

PREFACE

Molecular phylogenetics is science to reconstruct evolutionary relationships of life based on comparisons of structures of molecular carriers of information, the semantids. In contrast to classic approaches that were limited by available phenotypic features, it opened the new gateway to discover relationships robust to the misleading effects of parallel and convergent evolution. Although these bases nowadays seem universally recognized, early phylogenetics was severely opposed by traditionalists. Roots of phylogenetic science can be traced back to early XX century to studies of similarities between immune systems, and contemporary phylogenetics conceived in early 1960s has made a long way from comparisons of bacterial DNA and a few vertebrate proteins toward today's phylogenomics and metagenomics. It has now become the central paradigm of evolutionary biology and a key framework for making sense of a wide range of disciplines such as genomics, community ecology, epidemiology, conservation biology, population dynamics, to name just a few. It is a testament to the power of phylogenetic methods that its application has expanded far beyond its original inception, now including the study of human culture such as language and cultural memes.

Among milestone breakthroughs based on phylogenetic information are outlining the global Tree of Life, discovery of the superkingdom Archaeobacteria, and the understanding of symbiotic origins of double-membrane cellular organelles, like plastids and mitochondria, and ultimately the eukaryotic life. Over time, science witnessed an incredible progress in both experiment and theory of generating and analyzing molecular data. A rare evolutionary discipline nowadays dispenses with concepts of molecular phylogenetics. This can be judged by the sheer volume of published results. According to PubMed, 543 articles published since 2015 directly include terms “molecular phylogeny” or “molecular phylogenetics” in the title.

Keyword-based statistics is thousands of papers. New concepts are developing that tackle various aspects of coevolution, including approaches to define and algorithmically construct complex evolutionary scenarios for genetic systems, their regulations, epigenetic and intrinsic factors, noncoding genome elements, etc. Phylogenetics permeated into and fueled studies of global biodiversity laying out appropriate conservation strategies, biogeography, population genetics, agrobiolgy, and other fields.

This conference presents a gentle slice of this immense knowledge influx. It is the fifth in the “Molecular Phylogenetics” conference series that is run in Lomonosov Moscow State University since 2007. We place our hope in future development of this good tradition to gather bright researchers for a fruitful meeting.

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Editors