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Research Article
Phylogeny and DNA Barcoding of the Family Sparidae Inferred from Mitochondrial DNA of the Egyptian Waters

[1]Eman M. Abbas, [1]Taha Soliman, [2]Mohammed A. El-Magd, [3]Mahmoud M.S. Farrag, [4]Rania F. Ismail and [5]Mikio Kato

[1]Laboratory of Genetics, Division of Aquaculture, National Institute of Oceanography and Fisheries (NIOF), Kayed Bey, Anfushi, Alexandria, Egypt
[2]Department of Anatomy, Faculty of Veterinary Medicine, Kafrelsheikh University, Egypt
[3]Marine Science and Fishes Branch, Department of Zoology, Faculty of Science, Al-Azhar University, Assiut, Egypt
[4]Laboratory of Fish Reproduction and Spawning, Division of Aquaculture, National Institute of Oceanography and Fisheries (NIOF), Kayed Bey, Anfushi, Alexandria, Egypt
[5]Laboratory of Biology, Faculty of Liberal Arts and Sciences, Osaka Prefecture 14 University, 1-1 Gakuencho, Naka-ku, 599-8531 Sakai, Japan

Abstract

Background: The family Sparidae includes about 115 species divided into 33 genera that inhabits tropical and temperate coastal waters of the Pacific, Indian and Atlantic oceans. Herein, fish of family Sparidae were molecularly barcoded using the mitochondrial gene, cytochrome oxidase subunit I (*COI*). **Materials and Methods:** Fish samples from 22 fish species of the family Sparidae were collected from Abo Qir Bay, West of the Mediterranean sea and the Gulf of Suez, North of the Red Sea. Genomic DNA was extracted from fish muscles of these species and partial coding region of the *COI* gene was amplified then sequenced and their sequences were deposited into the GenBank database. **Results:** The results of the phylogenetic tree showed that monophyly of Sparidae species. The tree was divided into two distinct clades and some sub-clades. The two major clades are including all the species under the study except *Crenidens crenidens* in a separate branch. **Conclusion:** Our results confirm the phylogenetic relationship of these Sparidae species in Egyptian Mediterranean and Red Sea and support the previous finding which concluded that the Sparidae is composed by two major lineages.

Key words: Sapridae, DNA barcoding, phylogeny, *COI* gene

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Corresponding Author: Eman M. Abbas, Laboratory of Genetics, Division of Aquaculture, National Institute of Oceanography and Fisheries (NIOF), Kayed Bey, Anfushi, Alexandria, Egypt Tel: +201124852279

Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

The family Sparidae has historically been classified into six subfamilies, primarily on the basis of dentition[1,2]. This family includes about 115 species divided into 33 genera[3]. Fishes from this family are carnivorous, feeding on benthic invertebrates and inhabit tropical and temperate coastal waters of the Pacific, Indian and Atlantic oceans[2,4]. They swim near the shore in shallow inlet and bays at moderate depth[5] and can be used in mariculture and cultivated in cages[6]. In the Mediterranean countries *Sparus aurata* is so far, the most extensively cultured species[7]. Cultivation of other species such as *Pagrus pagrus*, *Diplodus sargus* and *Diplodus puntazzo* are envisaged[8].

Thirty three Sparidae species were recorded in the Egyptian coasts[9], most of them are economically important and commonly used as a food due to their good taste and rich flesh. Twenty one out of these 33 species found in the Egyptian Mediterranean water[10]. Twelve out of these 21 species are most frequent in the landed catch from Alexandria water on the Northern coast of Egypt. Seabreams represent about 15% of these landed catch fishes[11]. On the other hand, only 14 species of this family exist in the Red Sea[12], but they are less economically importance than those of the Mediterranean Sea.

The determination and identification of the different species are considered as the initial basic steps for biodiversity monitoring and conservation[13]. Fish identification is traditionally based on morphological features. However, due to high diversity and morphological plasticity, in many cases, fish and their diverse developmental stages are difficult to identify by using morphological characteristics alone[14]. The DNA-based identification techniques have been developed and proven to be analytically powerful[15-17]. For ensuring rapid and accurate identification of a broad range of biological specimens[18] proposed "DNA barcoding" technique, using the *COI* gene, because its mutation rate is often fast enough to distinguish closely related species and also its sequence is conserved among conspecifics. For many animal taxa, nucleotides sequence divergences within the *COI* gene are generally much greater between species than within species. However, changes in its amino acid sequence occur more slowly than those in any other mitochondrial gene[19]. Therefore, this gene is conserved and less subjected to external forces. Many studies have shown that intraspecific variation of *COI* barcodes is generally pretty small and clearly discriminable from interspecific variation[20-22]. Consequently, many researchers have investigated the use of DNA barcoding to enforce traceability regulations and to fight illegal fishing and frauds[21,23,24].

From the available literature, it was found that some studies have been published on the phylogeny of Sparid fishes using mitochondrial genes[2,25,26]. In addition, genetic variations between five Sparid species from the Northern coastal waters of Egypt were analyzed using sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) of sarcoplasmic proteins and Random Amplified Polymorphic DNA (RAPD) analyses[27]. In the present study, DNA barcoding technique based on mitochondrial *COI* gene was adopted to identify 22 fish species of family Sparidae inhabiting the Egyptian costs of Mediterranean and Red Seas.

MATERIALS AND METHODS

Sample collection: Fish samples were collected from two locations from Abo Qir Bay, West of the Mediterranean Sea and from the Gulf of Suez, North of the Red Sea in Egypt (Fig. 1). Samples were transferred to National Institute of Oceanography and Fisheries (NIOF) Alexandria Branch, in ice box. Twenty two fish species from family Sparidae were analyzed (Table 1). Fish samples were photographed and identified *in situ* by visual inspection and taxonomically classified employing standard taxonomic guides following the FAO fish identification sheets[9]. For DNA samples, pieces of flesh muscle were sliced and preserved in 99% ethanol.

DNA samples and analysis: Total genomic DNA was extracted from fish muscles using conventional phenol-chloroform procedures described by Ward *et al.*[28]. In brief, tissues were first homogenized in the DNA isolation buffer TES [10 mM tris-HCl (Wako, Japan), 140 mM NaCl (Wako, Japan), 25 mM EDTA (Bio-Rad), pH 7.8] containing 1% SDS-Wako, Japan and 0.5 mg mL^{-1} proteinase K (Biolabs, New England) and the reaction mixtures were incubated for 1 h at 50°C.

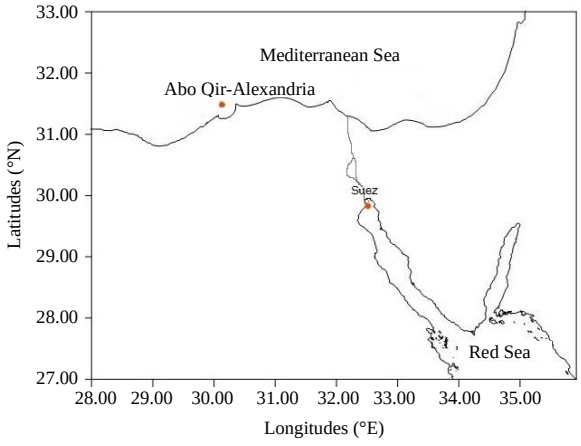

Fig. 1: Location map showing the sampling areas

Table 1: Collected samples used in the present study and the retrieved sequences of the relatives species from the GenBank database

Species	Sampling location	GenBank accession No.	Species	Sampling location	GenBank accession No.
Diplodus sargus	Turkey	KC500582	*Oblada melanura*	Abu Qir-Alexandria, Mediterranean Sea	LC163889*
Diplodus sargus	Central Mediterranean Sea from the European marine	KJ709518	*Oblada melanura*	Turkey	KC501013
Diplodus sargus	Italy	KJ012352	*Oblada melanura*	Turkey	KC501014
Diplodus sargus	Abu Qir-Alexandria, Mediterranean Sea	KP308274*	*Pagellus acarne*	Italy	KJ012382
Diplodus sargus	Turkey	KC500578	*Pagellus acarne*	Portugal	JQ775090
Diplodus noct	Suez, Red Sea	KP308273*	*Pagellus acarne*	Abu Qir-Alexandria, Mediterranean Sea	KU757073*
Diplodus argenteus	Brazil	JQ365343	*Pagellus acarne*	Portugal	JQ775092
Diplodus bermudensis	USA	KT883620	*Diplodus annularis*	Turkey	KC500526
Diplodus holbrookii	USA	JQ842442	*Diplodus annularis*	Turkey	KC500531
Diplodus puntazzo	Turkey	KC500553	*Diplodus annularis*	USA	KT883619
Diplodus cervinus	Canada	HQ945933	*Diplodus annularis*	Turkey	KC500521
Diplodus cervinus	USA	KF929819	*Diplodus annularis*	Italy	KJ012339
Diplodus cervinus	Turkey	KC500545	*Diplodus annularis*	Israel	KM538326
Diplodus cervinus	Abu Qir-Alexandria, Mediterranean Sea	KU757074*	*Diplodus annularis*	Italy	KJ012337
Diplodus vulgaris	Italy	KJ012359	*Diplodus annularis*	Abu Qir-Alexandria, Mediterranean Sea	LC152205*
Diplodus vulgaris	Italy	KJ012358	*Acanthopagrus latus*	South China sea	EU871695
Diplodus vulgaris	Turkey	JQ623934	*Acanthopagrus bifasciatus*	Suez, Red Sea	LC150892*
Diplodus vulgaris	Abu Qir-Alexandria, Mediterranean Sea	KP308275*	*Acanthopagrus bifasciatus*	Canada	GU805011
Oblada melanura	Italy	KJ012379	*Acanthopagrus catenula*	USA	KT883596
Rhabdosargus sarba	Australia	DQ107830	*Boops boops*	Turkey	KC500342
Rhabdosargus haffara	Italy	KJ012422	*Boops boops*	Italy	KJ012296
Rhabdosargus haffara	Suez, Red Sea	KP308279*	*Sarpa salpa*	Canada	JF494420
Lithognathus mormyrus	Israel	KM538409	*Sarpa salpa*	Turkey	KC501256
Lithognathus mormyrus	Abu Qir-Alexandria, Mediterranean Sea	KP308276*	*Sarpa salpa*	Abu Qir-Alexandria, Mediterranean Sea	KU757071*
Lithognathus mormyrus	Israel	KM538408	*Sarpa salpa*	Turkey	KC501255
Sparus aurata	Turkey	KC501554	*Sarpa salpa*	Italy	KJ012425
Sparus aurata	USA	KT883618	*Sarpa salpa*	Italy	KJ012429
Sparus aurata	Turkey	KC501557	*Argyrops spinifer*	Iran	HQ149794
Sparus aurata	Central Mediterranean Sea from the European marine	KJ709635	*Argyrops spinifer*	Suez, Red Sea	LC151617*
Sparus aurata	Abu Qir-Alexandria, Mediterranean Sea	KP308280*	*Argyrops spinifer*	Australian and South African waters	DQ884968
Pagellus bogaraveo	Italy	KJ012387	*Argyrops spinifer*	Australia	DQ107836
Spondyliosoma emarginatum	Canada	JF494575	*Argyrops spinifer*	Australia	DQ107839
Spondyliosoma cantharus	Turkey	KC501615	*Argyrops filamentosus*	Italy	KJ012287
Spondyliosoma cantharus	Abu Qir-Alexandria, Mediterranean Sea	KP308281*	*Pagrus pagrus*	Alabama Deep Sea in USA	KF461214
Spondyliosoma cantharus	Turkey	KC501622	*Pagrus pagrus*	USA	KF930219
Spondyliosoma cantharus	Turkey	KC501618	*Pagrus pagrus*	Italy	KJ012417
Spondyliosoma cantharus	Turkey	JQ624002	*Pagrus pagrus*	Abu Qir-Alexandria, Mediterranean Sea	LC177762*
Spondyliosoma cantharus	Turkey	KC501613	*Pagrus pagrus*	Turkey	KC501089
Boops boops	Israel	KM538238	*Pagrus major*	South China sea	EU871693
Boops boops	Abu Qir-Alexandria, Mediterranean Sea	LC151618*	*Pagellus erythrinus*	Europe sea	JQ178368
Pagellus erythrinus	Abu Qir-Alexandria, Mediterranean Sea	KP308278*	*Pagrus caeruleostictus*	China sea	KF857268
Dentex dentex	Turkey	KC500455	*Pagrus caeruleostictus*	Israel	KM538478

Table 1: Continue

Species	Sampling location	GenBank accession No.	Species	Sampling location	GenBank accession No.
Dentex dentex	Turkey	KC500460	*Pagrus caeruleostictus*	China sea	KF857267
Dentex dentex	Abu Qir-Alexandria, Mediterranean Sea	KP308272*	*Pagrus caeruleostictus*	Italy	KJ012409
Dentex dentex	Turkey	KC500467	*Pagrus caeruleostictus*	Israel	KM538481
Pagrus auriga	Turkey	KC501053	*Pagrus caeruleostictus*	Abu Qir-Alexandria, Mediterranean Sea	KU757072*
Pagrus auriga	Turkey	KC501054	*Crenidens crenidens*	Canada	JF493279
Pagrus auriga	Italy	KJ012405	*Crenidens crenidens*	Suez, Red sea	LC155797*
Pagrus auriga	Abu Qir-Alexandria, Mediterranean Sea	KP308277*	*Crenidens crenidens*	Italy	KJ767818
Dentex gibbosus	Abu Qir-Alexandria, Mediterranean Sea	LC152206*	*Crenidens crenidens*	Mediterranean Sea off the coast of Lebanon	KR861522
Pagrus caeruleostictus	Italy	KJ012407	*Morone chrysops*	Mediterranean BH	KJ553987

*Fish under the study

Following application of phenol and chloroform, genomic DNA was then recovered by standard precipitation with ethanol and the resulting DNA was dissolved in TE buffer (100 mM tris-HCl, 10 mM EDTA, pH 8). The concentration of the extracted DNA was spectrophotometrically assessed (Eppendorf, Hamburg, Germany) and DNA stored at 4°C till use.

The partial coding regions of the *COI* gene was then amplified by PCR using the following primers: FishF1-5'TCAACCAACCACAAAGACATTGGCAC3' and FishR1-5'TAGACTTCTGGGTGGCCAAAGAATCA3'[29]. The PCR was carried out in a GeneAmp PCR system 9700 (Applied Biosystems, California, USA) with a reaction volume of 25 µL, containing 2.0 µL DNA template (approximately 20 ng), 1.0 µL 10 µmol L^{-1} forward primer, 1.0 µL 10 µmol L^{-1} reverse primer and 21 µL1×RBC SensiZyme® HotstartTaq Premix (RBC Bioscience, Taipei, Taiwan). The following thermal cycling conditions were used: Initial denaturation at 94°C for 5 min, 35 cycles of amplification (94°C for 30 sec for DNA denaturation, 55°C annealing temperatures for 30 sec, extension at 72°C for 2 min) and final extension at 72°C for 7 min. The products were then purified using Hi-Yield Gel/PCR DNA fragments extraction kit (RBC Bioscience, Taipei, Taiwan). The purified DNA fragments were sequenced using the BigDye Terminator version 3.1 cycle sequencing kit (Applied Biosystems, California, USA) and ABI3730 sequencer (Applied Biosystems, California, USA). The sequencing PCR reaction was performed at 96°C for 2 min, followed by 25 cycles of 10 sec at 96°C, 5 sec at 50°C and 4 min at 60°C[30].

The raw sequence data of *COI* was edited by a free software Chromas Lite version 2.1 (Technelysium Pty Ltd., available from the URL http://technelysium.com.au/). The partial coding sequences of *COI* for 22 fish species of family Sparidae were deposited in GenBank/EMBL/DDBJ International databases with accession numbers are shown with asterisks in Table 1. Eighty six *COI* sequences belonging to the same family retrieved from the databases are given the similarities with the Egyptian Sparidae species (Table 1). Best fitting model were applied for the *COI* datasets of nucleotide composition and divergence values depending on Kimura 2-parameter model[31] with gamma distribution among invariant sites (G+I) with a tool from MEGA7 software[32]. Phylogenetic tree was constructed by MEGA7 using Maximum Likelihood (ML) method with 1000 replicates of bootstrapping.

RESULTS AND DISCUSSION

The DNA barcoding considered to be a tool to identify, invent and study specimens in order to understand the diversity of species within an ecosystem and also to evaluate the genetic variability within species[33]. In the present study, the universal DNA primers, FishF1 and FishR1, amplified about a 650 bp region of the *COI* gene from 22 fish species of the family Sparidae without stop codons, insertions or deletions. Multiple alignments resulted in a consensus length of 612 positions (base-pair sand gaps). While performing BLAST, the sequences of *Dentex dentex*, *Dentex gibbosus*, *Diplodus annularis*, *Lithognathus mormyrus*, *Oblada melanura*, *Pagellus acarne*, *Pagrus pagrus*, *Sarpa salpa*, *Spondyliosoma cantharus*, *Argyrops spinifer* and *Diplodus noct* showed 100% similarity with the existing data in the GenBank databases. However, *Boops boops*, *Diplodus cervinus*, *Diplodus sargus*, *Diplodus vulgaris*, *Pagellus erythrinus*, *Pagrus Auriga*, *Pagrus caeruleostictus*, *Sparus aurata*, *Crenidens crenidens* and *Rhabdosargus haffara* resulted in 99% identity with their counterparts in the GenBank databases. *Acanthopagrus bifasciatus*, however, showed 97% sequence similarity. Accession numbers for *Dentex gibbosus* (LC152206) and *Acanthopagrus bifasciatus* (LC150892) in the current study considered to be the second one for the same species in the GenBank. The GenBank accession numbers of all Sparidae species under the study and other related species retrieved are presented in Table 1. These accession numbers were retrieved depend on the similarity and haplotype sequences. The maximum likelihood analysis of the concatenated sequence of the 22 species resulted in the phylogenetic tree shown in Fig. 2. The ML tree showed monophyly of Sparidae species. This matches with a previous report of molecular analysis for some Sparidae species[34]. The tree was divided into two distinct clades and some sub-clades. The two major clades, that include all the species under the study except *Crenidens crenidens* in a separate branch were supported by 53 and 98 bootstraps. The clade one was divided into some subclades, first one that has genus *Diplodus* was clustered with the two different species *Oblada melanura* and *Acanthopagrus bifasciatus*, the second one for *Lithognathus mormyrus* and *Sparus aurata* was clustered in another subclade and the third one for *Spondyliosoma cantharus, Sarpa salpa* and *Boops boops* were clustered together. Both *Rhabdosargus haffara* and *Pagellus acarne* were paraphyletic and placed in the first major clade. The clade two was divided into two clades, first one that was for *Argyrops spinifer* as a paraphyletic species, while the second was for three species from genus *Pagrus*, two species from genus *Dentex* and *Pagellus erythrinus. Pagrus pagrus* and *Pagellus erythrinus* were clustered in one sub-clade and the other two species from genus *Pagrus* and the two species of genus *Dentex* were clustered together in the second sub-clade. These results are in agreement with the results of De la Herran *et al.*[34] that their phylogenetic analysis suggested that the Sparidae can be

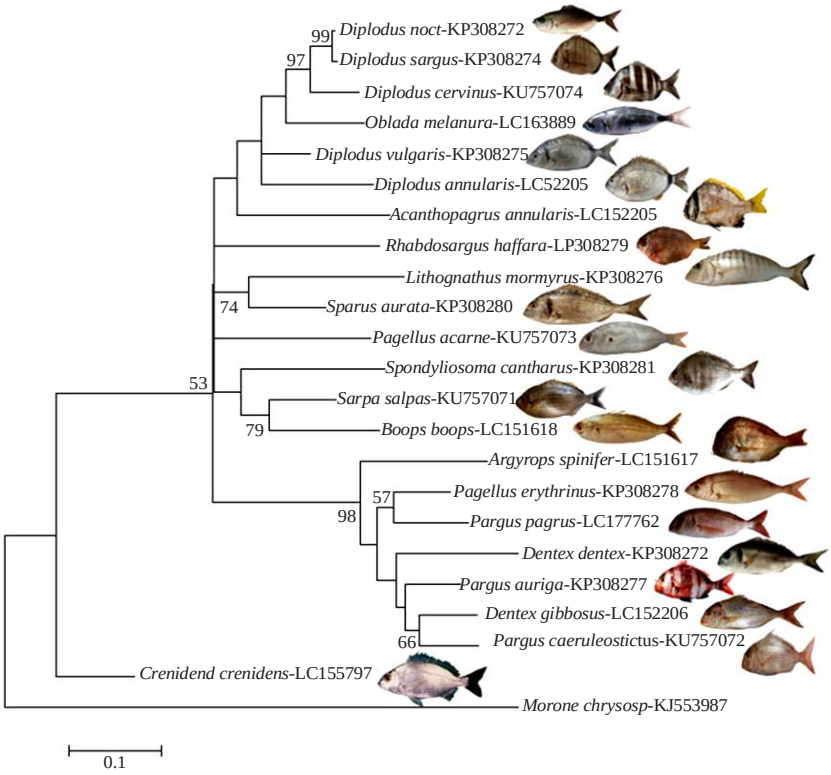

Fig. 2: Maximum Likelihood (ML) phylogenetic tree for the *COI* gene sequences for the common Egyptian Sparidae fish species

assigned into two major lineages: Lineage one, composed of the species of the genera *Sparus*, *Diplodus*, *Lithognathus*, *Spondyliosoma*, *Boops* and *Sarpa* and lineage two composed of the genera *Pagrus* and *Dentex*, plus *Pagellus erythrinus*. The phylogenetic relationship of the family Sparidae is also supported by previous data obtained from the analysis of using satellite DNA found within the genome of some Sparidae species[35,36]. Their study with the different phylogenetic inferences methods provisions the existence of two monophyletic groups within the family Sparidae. On the other hand, our data contradict the results that have considered the family Sparidae as non-monophyletic on the basis of mitochondrial cytochrome b (*Cyt-b*) gene and 16S ribosomal RNA data[2,25,37]. The species of *Diplodus* appeared as a monophyletic group as also presented by De la Herran *et al.*[34]. The more closely related species within this genus were *D. noct* that was collected from the Red Sea and *D. sargus* from the Mediterranean Sea. Special consideration should be given to the species *Oblada melanura*, which appeared in our results clustered with the genus *Diplodus* in a sub-clade and this results are in the agreement with Orrell *et al.*[2] and Chiba *et al.*[37]. Our results showed that the genus *Pagrus*, *Dentex* are closely related with *Pagellus erythrinus*[34] while *Pagellus acarne* separated in the other group and associates with species of *Boops*, *Sarpa* and *Spondyliosoma*. This means that the two species from genus *Pagellus* are monophyletic and appeared in our study as highly divergent species. *Spondyliosoma cantharus*, *Sarpa salpa* and *Boops boops* separated in a sub-clade. Another phylogenetic analysis based on mitochondrial DNA[38] suggested that the existence of a third lineage within the Sparidae composed of last three species. As considered traditionally, *S. salpa* and *B. boops* are closely related species (the common synonym of *S. salpa* was *Boops salpa*[39] and the genetic distance between these two species is 0.11. *Acanthopagrus bifasciatus* is clustered with genus *Diplodus* in one sub-clade and the genetic distance between this species and the species from genus *Diplodus* is ranged from 0.119-0.139. Therefore, our molecular results suggested that *A. bifasciatus* is closely related *Diplodus* spp. *Lithognathus mormyrus* and *Sparus aurata* are clustered in another sub-clade and the genetic distance between them is 0.125. Our results also showed genetic relationship between *Rhabdosargus haffara* and the latter two species, but no support for this finding.

For *COI* gene-based pairwise distances among all 22 Sparidae species showed the highest genetic distance (0.210) between *Diplodus cervinus* and *Argyrops spinifer* and the lowest genetic distance (0.010) between *Diplodus noct* and *Diplodus sargus* (Table 2). Taking into consideration that

Table 2: Pairwise genetic distances among family Sparidae inferred from *CO1* gene of the Egyptian waters

Parameters	*Morone chrysops*-KJ553987	*Spondyliosoma cantharus*-KP308281*	*Dentex gibbosus*-LC152206*	*Diplodus annularis*-LC152205*	*Diplodus cervinus*-KU757074*	*Diplodus noct*-KP308273*	*Diplodus sargus*-KP308274*	*Diplodus vulgaris*-KP308275*	*Lithognathus mormyrus*-KP308276*	*Oblada melanura*-LC163889*	*Pagellus acame*-KU757073*	*Pagellus erythrinus*-KP308278*	*Pagrus auriga*-KP308277*	*Pagrus caeruleostictus*-KU757072*	*Pagrus pagrus*-LC177762*	*Rhabdosargus haffara*-KP308279*	*Sarpa salpa*-KU757071*	*Sparus aurata*-KP308280*	*Acanthopagrus bifasciatus*-LC150892*	*Argyrops spinifer*-LC151617*	*Boops boops*-LC151618*	*Crenidens crenidens*-LC155797*	*Dentex dentex*-KP308272*
Morone chrysops-KJ553987																						
Spondyliosoma cantharus-KP308281*	0.223																					
Dentex gibbosus-LC152206*	0.254	0.187																				
Diplodus annularis-LC152205*	0.211	0.162	0.189																			
Diplodus cervinus-KU757074*	0.229	0.157	0.203	0.122																		
Diplodus noct-KP308273*	0.230	0.145	0.189	0.108	0.058																	
Diplodus sargus-KP308274*	0.230	0.141	0.180	0.105	0.064	0.010																
Diplodus vulgaris-KP308275*	0.230	0.134	0.162	0.110	0.093	0.084	0.080															
Lithognathus mormyrus-KP308276*	0.229	0.188	0.194	0.158	0.175	0.156	0.153	0.135														
Oblada melanura-LC163889*	0.229	0.153	0.176	0.122	0.101	0.092	0.094	0.095	0.170													
Pagellus acame-KU757073*	0.225	0.147	0.169	0.144	0.169	0.149	0.153	0.138	0.164	0.141												
Pagellus erythrinus-KP308278*	0.239	0.183	0.106	0.171	0.177	0.153	0.157	0.153	0.176	0.165	0.151											
Pagrus auriga-KP308277*	0.233	0.176	0.097	0.172	0.180	0.163	0.153	0.136	0.178	0.158	0.159	0.112										
Pagrus caeruleostictus-KU757072*	0.262	0.197	0.089	0.182	0.181	0.184	0.177	0.151	0.192	0.184	0.185	0.112	0.095									
Pagrus pagrus-LC177762*	0.241	0.194	0.120	0.179	0.196	0.184	0.178	0.153	0.178	0.160	0.176	0.096	0.124	0.107								
Rhabdosargus haffara-KP308279*	0.222	0.169	0.190	0.146	0.135	0.143	0.141	0.144	0.173	0.151	0.161	0.165	0.165	0.183	0.188							
Sarpa salpa-KU757071*	0.227	0.132	0.176	0.137	0.148	0.126	0.126	0.144	0.154	0.152	0.144	0.142	0.150	0.187	0.177	0.147						
Sparus aurata-KP308280*	0.242	0.155	0.166	0.134	0.158	0.138	0.129	0.116	0.125	0.137	0.149	0.155	0.157	0.161	0.140	0.126	0.144					
Acanthopagrus bifasciatus-LC150892*	0.254	0.167	0.202	0.139	0.119	0.119	0.119	0.130	0.180	0.149	0.169	0.181	0.179	0.213	0.200	0.148	0.161	0.157				
Argyrops spinifer-LC151617*	0.232	0.183	0.143	0.178	0.210	0.199	0.201	0.177	0.175	0.172	0.183	0.132	0.119	0.141	0.129	0.186	0.178	0.172	0.202			
Boops boops-LC151618*	0.216	0.146	0.195	0.170	0.157	0.141	0.135	0.149	0.179	0.147	0.156	0.152	0.169	0.178	0.175	0.146	0.110	0.151	0.161	0.177		
Crenidens crenidens-LC155797*	0.217	0.170	0.200	0.151	0.163	0.163	0.163	0.164	0.199	0.187	0.187	0.178	0.173	0.203	0.188	0.189	0.158	0.179	0.176	0.182	0.183	
Dentex dentex-KP308272*	0.244	0.206	0.105	0.176	0.194	0.199	0.199	0.172	0.207	0.172	0.176	0.130	0.117	0.138	0.139	0.168	0.177	0.189	0.201	0.138	0.199	0.183

Orrell *et al*.[2] and Hanel *et al*.[38] found that subfamilies of Sparidae are defined mostly by trophic levels. The interpretation of the agreement between our results and De la Harran *et al*.[34] that might be due to they investigated the family under study in the same water body, Mediterranean Sea with quite similar surrounding ecological factors including the available food items.

CONCLUSION

So far, this is the first study to report the molecular identification and DNA barcoding of the available and commercial fish of family Sparidae in Egyptian Mediterranean and Red Sea using *COI* gene as a genetic marker. This will provide a complete vision of the phylogenetic, evolutionary relationships of the Egyptian Sparidae and will enrich all the genetic database with the sequences from the Egyptian fauna for their biodiversity and conservation.

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