

BOOK REVIEW

Genome of eukaryotes: on efforts to read it from to

(Review of the book: “Mechanisms and control of eukaryotic genome rearrangements” written by T.U. Kolotova, B.T. Stegnii, I.U. Kouchma, N.V. Dubinina, A.N. Golovko, U.B. Chaikovski and U.L. Volyanski, Kharkov, Collegium Press, 2004, 263 p.)

In 1984 two publications attracted attention of geneticists in Slavonic countries. One of them was that of B. McClintock who published in *Science* her Nobel speech dedicated to the discovery of mobile elements [1]. The other one was a book written by Moscow professor R.V. Khesin who summarized multitudinous results that could be united under the title “Genome mobility” [2]. These publications marked the point of a shift in genome research paradigm from treating genome as a static structure containing genes like beads in a necklace (initially studied also as separate units in frame of «one gene one enzyme» conception) to a highly dynamic organization. The latter obeys some special laws governing the genome status depending on cell requirements and environmental conditions. The genome dynamic properties are endowed with a host of biological functions including homeostasis maintaining, genetic diseases, including malignancies emergence, and finally species formation and evolution.

20 years later, at the heart of post-genomic era dealing with the knowledge of full genetic text of many organisms that could be referred to as an letter in genome deciphering this book appeared in Kharkov, Ukraine. Written cooperatively by many specialists it is a timely survey of results on the way of studying the alpha bite of the genome as Book of Life.

As the following letter of genomic alpha bite the reader could interpret the described ability of genome

to dynamic reorganization of the structure initially considered as canonic. When, why and how do these organizations occur? What aftereffects of such reorganizations follow? If some special code to do it exists then what elements of this code might be? Studying the possibility to answer these questions was a motive force for the authors to compose this book.

Different positions at the genome of the mobile element result in different phenotypes and, therefore, the genome coding capacity depends on not only the size of coding sequences but also combinations of genome different parts inside the nucleus. Not only mobile elements attracted much attention but also different cis- and trans-factors involved into site-specific processes of genomic level, including mechanisms of these factors activation, their ability to form complexes and recruit only special factors active with these elements as well as their role in silencing the appropriate genes. This shows that the ability of genome to reorganize itself must be programmed. That this is the fact, the first chapter of the book demonstrates in details of immune response as a result of the right cis- and trans-elements activation at the right time and at the right place. Hypermutability inherent to this type of rearrangements elevates the level of an output product (antibodies) diversification that allow better to choose variant required for the case.

The second example demonstrating the role of a wider range of phenotypes for the selection of the most suitable one among them is the meiotic recombination.

It is described in the second chapter. It was shown that in yeast the meiotic recombination is developed as a stress reaction of the genome that could survive due to the possibility of appearance of the fitted phenotype. Structural and functional peculiarities of this process in yeast and other higher organisms are characterized.

The programmed genome rearrangements meet the requirements not only to be highly diverse but also effectively used during the life span. About 10 millions of species comprise our ecosystem and among them there is one very simple organism called 'ciliates'. The main feature of their genome is labor division between macro- and micronucleus. This is justified because ciliates can multiply themselves both asexually and sexually. In the first case no sex determinants are necessary and genome of the macronucleus is processed in such a manner that not needed genetic material is discarded due to specific reactions. This model is described in details in the book as the best to study the process of chromatin diminution where it can occur.

How can genome sense the threatening situation and prepare to face it using its potential for rearrangements? In her Nobel speech B. McClintock said, «We know nothing, however, about how the cell senses danger and instigates responses to it that often are truly remarkable». 20 years later the authors of the reviewed book showed that genome can sense danger due to alterations in pattern of specific epigenetic modifications resulting from environmental and endogenous conditions. This, currently especially intense, field of researches might be designated as letter of genome alpha bite according to the used cliché. Data on both DNA and histone code elements modifications are summarized in the book, the mechanisms of modification emerging and erasing as well as the mechanisms of possible epigenetic inheritance are discussed.

The book shows that genome rearrangement is a programmed process. Could rearrangements happen as a non-programmed event? The data analyzed in the book allow answering positively. First, the programmed processes could sometimes loose the control and enter the wrong way of fulfillments. Second, genome could face any environmental or endogenous assault using the inherent mechanisms of genetic plasticity. Special chapter of the book shows that these mechanisms are exactly the same as those for the programmed

events. (Surprisingly, this genome behavior resembles that of the whole stressed organism changing the pattern of activity of different physiological systems and developing general adaptive syndrome described by Hans Selye). The book allows raising a question if mammal liver regeneration is also accompanied by genome rearrangements.

The book covers the vast majority of experimental data obtained using yeast, drosophila, plants, ciliates, and mammals. In rather short writing the reader (even a student) is tacitly taken as familiar with the main peculiarities of these models. Otherwise, no details in many cases analyzed (*e.g.* why and how antibodies are divided into classes) make the book difficult to absorb. The same effect is produced because no list of abbreviations (that are in fact the second language of the book) is supplied. Moreover, it is not always clear what the abbreviations used stand for. There are some technical errors in spelling, legend explanation (Fig.VIII with P-nucleotide meaning omitted) as well as inefficiency of finding many good points of the book because no index of material analyzed is used at all. This, however, does not lower much the value of the book.

Besides the analysis of data obtained the book instigates raising novel questions in studying the alpha bite of genome. One of them concerns the appearance of mutations accompanying the process of rearrangements. The known «mutagenases», terminal and translesion polymerases may not exhaust cell potential to alteration. Capacity of DNA bases to form tautomers due to proton ability to migrate from one to another atom inside the molecule and being especially active under stress conditions could come into operation as a source of mutation emergence.

Also, study of genetic plasticity in prokaryotes could open novel insights on the study of genome alpha bite. In prokaryotes the phenomenon of protein splicing is widespread. On the one hand, inteins with their properties of genome homing could be an element important for genome rearrangements. On the other hand, if inteins could turn out to be those proteins that are capable of protecting targets from lethal ligands (antibiotics) [3] they could belong to the cell sensing machinery and participate in induction of genome reorganization, in case of eukaryotes in some specific way.

No doubt the book is a conspicuous event in genetics in our country and can be enthusiastically recommended for many specialists and students.

REFERENCES:

1. McClintock B/ The Significance of Responses of the Genome to Challenge // Science, 1984. 226, 792-801.
2. Khesin R.V. Genome Mobility// 1984, "Nauka" Press, Moscow 472 p.
3. Sidorenko S.V.and V.I.Tishkov. Molecular basis of resistance to antibiotics. // Uspechi biol. khimii , 2004.v.44.p.263-306 .

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