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Trying to resolve the taxonomic confusion of *Paracalanus parvus* species complex (Copepoda, Calanoida) in the Mediterranean and Black Seas through a combined analysis of morphology, molecular taxonomy and DNA metabarcoding.

Panagiotis Kasapidis[1], Ioanna Siokou[1], Meriem Khelifi Touhami[2], Maria Grazia Mazzocchi[3], Epaminondas Christou[1], Maria Luz Fernandez de Puelles[4], Alexandra Gubanova[5], Iole Di Capua[3], Mar Santandreu[4], Vassiliki Terzoglou[1], Efstratios Batziakas[1], Constantin Frangoulis[1]

[1]Hellenic Centre for Marine Research, Greece
[2]Badji Mokhtar University, Algeria
[3]Stazione Zoologica Anton Dohrn, Italy
[4]Centro Oceanográfico de Baleares (IEO), Spain
[5]Institute of Biology of the Southern Seas, Russia

Paracalanus parvus is reported as the most abundant representative of the genus and one of the main components of the coastal zooplankton in the Mediterranean and Black Seas. However, the subtle taxonomic differences between *P. parvus* and the congeneric species *P. indicus* and *P. quasimodo*, in combination with the ample morphological variation found in Mediterranean specimens, render problematic the correct identification. A recent molecular study by Cornils and Held (2014) provided evidence of cryptic speciation in the *P. parvus* complex and indicated that *P. parvus* s.s. does not have global distribution, but may be restricted to the northeastern Atlantic. In order to clarify the taxonomic status and distribution of this species complex in the Mediterranean and Black Seas, a study was conducted on *Paracalanus* specimens collected from different locations across the aforementioned marine basins and sequenced for portion of the COI mitochondrial gene. An accurate taxonomic analysis was also carried out to correlate morphological characteristics with the molecular species' assignation. The phylogenetic analysis of the specimens together with the publicly available sequences of *P. parvus* complex revealed the presence of four molecular operational taxonomic units (MOTUs) in the Mediterranean, which differed in abundance and geographic distribution. The combination of morphological and molecular data revealed great inconsistencies between morphospecies and MOTUs. Moreover, several bulk zooplankton samples were analyzed through DNA metabarcoding in the frame of the “MetaCopepod” project to provide more extensive information on the spatiotemporal distribution and abundance of the target species.

Keywords: *Paracalanus parvus* species complex, phylogenetic analysis, cyrochrome oxidase I, taxonomy, next generation sequencing

Contact author: Panagiotis Kasapidis, Hellenic Centre for Marine Research (HCMR), Institute of Marine Biology, Biotechnology and Aquaculture, P.O.Box 2214, 71003 Heraklion, Crete, Greece