Molecular Phylogenetics

Contributions to the 5th Moscow
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"Molecular Phylogenetics
and Biodiversity Biobanking" (MolPhy-5)
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Knowledge of phylogeny is of fundamental importance in evolutionary studies, from the reconstruction of the Tree of Life to revealing and understanding the laws of body plan formation (the evo-devo realm) and to describing the patterns and processes of microevolution. The discipline of phylogenetics has evolved radically in the new millennium, capitalizing on theoretical and methodological breakthroughs in analysis and algorithms, on the exponential increase in molecular data, and on the availability of vast computing power to enter the phylogenomic era. An integral part of contemporary phylogenetics is the development of mathematical models and effective algorithmic solutions to tackle high-complexity computational problems of building evolutionary scenarios across the levels from genes to species, bioinformatics of next-generation sequencing data, and metagenomic assays. A solid methodological framework of phylogenomic analysis is emerging, applying data derived from whole genomes to problems in deep phylogeny, functional genomics, speciation and divergence, large-scale biodiversity studies, and phylogeography. The mission of the 5th Moscow International Conference "Molecular Phylogenetics and Biodiversity Biobanking" (MolPhy-5) is to provide a stimulating platform for the exchange of ideas and experiences in contemporary phylogenetics, evolutionary genomics and conceptually integrated disciplines. This round the program also places emphasis on genomics of biodiversity and aspects of utilizing molecular data for biodiversity research. The acknowledged focus is to bridge new fundamental knowledge with various applications of phylogenetics in metagenomics, barcoding of biological objects, molecular ecology, and epidemiology.

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Conservatism of miRNA binding site in mRNA of *IGFBP3* gene and its orthologous genes

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miRNAs regulate gene expression and are often the cause of cancer development. The *IGFBP3* gene is involved in esophageal, lung, prostate, breast cancer, etc. Presumably, the *IGFBP3* gene is a target of miR-7-20589-3p (AGCAGCGCCUGCAGCGGUCGC), which binds to its mRNA in the protein-coding region. The search for miRNA binding sites in mRNA using the MirTarget program determines the beginning of miRNA binding sites, the free interaction energy, and makes up the nucleotide interaction schemes. A feature of miR-7-20589-3p interaction with mRNA of *IGFBP3* gene is the complete complementarity of all miRNA nucleotides with nucleotides of the binding site in mRNA of *IGFBP3* gene. One way to confirm the interaction of miRNA with mRNA is to establish the evolutionary conservatism of miRNA binding site in orthologous genes.

We have shown that miRNA binding site exists in mRNA of orthologous *IGFBP3* genes of 28 studied animal species. Accordingly, these binding sites encoded in IGFBP3 protein conserved the RPLQALL heptapeptide within a few hundred million years of divergence of the species studied, including *Gallus gallus* and *Alligator mississippiensis*. At the same time, oligopeptides adjacent before and after the RPLQALL heptapeptide are variable. Note that the heptapeptide is absent in the IGFBP3 protein of laboratory mouse and rat species. Therefore, these objects cannot be an adequate model for the study of miR-7-20589-3p interaction with mRNA of *IGFBP3* gene.

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