

A 28S rNA-based phylogeny of the Gnathostomes : first steps in the analysis of conflict and congruence with morphologically based cladograms
H.L. Van Lê, G. Lecointre and R. Perasso. 1993. *Molecular Phylogenetics and Evolution* 2 : 31-51.

Approximately 500 nucleotides of 28S rNA-based phylogeny of 31 species of gnathostomes have been sequenced in order to study the phylogeny of the major fish lineages. In maximum parsimony trees, nodes congruent with those of the morphologically based cladogram were found to be robust (chondrichthyans, neopterygians, euteleosteans), but some expected monophyletic groups were not found to be so (lissamphibians, tetrapods, osteichthyans). Possible causes for these discrepancies are discussed. Some non congruent nodes were significantly supported (elomorph-osteoglossomorph sister-group relationships) and the need for new morphological character analysis is discussed. In addition, the relationships of major gnathostome lineages (chondrichthyans, actinopterygians, sarcopterygyans) could not be resolved and the possibility of their rapid evolutionary radiation is examined. This result is strikingly similar to those obtained from approximately 1800 nucleotides of 18S rNA. Variations in the robustness of some nodes depending on the species sample were observed. This has led to a systematic study of the effect of species sampling on bootstrap values described in a companion paper (G. Lecointre, H. Philippe, H.L.V. Lê, and H. Le Guyader, 1993).