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A morphological evaluation of *Chrysaora chinensis* of Peninsular Malaysia and distinguishing its populations using geometric morphometrics

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Abstract

The morphology of seven specimens of *Chrysaora chinensis* (Scyphomedusae, Semaestomae) obtained from four sites off the coast of Peninsular Malaysia was examined. Morphological characteristics of *C. chinensis* that encompasses structures such as the bell, tentacles, oral arms, stomach, manubrium, radial canals and gonads were described in detail. A total of 107 specimens that represented *C. chinensis* populations of four coastal areas of Peninsular Malaysia (East-Central, East-North, West-Central, and West-North) were also analysed for shape variation using geometric morphometric analysis. Procrustes superimposition, Principal Component Analysis (PCA) and Canonical Variate Analysis (CVA) were applied to the images of gastrovascular pouches of *C. chinensis* to extract the shape information. Independent contrasts were used for comparisons between shapes. There were no significant differences in shape variation between all the specimens based on the PCA results. However, CVA results showed shape variations between specimens taken from the four areas of Peninsular Malaysia, especially with higher magnitudes of Mahalanobis distances between the east and west coast areas, including between East-Central and East-North, but lower magnitudes were detected between the West-Central and West-North.

Key words: geometric morphometrics, Scyphozoa, jellyfish, morphology, Malaysia

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1 Introduction

The sea nettle jellyfish of the genus *Chrysaora* are classified under the family Pelagidae (order Semaeostomeae) and are typically recognized by having 32–48 lappets, with eight marginal sense organs, with three or more tentacles per octant, with 16 gastrovascular pouches, and with numerous warts on the exumbrella (Kramp, 1961). Species of sea nettle have a worldwide distribution and have been reported to occur in the South China Sea, North, Central and South America, Africa, Europe and Australia (Morandini and Marques, 2010; Yap and Ong, 2012). According to the World Register of Marine Species (http://www. marinespecies.org) there are possibly 15–18 species, whereby 5 species have been verified: *Chrysaora achlyos, Chrysaora hysoscella, Chrysaora pacifica, Chrysaora quinquecirrha* and *Chrysaora chinensis*.

Although some regions of Southeast Asia have been reported to harbour Chrysaora species such as *Chrysaora quinquecirrha* and *Chrysaora melanaster* (Kramp, 1961; Yap and Ong, 2012), there is the possibility they were misidentified base on colour variations and this possibility warrants verification. In the past, jellyfish species were notoriously difficult to identify as there were no reliable taxonomic keys, specimens were badly preserved, and confounded by the existence of cryptic species complexes that could be detected only by the application of molecular genetic techniques. For example, C. chinensis in Malaysia has been previously identified as C. hysoscella or C. quinquecirrha based on reports of envenomation and toxicology studies of jellyfish stings (Azila and Othman, 1993) and those in the Singapore Straits as C. melanaster (Yap and Ong, 2012)- possibly misidentified due to the colour variations. Some features, such as nematocysts have been used to aid in the species identification, hence sea nettles from the South China Sea were believed to be C. chinensis (Morandini and Marques, 2010; Yap and Ong, 2012). More recently, applications of DNA sequence analysis and phylogenetics have helped identify and barcode some of the Malaysian jellyfish species, including C. chinensis (Rizman-Idid et al., 2016), which concurred the notion that specimens with different colour morphs are often genetically similar and regarded as the same species. However, it is important to realize that the efficiency of such DNA barcoding method depends on the availability of reference sequences of correctly identified voucher specimens in the GenBank database. Although the study provided 16S and ITS1 sequences, it did not have the required COI sequences to definitively barcode C. chinensis. Furthermore, the morphological description of the species in the study was relatively simple and preliminary. Hence a more detailed morphological evalu-

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