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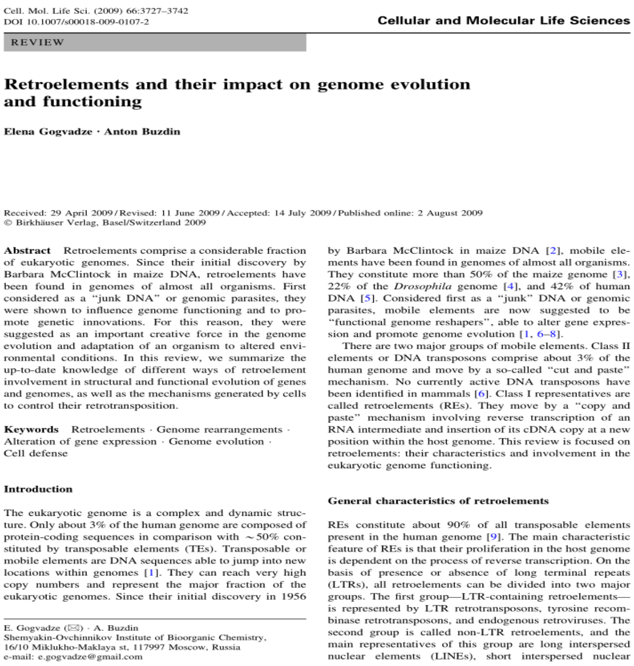

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REVIEW

Retroelements and their impact on genome evolution and functioning

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Abstract Retroelements comprise a considerable fraction of eukaryotic genomes. Since their initial discovery by Barbara McClintock in maize DNA, retroelements have been found in genomes of almost all organisms. First considered as a "junk DNA" or genomic parasites, they were shown to influence genome functioning and to promote genetic innovations. For this reason, they were suggested as an important creative force in the genome evolution and adaptation of an organism to altered environmental conditions. In this review, we summarize the up-to-date knowledge of different ways of retroelement involvement in structural and functional evolution of genes and genomes, as well as the mechanisms generated by cells to control their retrotransposition.

Keywords Retroelements · Genome rearrangements · Alteration of gene expression · Genome evolution · Cell defense

Introduction

The eukaryotic genome is a complex and dynamic structure. Only about 3% of the human genome are composed of protein-coding sequences in comparison with ~50% constituted by transposable elements (TEs). Transposable or mobile elements are DNA sequences able to jump into new locations within genomes [1]. They can reach very high copy numbers and represent the major fraction of the eukaryotic genomes. Since their initial discovery in 1956 by Barbara McClintock in maize DNA [2], mobile elements have been found in genomes of almost all organisms. They constitute more than 50% of the maize genome [3], 22% of the *Drosophila* genome [4], and 42% of human DNA [5]. Considered first as a "junk" DNA or genomic parasites, mobile elements are now suggested to be "functional genome reshapers", able to alter gene expression and promote genome evolution [1, 6–8].

There are two major groups of mobile elements. Class II elements or DNA transposons comprise about 3% of the human genome and move by a so-called "cut and paste" mechanism. No currently active DNA transposons have been identified in mammals [6]. Class I representatives are called retroelements (REs). They move by a "copy and paste" mechanism involving reverse transcription of an RNA intermediate and insertion of its cDNA copy at a new position within the host genome. This review is focused on retroelements: their characteristics and involvement in the eukaryotic genome functioning.

General characteristics of retroelements

REs constitute about 90% of all transposable elements present in the human genome [9]. The main characteristic feature of REs is that their proliferation in the host genome is dependent on the process of reverse transcription. On the basis of presence or absence of long terminal repeats (LTRs), all retroelements can be divided into two major groups. The first group—LTR-containing retroelements—is represented by LTR retrotransposons, tyrosine recombinase retrotransposons, and endogenous retroviruses. The second group is called non-LTR retroelements, and the main representatives of this group are long interspersed nuclear elements (LINEs), short interspersed nuclear

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