

## Channichthyid phylogeny based on two mitochondrial genes.

CHEN, W.J., BONILLO, C., LECOINTRE, G. 1998

In di Prisco, G., Pisano, E. and Clarke, A. (eds). Fishes of Antarctica. A biological Overview. Springer Verlag. pp. 287-298.

Our nucleotide sequence data from two mitochondrial genes of 14 species of Channichthyidae allowed reconstruction of a complete and reliable phylogeny of the family except for the relationships of *Chaenocephalus*. This study offered an example of obtaining a better resolution when the total evidence strategy is chosen. Only one node over 13 has a bootstrap proportion below 50% and 9 above 70%. Our molecular tree supports most of the clades proposed by Iwami on the basis of morphological characters. For the differing points, the principle of parsimony shows that there is no real contradiction between morphology and molecules. Indeed, the molecular position of *Channichthys* requires no extra step in the morphological matrix of Iwami. A reinterpretation of Voskoboinikova's developmental data shows that the most advanced channichthyids are the most pedomorphic. Assuming a molecular clock and a calibration based on the perciform fossil record, the channichthyid family dates back to the time of the polar front formation.