

## Molecular phylogenetics and the evolution of Antarctic Notothenioid fishes

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The monophyly of the Antarctic fish suborder Notothenioidei and the monophyly of its earliest family the Bovichtidae have been investigated with 12S and 16S mitochondrial DNA sequences. New data from *Cottoperca*, *Pseudaphritis*, *Harpagifer* and several outgroups, in addition to available sequences, show that the bovichtids are paraphyletic. *Pseudaphritis* is the sister group of all the non-bovichtid notothenioids. The same results are found from two independent genetic markers, the nuclear 28S rDNA and the 12S and 16S mitochondrial rDNA. This reliably refutes a previous hypothesis that placed *Pseudaphritis* as the sister group of all the remaining notothenioids (including *Cottoperca* and *Bovichtus*). Bootstrap analyses show that the Notothenioidei are monophyletic (although members of the suborder Trachinoidei have not been surveyed). Subsequent data from hemoglobin composition confirm the present relationships. After discussions between members of the European Science Foundation (ESF) network during its last two meetings, we point out here some fundamental aspects of comparative biology to improve understanding between the physiologist community and phylogeneticists. The most important points are differences in how the concept of homology is used and differences in the consideration of adaptation. When adaptation is evoked or questioned, endless speculations and untestable scenarios are often developed. We strongly advocate the use of phylogenetic trees for testing hypotheses of adaptation (through multiple character mapping). Such a "research program" in comparative biology has the power to improve knowledge because it can potentially lead to new experiments for testing adaptive hypotheses.