

PREFACE

Molecular phylogenetics has faced thriving development over recent years at the interface of molecular biology, genetics, computer science, and mathematics. Today it is among top areas of the new-age biology that uses computational approaches to interpret volumes of genetic information to generate new knowledge and evolutionary hypotheses with implications in fundamental and applied aspects of physiology, embryology, molecular ecology, comparative anatomy, etc. Armed with the power of modern computing and next-generation sequencing, phylogenetic methodology gave rise to phylogenomics, the comparison of partial or entire genomes to infer evolutionary relationships back to the deepest branches of life, predict gene function, and reconstruct patterns of ancient and recent lateral gene flows that shaped living genotypes. Molecular phylogenetics offers powerful tools to study biodiversity, and has become the framework of ambitious approaches to barcode the Tree of Life. Phylogenetic techniques are the today's basis of molecular medicine and epidemiology, genotyping in agriculture and breeding, forensic science, etc.

The Moscow Conference on Molecular Phylogenetics (MolPhy) is organized jointly by the Science & Education Centers "Evolutionary Genomics and Bioinformatics" (Moscow State University: Belozersky Institute for Physicochemical Biology, Faculty of Biology, Faculty of Bioengineering and Bioinformatics) and "Bioinformatic and Computational Technologies" (the Institute for Information Transmission Problems, Russian Academy of Sciences) with the support by leading academic organizations and scientific funds.

The conference program features contributions in the broad area of molecular evolution and its applications: ancient genetic history of life, algorithms and methodology to analyze molecular genetic data, evolutionary genomics, phylogenomics, fundamental and applied phylogenetics.