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Species Composition and Genetic Characterisation of *Acetes intermedius* and *Acetes japonicus* from the Coastal Waters of Terengganu, Malaysia

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ABSTRACT

This study investigates the diversity and species composition of *Acetes* sp. from selected coastal waters of Terengganu, Malaysia. Morphological and molecular identification using mitochondrial DNA COI genes were employed to differentiate species and assess genetic variation. The results revealed the presence of two species, *Acetes intermedius* and newly discovered *Acetes japonicus* in Terengganu waters. *A. intermedius* was found in four locations, Pengkalan Gong Batu, Jeti Marang, Jeti Seberang Takir, and Rhu Muda, while *A. japonicus* was more prevalent in two locations, Pantai Air Tawar and Pengkalan Gong Batu. Genetic analysis identified 10 haplotypes in *A. intermedius* and 8 haplotypes in *A. japonicus*, indicating a relatively high level of genetic diversity within both species. These findings contribute to enhancing our knowledge of *Acetes* diversity along the eastern coast of Peninsular Malaysia, serving as a foundation for future investigations into the ecology and fisheries management of this significant genus.

Keywords: Acetes intermedius, *Acetes japonicus*, identification, Malaysia, species diversity

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INTRODUCTION

The genus *Acetes* (Sergestidae) comprises a group of small shrimps inhabited the coastal and estuarine waters across the Indo-Pacific

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waters (Omori, 1975). Known for their ecological significance and economic value, *Acetes* species are frequently harvested for use in various regional fisheries, particularly in the production of shrimp paste and as an ingredient in local cuisine (Food and Agriculture Organisation of the United Nations [FAO], 2008; Vase et al., 2021). Despite their widespread occurrence in Malaysian waters, studies on *Acetes* have primarily focussed on the west coast of Peninsular Malaysia, where aspects such as population dynamics and ecology (Arshad et al., 2012; Arshad et al., 2007; Amani et al., 2011a; Amani et al., 2011b; Nurul Amin et al., 2009; Nurul Amin, 2008; Nurul Amin et al., 2008) and environmental impacts (Rahouma et al., 2012; Rahouma et al., 2013) have been well documented. However, relatively low knowledge of the diversity and species composition of *Acetes* in the east coast region, particularly in Terengganu waters.

Eight out of the sixteen described *Acetes* species were recorded in Malaysian coastal waters: *Acetes erythraeus* Nobili, 1906*, Acetes indicus* H. Milne Edwards, 1830, *Acetes intermedius* Omori, 1975*, Acetes japonicus* Kishinouye, 1905, *Acetes serrulatus* Krøyer, 1859*, Acetes sibogae Hansen, 1919, Acetes vulgaris* Hansen, 1919 and *Acetes omori* Hanamura, Imai & Hardianto, 2024 (Amani et al., 2011a, 2011b, 2011c; Arshad et al., 2012, 2013, 2014; Hanamura et al., 2024; Nurul Amin, 2011; Nurul Amin et al., 2012; Omori, 1975). Most studies on *Acetes* have concentrated on the west coast of Peninsular Malaysia, addressing topics such as population dynamics and ecological aspects (Amani et al., 2011a, 2011b; Arshad et al., 2012; Arshad et al., 2007; Nurul Amin et al., 2009; Nurul Amin, 2008; Nurul Amin et al., 2008) as well as environmental impacts (Rahouma et al., 2012). Molecular studies on *Acetes* remain limited, primarily focussing on the west coast of Peninsular Malaysia (Aziz et al., 2010; Maktar, 2013; Wong et al., 2017; Wong, 2013) and Sarawak (Hassan & Othman, 2021). In contrast, research on *Acetes* species in Terengganu has been sparse, with only a few studies investigating heavy metal content (Rahouma et al., 2013). Earlier works by Omori (1975) and Pathansali (1966) documented the presence of *Acetes* species in this region. However, no recent studies have examined the species composition of *Acetes* in Terengganu.

According to the report by the Department of Fisheries Malaysia, the total catch of *Acetes* in Malaysia experienced significant fluctuations from 2013 to 2023. It started at 36,207 tonnes in 2013, increasing to a peak of 43,001 tonnes in 2015. Subsequently, there was a decline until 2021 (41,968 tonnes), followed by a slight recovery in 2022 (27,957.48 tonnes) and 2023 (33,620.14 tonnes). The overall *Acetes* landings in Terengganu have been very low from 2013 to 2023. From 2013 to 2021, there were no recorded *Acetes* landings except for a small catch of two tonnes in 2015. A slight increase in landings was observed in 2022 (0.2 tonnes) and 2023 (2.4 tonnes). The overall trend for *Acetes* landings in both Malaysia and Terengganu is similar, with an initial increase followed by a decline and then a recent recovery. Both Malaysia and Terengganu have seen an increase in *Acetes* landings in recent years (2021-2023). The west coast of Malaysia is the main source of *Acetes*, with Perak generally leading in production but in 2013, Selangor surpassed

Perak as the top producer (Department of Fisheries Malaysia, 2013; 2014; 2015; 2016; 2017; 2018; 2019; 2020; 2021; 2022; 2023).

The goal of the present study is to address the knowledge deficiency by examining the diversity and species composition of *Acetes* in Terengganu waters, combining both morphological and molecular approaches. By identifying the species present and analysing their distribution, this research seeks to contribute valuable information to the understanding of *Acetes* diversity on the east coast of Peninsular Malaysia and provide a baseline for future studies on the ecological and fisheries management of this important genus.

MATERIALS AND METHODS

Acetes Sampling

During the present study, samples of *Acetes* were collected with the help of local fishermen from Pengkalan Gong Batu, Jeti Seberang Takir and Jeti Merang in April 2023, while from Pantai Air Tawar and Rhu Muda in February 2024 (Figure 1). *Acetes* shrimps were collected from inshore push nets and bottom trawling. All geographic locations were listed using their original language names (Table 1). *Acetes* samples were purchased from the local fishermen. The samples were immediately kept in 4% formalin and absolute ethanol for morphological identification and molecular identification, respectively. The samples were then taken to the laboratory for further analysis.

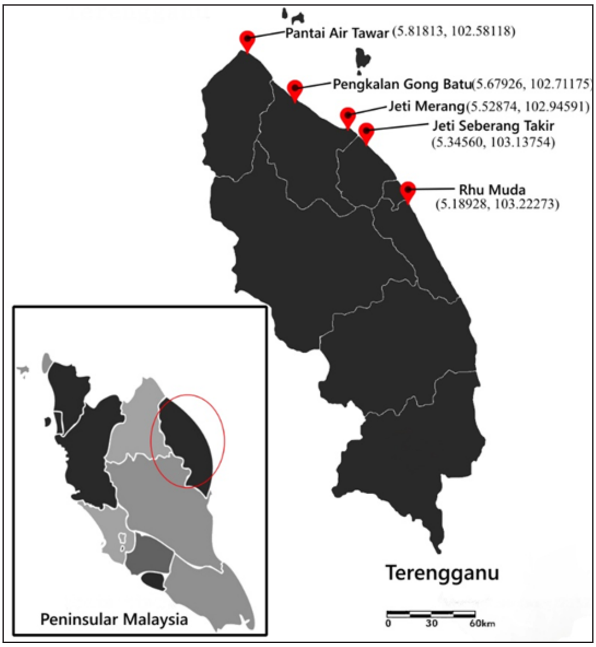

Figure 1. Sampling location of *Acetes* in Terengganu waters

Table 1
Sampling locations of Acetes in Terengganu waters

Sampling Location (Abbreviation)	Coordinate	Sampling Method
Pantai Air Tawar (PAT)	(5.81813, 102.58118)	In-shore
Pengkalan Gong Batu (GB)	(5.67926, 102.71175)	Off-shore
Jeti Merang (M)	(5.52874, 102.94591)	Off-shore
Jeti Seberang Takir (ST)	(5.34560, 103.13754)	Off-shore
Rhu Muda (RM)	(5.18928, 103.22273)	Off-shore

Species Identification, Sex Ratio, and Species Composition

Acetes were examined using a stereo microscope (Olympus SZ51, Japan) and identified according to Omori's (1975) keys and terminology. Antennular, carapace and total length of each *Acetes* were measured. The images were captured using a compound microscope (Leica Microsystems DM750, Germany) attached with a camera (Leica Microsystems ICC50 E, Germany). Drawings were made using a digital inking method using Krita drawing software in Samsung Galaxy Tab S7 FE. The petasma, genital coxae and clasping spines on the lower antennular flagellum were present in males in accordance with Omori (1975). Species composition was determined by calculating the percentage of each *Acetes* species among 30 randomly selected tails from each location (N=30) (Simões et al., 2013).

Statistical Analysis

Chi-square tests were used to determine the sex ratio for each species (Sokal and Rohlf, 1995) and were carried out using Minitab 17. The significance level was set at $P<0.05$.

DNA Extraction, Amplification, and Sequencing

A total of 55 individuals were used in the molecular study, as shown in Table 2. Following morphological identification, *Acetes intermedius* and *A. japonicus* were identified from the Terengganu samples. For molecular analysis, 10 specimens of each species from every location were selected. However, there were insufficient *A. intermedi*us samples from GB and RM for analysis due to a lack of specimens in the collected samples.

DNA was extracted using PrimeWay Genomic DNA Extraction Kit (Apical Scientific Sdn. Bhd., Malaysia). The extraction methods were carried out according to the manufacturer's manual. The amplification of the 634 bp mitochondrial DNA cytochrome c oxidase subunit I (COI) gene was performed using PCR using the universal primer LCO1490 (5’-GGT CAA CAA ATC ATA AAG ATA TTG G-3’) and HCO2198 (5’-TAA ACT TCA GGG TGA CCA AAA AAT CA-3’) (Folmer et al., 1994).

Each PCR reaction mixture contained 12.5 μL of MyTaq™ Red Mix (Bioline), 0.5 μL of each primer (Integrated DNA Technologies Pte. Ltd., Singapore), 2 μL of DNA template

Table 2
Sampling locations, number of samples and field voucher of Acetes for molecular study

Species	Sampling Locations*	No. of Samples	Field Voucher
Acetes intermedius	GB	7	GBI2-GBI5, GBI7-GBI9
	M	10	M1-M10
	ST	10	ST1-ST10
	RM	8	RM1-RM5, RM7, RM9, RM10
Acetes japonicus	PAT	10	PAT1-PAT10
	GB	10	GBJ1-GBJ3, GBJ6-GBJ10, GBI1, GBI6

and the volume was filled to 25 µL with ultra-pure water. The PCR protocols was carried out using Applied Biosystems Veriti 96-well Thermal Cycler (Thermo Fisher Scientific, USA) according to the following profile: initial denaturation at 94°C for 60 seconds, followed by five cycles of denaturation at 94°C for 30 seconds, annealing at 45°C for 90 seconds, and extension at 72°C for one minute which was followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 51°C for 90 seconds, and extension at 72°C for 60 seconds and a final extension at 72°C for five minutes (Costa et al., 2007; Hebert et al., 2003; Wong et al., 2017). The PCR products were submitted to Apical Scientific Sdn. Bhd. for Sanger sequencing.

Phylogenetic Analysis

The sequences were aligned using Multiple Alignment using Fast Fourier Transform (MAFFT) and queried in the Basic Local Alignment Search Tool (BLAST) of the National Centre for Biotechnology Information (NCBI) GenBank. The aim was to assess the sequence similarity between current study sequences and existing GenBank entries (Norshida et al., 2021). In order to avoid false positives, only top matches with ≥ 94% sequence similarity were retained (Khaleel et al., 2020). Haplotype (*h*) and nucleotide (π) diversities (Nei, 1987) were calculated using DnaSP v.6 (Rozas et al., 2017) based on segregating sites (*S*). Analysis of molecular variance (AMOVA) and pairwise F_{ST} was conducted in ARLEQUIN v3.5 (Excoffier & Lischer, 2010) to assess genetic population differentiation, using 1000 permutations. Two neutrality tests, Tajima's D (Tajima, 1989) and Fu's Fs (Fu, 1997), were examined in ARLEQUIN v3.5 to determine the deviation of studied populations from genetic equilibrium (Kamarudin et al., 2017).

A maximum likelihood (ML) tree was constructed using IQ-TREE (Trifinopoulos et al., 2016) under the best-fit substitution model selected by Bayesian information criterion (BIC) in ModelFinder (TIM+F+G4) (Kalyaanamoorthy et al., 2017). The bootstrapping was set for 1000 replications. A maximum parsimony (MP) tree was inferred using a heuristic search with TBR optimisation in PAUP (Swofford, 2021). The dataset was subjected to 1000 bootstrap replications. Nodal support values were retrieved using non-parametric bootstrapping with 1000 replicates and 10 random addition sequence replicates. *Belzebub faxoni* (Borradaile, 1915), the outgroup, was set as the root for all trees (GenBank Accession Number: KY449077), which follows the latest global phylogeny (Simões et al., 2023; Vereshchaka et al., 2016; Vereshchaka, 2017). Other sequences retrieved from NCBI GenBank included *Acetes japonicus* (acc. no: HQ630564, KF977240, OP420186 and OP420185), *A. indicus* (acc. no: LC804564 - LC804567), *A. omorii* (acc. no: LC804570 - LC804574), *A. spiniger* (acc. no: LC804568 and LC804569), *A. serrulatus* (acc. no: LC804579, HQ630498 and HQ630499) and *A. sibogae* (acc. no: HQ630582 and HQ630583). The tree was visualised using FigTree (Rambaut, 2018).

RESULTS AND DISCUSSION

Taxonomic Accounts

The "Material Examined" sections detail the number of specimens examined, which are broken down by sex. Additionally, the total length (in millimetres) is provided, where this measurement is taken from the tip of the rostrum to the apex of the telson.

Acetes intermedius Omori, 1975

Material Examined from Terengganu, Malaysia. – Pengkalan Gong Batu (GB): 6 ♂, 12.70-18.80 mm, 7 ♀, 15.20-20.20 mm Jeti Merang (M): 17 ♂, 13.40-24.70 mm, 13 ♀, 15.20-27.80 mm; Jeti Seberang Takir (ST): 16 ♂, 17.30-22.30 mm, 14 ♀, 16.40-23.70 mm; Rhu Muda (RM): 23 ♂, 14.60-23.70 mm, 7 ♀, 15.50-22.80 mm (Figures 2 and 3).

Diagnosis – Male antennular flagellum consisted of 11-13 segments and a single clasping spine (Figure 2). The clasping spine exhibited a row of small teeth, differing from the large teeth described by Omori (1975). The main branch's first segment bore 3 marginal spinules, while the segment opposing the clasping spine tip had 4 spinules. The clasping spine was longer, and the number of setae was fewer than those reported by Omori (1975). Similar to Omori (1975), the petasma was equipped with 3 large falcate hooks and several smaller ones. The large hooks exhibited a gradual increase in size towards their distal end. There was no clasping spine present on the female antennular flagellum. Petasma was absent in the female. The anterior part of the third thoracic sternite displayed a pair of protuberances (Figure 3). Unlike the significantly concave sternite described by Omori (1975), the present specimen showed only a slight concavity in the median part. The apex of the telson was truncated. In general, females tend to be larger than males in terms of all three measurements, suggesting potential sexual dimorphism. However, in GB, the males have a slightly larger average carapace length. *A. intermedius* from M tends to be larger in all measurements compared to other locations. ST also shows relatively larger sizes compared to RM and GB. This indicates potential geographical variations in *A. intermedius* size. The total length ranges in the current study were generally consistent with those reported by Omori (1975). There was a slight overlap in the female size ranges, but the male size range in the current study was slightly narrower.

Distribution – Melaka (Klebang Besar), Terengganu (Seberang Takir and Marang) and Sarawak (Bintulu and Miri).

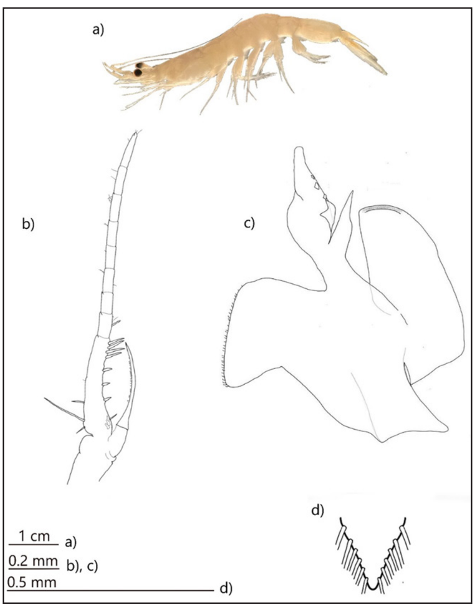

Figure 2. Acetes intermedius. Male: a) dorsal view; b) lower antennular flagellum; c) petasma; d) apex of telson. a), d) from Rhu Muda; b) from Jeti Merang; c) from Jeti Seberang Takir

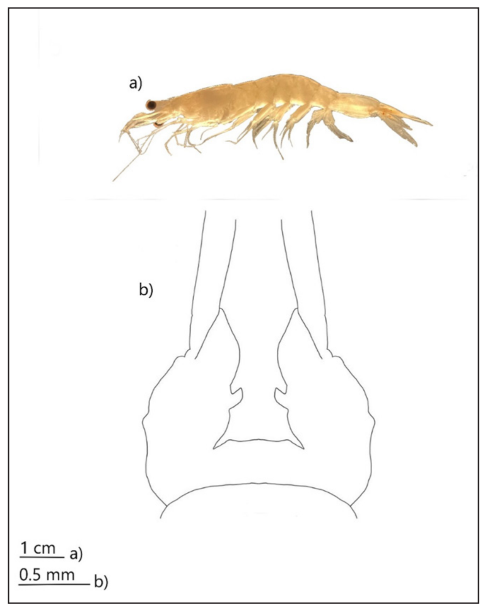

Figure 3. Acetes intermedius. Female: a) dorsal view; b) third thoracic sternite, ventral view. a) from Rhu Muda; b) from Jeti Seberang Takir

***Acetes japonicus* Kishinouye, 1905**

Synonym: *Acetes cochinensis* Rao, 1970; *Acetes dispar* Hansen, 1919

Material Examined from Terengganu, Malaysia. – Pantai Air Tawar (PAT): 10 ♂, 8.60-12.20 mm, 20 ♀, 7.90-17.30 mm; Pengkalan Gong Batu (GB): 14 ♂, 12.30-22.80 mm, 3 ♀, 14.90-15.10 mm (Figures 4 and 5).

Diagnosis – The male has 9-11 segments of the antennular flagellum, with a double clasping spine (Figure 4). The longer clasping spine has a row of teeth on its inner surface near the tip. The first segment of the main branch has a single basal spinule, while the segment opposite the clasping spine tip has 3-4 spinules. The remaining segments lack minute spinules, unlike those described by Omori (1975). The distal part of the capitulum of the petasma is bulbous and has numerous hooks of varying sizes. The processus ventralis extends beyond the capitulum, unlike in Omori's (1975), which was shorter. These differences may be related to the stage of development (Omori, 1975). There was no clasping spine present on the female antennular flagellum. Petasma was absent in the female. The third thoracic sternite of females were produced posteriorly as shown in Figure 5, with a deeper emargination on the posterior margin than described by Omori (1975). The apex of the telson was rounded. Males tend to be slightly larger than females in terms of antennular length and carapace length, while there is no significant difference in total length. However, this trend is not consistent across all locations. *A. japonicus* from GB tends to be larger in all aspects compared to other locations. PAT has the smallest average size for all measurements. This indicates potential geographical variations in *A. japonicus* size. The total length range in the current study was significantly smaller than that reported by Omori (1975), especially for the winter populations.

Distribution – Melaka (Klebang Besar), Perak (Kuala Gula, Kuala Kurau, Kuala Sepetang and Matang Mangrove Forest Reserve), Pulau Pinang (Gelugor, Batu Maung, Bagan Ajam, Teluk Bahang and Pantai Bersih), Kedah (Kuala Sala, Sungai Udang, Tanjung Dawai and Sungai Merbok), Perlis (Sungai Berembang and Sungai Baharu), Sarawak (Miri) and Johor (Pontian).

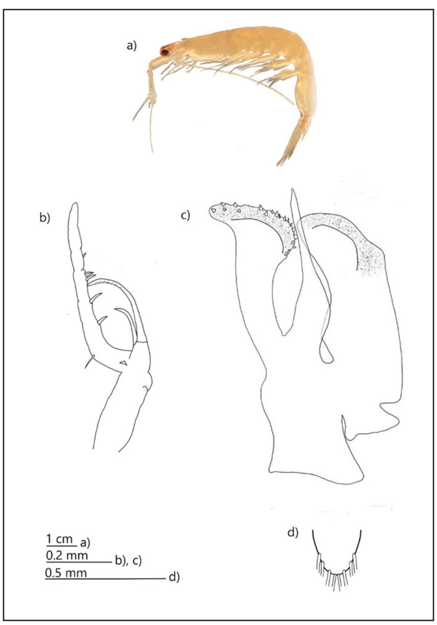

Figure 4. Acetes japonicus. Male: a) dorsal view, b) lower antennular flagellum; c) petasma; d) apex of telson. a), b), c) from Pengkalan Gong Batu; d) from Pantai Air Tawar

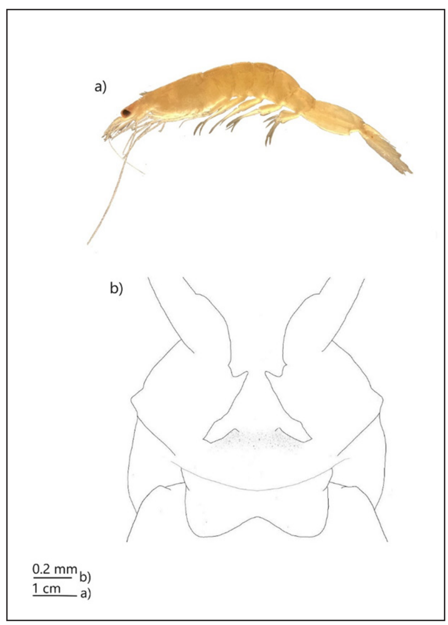

Figure 5. Acetes japonicus. Female: a) dorsal view, b) third thoracic sternite, ventral view. a), b) from Pengkalan Gong Batu

Species Composition

The species composition of *Acetes* in the study is shown in Figure 6. *Acetes intermedius* is the dominant species, with a composition of 100% in locations ST, M and RM. *A. japonicus* is present in locations GB and PAT, with a composition of 43.33% in GB and 100% in PAT. The species composition varies across locations. While *A. intermedius* is dominant in most areas, *A. japonicus* is present in GB and PAT.

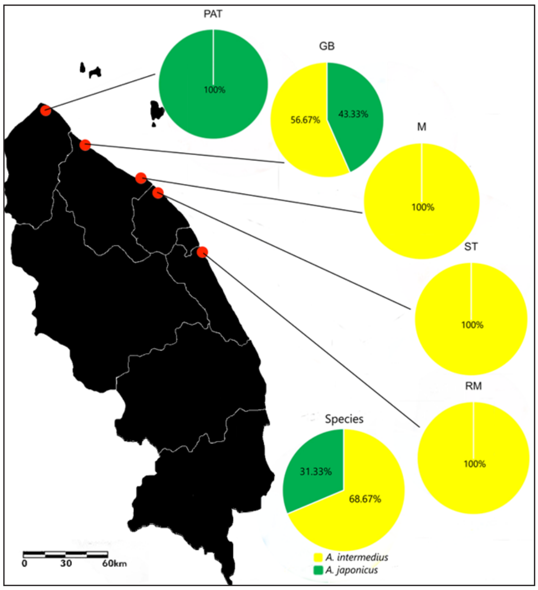

Figure 6. The species composition of *Acetes* in Terengganu waters

Sex Ratio

A mean sex ratio was observed with 0.74♀:1♂, favouring males as in Table 3. Pianka (2011) suggested a balanced sex ratio in dioecious organisms; however, Wenner (1972) found that crustaceans often exhibit skewed sex ratios due to factors such as differential growth, migration patterns, sex changes, and feeding habits. The factors should be further investigated to determine their roles which resulted in the observed sex ratio. Our results align with those of Amin et al. (2008) for *A. intermedius* and Arshad et al. (2008) for *A. vulgaris*.

Table 3
Number of males and females of A. japonicus and A. intermedius, with the resulting sex ratio and χ2 tests

Species	F	M	Total	Sex Ratio (♀: ♂)	x^2 Test	P-value
A. japonicus	23	24	47	0.96:1	0.02	>0.05
A. intermedius	41	62	103	0.66:1	4.28	<0.05
Total	64	86	150	0.74:1	3.23	>0.05

Molecular Analysis

Genetic Diversities

The haplotype composition, segregating sites (*S*), number of haplotypes (N_{hap}), haplotype (gene) diversity (*h*), and nucleotide diversity (π) for *Acetes intermedius* were tabulated in Table 4, and *A. japonicus* were tabulated in Table 5. Ten haplotypes are present for *A. intermedius,* as in Table 4. The Ai1 haplotype occurred most in four sampling locations. Samples from RM recorded the highest haplotype and nucleotide diversities with 0.8095 and 0.0085, respectively. The high haplotype and low nucleotide diversities resulted from a fast population growth from a small ancestral population, allowing for an increase in haplotype diversity through mutations, but limiting the accumulation of significant sequence differences (Chanthran, et al., 2020).

There were eight haplotypes present for *Acetes japonicus,* as in Table 5. The Aj1 haplotype was the most common and occurred in two sampling locations. Samples from GB recorded the highest haplotype (0.8667) and nucleotide (0.0038) diversities. The overall genetic diversity in the present study was 0.5898, surpassing the 0.5386 reported by Wong et al. (2017). Similarly, the nucleotide diversity in the current study, 0.0026, was

Table 4
Haplotype and molecular diversity in Acetes intermedius

Haplotype	Sampling Locations*				Total
	GB	M	ST	RM	
Ai1	5	8	6	3	22
Ai2	1		2		3
Ai3			2		2
Ai4	1				1
Ai5				1	1
Ai6		1			1
Ai7		1			1
Ai8				2	2
Ai9				1	1
Ai10				1	1
n	7	10	10	8	35
S	2	5	3	14	21
N_{hap}	3	3	3	5	10
h	0.5238	0.6444	0.7556	0.8095	0.6706
π	0.0009	0.0028	0.0017	0.0085	0.0043

Note. *Abbreviations for sampling locations: refer to Table 1 [*n*: number of sequences; *S*: number of segregating sites; N_{hap}: number of haplotypes; *h*: haplotype diversity; and π: nucleotide diversity]

Table 5
Haplotype and molecular diversity in Acetes japonicus

Haplotype	Sampling Locations		Total
	PAT	GB	
Aj1	8	5	13
Aj2		1	1
Aj3		1	1
Aj4		1	1
Aj5		1	1
Aj6		1	1
Aj7	1		1
Aj8	1		1
n	10	10	20
S	4	10	13
N_{hap}	3	6	8
h	0.3778	0.8667	0.5898
π	0.0013	0.0038	0.0026

Note. *Abbreviations for sampling locations: refer to Table 1 [n: number of sequences; S: number of segregating sites; N_{hap}: number of haplotypes; h: haplotype diversity; and π: nucleotide diversity]

notably higher than the 0.0010 found in the earlier study. In comparison to a previous study by Wong et al. (2017), which identified only two haplotypes of *A. japonicus* from three sampling locations, the current study shows a significantly higher genetic diversity in *A. japonicus*. A larger sample size in the current study might have revealed more haplotypes and increased the overall genetic diversity.

Population Differentiation

The AMOVA of every *Acetes* species were shown in Table 6. The F_{ST} value for *Acetes japonicus* was low (0.0584) and not significant ($P > 0.05$). This shows that there was a small genetic differentiation among the populations.

The percentage variation within the populations of *A. japonicus* was high (94.16%). This suggests that the majority of genetic variation occurred within the populations. In contrast to a previous study by Wong et al. (2017), which reported a significantly higher within-population variation (120.28%) and a significantly lower among-population variation (-20.28%), the current study found a higher percentage of variation among populations (5.84%) and a lower within-population variation (94.16%). It is noteworthy that the F_{ST} values in both studies were not significant, suggesting that the observed genetic differences among populations were not statistically significant. The F_{ST} value for *A. intermedius* was

Table 6
AMOVA of Acetes species

Species	Source of Variation	df	Sum of Squares	Variance Components	Percentage Variation	F_{ST} Value	P-value
Acetes japonicus	Among populations	1	0.900	0.0344	5.84	0.0584	P>0.05
	Within populations	18	10.000	0.5556	94.16		
	Total	19	10.900	0.5900			
Acetes intermedius	Among populations	3	12.860	0.389	28.11	0.2811	P<0.05
	Within populations	30	29.875	0.9959	71.89		
	Total	33	42.735	1.3852			

higher (0.2811) and significant ($P < 0.05$). This suggests moderate genetic differentiation among populations of *A. intermedius*. The percentage variation within populations of *A. intermedius* was lower (71.89%), which indicates that a smaller proportion of genetic variation is found within populations compared to *A. japonicus*. *A. japonicus* exhibits a lower F_{ST} than *A. intermedius*, suggesting greater gene flow and less genetic divergence, which confirms no variations among populations of *A. japonicus* (Jose et al., 2022).

The pairwise F_{ST} analysis of *Acetes intermedius* in Table 7 revealed a low genetic differentiation between the studied populations. The genetic similarity observed between the populations was high, which implies significant gene flow, which shares genetic material likely due to migration.

Tajima's D and Fu's Fs neutrality tests were shown in Table 8. All the Neutrality Tests in Table 8 were significant for *Acetes japonicus,* while *A. intermedius* showed only significance in Tajima's D. The negative values of Tajima's D, -1.5426, and Fu's Fs, -4.8112, of *A. japonicus* were indicative of population expansion. The negative value of Tajima's D and Fu's Fs suggests an excess of rare alleles in the population that is often

Table 7
The pairwise F_{ST} of Acetes intermedius

	GB	M	RM	**ST**
GB	-			
M	-0.02661	-		
RM	0.05185	0.03536	-	
ST	-0.0453	0.01688	0.03962	-

Note. *Abbreviations for sampling locations: refer to Table 1 (P<0.05)

Table 8
Neutrality statistics (Tajima's D and Fu's Fs)

	Tajima's D	Tajima's D P-value	Fu's Fs	Fu's Fs P-value
A. japonicus	-1.5426	0.0250	-4.8112	0.0000
A. intermedius	-1.6600	0.0290	0.1290	0.0645

shown as a recent population bottleneck (Eckshtain-Levi et al., 2018; Jose et al., 2022). However, the statistical significance of these findings differs when the P-value for Tajima's D, 0.0250, and for Fu's Fs, 0.0000, suggests a statistically significant deviation from neutrality. These results contrast with a previous study by Wong et al. (2017); Tajima's D, 1.4754, and Fu's Fs, 1.2350, were not significant.

Phylogenetic Tree

Phylogenetic analyses of *Acetes* samples from Terengganu using maximum likelihood (ML) and maximum parsimony (MP) methods yielded consistent tree structures, supporting the division of the genus into two primary clades: *Acetes intermedius* and *Acetes japonicus* (Figure 7). These findings aligned with morphological species identification. Both clades exhibited strong statistical support, with bootstrap values exceeding 70% for both ML and MP. However, subclades within these clades displayed lower bootstrap values, suggesting that a larger sample size might be necessary to enhance their statistical support (Hassan and Othman, 2021).

Notably, an individual of the *A. japonicus* specimen from Malaysia (HQ630564) clustered with the Terengganu *A. japonicus* group, suggesting a genetic connection between the two populations. *A. japonicus* reveals two clades, *A. japonicus* 1 and *A. japonicus* 2, which potentially suggest cryptic species. The *A. japonicus* (1) individuals from PAT and GB shared haplotypes, indicating gene flow between these populations. Similarly, *A. intermedius* individuals from GB, M, ST, and RM also exhibited evidence of gene flow. These results are in agreement with previous studies on *A. americanus* (Brazil 1) (Simões, et al., 2023) and *A. erythraeus* (Sarawak) (Hassan & Othman, 2021), which also demonstrated the presence of genetic variation and cryptic lineages within *Acetes* species.

The population's homogeneity may be attributed to the widespread dispersal of planktonic larvae and the absence of factors that restrict gene flow (Simões, et al., 2023). More detailed research is required to establish the cryptic species status of *A. japonicus*. This would involve combining in-depth morphological analyses with molecular techniques that utilise both mitochondrial and nuclear DNA markers (Kerkhove, et al., 2019).

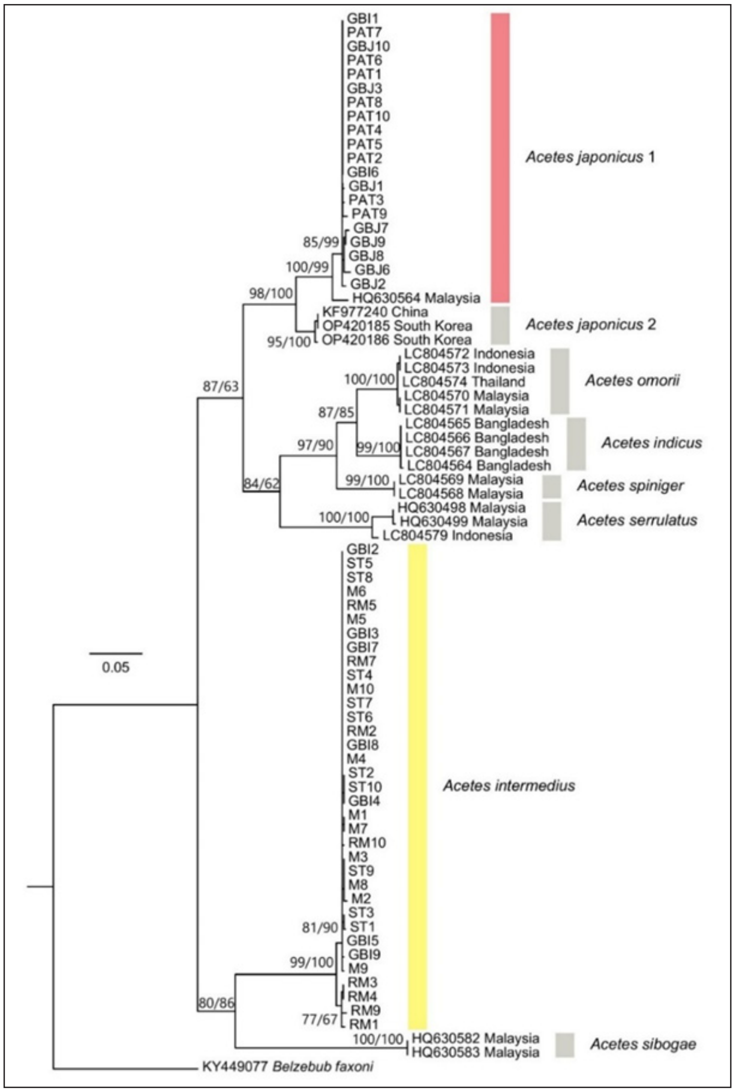

Figure 7. Bootstrap 50% majority rule consensus ML tree of Acetes intermedius and A. japonicus from Pantai Air Tawar, Pengkalan Gong Batu, Jeti Merang, Jeti Seberang Takir and Rhu Muda with species of Acetes acquired from GenBank, Belzebub faxoni as outgroup. The values at the node represent ML (%) and MP (%)

CONCLUSION

In conclusion, two *Acetes* species were identified from five *Acetes* landing sites in Terengganu, which are *Acetes intermedius* and *A. japonicus*. *A. japonicus* recorded in the current study is the new record on the east coast of Peninsular Malaysia. *A. intermedius* dominated the *Acetes* population in Terengganu and was present in all sampling sites except for PAT, while *A. japonicus* is only present in GB and PAT. Phylogenetic analysis revealed two distinct clades: *A. japonicus* and *A. intermedius*. Genetic diversity was higher in

A. intermedius with 10 haplotypes compared to 8 in *A. japonicus*. The findings presented in this study represent a preliminary exploration. Further research is suggested to expand upon these results and consider broader sampling locations.

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