

GENE STRUCTURE EVOLUTION

Summary

With the growing number of sequenced genomes comparative studies of lineage specific genomic features become both very rewarding and challenging. Large scale multiple genomes analyses allow to decipher many genomic features. They show that main differences between related species concern not as much the number of genes or the presence of species specific genes as the differences in the gene structure organization. Although much has been learned about gene structure evolution many problems remain unsolved. Alternative splicing is one of the main mechanisms leading to the proteome diversification. The raise of new splice variants is strictly connected with the exon and intron loss and gain. Main mechanisms of how the new exons originate are known, but question which of them, if any,

plays the main role remains open. Another unsolved mystery is the intron origination. The dispute between “intro-early” and “intron-late” hypotheses supporters leads us to many interesting findings but the problem remains unsolved. One of the most fascinating discoveries in the genome studies is the role of so called ‘junk DNA’ in the evolution of human and other vertebrates. Repetitive elements and retrogenes are one of the most important elements in the gene structure evolution. They provide signals, motifs and coding sequences for new exons, splice sites or regulatory elements. Another phenomenon discovered in the process of whole genomes analyses is the common presence of overlapping genes and, at the same time, their low conservation level.