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Volume 40, Issue 2, May 2017, Pages 305-318**Comparison of ossicle shape and 12S rRNA gene sequencing techniques for species identification of Gamat-based beche-de-mer from Langkawi Island, Kedah** (Article)Kamarudin, K.R.² [ORCID](#), Rehan, M.M.² [ORCID](#), Noor, H.M.² [ORCID](#), Ramly, N.Z.² [ORCID](#), Rehan, A.M.² [ORCID](#) [ORCID](#)²Food Biotechnology, Faculty of Science and Technology, Universiti Sains Islam Malaysia, USIM, Bandar Baru Nilai, Nilai, Negeri Sembilan, Malaysia²Department of Biotechnology, Kuliyah of Science, International Islamic University Malaysia, IIUM, Kuantan, Pahang, Malaysia

Abstract

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Due to the issues of species substitution and product mislabelling of beche-de-mer worldwide, this study aimed to identify the species of seven gamat-based beche-de-mer specimens from Kuah, Langkawi Island, Kedah, Malaysia based on ossicle shapes and non-protein-coding 12S mitochondrial rRNA gene sequences. In general, ossicles were well extracted from the specimens. At least eight ossicle shapes were observed i.e. large I-shaped rod, perforated plate, table, C-shaped rod, button, rosette, I-shaped rod and X-shaped rod. Except for button, I-shaped rod and X-shaped rod, the other five ossicle shapes are common in *Stichopus horrens*. However, the species status could not be resolved at this level due to the presence of uncommon ossicle shapes and the physical features of the specimens could not be used as supporting data as they were different from the live or unprocessed sea cucumber. In this study, 12S mitochondrial rRNA gene sequences were analysed using the Basic Local Alignment Search Tool programme for Nucleotides (blastn), resulting in the species identification of the beche-de-mer specimens as *S. horrens*, known locally as gamat emas (golden sea cucumber) with 96-99% similarity (an average of 98%). The phylogenetic trees based on the Neighbour-joining method, Maximum Parsimony method and Maximum Likelihood method indicated that all 12S mitochondrial rRNA gene sequences of the beche-de-mer specimens clustered with the reference samples of *S. horrens* from Pangkor Laut, Pangkor Island, Perak, Malaysia, supporting the BLASTN results and confirming their species status as *S. horrens*. Furthermore, 10 partial 12S mitochondrial rRNA gene sequences of the reference samples and the beche-de-mer specimens of *S. horrens* were registered with the GenBank (Accession No.: KX879628-KX879637). Overall, the findings suggested that the species identification of the beche-de-mer specimens using 12S mitochondrial rRNA gene sequence gave better inference than ossicle-shape identification. The outcomes of this study benefit enforcement agencies in their work of monitoring and overcoming the issues of species substitution and product mislabelling of beche-de-mer or commercial dried sea cucumber in Malaysian markets as well as in global markets. © Universiti Putra Malaysia Press.

Author keywords

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