Taxonomic and phylogenetic studies on coastal marine and brackish-water calanoid copepods in the tropical Indo-West Pacific, especially in territorial waters of Thailand

Abstract

In Thailand, only a limited number of taxonomic studies on marine calanoid copepods have been conducted. The surveys that have been conducted have not always been sufficiently detailed to reveal new species or to identify new location records. While it has been suggested that there are faunal differences between the populations of marine copepods in the Andaman Sea (the Indian Ocean) and the Gulf of Thailand (the West Pacific Ocean), these have never been considered zoogeographically. Recent molecular-based taxonomic studies of copepods has revealed the presence of many sibling/cryptic species even within common species and therefore the objectives of the current study were to investigate the taxonomy and phylogeny of coastal and brackish calanoid copepods in Thailand using an array of modern morphology and molecular-based techniques.

A review of the literatary records of coastal marine and brackish-water calanoid copepods found in Thai coastal and estuarine waters suggests that from the 30 known published studies, a total of 123 species belonging to 29 genera, and 18 families have been documented. From the present study on the taxonomy of calanoid copepods on samples collected between 2001 and 2015, I report on the discovery of one new species and four new location records for Thailand. The new species belongs to the family Pseudodiaptomidae, genus *Pseudodiaptomus* and following its publication is formerly known as *Pseudodiaptomus siamensis* Srinui, Nishida & Ohtsuka, 2013. The new location records include: 1) *Acartiella nicolae* Dussart, 1985 (Family Acartiidae Sars, 1903; Genus *Acartiella* Sewell, 1914) which was collected from the brackish-waters of the Prasae River Estuary in Rayong Province in the eastern Gulf of Thailand; 2) *Centropages brevifurcus* Shen & Lee, 1963 (Family Centropagidae Giesbrecht, 1892; Genus *Centropages* Kröyer, 1849) found along the coast of Prachuap Khiri Khan Province in the western Gulf of Thailand; and, 3) *Acartiella kempi* Sewell, 1914 (Family Acartiidae Sars, 1903; Genus *Acartiella* Sewell, 1914) collected from the brackish-waters of the Kraburi Estuary within Ranong Province that borders the Andaman Sea.
Following analysis, this study separates the five species of copepods into two distributional patterns which are zoogeographically restricted by water temperature and salinity to either the West Pacific Ocean or to the Indian Ocean. Four species were restricted to the West Pacific Ocean, namely: *P. siamensis* which was found in waters ranging from 0.7 to 23.3 salinity; *Acartiella sinensis* Shen & Lee, 1963 occurred in waters of around 31.3 °C and approximately 5.0; *A. nicolae* which was found in waters ranging from 28.0–29.9 °C in temperature and 1.0–4.0 in salinity; and, *C. brevifurcus* which was collected in waters of around 31 °C and 32 in salinity. The only species restricted to the Indian Ocean was *A. kempi*, which was found in waters measuring 31.4–32.1 °C in water temperature and 13.0–22.0 in salinity.

To ascertain whether there were sibling/cryptic species among the three species complexes of marine calanoid copepods in the Indo-West Pacific waters, I analysed the nucleotide sequences of the mitochondrial genes of *Acartia* (*Odontacartia*) *pacificica* Steuer, 1915 collected from six populations (i.e. locations) across East and Southeast Asia. I also conducted similar analyses for *Tortanus* (*Tortanus*) *forcipatus* Giesbrecht, 1889, and *Labidocera rotunda* Mori, 1929 from various locations throughout Asian waters. For *A. (O.) pacifica sensu lato*, the two target genes were sufficient to reveal two species groups, one consisting of samples collected from brackish-waters (i.e. samples collected from China, the Gulf of Thailand and the Andaman Sea) and, a second group of specimens collected from coastal waters (i.e. those collected from Japan, Korea and the Philippines). From the phylogenetic trees that were constructed, the two clades could be further separated into four sub-groups, namely: 1) the Gulf of Thailand and China; 2) the Andaman Sea; 3) the Philippines; and, 4) specimens from Japan and Korea. This last sub-group also included specimens of *A. (O.) pacifica* deposited in Genbank (accession numbers DQ071177 and DQ071175). A 636 bp fragment of the *COI* gene sequenced and compared from 28 individual sequences revealed 23 haplotypes, while a 163 bp region of the *16S rRNA* gene from 29 individual sequences revealed 17 haplotypes. The maximum genetic divergence between the sub-groups was between the specimens collected from the Andaman Sea and those collected from the Philippines (i.e. divergence values = 33–34, and 19–20 % for the *16S rRNA* and *COI* genes, respectively). These four sub-groups most likely correspond to separate species, one of which is evidently different, based on both morphology and molecular evidence,
and represents an undescribed species. The specimens of *T. (T.) forcipatus*, however, require further examination using both DNA and morphology-based tools. From the study, a 591 bp fragment from the *COI* gene from 15 individual sequences were obtained, revealing 8 haplotypes, while a 258 bp region of the *16S rRNA* gene from 18 individual sequences revealed 7 haplotypes. The maximum genetic divergence between these sub-groups was between the specimens collected from the Andaman Sea and from the West Pacific (i.e. divergence values = 10–11 and 7–8 % for the *COI* and *16S rRNA* genes, respectively). For the species *L. rotunda*, a 621 bp fragment of the *COI* gene obtained from 18 individual sequences revealed 17 haplotypes, while a 271 bp region from the *16S rRNA* derived from 15 individual sequences revealed 10 haplotypes. The maximum genetic divergence between the sub-groups was between the specimens collected from the Andaman Sea and from the West Pacific (i.e. divergence values = 11–12 and 3–4 % for the *COI* and *16S rRNA* genes, respectively). Only one sequence for *L. rotunda* collected from the Andaman Sea was available, making it impossible to compare this sequence with those obtained from the other populations; more surveys and analyses, therefore, are needed for this locality.

The present data on calanoid copepods clearly indicates that there is zoogeographical separation of species between the Indian and West-Pacific Oceans. Even common species that are broadly distributed throughout the Indo-West Pacific region, therefore, require detailed study to assess their structure using modern morphology and molecular-based tools, and where necessary, to revise and update their taxonomy. From the current study, it is likely that certain species are composed of several sibling and/or cryptic species. Future work, therefore should not only set out to have a better understanding of species and the structure of copepod communities but also to clarify what vicariant events have led to their speciation and separation.