Molecular Phylogenetics

Contributions to the 4th Moscow
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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, inferring patterns of coevolution of molecules, pathways, regulation systems, and species, assembling of sequence and tree data, etc. 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, barcoding, and phylogeography. The mission of the IV Moscow International Conference "Molecular Phylogenetics" (MolPhy-4) is to provide a stimulating platform for the exchange of ideas in such top areas of evolutionary research as evolutionary genomics, molecular phylogenetics and systematics, studies of complex traits of coevolution of different genomic and proteomic elements and their ancestral reconstruction, modeling evolution in a contemporary framework of algorithmic and computer science. The acknowledged focus is to bridge new fundamental knowledge with various applications like biodiversity studies, barcoding of biological objects, molecular ecology, epidemiology and anthropology, and other actively developing fields.

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miRNAs binding sites in mRNAs of maize transcription factor genes

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Transcription factors of *MYB*, *AP2*, *bZIP*, *C2H2*, and *TCP* families in many aspects determine the productivity of plants. Maize genome encodes for 321 miRNAs. The free energy of hybridization (ΔG) miRNAs with mRNAs and the $\Delta G/\Delta G_m$ (%) values were defined using the MirTarget program. Twenty four miRNA families have binding sites in 113 from 203 mRNAs of MYB genes. The miR159a-3p has 90 binding sites with the $\Delta G/\Delta G_m$ values ranging from 87% to 92%. The miR159 binding sites encodes ELPSIQ peptide in nine mRNAs. Nineteen from 54 mRNAs of AP2 genes have binding sites with 14 miRNA families. The miR172-3p family has 25 binding sites. Four mRNA binding sites encode AASSGF peptide. mRNAs of 50 from 218 bZIP genes have sites with 26 miRNA families with $\Delta G/\Delta G_m$ values ranging from 85% to 92%. The miR169-3p family has binding sites in mRNAs of nine genes. These binding sites encode DYAKKAM peptide. Thirty one miRNA families have binding sites in mRNAs of 50 from 179 *C2H2* genes. miR164-3p and miR167-3p have 20 and 14 binding sites, respectively. The miR164-3p can bind with mRNAs of 16 genes and miR167-3p can bind with mRNAs of seven genes with $\Delta G/\Delta G_m$ values ranging from 86% to 90% and from 85% to 89%, repectively. Fourteen miRNA families have binding sites in mRNAs of 20 from 52 *TCP* genes. The miR319-3p has binding sites in mRNAs of seven genes and encode RGPLQS peptide. All considered miRNA sites are located in protein-coding sequence of target genes. It was revealed that 56%, 35%, 23%, 28%, and 38% of transcription factor genes of *MYB*, *AP2*, *bZIP*, *C2H2*, and *TCP* families, respectively, can be regulated by miRNAs. The evolutionary changes in the relationship of miRNAs with mRNAs of transcription factor genes were established.

Multiple miR-1322 binding sites in mRNAs of paralogous and orthologous genes

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MicroRNAs (miRNAs) are important translation repressors. Here, the 2,563 miRNAs binding sites have been researched in 17,494 mRNAs of human genes. Hsa-miR-1322 has more than two thousands binding sites in mRNAs of 1,058 genes. The free energy of hybridization (ΔG) miRNA with mRNA and the $\Delta G/\Delta G_m$ (%) values were defined using the MirTarget program. miR-1322 has 1,889 binding sites located in the protein-coding domains (CDS), 215 sites located in the 5′-untranslated regions and 160 sites located in the 3′-untranslated regions. The parts of mRNAs have from 2 to 28 arranged miR-1322 binding sites with start points located through three nucleotides. Oligonucleotides of miRNA sites encode polyglutamine, polyalanine, or polyserine depending on the open reading frame of CDS. The interconnecton between miRNAs and mRNAs of *MAMLD1*, *MAML2*, and *MAML3* paralogous human genes and their orthologous genes has been considered. mRNA of *MAMLD1* human gene has two regions with multiple miR-1322 binding sites and oligopeptides of *MAMLD1* that consist of 11 and 10 glutamine. Each mRNA of *MAML2* and *MAML3* genes has three regions with multiple miR-1322 binding sites encoding polyglutamine. The $\Delta G/\Delta G_m$ values range from 87% to 92%. mRNAs of orthologous *MAMLD1*, *MAML2*, and *MAML3* genes of 15 mammals have miR-1322 binding sites that encode polyglutamine. The number of glutamine residues changes from 7 to 38 in olygopeptides of *MAMLD1*, *MAML2*, and *MAML3* coding by one multiple site depending on animal. Polyglutamine olygopeptide is located between conserved domain of orthologous *MAMLD1*, *MAML2*, and *MAML3*. The variation of the number of amino acids residues in a polyglutamine olygopeptide causes various diseases.