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Types of self-assembling of lengthy intron RNA presented in the regions of homologue chromosomes somatic pairing

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In different types of chromosomes pairing the initiation stages are less elucidated. Frequent somatic pairing of homologs was established for diptera and recently also the homologs somatic pairing for other species was shown, although it was not so pronounced because of the more short-lived states in cell cycles particular in human organisms. The somatic homologs pairing appeared to be transcriptionally dependent. In *Drosophila melanogaster* the cases of pairing were well correlated with the regions of bi-directional transcription with the expression of long introns RNA products and in some cases with long RNA in the inter-gene regions. To study the probability to initiate pairing through RNA interference examination of their secondary structure folding was done computationally. Among two possibilities, stretched or coiled forms, the preferred forms were stretched ones. The propensity to kinetic folding and stability of folded pre-mRNA structures *in vivo* was discussed well. The folded RNA structures have characteristic lengths of nano-range values and may be presented as natural self-assembling objects. UNAFOLD resource was used as computing programs for RNA folding. Chromosome interactions due to pairing may play regulatory role in gene expression, regulation *in trans*, reparation of double stranded breaks. Inappropriate pairing or loss of normal pairing is associated with gene mis-regulation in some disease states.

Biography

Viya Fedoseyeva completed her thesis for PhD at Moscow Institute of Physics and Technology and for many years she worked as Research Scientist in Laboratory of Bioinformatics of Institute of Molecular Genetics (Russian Academy of Science) till the present time. She has published more than 25 papers in Russian and foreign reputed journals.

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