

ABSTRACT

Taxonomy status of razor clam, *Solen* spp. is unclear due to the presence of morphological variations in the arrangement of pallial muscle scars and adductor scars. Three species of razor clams have been reported in various locations in Malaysia. Previous classifications were done by observing differences in the pallial muscle scars and adductor scar on the specimen shell. This study incorporated morphological and molecular approaches to evaluate the systematic relationships of *Solen* spp. in Malaysia more effectively. Multivariate morphometric tools were applied in verifying the reliability of using shell variables in classifying *Solen* spp. Eight morphological shell characters were scored: total shell length (TSL), shell width (SW), shell weight (SWHT), distance innermost point of pallial sinus to posterior margin (DPSPM), length of abductor scar (LAS), ligament length (LL), length of anterior abductor scar (LAAS), length of ventral limb of pallial sinus. Discriminant function analysis (DFA) and Principal Component Analysis (PCA) were applied to examine these eight morphometric variables of the *Solen* sp. The results showed the existence of four distinct morphospecies in the samples collected, indicating DFA morphometric analysis as useful tools for discriminating *Solen* spp. PCA managed to extract SW and LAAS as suitable variables to discriminate the three forms of *Solen* as *Solen regularis* (Ambal Biasa), *Solen lamarckii* (Ambal Jernang) and *Solen sarawakensis* Type I and Type II (Ambal Riong). As for the molecular aspects, phylogenetic relationship study was conducted among the Malaysian razor clam of family, *Solenidae* using partial 16S ribosomal RNA gene, ITS region of ribosomal DNA and CO1 mitochondrial gene sequences. This paper attempted to

combine both ecological aspect and molecular approaches to further clarify the issue on *Solen* spp. taxonomic relationship in species level. The obtained results manage to shed some light in the taxonomy of bivalve especially *Solenids*. Twenty-three samples from three species of the Peninsular and Sarawak razor clams (Family: *Solenidae*) was used in this study to examine on the phylogenetic relationship between species of razor clams based on three targeted genes. Phylogenetic analysis using neighbour-joining, maximum parsimony and maximum likelihood methods support the monophyly of the four different taxa found in Sarawak namely *Solen regularis*, *Solen lamarkii*, *Solen sarawakensis* Type I and Type II. The results obtained from the phylogenetic trees generated from the three studied genes revealed that *Solen sarawakensis* Type II that was collected from Peninsular Malaysia could belong to a distinct species and failed to show any similarity in its morphological characters. Overall, this study has provided a significant contribution in clarifying the phylogenetic and relationships of *Solenidae* in Malaysia.

Keywords: Discriminant Function Analysis, Principal Component Analysis, Phylogenetic Analysis, 16S ribosomal RNA gene, ITS ribosomal DNA gene, CO1 mitochondrial genes sequences

ANALISIS MORFOLOGI DAN MOLEKULAR SIPUT AMBAL *Solen* spp. DARI
MALAYSIA

ABSTRAK

*Status taksonomi Solen spp. masih kabur atas kewujudan pelbagai variasi dalam susunan 'palium parut otot' dan 'parut aduktor'. Tiga spesies ambal atau lebih dikenali sebagai siput pahat-pahat dijumpai di Malaysia. Klasifikasi tradisional dilaksanakan berdasarkan pemerhatian terhadap perbezaan susunan 'palium parut otot' dan 'parut aduktor' yang terdapat pada cangkerang spesimen. Kajian ini menggunakan pendekatan morfologi dan molekular bagi menilai sistematik Solen spp. dengan lebih berkesan. Aspek morfologikal menggunakan kaedah multivariate morfologikal dalam mengesahkan kebolehppercayaan bagi menggunakan ukuran-ukuran cangkerang yang diperolehi dalam mengklasifikasikan Solen spp. Lapan jenis pengukuran cangkerang diperolehi: panjang cangkerang (TSL), kelebaran cangkerang (SW), berat cangkerang (SWHT), jarak dari dalaman palium sinus ke pinggir posterior (DPSPM), panjang parut aduktor (LAS), panjang ligamen (LL), panjang parut aduktor anterior (LAAS), dan sebagainya. Analisis Fungsi Diskriminasi (DFA) dan Analisis Komponen Utama (PCA) digunakan untuk mengkaji kelapan-lapan ukuran yang diukur dan DFA berjaya dalam membezakan Solen spp. PCA dapat mengekstrak SW dan LAAS sebagai karakter yang sesuai digunakan untuk mengenalpasti keempat-empat jenis *Solen* kepada Solen regularis (Ambal Biasa), Solen lamarckii (Ambal Jernang), Solen sarawakensis Jenis I (Ambal Riong) dan *Solen sarawakensis* Jenis II (Ambal Riong). Selain itu, kajian hubungan filogenetik telah dikendalikan antara siput ambal yang terdapat di Malaysia (Family: Solenidae) dengan*

menggunakan jujukan 16S ribosomal RNA gen, ITS and CO1 mitokondrial gen. Bahagian ini menggabungkan kedua-dua aspek ekologi dan molekular bagi melanjutkan penjelasan isu pertalian taksonomi Solen spp. dalam tahap spesies. Dua puluh tiga spesimen daripada tiga spesies yang terdapat di Semenanjung Malaysia dan Sarawak (Family: Solenidae) telah digunakan dalam kajian ini bagi meneliti hubungan filogenetik antara spesies ambal berdasarkan tiga gen yang disasarkan. Hasil analisis filogenetik menggunakan kaedah pengikatan-jiran, parsimoni maxima dan pendekatan maxima menyokong monophyletik tiga spesis berbeza yang terdapat di Sarawak iaitu Solen regularis, Solen lamarckii dan Solen sarawakensis. Bagaimanapun, keputusan yang diperoleh dari analisis filogenetik yang dihasilkan dari tiga gen menunjukkan Solen sarawakensis Jenis II yang diperolehi dari semenanjung Malaysia telah dibezakan sebagai spesis yang berlainan dan gagal memaparkan sebarang persamaan dalam aspek morfologi. Secara keseluruhannya, keputusan kajian ini telah menyumbangkan kepada kefahaman hubungan filogenetik Solenidae di Malaysia.

Kata kunci: Analisis Diskriminasi Fungsi, Analisis Komponen Utama, hubungkait filogenetik, 16S ribosom RNA gen, ITS gene, CO1 mitokondrial gen