

Alexey V. Troitsky

Department of Evolutionary Biochemistry
A. N. Belozersky Institute of Physicochemical Biology
M. V. Lomonosov Moscow State University

Leonid Yu. Rusin

Laboratory for Mathematic Methods and Models in Bioinformatics
Institute for Information Transmission Problems
Russian Academy of Sciences
Phylogenetics Laboratory, Faculty of Biology
M. V. Lomonosov Moscow State University

Nikolay B. Petrov

Department of Evolutionary Biochemistry
A. N. Belozersky Institute of Physicochemical Biology
M. V. Lomonosov Moscow State University

ББК 28

М 97

УДК 57.06; 577.2; 575.8

M97 **Molecular Phylogenetics: Contributions to the 4th Moscow International Conference “Molecular Phylogenetics” (Moscow, Russia, September 23–26, 2014)** / [Compiled by A. Troitsky, L. Rusin, and N. Petrov]. — Moscow: TORUS PRESS, 2014. — 90 p.: ill.

ISBN 978-5-94588-153-2

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.

ББК 28

ISBN 978-5-94588-153-2

© TORUS PRESS, 2014

Financial support to the Conference was partially provided by the Russian Foundation for Basic Research (grant No. 14-04-20170), Federal Agency of Scientific Organizations, and commercial sponsors (the companies SkyGen and Genotek).