 Int J Hum Genet, 6(4): 281-285 (2006)

Chromosomal Q-Heterochromatin Variability in Neonates Deceased During First Year of Age

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KEYWORDS chromosomal Q-heterochromatin; age; neonates

ABSTRACT There is analyzed the amount of chromosomal Q-heterochromatin regions (Q-HR) in a genome of neonates deceased during first years of life. Chromosome preparations were made from umbilical-cord blood with the subsequent Q-staining in 145 Kyrghyz and 37 Russian neonates. During the first 3 years of life 17 Kyrghyz and 5 Russian neonates have died of various diseases. Mean numbers of Q-HRs per one individual ($\bar{x}$) in newborn population were 3.16 ± 0.13 in Kyrgyz and 3.59 ± 0.23 in Russian, whereas in neonates died 4.58 ± 0.23 and 4.80 ± 0.37 respectively. In no group there was not preferential Q-HRs localization on seven Q-polymorphic autosomes. It is supposed that individuals with the greatest amount of Q-HRs in the newborn population have greater probability to die in the first years of life other conditions being equal.

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, differing only on size and very rarely in location (inversion), while Q-heterochromatin can only be detected on seven autosomes and the Y chromosome (Paris Conference, 1971, 1975).

Individuals in a population differ from each other in the number, location, size and intensity of staining (fluorescence) of chromosomal Q-heterochromatin regions (Q-HR) (Geraedts and Pearson 1974; McKenzie and Lubs 1975; Müller et al. 1975; Buckton et al. 1976; Yamada and Hasegawa 1978). It has been shown that certain human populations differ significantly as concerns this feature (Müller and Klinger 1975; Buckton et al. 1976; Lubs et al. 1977; Al-Nassar et al. 1981; Verma and Dosik 1981; Ibraimov and Mirrakhimov 1982a, 1985; Stanyon et al. 1988; Ibraimov 1993; Ibraimov et al. 1986, 1990; Kalz et al. 2005).

There was received an affirmative answer of a question, whether there are distinctions in amount of chromosomal Q-HRs in a genome of individuals belonging to different age groups in population. It was shown that chromosomal Q-HRs are most numerous in the genome of neonates, while they are the least numerous in the genome of elderly subjects (aged 60 years and older) regardless of the climatic and geographic, racial and ethnic features of the individuals studied (Buckton et al. 1976; Nazarenko 1987; Ibraimov and Karagulova 2006). The nature of this phenomenon is not quite clear yet.

OBSERVATIONS AND DISCUSSION

The purpose of present communication is for the first time to pay attention to features of distribution of amount of chromosomal Q-HRs in neonates died in first year of age. The fact is that we from 2003 till 2005 have analyzed chromosomal Q-HRs in 145 Kyrghyz and 37 Russian neonates in Bishkek. 22 neonates have deceased from various diseases in stationary conditions during this time, and from them 17 Kyrgyz and 5 Russian ones, the diagnosis of which is confirmed by pathological-anatomical dissection. Here it is necessary especially note that we unfortunately have not observed for a destiny of all neonates investigated by us, as the transit economics which is in post-soviet Kyrghyzstan, compels a large part of the population to change permanently a place of residence in searches of job and often far outside the country. But nevertheless even this small actual material, as we believe, can present an interest.

In Table 1 the distribution and mean number of Q-HRs ($\bar{x}$) on autosomes in neonates is shown

(Ibraimov and Karagulova 2006) and in individuals died. As can be seen from this Table, neonates are characterized by a high range of variability in the distribution of Q-HRs (from 0 up to 7). But died neonates, besides high value differs by extremely narrow diapason of variability of Q-HRs in population: number of Q-HRs in a karyotype changes from 4 up to 6, with = 4.58 ± 0.23 and = 4.80 ± 0.37 in Kyrgyz and Russian respectively.

Table 2 shows the frequency of the Q-HRs in seven Q-polymorphic autosomes in the samples studied. As can be seen from this Table, Q-HRs in all samples studied are encountered with an expected frequency on all the potentially Q-polymorphic autosomes, i.e. in no group there was preferential Q-HR localization, and this is again suggesting that Q-heterochromatin is not locus-specific material in the genome (Ibraimov 1993; Ibraimov et al. 1986).

There is no agreement as to the nature of such Q-HRs variability. It is possible that a decrease in the number of Q-HRs with age in a population is not an ontogenetic process, but rather the results of natural selection where individuals with a greater amount of chromo-somal Q-HRs in their genome than on the average in a population "fall out" (Ibraimov and Karagulova 2006).

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. This hypothesis can be checked at the level of cells or organisms (Ibraimov 2003). 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 2002a, b, 2004).

Thus, how do we explain age-related differences 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, 2002b, 2004) and consider all this using as an example neonates

Table 1: Distribution and mean number of Q-HRs per individual in neonates and infants died.

	Kyrghyz		*Russians*	
Number of Q-HRs	*Neonates* *I* *(n = 145)*	*Infants died* *II* *(n = 17)*	*Neonates* *III* *(n = 37)*	*Infants died* *IV* *(n = 5)*
0	4			
1	19		3	
2	23		7	
3	38		5	
4	37	9	12	2
5	16	5	7	2
6	5	3	3	1
7	3			
Total number of Q-HRs	458	79	133	24
	$\chi^2_{I,II}$=9.03 df=2 P<0.05	$\chi^2_{I,III}$=2.18 df=2 P>0.05	$\chi^2_{I,IV}$=6.18 df=2 P<0.05	
	$\chi^2_{II,III}$=2.23 df=2 P>0.05	$\chi^2_{II,IV}$=0.28 df=2 P>0.05	$\chi^2_{III,IV}$=2.26 df=2 P>0.05	
Mean number of Q-HRs	3.16 ± 0.13	4.65 ± 0.19	3.59 ± 0.23	4.80 ± 0.37
	$t_{I,II}$=6.47 df=36 P<0.000	$t_{I,III}$=1.52 df=180 P> 0.100	$t_{I,IV}$=2.33 df=148 P<0.021	
	$t_{II,III}$=3.55 df=52 P>0.001	$t_{II,IV}$=0.37 df=20 P> 0.500	$t_{III,IV}$=1.88 df=40 P>0.050	

Table 2: Q-HR frequencies in seven Q-polymorphic autosomes in Kyrghyz newborns* and infants died.

Locations of Q-HRs	*Neonates (n=145)*	*Neonates died (n=17)*
3	145 (0.500)** (31.7)***	19 (0.559)** (24.1)***
4	16 (0.055) -3.5	2 (0.059) -2.5
13	156 (0.538) -34.1	27 (0.794) -34.2
14	21 (0.072) -4.6	6 (0.176) -7.6
15	55 (0.189) -12	14 (0.412) -17.7
21	36 (0.124) -7.9	6 (0.176) -7.6
22	29 (0.100) -6.3	5 (0.147) -6.3
Total number of Q-HRs	458	79

* - Ibraimov and Karagulova 2006;
** - Q-HR frequency from the number of chromosomes analyzed;
*** - Q-HR frequency as percentage of the overall number of chromosomal Q-HR.

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. 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).

Indirectly other known medical-biological data justify our point of view:

1) the level of infant mortality and morbidity is higher with boys than girls. This trend especially expressed in high mountain climate conditions (Baker 1978);
2) apparently, girls are better than boys "protected" from hunger and diseases, and the trend of curve of their physical growth breaks very rarely (Harrison et al. 1977);
3) mortality from infectious diseases in males is, on average, two times higher than in females;
4) in all ethnic groups males almost 2 times more often are sick with tuberculosis (TBS) than females. For example, in the USA the Afro-Americans are more susceptible to TBS that determines quick progress of the disease. Vice versa, in "whites" the TBS more often acquires chronic than acute form;
5) also it is known that among the animals only apes get our common cold and stand it very badly.

Aside from effects of hypothetical sex-chromosome factors, the increased disease stress in males is poorly understood (Green 1992; Synnes et al. 1994). The increased susceptibility of males to nutritional insult in early life, reported in both human and other animals (Smart 1977; 1986; Katz 1980; Lucas et al. 1990, 1998), is also generally assumed to be an unresolved biological issue (Lucas et al. 1998). Both morbidity and mortality are consistently reported to be higher in males than in females in early life, but no explanation for these findings has been offered. The latest attempt to explain this phenomenon belongs to Wells (2000), who argues that "the sex difference in early vulnerability can be attributed to the natural selection of optimal maternal strategies for maximizing lifetime reproductive success" and "that whatever improvements are made in medical care, any environmental stress will always affect males more severely than females in early life."

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.

In any case in search for the reasons of the above phenomenon, one hardly can ignore the facts of Q-HRs presence in the genomes of gorilla and chimpanzee (Pearson 1973, 1977; Seuanez 1976), high Q-HRs content in the genome of the sub-equatorial Africa residents (Ibraimov Mirrakhimov 1982b) and tropical zones of India (Ibraimov et al. 1997; Kalz et al. 2005) than in the genome of populations from the moderate Euro-Asia zones, as well as availability of the largest Q-heterochromatin region on Y chromosome in male karyotype (Paris Conference 1971).

At last as early as 70-th years of XX century chromosomal Q-polymorphism was investigated by one or another reasons in hundreds and thousand of neonates in the world (Müller et al. 1975; Buckton 1976; Lin et al. 1976), destiny of which can be observed at present time, though in developed countries. We are going continue our observations. In this connection it would be helpful if the authors studying the amount of Q-HRs in neonates did the same, for facts obtained under different ethnic, climatic, and socio-economic conditions will be exceptional importance if the different amount of Q-HRs in the genome of individuals in different age groups (Buckton et al. 1976, Ibraimov and Karagulova 2006), is not really fortuitous.

ACKNOWLEDGEMENTS

The research described in this paper was made possible, in part, by grant number MYR 000 from the International Science Foundation.

I am grateful to Dr. S. Tabaldiev for excellent technical assistance, and to an anonymous reviewer for constructive comments.

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