Phylogenetic study and barcoding of the blood cockle, *Tegillarca granosa*, found on the west coast of peninsular Malaysia using the COI gene

S.Y. Chee[1], M.N. Devakie[2] and M.N. Siti Azizah[1]

[1]School of Biological Sciences, Universiti Sains Malaysia, Penang, Malaysia
[2]Fisheries Research Institute, Batu Maung, Penang, Malaysia

Corresponding author: S.Y. Chee
E-mail: suyinchee@gmail.com

ABSTRACT. Blood cockles are among the most economically important brackish water invertebrates found in Malaysia. However, our knowledge of blood cockle phylogeny and systematics is rudimentary, especially for the species *Tegillarca granosa*. It is unclear, for instance, whether the cockles occurring on the west coast of peninsular Malaysia constitute a single species, or multiple, phylogenetically distinct species. We performed the first DNA molecular phylogenetic analysis of *T. granosa* to distinguish it from other related species found in other parts of the world and to create a DNA database for the species. An approximately 585-nucleotide fragment of the mitochondrial DNA (cytochrome oxidase I, COI) was sequenced for 150 individual cockles, representing 10 populations: three from the north, four from the central part and three from the southern part of peninsular Malaysia. Phylogenetic analyses of the resulting dataset yielded tree topologies that not only showed the relationship between *T. granosa* and its closest relatives but its position in the evolutionary tree. Three mitochondrial clades were evident, each containing an individual genus. Using the

mutation rate of the COI gene, the divergence time between *T. granosa* and its closest related species was estimated to be 460 thousand years ago. This study provides a phylogenetic framework for this ecologically prominent and commercially important cockle species.