymorphism studying shows: 1) despite the fact that Q-HRs exist in the genome of three higher primates, their broad variability is only inherent in human populations; 2) individuals in population differ in

the number (from 0 to 10), location, size, and intensity of fluorescence of these regions [16-35].

Facts and their interpretation.

The distribution of chromosomal Q-HRs in human populations described in the form of two main quantitative characteristics: l) the frequency of Q-HRs in seven Q-polymorphic autosomes; 2) the distribution of Q-HRs in a population, i.e., distribution of individuals having different numbers of Q-HRs in the karyotype regardless of the location; 3) the mean number of Q-HRs.

Table 1 presents data on the frequencies and mean numbers of chromosomal Q-HRs in human populations living in various climatic and geographic conditions of Eurasia and Africa (columns I-VI), as well as in patients (columns VII-IX) suffering from purely human forms of pathologies (drug addiction, alcoholism, and dietary obesity).

Location of Q-HRs	I (n = 520)	II (n = 1122)	III (n = 449)	IV (n = 297)	V (n = 48)	VI (n = 327)	VII (n = 100)	VIII (n = 105)	IX (n = 100)
3	358 (0.344) *	759 (0.354)	378 (0.420)	236 (0.397)	53 (0.552)	425 (0.649)	134 (0.670)	64 (0.305)	49 69 (0.345)
	34.3**	**31.0**	**34.4**	**22.6**	**29.8**	**27.8**	**32.6**	**45.1**	**53.1**
4	32 (0.031)	130 (0.058)	29 (0.022)	16 (0.027)	5 (0.052)	18 (0.027)	10 (0.050)	2 (0.010)	6 (0.030)
	3.1	**5.0**	**1.8**	**1.5**	**2.8**	**1.2**	**2.6**	**1.4**	**4.6**
3	332 (0.319)	769 (0.343)	379 (0.422)	309 (0.520)	55 (0.573)	573 (0.821)	145 (0.725)	42 (0.200)	29 (0.120)
	31.8	**30.0**	**34.4**	**29.6**	**30.9**	**35.1**	**35.3**	**29.6**	**18.5**
14	63 (0.060)	113 (0.059)	69 (0.077)	93 (0.156)	10 (0.104)	112 (0.171)	23 (0.005)	11 (0.052)	7 (0.035)
	6.0	**5.2**	**6.3**	**8.9**	**5.6**	**7.3**	**5.6**	**7.7**	**5.3**
15	86 (0.083)	262 (0.117)	86 (0.094)	140 (0.235)	24 (0.250)	147 (0.224)	34 (0.170)	5 (0.024)	11 (0.055)
	8.2	**10.2**	**7.7**	**13.4**	**13.5**	**9.6**	**8.3**	**3.5**	**8.4**
21	125 (0.120)	260 (0.116)	105 (0.116)	135 (0.230)	18 (0.188)	155 (0.237)	40 (0.200)	14 (0.067)	21 (0.105)
	12.0	**10.1**	**9.5**	**13.1**	**10.1**	**10.1**	**9.7**	**9.9**	**7.4**
22	48 (0.046)	214 (0.095)	64 (0.071)	113 (0.190)	13 (0.135)	136 (0.207)	25 (0.125)	4 (0.019)	7 (0.035)
	4.6	**8.3**	**5.8**	**10.8**	**7.3**	**8.9**	**6.1**	**2.8**	**5.3**
Total	1044	2563	1100	1044	178	1530	411	152	130
Mean number of Q-HRs	**2.1**	**2.28**	**2.45**	**3.52**	**3.71**	**4.68**	**4.10**	**1.45**	**1.30**

Table 1: The frequency of chromosomal Q-heterochromatin regions (Q-HRs) in human populations living in Eurasia and Africa.

n -- sample size; * Q-HR frequency of the chromosomes analyzed; ** Q-HR frequency as a percentage of the overall number of chromosomal Q-HRs. I – northern Mongoloids of Siberia; II – highland Mongoloids of the Pamirs and Tien-Shan; II – steppe Mongoloids of Central Asia; IV – Russians; V – Indians of northern India; VI – lowland Negroids of subequatorial Africa; VII - drug addicts; VIII – alcoholics; IX – obese females. Even brief analysis of Table 1 convinces that Q-HRs are distributed in seven potentially Q-polymorphic autosomes far from by accident: more than a half of Q-HRs are localized in autosomes 3 and 13, and the rest more or less evenly are distributed in autosomes 4, 14, 15, 21 and 22. In the Table there also presented a data on Q-HRs distribution, where their frequencies are expressed in percentage from the number of analyzed chromosomes and from the overall number of chromosomal Q-HRs found in a sample. Data presented in Table 1 testify that at the level of human populations each of seven Q-polymorphic autosomes contains comparable "portion" of the overall number of Q-HRs in population genome irrespective of their race, ethnic peculiarities or pathology. Hence, if Q-HRs frequencies to be expressed in relative numbers (in percentage from the overall number of chromosomal Q-HRs found in a sample), then it became obvious that inter-population heterogeneity is formed due to proportional increase or decrease of the absolute number of Q-HRs in all potentially Q-polymorphic loci of seven autosomes simultaneously.

That is why, there are reasons to assume that human population heterogeneity according to distribution of Q-HRs is formed not due to various polymorphic degree of any loci in different samples, but due to simultaneous proportional increase or decrease of Q-HR contents in all potentially Q-polymorphic loci of seven autosomes, the change of which the best of all is reflected by as such quantitative characteristic of Q-HR variability as the mean number of Q-HRs (*m*) calculated per individual in population.

On the Table 1 presented the values of the *m* in populations from different climate-and-geographic provinces of Africa and Eurasia (columns I-VI). As can be seen from the Table, studied populations significantly differ from each other. First of all, draws attention the fact that the value of the *m* is considerably decreased in human populations living in the Far North of Siberia, in high-altitude areas of the Pamirs and the Tien-Shan, compared to those of steppe zones of Central Asia, low mountain subequatorial Africa (negroes of Mozambique, Angola, Zimbabwe and Guinea-Bissau). The same table presents the distribution patterns of chromosomal Q-HRs in samples of patients suffering from drug addiction, heavy alcohol abuse, and alimentary obesity (columns VII-IX). If the *m* values are not taken into account, these samples do not differ from the "natural" populations of Eurasia and Africa in terms of the distribution of the frequency ("portion") of Q-HRs across seven chromosomes in human populations. As is known among the climatic conditions where men have to live, the most difficult is the high-altitude areas. Therefore, the study of men at highland is important because living at high-altitude has a significant impact on the human body, particularly on physiology, adaptation, health, and disease. We managed to obtain data indicating the adaptive changes in the chromosomal of Q-HRs in the human population, which due to circumstances beyond their control migrate to the territory with extreme climatic conditions.

This is what happened to one Kyrgyz population after the Bolshevik Revolution in Russia in 1917. To avoid physical extermination and political persecution one Kyrgyz tribe fled to Afghanistan in the 1920s and appealed to give them asylum. The Afghan government offered them an almost uninhabited and inaccessible high-altitude area in the northeastern Pamirs, which is characterized by an extremely harsh climate. During more than five generations that the Kyrgyz have lived in complete genetic isolation in the extreme conditions of the Pamir high-altitudes (4200 m and higher above sea level).

The material was Kyrgyz sample, who returned to his historic homeland a few years ago by consent of the governments of the two countries due to extremely difficult living conditions at the high-altitude of Afghanistan Pamirs: high morbidity and child mortality, short life expectancy (~35 yrs.), lack of school education, medical services and many others. The sample included repatriates, who moved to live in their historical homeland, which their ancestors left more than 100 years ago (the Alay mountains of Kyrgyzstan). As a control, we used a sample of Kyrgyz who are indigenous inhabitants of the Alay highland region (2,600 m and above sea level). For comparison, we studied a sample of students from the North India, who study at Bishkek, Kyrgyzstan. The aim of the study is find out whether the number of chromosomal Q-HRs in the genome may change if it is forced to exist in extreme climatic conditions of the high-altitude for several generations (Table 2).

Location of Q-HRs	Populations		
	Kyrgyz repatriates (n = 58) I	Kyrgyz natives (n = 112) II	Indians (n = 97) III
3	50 (43,10)* 44,64**	68 (30.4)* 21.9**	93 (50.5)* 23.6**
4	7 (6,03) 6,25	12 (5.4) 3.9	17 (8.2) 4.1
13	31 (26,72) 27,68	84 (37.5) 27.1	128 (62.3) 30.7
14	8 (6,9) 7,14	29 (13.0) 9.3	27 (13.9) 6.9
15	6 (5,17) 5,36	34 (15.2) 10.9	39 (19.6) 9.6
21	3 (2,59) 2,68	42 (18.7) 13.5	52 (26.8) 13.2
22	7 (6,03) 6,25	41 (18.3) 13.2	48 (24.2) 11.9
Total Q-HRs	112 (96,52) 100.0	310 (138.5) 99.9	404 (203.1) 100.0
Mean number of Q-HRs	**1.9±0.123**	**2.78±0,083**	**4.12±0.149**
Statistics	$\chi^2_{I, II} = 67.3$; df = 168; P = 0.002;	$\chi^2_{I, III} = 115.2$; df = 155; P < 0.001;	$\chi^2_{II, III} = 90.56$; df = 207; P < 0.001;

Table 2: The frequency of chromosomal Q-heterochromatin regions (Q-HRs) among Kyrgyz and Indians.

* Q-HR frequency of the chromosomes analyzed.

** Q-HR frequency as a percentage of the overall number of chromosomal Q-HRs.

Table 3 shows the distributions of the numbers of Q-HRs in individuals at the population. The studied samples differ significantly from each other both in the distribution of the numbers of Q-HRs and in the mean numbers of Q-HRs. The highest number of Q-HRs is found in the genome of Indians, and the lowest in Kyrgyz repatriates. At the same time, the Kyrgyz repatriates differ with the predominance of individuals with a low number of Q-HRs and a very narrow range of Q-HRs amount variability in the population (from 0 to 4).

Number of Q-HRs	Populations		
	Kyrgyz repatriates (n = 58) I	Kyrgyz natives (n = 112) II	Indians (n = 97) III
0	3	1	
1	15	6	1
2	25	35	7
3	13	48	25
4	2	20	32
5		2	14
6			13
7			3
8			1
9			1
Total Q-HRs	112	310	404
Statistics	$\chi^2_{I,II}=34.7$; df = 169; P = 0.002;	$\chi^2_{I,III}=115.2$; df = 155; P < 0.001;	$\chi^2_{II,III}=59.7$; df = 208; P < 0.001;
Mean number of Q-HRs	**1.9±0.123**	**2.78±0.083**	**4.12±0.149**
Statistics	$t_{I,II}=6.07$; df = 169; P < 0.001;	$t_{I,III}=10.38$; df = 155; P < 0.001;	$t_{II,III}=8.16$; df = 208; P < 0.001;

Table 3: The distribution and the mean numbers of chromosomal Q-HRs per individual in Kyrgyz and Indians.

So far, the lowest amount of the chromosomal Q-HRs in the genome of human populations was found in the natives of Eastern Siberia, Pamir and Tien-Shan. In the aborigines of the Far North of Eastern Siberia, the mean number of Q-HR in the samples was: Chukchi - 2.2; Nenets - 2.2; Khanty - 1.8; Yakuts - 1.8; Selkups - 1.8 [30,36,37], and in the highlanders of the Pamirs and Tien-Shan (2.7 and 2.1, respectively) [24,30,37]. Among non-indigenous people, such low mean numbers of Q-HRs have been found in mountaineers and oil workers working in polar Eastern Siberia (1.60 and 1.72, respectively). It is noteworthy that in the genome of newcomers, but successfully adapted individuals the number of Q-HRs was lower than in the native populations of the high mountains Pamir and Tien-Shan and the Far North of Siberia [29,30]. The peculiarity of this study is that, for the first time, a decrease in the number of Q-HRs was found in a population that lived for a short time (about 100 years) in extremely harsh climatic conditions at high-altitude.

Discussion

Anthropologists have been divided as to whether modern humans evolved as one interconnected population, or evolved only in East Africa, speciated, then migrated out of Africa. In their conclusions, anthropologists rely on data, which were received by analyzing fossil remains and mitochondrial DNA.

Our data on variability of chromosomal Q-HRs testifies that apparently modern human originated according to Out of Africa Model. Moreover, cytogenetic data show that modern humans most likely originated from a single population, whose members had a karyotype with 46 chromosomes. Indeed, it is difficult to imagine that in genome of populations represented different racial and ethnic groups and residing tens of thousands of years in such diverse climatic and geographic conditions of Eurasia and Africa, chromosomal Q-HRs on seven Q-polymorphous autosomes distributed equally randomly. If the Multiregional Continuity Model were true then probably, we will see different patterns of chromosomal Q-HRs distribution in seven Q-polymorphic autosomes in population's genome. When talking about the fact that modern humans could have arisen from a single population, we mean the emergence of individuals who have 46 chromosomes in their karyotype instead of 48. It does not matter what populations these individuals came from, how many there were, or where and when they lived. Therefore, we will only consider the question of how such individuals could have arisen, and then the population with 46 chromosomes.It has been established that a decrease in the number of chromosomes by two in humans is a result of the fusion of two autosomes into one chromosome in his karyotype ancestors. It is curious that the question of why a man has 46, and not 48 chromosomes, like other higher primates, the cause of their origin and biological consequences is still not the subject of special studies [37]. We believe that changes in the composition, amount and localization of chromosomal HRs in the human karyotype led to the fact that he became a unique biological species, with all its distinctive features. Distribution of chromosomal Q-HRs on Q-polymorphic autosomes in population of a chimpanzee and a gorilla are absolutely the other. The mean number of Q-HRs in the chimpanzee is considerably higher than in man; in man, their incidence averages from about 2.9-4.2, while in the chimpanzee it has been estimated to be equal to 8.77, and to 8.85. The number of Q-HRs accounted for 14.8 in specimens of gorilla, which is approximately five times the number observed in man [38-43].

We think it highly probable, that the causes of origin of individuals with 46 chromosomes were climate in the East Africa. Middle and Late Miocene ecology was far from being uniform, and such climatic changes as cooling, aridity, seasonal and diurnal temperature fluctuations gradually became dominant environmental factors [51]. Thus, even before they left Africa our ancestors were probably faced with the problem of adaptation to new, more rigorous natural conditions differing from those of the savannah. As the amount of food decreases, populations of the common ancestor of the modern man began to expand the territory of their habitat to more severe, including cold areas. Perhaps, just at this stage in the life history of our ancestors, the adaptive changes appeared in their karyotype, which, ultimately, resulted to the emergence of the modern human. In particular, the

individuals with a number of chromosomal Q-HRs in the karyotype closest to the modern Africans became adapted better in the new climate conditions (for details see [45,50,51]). We postulate that two pairs of acrocentric chromosomes in the genome of the ancestral population, which generated the chromosome 2 of the modern human, were bearers of Q-HRs with a very high frequency. In the genome of the population of the modern human only two pairs of autosomes (3 and 13) are the high frequency, and for more than half of the total amount of chromosomal Q-HRs belongs to their share, and the rest amount of Q-heterochromatin is distributed on the other Q-polymorphic chromosomes (4, 14, 15, 21 and 22) with frequency from 3% to 10% (see above). Apparently, our ancestors had the number of high Q-polymorphic chromosomes by two pairs more than the modern human. But it wasn't enough.

We assume that the human adaptive evolution became possible when in a population began to born individuals with different Q-heterochromatin material, as it occurs now as well. It has become possible just because: 1) the number of potentially Q-polymorphous loci in the karyotype was great enough (25 loci) to ensure the appearance in the population of individuals with various amount of Q-HRs in the genome; 2) the relative frequencies of Q-HRs in these loci were different, due to which the same Q-HRs number in different individuals could be provided with a very various combinations of Q-HRs [44,45]. It is imperative that chromosomal Q-HRs was not distributed equally to all potentially Q-polymorphic autosomes. If the population have uniform distribution of chromosomal Q-HRs with high frequency as in modern chimpanzees and gorillas, then it will be difficult, if not possible, to birth the individuals with different numbers of Q-heterochromatin in the karyotype. The presence of individuals in human population with different numbers of Q-HRs in the karyotype (from 0 to 10) is due to the fact that Q-HRs is unevenly distributed on seven potentially Q-polymorphic autosomes [16-35,37].

Thus, the essence of our hypothesis is that natural selection caused merger of two pairs of autosomes into one chromosome. In the changed climate of the East Africa individuals with less number of chromosomal Q-HRs in genome were the most adapted. Two pairs of acrocentrics in the genome the common ancestor, which merged into a single chromosome, apparently, carried on their short arms of Q-HRs with a very high frequency, preventing the birth of individuals with a low number Q-heterochromatin. With the merger of these two pairs of acrocentrics into one, the number of autosomes bearing the Q-HRs reduced from nine to seven pairs, as in the modern human. Such chromosome rearrangement resulted in two important consequences: a) chromosomal Q-HRs distributed into seven Q-polymorphic autosomes, so that it was possible to give birth to the individuals with different, including the low, number of Q-heterochromatin; b) in the population individuals with low number of Q-HRs appeared, able to adapt to new, harsher climatic conditions. With the lapse of time, these individuals formed a new population in the new territory, where individuals with a number of chromosomal Q-HRs like the modern natives of Africa, and with the number of 46 chromosomes in the genome began to dominate (for details see [50,51]). 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-HRs frequencies on all the variable loci proved to be high enough to produce of individuals with significantly different numbers of chromosomal Q-HRs. In other words, the chimpanzee and the gorilla were initially unable to vary the number of Q-HRs of their genome as much as man could. The following facts are in favor of this assumption: I) the range of variability in the number of Q-HRs in the chimpanzee genome is from 5 to 7 [10,11], whereas in the human population it is from 0 to 10, i.e., considerably wider [44,46]; 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. Finally, individuals with 46 chromosomes could not interbreed with members of the original population with 48 autosomes, and therefore, for reproduction, they were forced to seek mates with a compatible (similar) karyotype. The emergence of individuals in a population with a number of chromosomes different from the original was a turning point in human evolution. This is precisely what we mean when we say that the search for populations that gave rise to individuals with 46 chromosomes is of little prospect, as there could have been not just one, but several. The most important thing here is that they lived in the same territory and experienced the same selective pressure from the environment.

The biological meaning of a broad variability in the content of chromosomal Q-HRs in the human genome can be explained within the framework of cell thermoregulation (CT) hypothesis [47,48]. The essence of the hypothesis is that chromosomal HRs, as the densest structure around the interphase nucleus, known as condensed chromatin, participate in CT by eliminating of excess metabolic heat from the nucleus into the cytoplasm due to its highest heat conductivity. The phenotypic manifestation of CT on the organism level is human body heat conductivity (BHC), the magnitude of which depends on the number of chromosomal C- and Q-HRs in his genome. Since human populations do not differ significantly from each other in the number of C-HRs [13,14], it is obvious that the differences of individuals in the population at the level of BHC depends on the number of Q-HRs in their genome. It has been shown that the more Q-HRs in the karyotype of an individual, the higher the level of his BHC and *vice versa* [37,49]. We do not yet know how the number of Q-HRs in the genome or its physiological phenotype (BHC) affects human adaptation to cold and high-altitude climate. Nevertheless, we consider as highly probable that humans in the struggle with cold and high-altitude hypoxia, in addition to the known morphological and physiological mechanisms use low BHC as a means of defense. Perhaps individuals with low BHC are relatively better at maintaining temperature homeostasis, by more effectively retaining metabolic heat in the body under conditions of permanent high-altitude cold and limited food resources in high altitude regions.

Regarding questions about the ancestors of modern humans: 1) who were they? 2) why did they vanish? and 3) why were they able to colonize the entire landmass of the Earth? one could answer as follows: a) they were individuals with 46 chromosomes; b) they disappeared because few or no children were born in the population with varying numbers of Q-HRs, and c) thanks to the birth of children with different numbers of Q-HRs, the population made it possible for individuals with different levels of BHC to emerge, allowing it (the population) to adapt to different climatic and geographical conditions (for details see [37,44,45]).

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