

Article

Novel Comprehensive Molecular and Ecological Study Introducing Coastal Mud Shrimp (*Solenocera Crassicornis*) Recorded at the Gulf of Suez, Egypt

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Abstract: *Solenocera crassicornis* is a commercially important shrimp of the Solenoceridae family. The current study investigated the morphology, molecular identification, phylogenetic relationships, and population dynamics of *S. crassicornis* in Egypt. Samples were collected monthly (total, 1722; male = 40.19%, wet weight, 0.89–10.77 g; female = 59.81%, wet weight, 1.55–19.24 g) from Al-Attaka commercial catch in the Gulf of Suez in the Red Sea. Two barcode markers, 18S rRNA and cytochrome c oxidase subunit I (COI), were used for molecular identification. COI partial sequences were used to construct the phylogenetic relationships among different species of genus *Solenocera* and to infer the origin of the studied *Solenocera crassicornis*. The applied molecular markers successfully identified the studied species to the species level. The genetic distances among *S. crassicornis* sequences from different countries revealed the Indo-West Pacific origin of *S. crassicornis*. The relationship between total length (TL) and total weight (TW) was $TW = 0.035TL^{2.275}$ and $r^2 = 0.805$ for males and $TW = 0.007TL^{3.036}$ and $r^2 = 0.883$ for females, indicating that females were heavier than males. Despite its social and economic relevance in the area, information on the hatching, larval rearing, and farming of *S. crassicornis* is scarce and requires future studies under Egyptian conditions.

Keywords: Penaeoidea; Solenoceridae; shrimp; Suez Gulf; Red Sea; DNA barcoding; 18S rRNA; COI



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1. Introduction

Shrimp is presently the foremost important globally traded fishery product in terms of value. In numerous tropical developing countries, it is the most profitable fishery trade [1,2]. Shrimp fisheries are not only valuable food resources, but also major economic resources in Egypt and other developing countries. Worldwide, the commercial shrimp species is a one of the superfamily Penaeoidea, which is classified into five Penaeidean families: Penaeidae, Solenoceridae, Sicyoniidae, Aristeidae, and Sergestidae [3,4]. The Solenoceridae family has the economic importance for the commercial catch. All individuals are marine species, despite some juvenile Penaeidae species inhabiting brackish water and being occasionally found in almost fresh water. A significant species of the Solenoceridae family is *Solenocera crassicornis*, a member of the genus *Solenocera* Lucas, 1849, which comprises 38 species [5]. The common name of *S. crassicornis* (H. Milne Edwards, 1837), also identified as *S. indicus* (Nataraj, 1945), is the costal mud shrimp. It is an important commercial shrimp of Indian waters [6] and the main aquatic product for export in China [7]. This species is distributed along the West and East coasts of India; the coast of Malaysia,

Mergui Archipelago, and Singapore, North Borneo, and Hong Kong; and the Indo-West Pacific (from the Malay Archipelago to India and Pakistan), Japan, and China. Its habitat depth is 40 m, preferring the mud and sandy bottoms [5,8]. Several studies have been conducted on *S. crassicornis* dealing with some aspects of its fisheries and biology, such as age, growth, food, and feeding, breeding, and migration [8–10]; sustainable yield and population dynamic for *S. crassicornis* species in the East China Sea [11] and in the waters of Versova, Mumbai [10]. Furthermore, Rajkumar et al. [12] investigated the morphological and molecular identification of *S. crassicornis* inhabiting the Coromandel Coast of Tamil Nadu, India. The developing countries, including Egypt, are the primary producers of shrimp, due to extensive shrimp activities and overfishing. The demand for shrimp production and subsequent overexploitation can negatively impact shrimp stocks in water bodies in these countries. Therefore, regular assessment and management of fishery stock, particularly shrimp species of economic interest, is necessary. It is necessary to understand genetic structures to start breeding programs domestication and selection for aquaculture. Approximately 610 tons of shrimp are produced annually, and Penaeidae shrimp contribute to 8% of the total trawl landings [13]. The unparalleled geographic location of the Red Sea makes it highly sensitive to biodiversities, communities, and distributions [14]. Since the operation of the Suez Canal in 1872, the shrimp fauna in the Mediterranean has been enriched due to the changes and disturbances caused by the migration of some fish species and the partial change in the ecosystem. *S. crassicornis* was first recorded in the Mediterranean shelf of Egypt in 1981 by Abdel-Razek et al. [15], identified as *S. indicus* (Nataraj, 1945). However, there are no published data recording *S. crassicornis* in the Red Sea in Egypt. Additionally, there are no data available regarding the identification, occurrence, distribution, stock assessment, hatching, larval rearing, and farming of *S. crassicornis* in Egypt, despite it being an economically important species. The identification and characterization of aquatic organisms are considered a basic step for monitoring biodiversity and conserving such species [16–18]. In the case of crustaceans, morphology-based identification is an extremely basic science. Crustaceans undergo various larval stages with alterable and changeable shapes and background coloration due to chromatophores [19]. Therefore, this identification tool can be ineffective and misleading [20,21]. In such cases, the application of molecular-based identification tools, including DNA barcoding, can resolve these problems. DNA barcoding applies universal primers to amplify a targeted genomic region. The efficiency of this method depends on the diverse nature of the targeted region among species [22,23]. In crustaceans, targeting the region of the cytochrome oxidase subunit I (COI) mitochondrial gene using the primer pairs described by Folmer et al. [24] was the most efficient. DNA barcoding is a perfect tool for identification and studying species diversity within an ecosystem. Several studies have used the COI region to identify various crustaceans [12,25–27]. Some of the shrimp species of economic interest in Egypt have been precisely characterized using morphological and genetic analyses [28–31]. Here, we conducted a comprehensive study of *S. crassicornis* collected from the Gulf of Suez in Egypt, including molecular identification, growth parameter assessments, and estimations of population dynamic parameters. We integrated two barcode regions, namely, 18S rRNA nuclear barcode and COI mitochondrial barcode, with morphological identification data to precisely characterize the studied species. Additionally, monthly variations in length frequency were used to determine *S. crassicornis* growth parameters and to estimate other population dynamic parameters.

2. Materials and Methods

2.1. Sample Collection and Morphology

Random *S. crassicornis* samples were collected monthly for 12 months starting from June 2019 by trawl nets from Al-Attaka commercial catch in the Gulf of Suez, the Red Sea. The collected shrimp samples were identified as *S. crassicornis* (H. Milne Edwards, 1837) based on morphological characteristics, as described in the literature [8,9,15]. The length

frequency for 1722 *S. crassicornis* individuals, comprising 692 males (2.3–11.0 cm) and 1030 females (3.9–13.3 cm), was estimated.

2.2. Growth Parameters and Population Dynamics

2.2.1. Population structure

To prevent prejudice due to various measuring tools for researchers and for a more accurate methodology, we estimated singular lengths to the closest 0.1 cm by using a MATLAB routine (MathWorks Inc., Natick, MA, USA) to singular shrimp snapshots taken with a MEGA 0.I.S USB camera (Leica, Wetzlar, Germany) outfitted with a DC VARIO-ELMARIT 1:2.8-49/6.3-25.2 A SPH lens (Leica). The snapshots created a record that could be easily stored and used for additional estimations and confirmatory checks if necessary. Manual fixation of singular shrimp with a complete rostrum on millimeter paper was done (to stay away from the natural warp of the shrimp body). The estimations were characterized as: (a) Total length (TL): The space from the tip of the rostrum to the end of the telson, cm; (b) carapace length (CL): The space from the posterior margin of the orbit to the posterior edge of the carapace, mm; and (c) total weight (TW): Weighed in grams by using an electronic digital balance (± 0.01 g; Sartorius, Göttingen, Germany).

2.2.2. Growth Parameters, Mortality, and Exploitation Rates

We applied the ELEFAN1 program to length frequency inputs to evaluate asymptotic length (L_∞) and to estimate the growth coefficient (K) for each sex separated utilizing von Bertalanffy growth function (VBGF) development work [32] as follows:

$$L_t = L_\infty [1 - e^{-K(t - t_0)}] \tag{1}$$

where: L_t is TL at age t , L_∞ is the asymptotic TL, K is the curvature value, and t_0 is the theoretical age when TL is zero.

To compare the growth performance of both males and females [33] as follows:

$$\phi = \log_{10} k + 2 \log_{10} L_\infty \tag{2}$$

where: K and L_∞ are Bertalanffy equation constant.

The instantaneous rate of natural mortality (M) was also estimated [33] as follows:

$$\log_{10}(M) = -0.0066 - 0.279 \log_{10}(L_\infty) + 0.6543 \log_{10}(K) + 0.4634 \log_{10}(T) \tag{3}$$

where: T is the temperature of water.

Total mortality instantaneous rate (Z) was evaluated by applying the FiSAT II program, using a length-converted fishing curve [34] according to the equation $\ln(N/\Delta t) = a + bt$, where N is the number of crabs in a particular size class, Δt is the time required to attain that class (years), t is the relative age (years), a is the intercept, and b is the regression coefficient ($b = Z$). Hence, fishing mortality (F) for both sexes were estimated as $F = Z - M$. Then, the exploitation rates (E) were estimated as the following: $E = F/Z$ [35]. As indicated by Pauly [36], the ascending left arm of the CL-converted catch curve was utilized to examine the probability of capture of every length class. The modified Beverton and Holt [37] relative yield per recruit (Y/R) model by Pauly and Soriano [38] was utilized and then incorporated into FiSAT II programming to gauge the degrees of exploitation that would give ideal yields. Investigations of E_{max} (the exploitation rate giving highest relative yield per recruit), $E_{0.1}$ (exploitation rate at which the marginal raise in Y/R is 10% of its value at $E = 0$), and $E_{0.5}$ (the identical exploitation to half of the unexploited relative biomass per recruit, B/R) were evaluated.

To assess the allometry, the TW-TL relationship, the equation of Le-Cren's [39] was used as follows:

$$TW = a TL^b \tag{4}$$

where: TL (cm): Is the carapace length, TW (g): Is the total body wet weight, while a is intercept parameter and b is allometric parameter.

2.3. Molecular Analysis

2.3.1. DNA Extraction and Polymerase Chain Reaction Amplification

Genomic DNA was extracted from the axial muscle of the collected samples, according to Sambrook et al. [40]. Briefly, 100–200 mg of muscle tissue sample was ground in TES buffer (10 mM Tris-HCl, 25 mM EDTA, 140 mM NaCl, and pH 7.8) containing 0.5 mg mL⁻¹ proteinase K and 1% SDS. The homogenates were incubated for 2 h at 56 °C. Total genomic DNA was extracted using a conventional phenol-chloroform procedure and precipitated with absolute ethanol. The DNA pellets were eluted in TE buffer (100 mM Tris-HCl and 10 mM EDTA, pH 8). The concentrations of DNA of all samples were measured using a Nanodrop spectrophotometer (Biodrop, Cambridge, England). Following DNA isolation, two barcode regions were amplified for species identification, namely, a 683-bp fragment from the coding region of the mitochondrial gene (COI) and a 469-bp partial fragment of the 18S rRNA nuclear gene. Polymerase Chain Reaction (PCR) was performed on a GeneAmp PCR System 9700 Thermal Cycler (Applied Biosystems, Foster City, CA, USA) utilizing the primer pairs LCO1490 (5'-GGTCAACAAATCATAAAGATATTGG-3') and HCO2198 (5'-TAAACTTCAGGGTGACCAAAAAATCA-3') [24], and Ebi18S-F (5'-CGCCTACAATGGCTATAACGGGTAAC-3'), and Ebi18S-R (5'-GGTTAGAACTAGGGCGGTATCTGATC-3') [29] for COI and 18S rRNA amplification, respectively. The PCR reactions were conducted in 25 µL as a total volume containing 12.5 µL of 1x MyTaqTM HS Red Mix (Bioline, London, UK), 30 ng of template DNA, and 0.4 µM of each primer. The PCR program for amplification of the COI region was: Initial denaturation for 5 min at 94 °C, followed by 40 cycles of denaturation for 1 min at 94 °C, annealing for 1 min at 45 °C, and extension for 1.30 min at 72 °C, and a final extension for 7 min at 72 °C. The cycling profile for 18S rRNA amplification was: Denaturation for 5 min at 95 °C, followed by 35 cycles of denaturation for 30 s at 95 °C, annealing for 30 s at 48 °C, and extension C for 2 min at 72°, and a final extension for 7 min at 74 °C. The amplicons were electrophoresed at 120 V on a 2.5% agarose gel and stained with ethidium bromide (25 µg mL⁻¹) for visualization. PCR products having single bands with the expected amplicon size were purified using Isolate II PCR and Gel Kit (Bioline). The purified PCR products were sequenced using a BigDye Terminator v3.1 Cycle Sequencing Kit [41] on an ABI 3730 Sequencer (both Applied Biosystems). The sequencing reaction was applied as follows: 96 °C for 2 min, followed by 25 cycles at 96 °C for 10 s, at 50 °C for 5 s, and at 60 °C for 4 min.

2.3.2. Sequencing and Phylogenetic Analysis

The raw data of sequences for COI and 18S rRNA were treated using the free software Chromas Lite v2.1 (Technelysium Pty Ltd., available from <http://technelysium.com.au/>) and compared with the available sequences in the databases of GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) using BLAST searches. The COI sequences were also compared using the Barcode of Life Data System (BOLD) species identification portal (<http://www.barcodinglife.org>). A Barcode Index Number (BIN) was assigned [42] for the COI sequences of the study specimens, to confirm their concordance with sequence clusters available in the BOLD database. The partial coding sequences of COI (683 bp) and 18S rRNA (469 bp) of the investigated samples were deposited in the GenBank, EMBL, and DDBJ global databases under the accession numbers LC477203–LC477205 and LC477340. Due to the abundance of the available COI sequences on the GenBank Database compared to 18S rRNA sequences, COI barcode region was used as a reference region for further molecular analysis. COI sequences for *Solenocera* species were retrieved from the GenBank database and aligned with the obtained sequences of the Egyptian *S. crassicornis* by CLUSTALW software in MEGAX [43]. To locate *S. crassicornis* in relation to its relatives from the same genus, the genetic distances among species of *Solenocera* were estimated based on Kimura two-parameter distance model (K2P) using Group Mean Distance software impeded in

MEGAX software package. MEGAX was used to apply the best fitting models to the COI datasets of nucleotide sequences and disparity estimates using the general time-reversible model [44]. Phylogenetic trees were constructed in MEGAX using the method of maximum likelihood (ML), with 1000 bootstrap replicates.

3. Results

3.1. Morphology, Population Dynamics, and Growth Parameters

3.1.1. Morphology

The body and legs of *S. crassicornis* are reddish (Figure 1). The antennules were banded with white and dark red. Except for some white areas, the uropods were dark red. The rostrum is short and extends to approximately 2-3 of the eyes, with an upper border with 7 to 8 teeth and a robustly convex lower border. The postrostral crest was obviously raised, slightly interrupted by a little notch over the cervical groove, and the height of the posterior section gradually decreases posteriorly. The orbital, antennal, hepatic spines, and postorbital were unmistakable on the carapace, however, without pterygostomian spines. The hepatic spine closes at the edge of a little round pit just behind the pterygostomian angle. The orbital edge sharp, there was a little postorbital pit over the postorbital spine, and the branchiocardiac carina and sulcus were well determined. The antennular flagella were sensibly long and tube-like. The telson has a couple of horizontal spines.



Figure 1. *Solenocera crassicornis* (H. Milne Edwards, 1837) caught from Al-Attaka, the Gulf of Suez, Red Sea of Egypt.

All shrimp samples were pooled by sex to determine relationships between TL-TW and TL-CL ($n = 1722$; male, 40.19%; female, 59.81%) were analyzed as shown in Figures 2 and 3. The TW were ranged from 0.89 to 10.77 g and from 1.55 to 19.24 g for males and females, respectively. While the TL ranged from 2.3 to 11.0 cm and from 3.9 to 13.3 cm for males and females, respectively. Meanwhile, CL were ranged from 0.9 to 3.2 and from 1.3 to 4.5 cm for males and females, respectively.

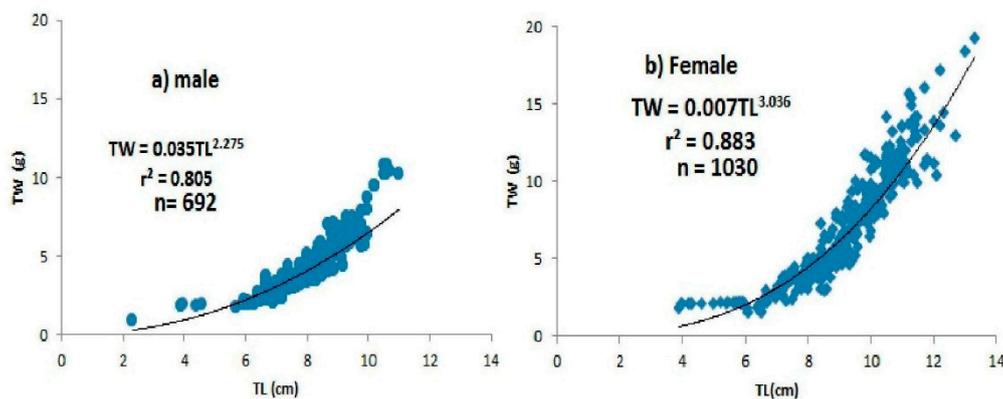


Figure 2. Length-weight relationship for males (a) and females (b) of *S. crassicornis* from the Gulf of Suez, Egypt.

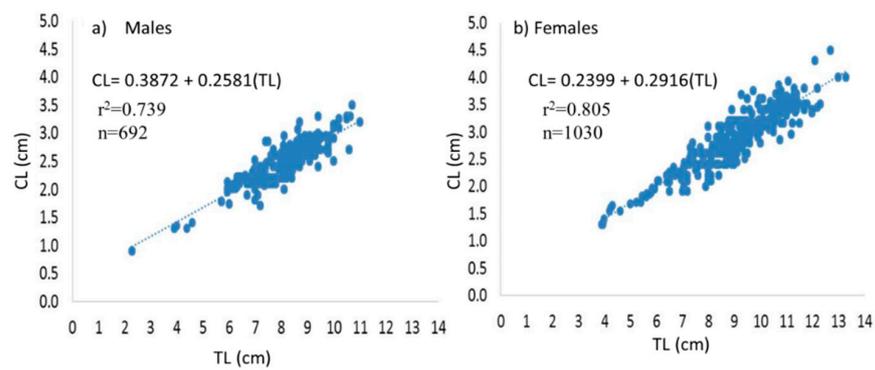


Figure 3. The relationship between total length and carapace length for males (a) and females (b) of *S. crassicornis* from the Gulf of Suez, Egypt.

3.1.2. TL-TW Relationship

The length-weight relationship between (TL) and total weight (TW) was $TW = 0.035TL^{2.275}$ and $r^2 = 0.805$ for males and $TW = 0.007TL^{3.036}$ and $r^2 = 0.883$ for females. Overall, TW regression analyses showed positive allometric growth ($b > 3$) in females in contrast with males (negative allometric growth), indicating that females were heavier than males with a growing length TL (Figure 2).

3.1.3. TL-CL Relationship

A linear equation was estimated for males as $CL = 0.3872 + 0.2581(TL)$, $r^2 = 0.7394$, and $CL = 0.2399 + 0.2916(TL)$, $r^2 = 0.805$ for females. The size of the female carapace was larger than that of the male (Figure 3).

3.1.4. Growth Parameters

The growth parameters evaluated using ELEFAN1 for males and females were $L_\infty = 115.5$ mm and 136.5 mm, respectively, with $K = 0.76 \text{ yr}^{-1}$ and $t_0 = -0.0366$ for males and $K = 1.1 \text{ yr}^{-1}$ and $t_0 = -0.08184$ for females.

The VBGF was $L_t = 115.5 [1 - e^{-0.76(t + 0.0366)}]$ for males and $L_t = 136.5 [1 - e^{-1.1(t + 0.08184)}]$ for females.

The obtained results of growth performance index (ϕ) were 4.01 and 4.31 for males and females, respectively.

3.1.5. Mortality Rate

Total mortality (Z) for males = 3.99 yr^{-1} and females = 3.05 yr^{-1} , while the natural mortality (M) was 1.91 yr^{-1} and 1.35 yr^{-1} for males and females, respectively. Fishing mortality (F) for males and females were 2.08 yr^{-1} and 1.70 yr^{-1} , respectively. Meanwhile, exploitation rates (E) were 0.52 and 0.56 for males and females, respectively (Figure 4).

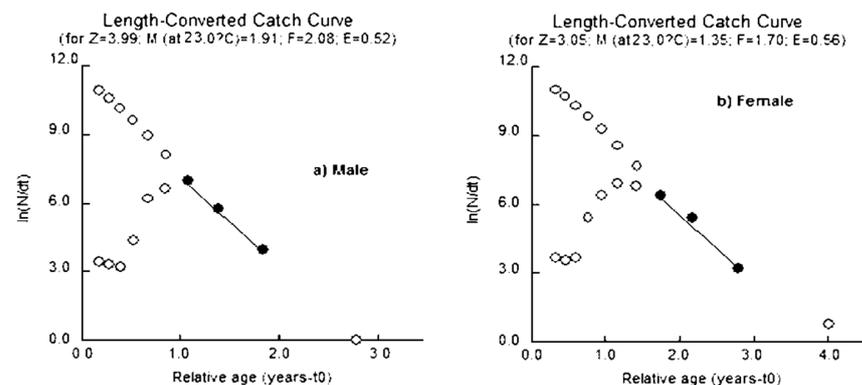


Figure 4. Cumulated catch curve based on length composition data for males (a) and females (b) of *S. crassicornis* from the Gulf of Suez, Egypt.

3.1.6. Length at First Capture

The length at first capture (LC), at which 50% of the shrimp are vulnerable to capture (L50%), was estimated as 72.3 mm and 94.6 mm for males and females, respectively (Figure 5).

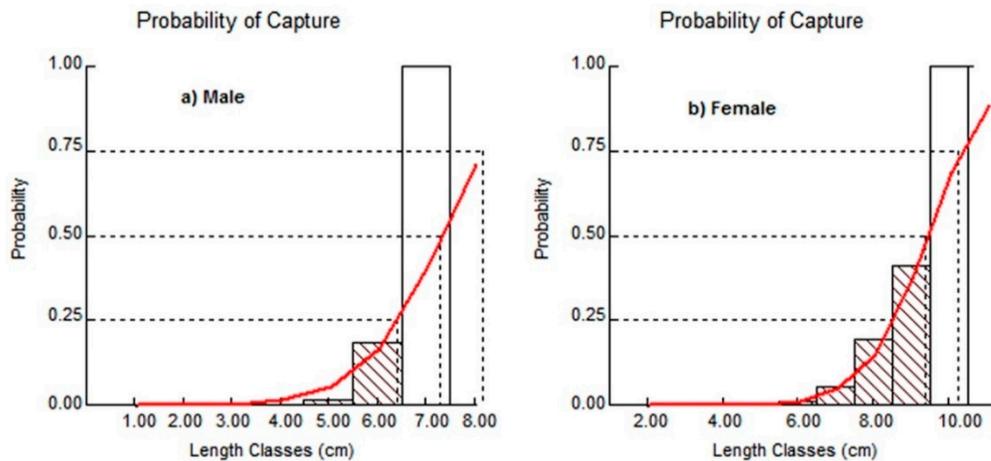


Figure 5. Probability of capture (L50% or LC) for males (a) and females (b) of *S. crassicornis* from the Gulf of Suez, Egypt.

3.1.7. Relative Yield per Recruit

The relationships between Y/R and B/R of both males and females showed that E_{max} , $E_{0.1}$, and $E_{0.5}$ were the same for males and females (0.421, 0.355, and 0.278, respectively) (Figure 6).

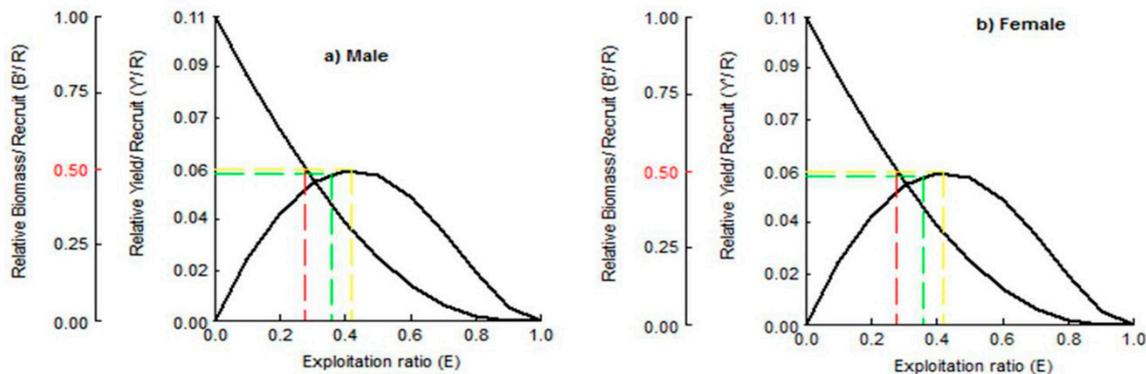


Figure 6. Relationship between the relative yield per recruit (Y/R) and biomass per recruit (B/R) applying knife-edge procedure for males (a) and females (b) of *S. crassicornis* from the Gulf of Suez, Egypt. “Red line = $E_{0.5}$ – Green = $E_{0.1}$ – Yellow = E_{max} ”.

3.2. Molecular Analysis

Positive PCR amplifications were manifested by the tested samples using the primer pairs of both eukaryotic 18S rRNA and COI mitochondrial genes. PCR amplicons of 469 and 683 bp were obtained for the 18S rRNA and COI target regions, respectively. BLAST comparisons of the resultant 18S rRNA sequences showed 99% similarity with *S. crassicornis*, which was confirmed by both the alignment of the obtained COI sequences (99% similarity with *S. crassicornis*) and the morphological examination results.

The COI sequences obtained for the specimens in our study were assigned a BIN (BOLD ABE7069). BOLD identified the nearest neighbor of the study species as *S. koelbeli* (BOLD ACS4793), with a p-distance of 0.32%. The analysis of Group Mean genetic distances among *S. crassicornis* from different countries (Egypt, China, and India) showed that the pairwise distances for the Egyptian *S. crassicornis* ranged from 0.024 in relation to its Indian

reference group to 0.048 in relation to the Chinese *S. crassicornis* counterparts. On the other hand, the estimation of the genetic distance among the species of *Solenocera* revealed that *S. melantho* was the closest to *S. crassicornis* with a genetic distance of 0.071. Where, *S. pectinata* was the most distant from *S. crassicornis* with a genetic distance of 0.27. Values of genetic distances among species of *Solenocera* genus are presented in Table 1.

COI-based ML tree (Figure 7) for *Solenocera* species (from different countries) grouped the studied *Solenocera* species into two distinct clusters. The first cluster branched into three clades that included *S. crassicornis* from different countries and *S. melantho* in the first clade; *S. chopraii*, *S. hextii*, *S. koelbeli*, and *S. annectens* in the second clade. The second cluster included *S. pectinata*, *S. rathbuni*, and *S. agassizi* in the first clade and *S. membranacea* in the second clade. COI-based ML phylogenetic tree among different species of *Solenocera* is shown at Figure 7.

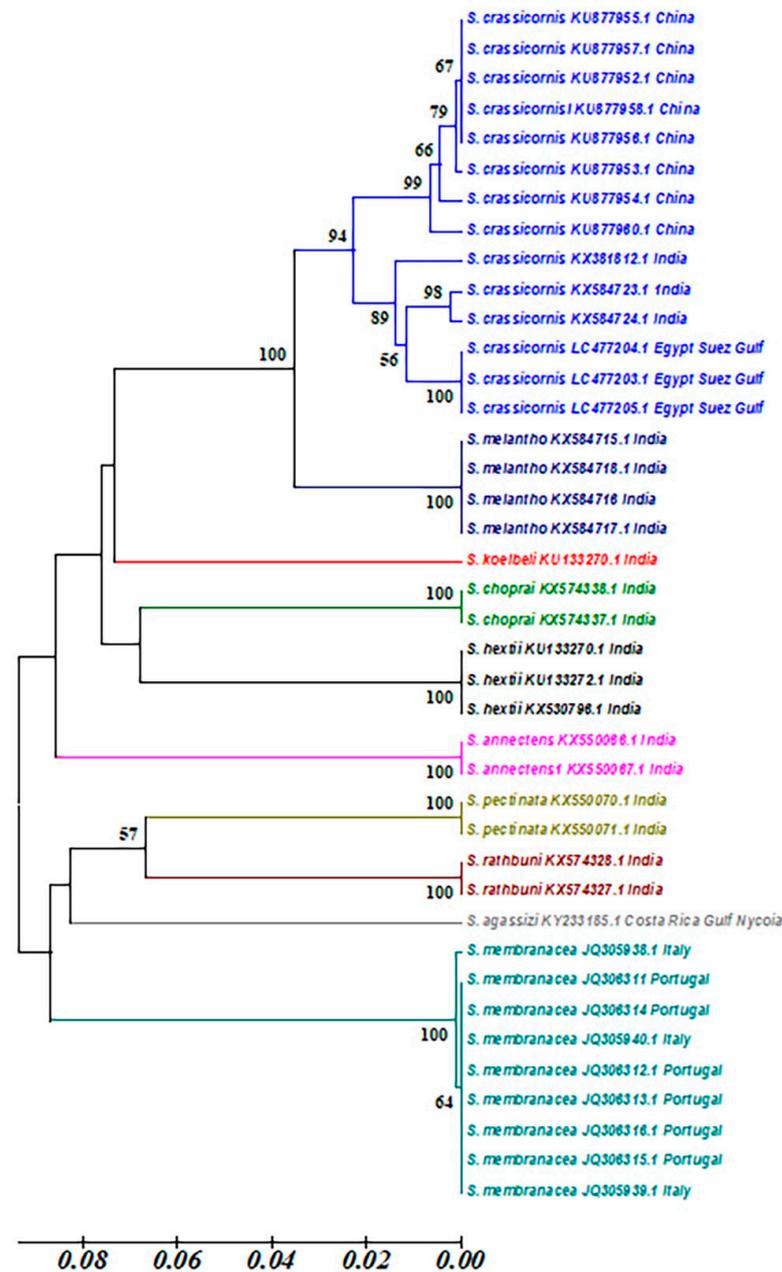


Figure 7. COI-based maximum likelihood (ML) phylogenetic tree among *Solenocera* species all over the world.

Table 1. COI (cytochrome oxidase subunit I)-based pairwise genetic distances among *Solenocera* species worldwide.

	<i>S. choprai</i>	<i>S. agassizi</i>	<i>S. annectens</i>	<i>S. crassicornis</i>	<i>S. hextii</i>	<i>S. koelbeli</i>	<i>S. melantho</i>	<i>S. membranacea</i>	<i>S. pectinata</i>	<i>S. rathbuni</i>
<i>S. choprai</i>										
<i>S. agassizi</i>	0.203									
<i>S. annectens</i>	0.152	0.194								
<i>S. crassicornis</i>	0.161	0.195	0.169							
<i>S. hextii</i>	0.136	0.181	0.162	0.137						
<i>S. koelbeli</i>	0.228	0.226	0.229	0.146	0.190					
<i>S. melantho</i>	0.175	0.190	0.181	0.071	0.148	0.148				
<i>S. membranacea</i>	0.204	0.172	0.174	0.192	0.190	0.233	0.195			
<i>S. pectinata</i>	0.169	0.170	0.181	0.188	0.179	0.270	0.192	0.176		
<i>S. rathbuni</i>	0.154	0.161	0.161	0.148	0.138	0.215	0.165	0.171	0.134	

4. Discussion

This novel study introduces *S. crassicornis*, the lone species of Solenocera in Egypt. Our results provide useful clues about its morphological and molecular characterization, growth parameters, and population dynamics. DNA barcoding has been established as universal tools to identify different species of organisms during the last decade. This molecular-based approach involves sequencing a short and standardized gene region to identify and recognize species such as fish [20]. DNA barcoding does not look to disregard the morphological assessment, and its general purpose is to build an alliance between molecular and morphological taxonomists for quick and unequivocal species identification [30].

Although Solenocera encompasses 38 species, DNA barcoding studies of these species are rare. This study is the first to integrate two molecular markers, namely, the nuclear marker 18S rRNA and the mitochondrial marker COI, to characterize *S. crassicornis*. The analysis of both markers showed 99% similarity with their reference sequences in the GenBank database, demonstrating a high discrimination level of both markers at a high taxonomic level, and molecular identification matched the morphological identification of the species under examination. The phylogenetic relationship between the Egyptian *S. crassicornis* and the other *S. crassicornis* from China and India revealed the close relationship between the specimens from Egypt and their counterparts from India (both of them were clustered in a sub-clade), while the specimens from China were grouped in a separate cluster of the ML tree. These phylogenetic relationships clarified the Indo-West Pacific origin of *S. crassicornis* [5,45] and suggested its existence in the Red Sea as a migratory species that translocated from the Indian Ocean. This may explain the high comparability despite the natural geographical barrier between these distant areas. Abbas et al. [28] reported that Penaeid shrimps are an effective migratory species that can migrate over vast distances. For instance, *Melicertus plebejus* was collected approximately 900 km from its origin in Australia [46]. Interestingly, our study is the first to construct a phylogenetic tree of species of *Solenocera* capable of separating them according to genetic distance and locating *S. crassicornis* in the correct position in relation to its close relatives of the same genus.

In the current work, monthly variations of length frequency were utilized to decide the growth parameters of *S. crassicornis*, and to evaluate other population dynamic parameters. The results of morphometric measurements in the present study clearly demonstrated that the female reached both larger size and higher growth rate than males showing sex-specific growth this is due to the higher growth performance index for females than males of the same age group. This observed growth difference is common for many shrimp species [29,47]. The population parameters are consistent with that of *S. crassicornis* estimated growth parameters reported from the same species in other regions [11,48,49]. Chakraborty et al. [48] studied the *S. crassicornis* in Maharashtra coast and reported that the population dynamics parameters for males and females individually was $L_{\infty} = 92$ mm, $K = 1.5 \text{ yr}^{-1}$, $Z = 6.00 \text{ yr}^{-1}$, $M = 3.20 \text{ yr}^{-1}$, $F = 3.60 \text{ yr}^{-1}$, and $E = 0.53$ for males and $L_{\infty} = 139$ mm, $K = 2.00 \text{ yr}^{-1}$, $Z = 10.36 \text{ yr}^{-1}$, $M = 6.92 \text{ yr}^{-1}$, $F = 3.44 \text{ yr}^{-1}$, and $E = 0.67$ for females. Such wide deviations in the growth parameters assessed by different researchers are due to differences in observed sizes, age, sample size, and environmental conditions [50–52]. Pauly et al. [36] cited that the equation could be utilized for shrimps or prawns and any marine invertebrates because these marine organisms share similar resources, habitats, and predators as fish, and they are probably not going to differ widely in their vital parameters [53]. Our results clearly indicated the overfishing situation in the Suez gulf ($E > 0.5$). These results agreed with Xue et al. [11] that studied *S. crassicornis* in the East China Sea and with Chakraborty et al. [48,49] in Maharashtra coast.

5. Conclusions

The current work is a novel study presents *S. crassicornis* (H. Milne Edwards, 1837), as a lone commercially important shrimp species of the *Solenoceridae* family (*Penaeoidea* superfamily) in the Red Sea, Egypt. This species is distributed in the Indo-West Pacific, Japan, China, Hong Kong, and North Borneo. The first record of this species in the

Mediterranean shelf of Egypt was in 1981, identified as *S. indicus* (Nataraj, 1945). Our study is the first report investigating this species in Al-Attaka, a commercial landing site of the Gulf of Suez, the Red Sea Shelf of Egypt. Morphological features, molecular identification, and DNA barcoding (18S rRNA nuclear markers and COI mitochondrial markers) were investigated of this species in the Gulf of Suez to precisely identify this Indian-water species as *S. crassicornis* (H. Milne Edwards, 1837). Despite the social and economic relevance of *S. crassicornis* in the area, information about the hatching, larval rearing, and farming of *S. crassicornis* is scarce. Finally, the current novel study is an opportunity to understanding the impacts on wild fisheries of this economic species in the Red Sea, as well as, it is a good opportunity to understanding genetic structures to start breeding programs domestication and selection for aquaculture of this economically commercial species under Egyptian conditions.

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