

A Phylogenetic analysis of Oplophoridae (Decapoda, Crustacea) based on molecular data.

Master thesis in Marine Biodiversity

By

Ole Kristian Larsen
Department of Biology
University of Bergen
January 2009

Abstract

Deep sea shrimps of the family Oplophoridae DANA, 1852 are conspicuous members of deep-sea ecosystems with 10 genera and about 70 species (Cardoso and Young, 2005). The Census of Marine Life associated Mar-Eco Cruise over the northern mid-Atlantic ridge in summer 2004 retrieved many species of Oplophoridae. Some of the samples were suitable for DNA extraction. I sequenced fragments of two mitochondrial genes, *Cox1* and *16S*, and two nuclear genes, *H3* and *18S* from representatives of the genera *Ephyrina*, *Oplophorus*, *Systemaspis*, *Acanthephyra*, *Hymenodora*, *Notostomus*, and *Meningodora* to compare sequence divergence and to initiate phylogenetic studies of the group. Maximum likelihood search, Bayesian estimations and the Bayesian integrated program BEST were employed. With few exceptions, the Bayesian estimation and the ML search results had similar outcome on the different genes. All but one of the phylogenetic inferences on the genes resulted in a paraphyletic *Systemaspis*, which is also supported by the species tree.