

Molecular Phylogenetics and Evolution

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GUIDE FOR AUTHORS

Molecular Phylogenetics and Evolution is dedicated to bringing Darwin's dream within grasp—to "have fairly true genealogical trees of each great kingdom of Nature." The journal provides a forum for molecular studies that advance our understanding of phylogeny and evolution by publishing the results of molecular studies that identify the actual clades to which different species and higher taxa belong. Such knowledge furthers the development of phylogenetically more accurate taxonomic classifications and ultimately a unified classification for all the ramifying lines of life. Molecular studies have already provided evidence—missing in Darwin's time—that a single primordial species in our ancient past was probably the source of the ramifying lines of evolution from which all present-day species have descended. With each present-day genome containing a range of DNA sequences from rapidly to extremely slowly evolving, it becomes possible to discover the phylogenetic relationships that exist among living species at all levels of the taxonomic hierarchy, from the most recently separated to the most anciently separated.

Papers that result from or encourage the collaboration of molecular biologists and computer scientists with the community of systematic and evolutionary biologists are of special interest. In addition, presentations of new findings on or insights into evolutionary processes and mechanisms as expressed at the molecular level are welcome, as are those that deal with the methodology of reconstructing evolutionary history from molecular data (such as descriptions of new or more powerful computer algorithms for constructing phylogenetic trees from homologous nucleotide sequences or from homologous amino acid sequences). A deeper understanding of the mechanisms and processes of molecular evolution should lead to more accurate models of molecular evolution, which in turn should facilitate the development of better algorithms for reconstructing evolutionary history from sequence data.

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Review papers are accepted. These papers do not contain much new data; rather, they are a status report of a specific field within molecular phylogenetics. Authors should relate molecular phylogeny to a broader audience by linking taxonomic group/names to common names so papers will have more general appeal.

Short communications of approximately 3000 words are also accepted. These papers should contain no more than two figures, two tables, thirty references, and should omit the abstract.

Letters to the editor should consist of about 1000 and contain no tables, no figures, and no new data.

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Williams, P.L., Fitch, W.M., 1989. Finding the minimal change in a given tree. In: Feraholm, B., Bremner, K., Jornvall, H. (Eds.), *The Hierarchy of Life*. Elsevier, Amsterdam, pp. 453–470.

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