

RESEARCH ARTICLE

Molecular phylogeny of Oncaeidae (Copepoda) using nuclear ribosomal internal transcribed spacer (ITS rDNA)

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Abstract

Copepods belonging to the Oncaeidae family are commonly and abundantly found in marine zooplankton. In the Mediterranean Sea, forty-seven oncaeid species occur, of which eleven in the Gulf of Naples. In this Gulf, several *Oncaea* species were morphologically analysed and described at the end of the XIX century by W. Giesbrecht. In the same area, oncaeids are being investigated over seasonal and inter-annual scales at the long-term coastal station LTER-MC. In the present work, we identified six oncaeid species using the nuclear ribosomal internal transcribed spacers (ITS rDNA) and the mitochondrial cytochrome c oxidase subunit I (mtCOI). Phylogenetic analyses based on these two genomic regions validated the sisterhood of the genera *Triconia* and the *Oncaea sensu stricto*. ITS1 and ITS2 phylogenies produced incongruent results about the position of *Oncaea curta*, calling for further investigations on this species. We also characterised the ITS2 region by secondary structure predictions and found that all the sequences analysed presented the distinct eukaryotic hallmarks. A Compensatory Base Change search corroborated the close relationship between *O. venusta* and *O. curta* and between *O. media* and *O. venusta* already identified by ITS phylogenies. The present results, which stem from the integration of molecular and morphological taxonomy, represent an encouraging step towards an improved knowledge of copepod biodiversity: The two complementary approaches, when applied to long-term copepod monitoring, will also help to better understanding their genetic variations and ecological niches of co-occurring species.