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Editorial

Often it is possible to hear, that we live in the epoch of molecular biology and genetics. Indeed, the achievements of these young disciplines in understanding the secrets of life are considerable and indisputable. Nevertheless, sometimes we run to extremes, attributing, for example, to genes of what is not present actually. Steven Rose has written well about it in his book "Lifelines. Life beyond the gene". From headlines in daily newspapers, or the titles of academic papers in major scientific journals it is possible to read such statements, for example: "There are genes available to account for every aspect of our lives, from personal success to existential despair: genes for health and illness, genes for criminality, violence and 'abnormal' sexual orientation-even for 'compulsive shopping'". Watson's view that "there is only one science, physics; everything else is social work" is a characteristically strong vision. These and other similar statements are a fruit of philosophical reductionism, a fashionable trend among of some biologists during the last decades [1].

However, other thoughts, the meaning of which still are not realised by many, were in the history of biology. So, for example, for Ch. Darwin, the organism was the central element of life and evolution. In many of his writings, E. Mayr rejected reductionism in evolutionary biology, arguing that evolutionary pressures act on the whole organism, not on single genes, and that genes can have different effects depending on the other genes present. He rejected the idea of a gene-centered view of evolution and asserted that "Evolution is change in the properties of populations of organisms over time. … Not its genes or genotype, because these are not visible to selection, but rather its phenotype. …All the findings of molecular biology relevant to evolution deal with the nature and the origin of genetic variation" [2].

So not to be unfounded, I will give an example from my personal experience. A major discovery of the past two decades is that many eukaryotic genomes contain vastly more noncoding DNA than coding DNA, with the typical figure for humans being more than 97% noncoding. A part of noncoding DNAs in chromosomes of the higher eukaryotes forms the so-called heterochromatic regions. Heterochromatin is universally distributed in the chromosomes of all the eukaryotes - plants, animals and man, accounting for 10% to 60% of their genome. Heterochromatin regions (HRs) account for about 15% to 20% of the human genome. They are localized in pericentric regions, telomere chromosome sections, as well as in regions forming nucleolar organizers. Broad interspecific and intraspecific variation according to quantitative contents [3].

Despite the over 80-year history of studying the heterochromatin part of the genome of higher eukaryotes, its biological role remains unclear. Existence of genes has been guessed on their phenotypes though they cannot be seen through a microscope. A paradoxical situation has formed: it is known incomparably more about the invisible genome part activity, than about its visible one [4].

Searching a biological role of chromosomal HRs scientists hoped for molecular approach as genes are absent in these areas. However, hopes of scientists were not justified. According to most hypotheses heterochromatin is a reservoir of "excess" DNA, and some investigators call DNA in the genome of eukaryotes useless and even "selfish" because these DNA consist of non-coding, short and highly repeated sequences. The maximum that it was possible to find out (learn) is that its renaturation kinetics suggests that it consists of repetitive nucleotide sequences [5].

We have refused the molecular approach, believing, that, probably, the chromosomal HRs participate in cell thermoregulation (CT). And at the level of the whole organism the effect of chromosomal HRs could be defined by estimation of human body heat conductivity (BHC) [6].

In our lab, these studies were developed in three directions: a) possible selective value of the amount of chromosomal Q-heterochromatin regions (Q-HRs) of man in their adaptation to certain extreme environmental factors; b) examining individuals of different sex, age and ethnic groups; c) studying of some exclusively human forms of pathology. These researches showed that in fact there are differences in the BHC between individuals in population. Results obtained show that individuals in population truly differ from each other in BHC and its level depends on the amount of chromosomal Q-HRs in human genome. Here we give some examples of possible cell thermoregulation participation in some stages of evolution and development. By studying chromosomal HRs variability in the human populations permanently living in various climatic-and-geographic conditions of Eurasia and Africa, in norm and pathology we have obtained the data indicating possible participation of chromosomal HRs in cell thermoregulation [7].

Hypothetically, we think of the CT mechanism as follows. For the known in the science reasons, at a certain stage of cell activity the thermal energy excessing the optimal physiological level may be accumulated in the nucleus. Such excessive heat energy is required to remove outside of the nucleus, so it would not harm the normal work of cellular metabolism and of the genetic apparatus. As it is known, high temperature, among other things, has a strong mutagenic effect. Since the nucleus in terms of removing heat surplus, the choice is not great (increase of the own volume and/or density), it is forced to use a dense layer of condensed chromatin, as the heat removal. Further, the thermal energy, using the cytoskeleton, membrane system and other dense structures of the cytoplasm as a "heat conductor", removed outside the cells in the intercellular space. Thus, for example, we found that in individuals with obesity the amount of Q-HRs in their genome proved to be extremely low. We once again feel that the reason for this

difference lies in the features of cell thermoregulation. Thus, in patients with alimentary obesity and therefore with a low BHC (even assuming that they use the same amount of calories as people with normal weight), we believe that a part of the calories accumulates in the body in the form of adipose deposits due to inadequate heat loss [9].

The problem of alcohol abuse is exclusively human. From the data obtained by us, of interest are the following results: 1) alcoholics have the lowest number of Q-HRs in their genome, and they do not differ from each other in all the quantitative characteristics of chromosomal Q-HRs variability despite their different ethnic affiliation; 2) in the genome of drug addicts the number of QHRs is significantly greater than in controls, especially in subjects abusing in strong alcoholic beverages [10].

Almost hundred years ago the outstanding American biologist E. B. Wilson wrote: "the key to every biological problem must finally be sought in the cell; for every living organism is, or at some time has been, a cell." This position remains unshakeable, despite impressing successes of molecular biology, genetics and unreasonable claims of philosophical reductionism. Let's hope, that on pages "Organismal Biology Journal" we see many works where authors show the adherences to the organismal approach of life research.

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