Project ID-609

Competitive Research Grant (CRG)

Sub-Project Completion Report
On

DNA Barcoding and Metabarcoding of Coral Associated Fish and Zooplankton Community of Saint Martin's Island for Effective Conservation of Marine Life

Project Duration
May 2017 to September 2018

Department of Fisheries Biology and Genetics
Faculty of Fisheries and Aquaculture
Sher-e-Bangla Agricultural University (SAU)
Sher-e-Bangla Nagar, Dhaka-1207.

Submitted to
Project Implementation Unit-BARC, NATP 2
Bangladesh Agricultural Research Council
Farmgate, Dhaka-1215

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Project Implementation Unit
National Agricultural Technology Program-Phase II Project (NATP- 2)
Bangladesh Agricultural Research Council (BARC)
New Airport Road, Farmgate, Dhaka-1215
Bangladesh

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Acronyms

BOLD- Barcode of Life Database

BLAST- Basic Local Alignment Search Tool

COI- Cytochrome c Oxidase Subunit I

DNA- Deoxyribonucleic Acid

DO- Dissolved Oxygen

SMI- Saint Martin’s Island

ECA- Ecological Critical Area

FAO- Food and Agriculture Organization of the United Nations

GPS- Global Positioning System

MPA- Marine Protected Area

BoB- Bay of Bengal

NCBI- National Center for Biotechnology Information

NGS- Next Generation Sequencing

OUT- Operational Taxonomic Unit

PCR- Polymerase chain reaction

PSS- Plasma sound source

SAU- Sher-e-Bangla Agricultural University

UV- Ultraviolet

16S rRNA- 16S Large Ribosomal RNA

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Executive Summary

Coral reef is exceptional biodiversity and home to thousands of marine species. The current rates of species description using traditional keys is extremely slow and typically require specialized expertise which have severely limited the understanding of coral reef biodiversity. DNA barcoding is an advance tool to identify unique, cryptic and new species from marine ecosystems and reveals undisclosed biodiversity than previously estimated. Saint Martin's Island (SMI) is the only place in Bangladesh where coral colonies are found and declared an Ecologically Critical Area (ECA) by the government of Bangladesh. There is lack of information on different biodiversity data such as a complete species inventory, genetic structure and diversity of species, recruitment process etc. for effective conservation of marine lives and for converting this ECA to a well planned marine protected area (MPA). Present study aims to assess the diversity and make an updated inventory of coral associated fishes of the island through morpho-molecular approach, and to build a reference library of DNA barcode data for coral associated fishes in Bangladesh. Collected samples were first identified by examining morphometric characteristics and then assessed by DNA barcoding. From May 2017 to July 2018, DNA barcoding was successfully completed and analysed for 111 coral associated fish species belonging to 9 orders, 49 families. Another 13 species were identified by underwater monitoring through scuba diving. The study provided a total of 32 species which had been detected as new distributional records in Bangladesh marine water. Among them, *Cryptocentrus maudae* (Fowler, 1937), *Stegastes apicalis* (De Vis, 1885) and *Apogonichthyoides pseudotaeniatus* (Gon, 1986) were documented for the first time in the Bay of Bengal (BoB).

In this study, Scalloped Hammerhead Shark, *Sphyrna lewini*is was found in abundance along continental margins and also occurred near shore, especially around submerged reefs; although this species was declared globally endangered by IUCN. The population genetic structure of *S. Lewini* collected from the sea area near SMI was assessed with partial sequences of the mtDNA control region from 33 individuals collected off SMI and Teknaf coast, and designated as BoB population. The nucleotide diversity was low as 0.002 while the haplotype diversy was high as 0.58. Estimates of F_{ST} values between BoB and each of the population of different global seas were ranged from 0.308 to 0.530 with significant difference (P = 0.00) from random mixing, indicating a unique population genetic structure (i.e. a single genetic stock) was established in the Bay of Bengal region. This genetic population in BoB indicates the presence of nursery of *S. lewini* in this sea.

In the assessment of zooplankton diversity of SMI through DNA metabarcoding by next generation sequencing technology, a total of 332 operational taxonomic units (OTUs) were found in 6 samples from two different sampling sites. Among them 137 OTUs had been ensured by 98% matching with NCBI reference database and 67 OTUs were identified up to species level under 9 phyla. Zooplanktons were collected from horizontal & vertical sampling methods from two spots of SMI.

Present study suggests that the SMI has still quite good diversity of fish and zooplankton in its marine habitat. However, the island is facing high level of ecosystem degradation due to anthropogenic causes. So, it is urgently needed to declare SMI as marine protected area (MPA) to save this only coral Island of Bangladesh.

CRG Sub-Project Completion Report (PCR)

A. Sub-project Description

1. **Title of the CRG sub-project:** DNA barcoding and metabarcoding of coral associated fish and zooplankton community of Saint Martin's Island for effective conservation of marine life.
2. **Implementing organization:** Department of Fisheries Biology and Genetics, Faculty of Fisheries and Aquaculture, Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207.
3. **Name and full address with phone, cell and E-mail of PI/Co-PI (s):**

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4. **Sub-project budget (Tk):**
   4.1 Total: Taka 39,58,039.00(Thirty nine lac fifty eight thousandsthirty nine)
   4.2 Revised (if any): N/A

5. **Duration of the sub-project:**
   5.1 Start date (based on LoA signed): 05 May 2017
   5.2 End date: 30 September 2018

6. Justification of undertaking the sub-project:

Coral reefs are complex and productive ecosystems in the ocean. Although covering less than one percent of the globe, coral reefs are the most diverse marine systems on the earth (Gray 1997, Hoegh-Guldberg 1999). Coral reefs are essential spawning, nursery, breeding, and feeding grounds for numerous organisms. Over 25 percent of the world's fish biodiversity, and between nine and 12 percent of the world's total fisheries, are associated with coral reefs (Spalding *et al.,* 2001). Of the 34 recognized animal Phyla, 32 are found on coral reefs, compared to only nine Phyla in tropical rainforests (Wilkinson 2002). To score of invertebrate species and macrofauna (Bony fish, Sharks, sea Turtles, etc.), the number of species found on coral reefs has been estimated at around 600,000 to over 9 million (Plaisance *et al*., 2011b). New cryptic species (morphologically similar but genetically distinct lineages) still continue to be uncovered in many marine fish and other taxa such as marine crustaceans, molluscs, cnidarians etc. (Thomas Jr 2014). Until now the estimates of reef fish and coral diversity stand at about 4000 and about 800 species, respectively (Hughes *et al.* 2002, Plaisance *et al*., 2011b).

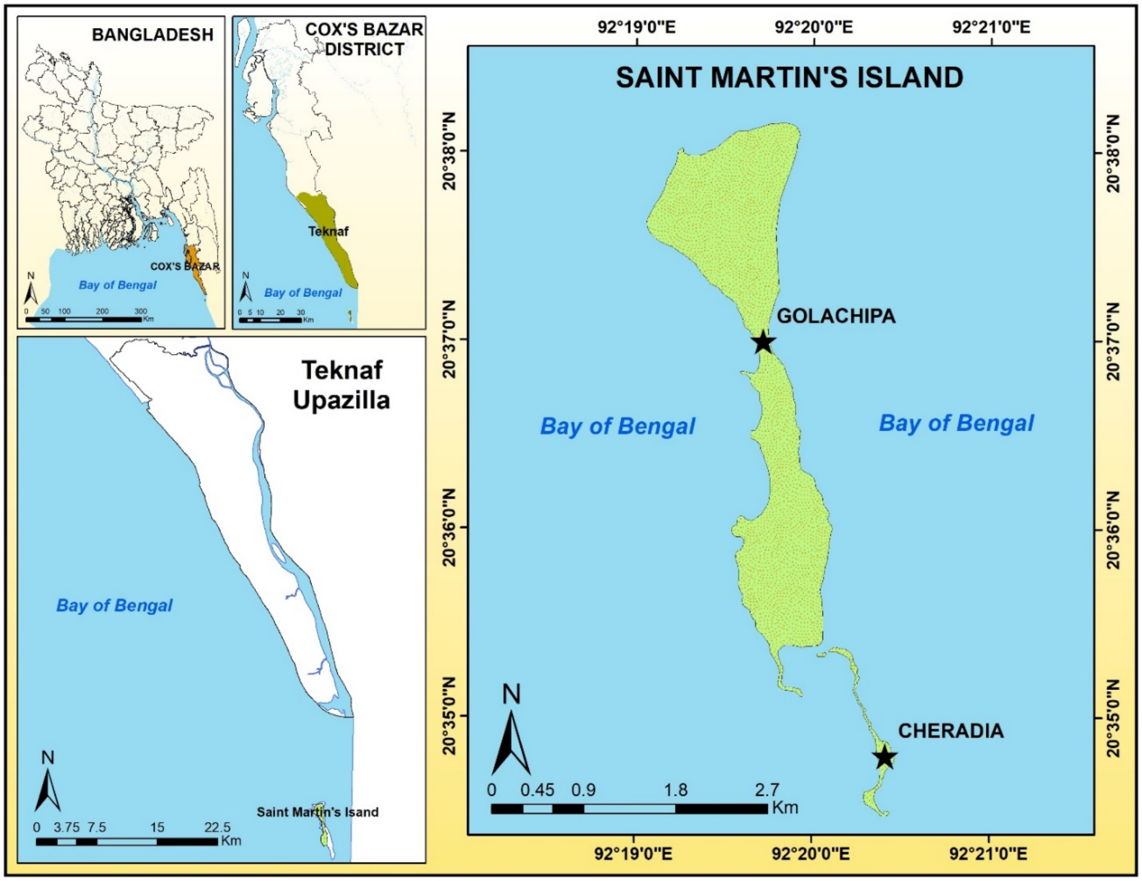


Figure 1. GIS map of St. Martin`s Island Bangladesh in the Bay of Bengal; coordination between 20°34’ -20°39’ N and 92°18’ - 92°21’ E.

Saint Martin's Island is about 08 sq. km (600 Ha.) island lying 10 km south of the southern tip of Teknaf peninsula in the Cox's Bazar District (20°36'N; 92°20'E; Figure. 1) separated from the mainland by a channel that is about 9 km wide (Figure 1). It is the only coral island in Bangladesh which is dumbbell shaped and characterized by large areas of sand dune and scattered mangroves. It is a natural treasure of Bangladesh that attracts thousands of tourists. The (biotic and abiotic) environmental conditions found in the St. Martin’s Island are unique in Bangladesh and perhaps in the world. There are only a few examples worldwide where coral communities dominate rock reefs. The co-occurrence and succession of corals, sea grasses and mangroves in the Island are little known example in the tropical areas (Tomascik 1997). The unique and dynamic nature of the inter-tidal and sub-tidal rocky habitats offers excellent research opportunities for the national and international scientists as a global interest of coral reef biodiversity (Mollah 1997; Hasan 2009).

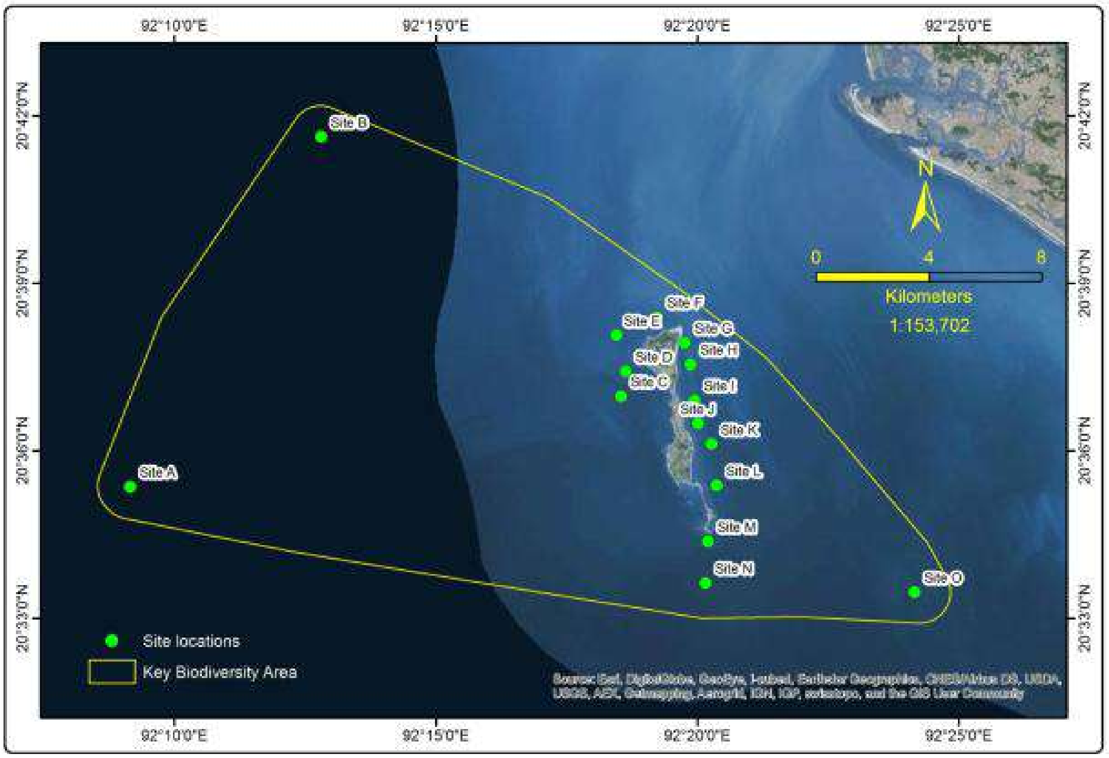


Figure 2. Map showing the possible biodiversity area and possible ecosystem boundary of Saint Martin's Island proposed in BOBLME (2015).

There have been only a few studies on the biodiversity of coral and associated marine organisms of the St. Martin's island which were not methodologically conducted with under water monitoring and not conclusive except the study of Tomasick (1997) and Hossain *et. al*. (2009). The study found coral communities extended to about 200m offshore of St. Martin's Island. These comprise 66 hard coral species including many soft corals, Sea fans, and Sea whips. The other macro-invertebrates were represented by 61 species of mollusks, 9 species echinoderms, 4 species zonathids and 4 species of Bryzoans. Reef fish diversity was found low (86 species) with Damselfish (Pomacentridae), Surgeonfish (Acanthuridae) and Parrotfish (Scaridae) being the most abundant. There were also 5 species of Butterfly fish (Chaetodontidae) and one Angel fish (*Pomacanthus annularis*). It is anticipated that at least 100 additional species might be discovered in the Island if properly surveyed (Tomascik 1997; Mollah 1997). Considering the relative isolation of the Island, there are high chances of presence of endemic fish species and genetic stock (population) in this island. Further, in a recent field survey (BOBLME 2015), it has been found that rocky habitats around Saint Martin's Island extends up to 16 km (Figure 2) and in many places offshore supports a diverse coral community. No biodiversity survey has been conducted throughout this extended habitat. Until now, species identification in Saint Martin's Island by different studies including the study of Tomascik (1997) was carried out based only on the morphological study but no genetic methods and DNA based taxonomy were employed. So, it is expected that more species and unique population genetic structure will be identified in the Island if modern genetic approach such as DNA barcoding, gene sequencing of mitochondrial and/or nuclear DNA, are used. Analysis of these genetic data by modern bioinformatics programs can reveal unique findings in the taxonomic and population genetic study.

Temporal and spatial distribution and diversity monitoring of zooplankton community including eggs and larvae of fish of SMI can contribute to understand the dynamics of biodiversity of this island. Zooplankton plays an important role in the ocean, in biogeochemical cycling and providing a food source for commercially important fish larvae. However, due to very tinny and microscopic size, separation and correct identification of zooplankton is very difficult job which hinder the understanding of their roles in marine ecosystem functioning, and can prevent detection of long term changes in their community structure. The state-of-art technology High-Throughput Sequencing (HTS) or Next Generation Sequencing (NGS) technologies open up new frontiers in marine biodiversity science by making it possible to read DNA barcodes for hundreds of specimens at a time. This approach, termed DNA metabarcoding, holds considerable promise for rapid and more comprehensive biodiversity monitoring of the ocean on a large scale, particularly when combined a number of tiny, microscopic mixed samples of zooplankton (Lindeque *et. al*. 2013) including fish eggs, larvae and fry. Quantification of richness and diversity study of coral associated organisms of this biodiversity hot spot of Bangladesh through NGS technology is very useful to understand the ecosystem structure and for determining it's conservation strategy.

Reefs are very sensitive and susceptible to environmental conditions. Human activities such as unplanned tourism, population stress, pollution, shipping, habitat destruction, overfishing, illegal harvesting of corals and infrastructure development along shorelines have made dramatic adverse impacts on coral population and associated reef organisms of the St. Martin's Coral Island. The island was declared an Ecologically Critical Area (ECA) in 1999 under the Bangladesh Environmental Conservation Act. Protection and rational use of the marine biological resources is important for livelihood, sustainable tourism and prosperity of the island. Establishment of an effective reef management and conservation plan for this biodiversity reservoir of the country is an urgent task such as declaration of marine protected area (MPA). This issue is under active consideration by the Department of Environment under the Ministry of Environment and Forest. A national frame work was also made where St. Martin's island has been proposed as the potential site for MPA declaration (IUCN 2015). Before planning and implementing such management strategy a systemic and complete inventory of aquatic organisms, population structure, recruitment process and biogeography of the aquatic organisms of this island are needed to depict especially using modern methods such as DNA barcoding and gene sequence analysis. Considering the above assumptions present study has been carried out.

7. **Sub-project goal:** Contribution to conservation of the only coral island of Bangladesh i.e. Saint Martin's Island as a biodiversity hotspot.

8. **Sub-project objective (s):**
   a. To build a precise inventory of coral associated fish based on DNA barcoding along with morphometrics
   b. To assess population genetic structure of biodiversitycally/ecologically important fish species found in the island area
   c. To assess the diversity of zooplankton by DNA metabarcoding through next generation sequencing (NGS)

9. **Implementing location:** Saint Martin's Island, Teknaf, Cox's bazar district, Bangladesh

10. Methodology:

10.1. DNA Barcoding of coral associated fishes found in Saint Martin's Island

10.1.1 Collection of fish samples:

Fish specimens were collected from local fishermen in St. Martin's Island between May 2017 to July 2018 while operating set gill net on the coral reef. Underwater survey was conducted to monitor coral fish species in its natural habitat and photographed through Scuba diving usually within 1.5 - 3 m depth in the north and east side of the island where coral colonies are found frequently. Collected samples were photographed after tagging in field for best living colour representation. Then the specimens were transferred and stored in the Aquatic Bioresource Research Lab. (ABR Lab.) in the Department of Fisheries Biology and Genetics, Sher-e-Bangla Agricultural University (SAU), Dhaka, Bangladesh for morphological and molecular analysis. After morphological analysis, a small piece of muscle tissue was cut and stored in a sterile 1.5 ml tube containing 98% alcohol for subsequent molecular work.

10.1.2 **Morphological identification:**

Species level identification was carried out at Aquatic Bioresource Research Lab., SAU using morphological characters according to original descriptions in a morphological data sheet for each individual. The Generic diagnosis was based on meristic counts and proportional measurements of collected specimens according to Talwar & Kacker (1984), Rahman *et al.,* (2009), Froese *et. al.* (2019), FAO species identification sheets, Fishes of Andaman Sea etc.

10.1.3 Molecular Identification

Genomic DNA extraction, PCR amplification and DNA sequencing

Genomic DNA was extracted from the collected muscle tissue using a TIANamp Marine Animals DNA Kit (TIANGEN) following the protocol provided inside kit box. The concentration of genomic DNA was then measured by Qubit 3.0 fluorometer. Polymerase chain reaction (PCR) was performed in a 50μl reaction mixture in small reaction tubes (0.2 ml) in Thermal cycler (2720 Thermal Cycler, Applied Biosystems). The partial sequence of mitochondrial DNA (mtDNA) COI and 16s rRNA gene regions of collected specimen was amplified by polymerase chain reaction (PCR) which was carried out under different thermal conditions that varies primer to primer as presented in table 1. After successful PCR, each sample was visualized on 10% agarose gel (EZ-Vision® In-Gel Solution, USA) stained with ethidium bromide in gel documentation chamber (Model: Syngene InGenius^3). The flow UV-ray is kept on to watch the band in the connected computer by using GeneSys software. PCR samples with a single and clear visible band were purified with the PCR Purification Kit (TIANGEN- Universal DNA Purification Kit) for sequencing. The concentration of the purified DNA was estimated with the help of Qubit 3.0 fluorometer. Sequencing was conducted with the PCR primers by Sanger standard method in a normal automatic sequencing (Model 3730xl DNA analyzer) at Macrogen Inc. (Korea).

Table 1. List of primers and thermal conditions used in PCR amplification for DNA barcoding

Name of Primer set		**Direction**	**Author**	**Thermal profile**
FishF1		Forward	Ward et al. 2005	95°C (2m), 94°C (40s), 35 cycles 54°C (40s), 72°C (1m) with final extension at 72°C for (10 min)
FishR1		Reverse		
FishF2		Forward		
FishR2		Reverse		
VF2_t1 **FR1d_t1**	**Primer cocktails**	Forward Reverse	Ivanova et al. 2007	95°C (3m), 95°C (30s), 35 cycles 57°C (40s), 72°C (1m) with final extension at 72°C for (10 min).
FishF2-t1 **FishR2-t1**		Forward Reverse		
16Sar-5′		Forward	Palumbi, 1996	94°C (3m), 94°C (30s), 35 cycles 52°C (40s), 72°C (1m) with final extension at 72°C for (10 min).
16Sbr-3′		Reverse		

10.1.4 Data analysis

The Software Geneious 9.0.5 was used for editing nucleic acid sequences. The obtained consensus sequences were edited based on the chromatogram peak clarities with the help of Chromas Lit. Sequences were matched using BLAST search engine provided by NCBI and Bold database. Sequences were also manually edited using the MEGA 6.0 program combined with manual proofreading; each base of the spliced sequences was ensured to be correct before submitting them to GenBank and BOLD database (annex 2). Next, the sequences were aligned using ClustalW in MEGA 6.0 software, and parameters including the sequence length, GC content, divergence and genetic distance were calculated. The distances within species and between species were calculated using the Kimura-2-parameter (K2P) model; phylogenetic tree was constructed using the neighbor-joining (NJ) method. The clade credibility in the tree that was obtained using the NJ method was tested by bootstrapping, in which 1000 repeated sampling tests were performed to obtain the support values of the clade nodes.

10.2. Assessing population genetic structure of *Sphyrna lewini*

10.2.1 Collection of samples

Globally endangered scalloped hammerhead Shark, *Sphyrna lewini*is was found abundant along continental margins and also occur near shore, especially around submerged reefs. Tissue samples of thirty-three *S. lewini* individuals were collected and preserved in 95% ethanol from whole Sharks (Figure 3) in 2018 from landing center of Cox’s Bazar of Bangladesh.

Figure 3: Scalloped hammerhead Shark (*Sphyrna lewini*)

These fishes were caught by local fishermen from off Cox’s Bazar of the Bay of Bengal near SMI (Figure 4). For comparing the samples of other seas and oceans, mitochondrial d-loop sequences (520 bp) of 504 samples from six regions viz. Arabian Sea Basin, Red Sea, Indo-Pacific, Pacific Ocean, Indian Ocean and Atlantic Ocean were used (Duncan *et al.* 2006 and Spaet *et al.* 2015; GenBank accession numbers of haplotypes: KR232952 to 232956; HQ916311, HQ916312; DQ438148 to DQ438172; DQ438189 to DQ438191). Sampling information is given in Table 2.

Figure 4. Sampling location in Cox's Bazar coast of Bangladesh

Table 2. Sampling information for *S. lewini* used in the present study

ID	Sampling regions	Year of collection/ References	Sampling size (N)
BoB	Bay of Bengal	2018 (present study)	33
RS	Red Sea	Spaet et al., 2015	81
AS	Arabian Sea		152
IP	Indo Pacific	Duncan *et al*. 2006	183
IO	Indian Ocean		10
PO	Pacific Ocean		35
AO	Atlantic Ocean		43

10.2.2 DNA extraction, PCR amplification and sequencing:

Genomic DNA was extracted from 95% alcohol fixed tissue samples using a DNeasy blood and tissue kit (Qiagen, Germany) following the manufacturer's protocol. The first hyper-variable portion of the mtDNA control (Figure 4) region was amplified from the genomic DNA through the polymerase chain reaction (PCR) using the forward and reverse primers, CRF6 (5'-AAGCGTCGACTTTGTAAGTC-3') and CRR10 (5'-CTTAGAGGACTGGAAATCTTGATCGAG-3') designed by Pinhal *et al*. (2012). PCR was performed in a 50 µl reaction mixture containing 2.5 unit of Taq DNA polymerase, 5 µl of 10 × PCR buffer, 10 mM each of the dNTPs (2.5 µl each), 25 pmoles of each primer, and 0.5 - 1.0 µg template DNA. The temperature profile was as follows: preheating at 95°C for 5 min followed by 35 cycles of denaturation at 95°C for 1 min, annealing at 58°C for the control region for 40 seconds, extension at 72°C for 1 min, and completion with final extension at 72°C for 7 min. PCR products were examined at an 1% agarose gel by electrophoresis with a standard size marker and purified by a QIAGEN QIA quick PCR Purification kit. The purified DNA was sequenced by an automated sequencer using the dye-termination method (Applied Biosystems, USA).

10.2.3 Genetic diversity and population genetic analysis

The sequence data were edited and aligned with ClustalW (Thompson *et al.* 1994) and DNAssist 2.5 (Patterton and Graves 2000). Molecular diversity indices such as haplotype diversity (h), nucleotide diversity (π), average number of nucleotide differences (k), number of haplotypes (N_h), polymorphic sites (S), transitions (ti) and transversions (tv) for each population were obtained using the program ARLEQUIN (version 3.5, Schneider *et al.* 2000). Pairwise genetic variation and structure between sampled populations were assessed using fixation index (F_{ST}) (Excoffier *et al.* 1992). The statistical significance of the estimates was assessed by 10,000 permutations. The null hypothesis of population panmixia was also tested using an exact test of haplotype differentiation among populations (Raymond and Rousset 1995). All the above calculations were performed in ARLEQUIN. The haplotype frequencies of the sequences used in the present study are given in table 3.

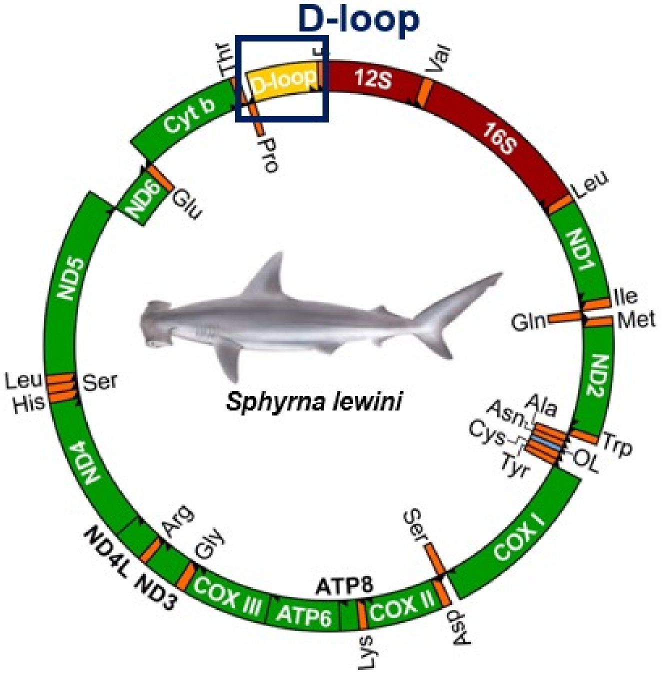


Figure 5. D-loop region of mitochondrial DNA

10.2.4 Haplotype network analysis

Genealogical relationship among haplotypes for mtDNA control region was assessed by generating the network of haplotypes using a statistical parsimony method TCS 1.18 (Clement *et al.* 2000). In the haplotype network, a haplotype is represented by a circle and a line indicates one mutational step between haplotypes.

10.2.5 Neutrality and demographic analyses

Genetic signature of population demography of the BB of population of *S. lewini* was investigated by Tajima's *D* statistics (Tajima 1989) and Fu's F_S test (Fu 1997) for selective neutrality implemented in ARLEQIN. The neutrality tests evaluate mutations for their deviation from neutrality and history of effective population size for its constancy following the Wright-Fisher population model. Significant large negative *D* and F_S values can be interpreted as signatures of demographic expansion. Historical demography of the BoB population was further examined by mismatch distribution analysis. The analysis evaluates the frequency distribution of pairwise differences between sequences. The distribution is usually unimodal in the population that has experienced recent demographic and/or range expansion but it is multimodal when the population is in demographic equilibrium or is subdivided into several units (Rogers and Harpending 1992; Excoffier 2004). In this analysis, historic demographic expansion was represented by three population genetic parameters: τ (tau, an index of time since expansion expressed in units of mutational time), ϑ_0 and ϑ_1 (mutational parameters of population size represent the population sizes before and after the expansion, respectively; Rogers 1995). The population expansion was further assessed by examining the concordance between the observed and the expected frequency distribution with sum of squared deviations (SSD) statistics (Rogers and Harpending 1992) and the Harpending's reggedness index (*Hri*) (Harpending 1994) under the sudden expansion model. The mutational time value of τ was converted into estimate of real time in years since expansion with the equation, $\tau = 2ut$, in which u is the mutation rate for the whole sequence and t is the time measured in generation since expansion. Mutation rate is required to convert the mutational time value of expansion (τ) to real time in years. In the present study, we used a divergence rate of 1.21% per MY for Sphyrnidae D-loop and the generation time of 15 years for *S. lewini* in calculation of the expansion time (Nance *et al*. 2011).

10.3. Assessing diversity of zooplankton by DNA metabarcoding technology through next generation sequencing (NGS)

10.3,1 Collection of samples

The collection of zooplankton samples were carried out by using conical net by a mechanical boat. A total of 6 samples from two different locations were collected using a cylindrical conical net (front half -cylindrical, connected rear half - conical; mouth diameter- 60 cm; mesh sizes- 100 µm for horizontal and 53 µm for vertical sample; length, 300 cm; vertical and horizontal towing) tied with a hard rope to the opposite side of the water current attached flowmeter from November, 2017 to January, 2018 in the St. martin's island of the Bay of Bengal. The difference in species number might occure depending on the inflow-quantity. We also used different instruments for measuring the water quality parameter such as CDT for measuring the water sound, GPS, salinity/PSS, temperature, conductivity; pH meter to measure the pH of water during collection of sample; Thermometer to measure air temperature; DO for estimating dissolve oxygen per liter of water.

Figure 6: Preparation for scuba diving in Saint Martin`s Island for collecting samples and capturing underwater photographs

Figure 7: Scuba diver diving near SMI for sampling and underwater observation

Figure 8: Underwater photographs of fish captured during scuba diving

10.3.4 Preservation of sample

After collecting the samples using zooplankton conical net, the sample were sieved by 100 µm 53 µm micron mesh net to get out of the saline water. After that, the zooplankton samples were preserved in 500ml sample bottle with 70%-98% of alcohol.

Figure 9: Mounted fish specimens arranged for morphological analysis

10.3.5 Molecular analysis

The zooplankton species were identified using DNA metabarcoding process to be explained in detail below and the number of zooplankton species were obtained after counting the available species number obtained. Firstly, the samples were centrifuged by 2 ml PBS buffer for extracting of remain saline water. The genomic DNA (gDNA) of zooplankton was extracted using the QIAGEN® DNeasy Blood & Tissue KIT (Qiagen, Inc., Valencia, CA). The concentration of genomic DNA was then measured by Qubit-3 fluorescent meter. Polymerase chain reaction (PCR) was performed in a 50 μl reaction mixture in small reaction tubes (0.2 ml) in Thermal cycler (2720 Thermal Cycler, Applied Biosystems). We amplify COI gene region of marine zooplanktons (313bp) as described in Leray *et al* (2014). The primers mlCOIintF and jgHCO2198 had been used for amplifying COI region of marine invertebrate phyla. The PCR reaction was carried out under the thermal conditions of 95°C (1 min), 95°C (10 sec), 62°C (30 sec), 72°C (60 sec), 16 cycles 52°C (40 sec), 72°C (1 min) with final extension at 72°C for (10 min). PCR products were visualized on 10% agarose gel (EZ-Vision® In-Gel Solution, USA) stained with ethidium bromide in gel documentation chamber (Model: Syngene InGenius^3). The flow UV-ray is kept on to watch the band in the connected computer by using GeneSys software. After getting our target gel band (313bp) under ingenious documentation system, we generated a library using refined PCR products. PCR samples with a single and clear visible band were purified with the PCR Purification Kit (TIANGEN- Universal DNA Purification Kit) for sequencing. The concentration of the purified DNA was estimated with the help of Qubit 3.0 fluorometer. After that next generation sequencing was conducted with standard protocol of MiSeq mini kit (Illumina Inc., San Diego, CA) by sequencing MiSeq analyzer at Macrogen Inc. (Korea). After getting result, the nucleotide sequences for low-quality reads and chimeras were removed using the Mothur program at Aquatic bioresearch research laboratory. Subsequently, clustering was performed based on the Molecular Operational Taxonomic Units (MOTUs) at the 98% similarity level (Li *et al.*

2012; Blaxter *et al.* 2005; Machida *et al.* 2009). After searching/comparing the NCBI non-redundant database and MegaBLAST MOTUs with these produced MOTUs, the zooplankton species were confirmed (Zhang *et al*. 2000).

The primer sequences are in the 5′~3′ orientation-
mlCOIintF: GGWACWGGWTGAACWGTWTAYCCYCC (Leray *et al,* 2014)
jgHCO2198: TAIACYTCIGGRTGICCRAARAAYCA (Geller *et al,* 2014)

11 Results and Discussion

11.1. Results and Discussion on Study 1: inventory of coral associated fish based on DNA barcoding along with morphometrics

In this study, we conducted morphologic analysis to confirm fish species before sequencing analysis of 125 coral associated fish species in St Martin`s Island belonging to 11 orders, 51 families and another 6 species that could only be reliably identified to genus level. Maximum number of 102 species (82%) of fishes were recorded from order Perciformes in St. Martin's island, Bangladesh. The frequency of number of fish species into 9 orders is given at figure 10.

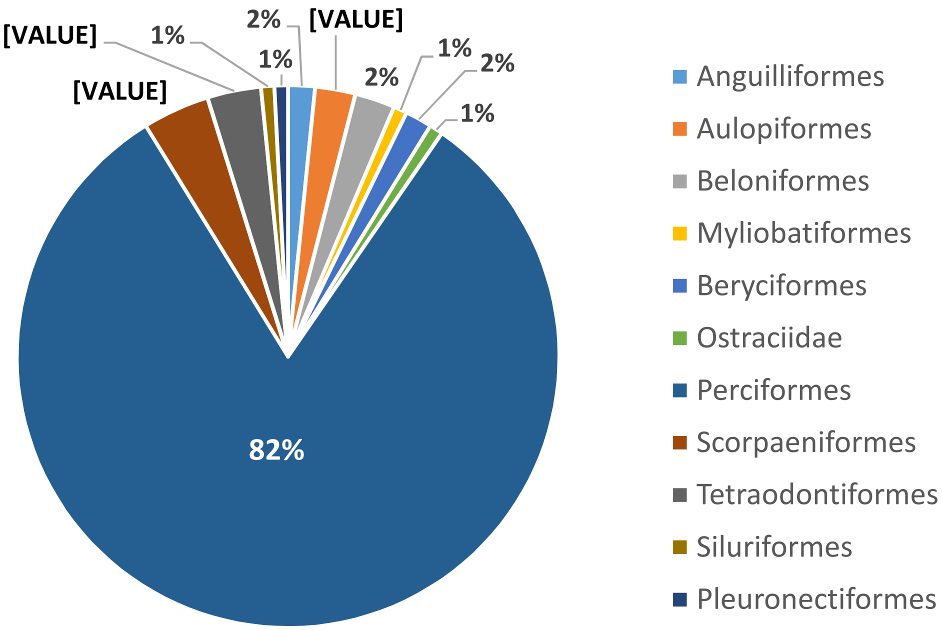


Figure 10. Family-wise distribution of listed fishes of the St. Martin's Island, Bangladesh

A total of 32 species had been recorded as new distributional records in Bangladesh water during the study, which were *Ostorhinchus cookie, Lepidamia kalosoma, Istiblennius dussumieri, Blenniella periophthalmus, Caranx heberi, Valenciennea muralis, Amblyeleotris downingi, Cryptocentrus cyanotaenia, Istigobius ornatus, Plectorhinchus macrospilus, Bodianus neilli, Pomadasys andamanensis, Pomadasys guoraca, Leiognathus daura, Leiognathus longispinis, Equulites leuciscus, Lethrinus crocineus, Lutjanus fulvus, Parupeneus indicus, Opistognathus variabilis, Parapercis clathrate, Filimanus similis, Chromis cinerascens, Chlorurus rhakoura, Chrysochir aureus, Plectropomus pessuliferus,Sphyraena putnamae, Saurida micropectoralis, Synodus variegatus, Apogonichthyoides pseudotaeniatus, Cryptocentrus maudae* and *Stegastes apicalis*. Among these species, the order Perciformes solely contributes 30 species (93%). However, three new record of fishes i.e.

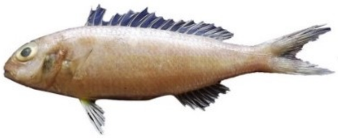
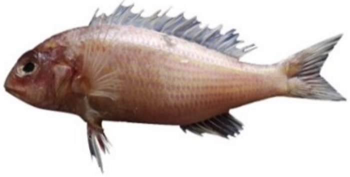
Apogonichthyoides pseudotaeniatus (Gon, 1986), *Cryptocentrus maudae* (Fowler, 1937) and *Stegastes apicalis* (De Vis, 1885) belonging to the family Apogonidae, Gobiidae and Pomacentridae respectively under the order of Perciformes were reported for first time from the Bay of Bengal as well as Bangladesh water. Detailed results of investigation and study including scientific name, English name, taxonomic classification, morphological characters and DNA barcode are presented as follows:

11.1.2 Pictures of the coral associated fishes collected from St. Martin's Island

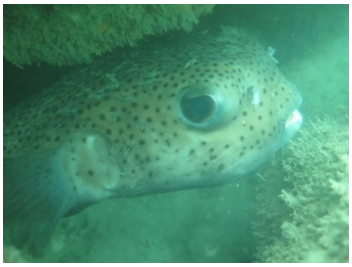
		
Neotrygon indica	*Ophisurus serpens*	*Gymnothorax favagineus*
		
Trachinocephalus myops	*Ablennes hians*	*Sargocentron rubrum*
		
Acanthurus xanthopterus	*Acanthurus mata*	*Caesio cuning*
		
Caranx sexfasciatus	*Alectis indica*	*Megalaspis cordyla*
		
Alepes kleinii	*Scomberoides tol*	*Scomberoides commersonnianus*

		
Scomberoides lysan	*Ulua mentalis*	*Gnathanodon speciosus*
		
Seriolina nigrofasciata	*Chaetodon decussatus*	*Heniochus acuminatus*
		
Chaetodon octofasciatus	*Drepane longimana*	*Echeneis naucrates*
		
Platax teira	*Pomadasys maculatus*	*Pomadasys argyreus*

		
Diagramma pictum	*Kyphosus cinerascens*	*Thalassoma lunare*
		
Halichoeres nigrescens	*Cheilinus chlorourus*	*Lactarius lactarius*
		
Lutjanus johnii	*Lutjanus russellii*	*Lutjanus lemniscatus*
		
Lutjanus lunulatus	*Lutjanus lutjanus*	*Lutjanus rivulatus*
		

Mene maculate	*Upeneus guttatus*	*Upeneus sulphureus*
		
Upeneus tragula	*Scolopsis vosmeri*	*Nemipterus peronii*
		
Nemipterus japonicas	*Pomacentrus tripunctatus*	*Chromis cinerascens*
		
Pomacanthus annularis	*Abudefduf sordidus*	*Abudefduf septemfasciatus*
		
Johnius amblycephalus	*Protonibea diacanthus*	*Otolithes ruber*
		
Otolithoides pama	*Chrysochir aureus*	*Pterotolithus maculatus*

		
Rastrelliger kanagurta	*Epinephelus erythrurus*	*Cephalopholis boenak*
		
Cephalopholis Formosa	*Cromileptes altivelis*	*Siganus javus*
		
Siganus canaliculatus	*Siganus vermiculatus*	*Sillago sihama*
		
Acanthopagrus berda	*Pampus argenteus*	*Terapon jarbua*
		
Terapon theraps	*Platycephalus indicus*	*Pterois volitans*

		
Pterois russelii	*Dactyloptena orientalis*	*Minous monodactylus*
		
Plotosus lineatus	*Tetrosomus gibbosus*	*Diodon hystrix*
		
Balistoides viridescens	*Chelonodontops patoca*	*Sufflamen fraenatum*
		
Hemiramphus far	*Chlorurus rhakoura*	*Heteromycteris oculus*

11.1.3 Pictures of the coral associated fishes recorded for the first time from St. Martin's Island and Bangladesh

		
Saurida micropectoralis	*Synodus variegates*	*Cheilopogon furcatus*
		
Myripristis hexagona	*Lepidamia kalosoma*	*Ostorhinchus cookie*
		
Apogonichthyoides pseudotaeniatus	*Istiblennius dussumieri*	*Blenniella periophthalmus*
		
Caranx heberi	*Cryptocentrus maudae*	*Valenciennea muralis*
		
Amblyeleotris downingi	*Istigobius ornatus*	*Cryptocentrus cyanotaenia*

		
Opistognathus variabilis	*Pomadasys guoraca*	*Pomadasys andamanensis*
		
Plectorhinchus macrospilus	*Bodianus neilli*	*Gazza dentex*
		
Leiognathus daura	*Leiognathus longispinis*	*Equulites leuciscus*
		
Lethrinus crocineus	*Lutjanus fulvus*	*Lutjanus madras*
		
Lutjanus erythropterus	*Parupeneus indicus*	*Parapercis clathrata*

		
Filimanus similis	*Stegastes apicalis*	*Epinephelus fuscoguttatus*
		
Plectropomus pessuliferus	*Sphyraena putnamae*	*Lobotes surinamensis*

11.2 Detailed description of the identified species from S. Martin's Island

Scientific name: *Neotrygon indica* **Müller & Henle, 1841**
English name: Bluespotted stingray
<u>Classification</u>
Class: Elasmobranchii
Order: Myliobatiformes
Family: Dasyatidae

Identification: Colour of body above dull-brown, white ventrally with numerous small black spots and blue black-edged ocelli. Tip of tail black, preceded by two obscure cross-bands. Disc kite-shaped, much broader than long. Spiracles greatly larger than eyes. Mouth undulated, with two buccal papillae on floor of mouth. Tail long, whip-like, exceeding length of disc, with upper and lower cutaneous folds, with 2 or 3 serrated spines. Back and head with small denticles in adult.

DNA Barcode: MK340668

MK340668 (mtDNA COI)
GGCACTGGCCTCAGTTTACTTATCCGAACAGAACTAAGCCAACCAGGCGCTTTACTGGGTGATGATCAAATTTATAATGTAATCGTCA
CTGCCCACGCCTTCGTAATAATCTTCTTTATAGTAATGCCAATTATAATTGGTGGATTTGGTAACTGGCTAGTGCCCCTGATAATTGG
GGCTCCGGACATAGCCTTTCCACGAATAAACAACATAAGTTTTTGGCTTCTGCCTCCCTCATTCCTATTACTACTAGCCTCAGCAGGA
GTAGAAGCCGGAGCCGGAACAGGTTGGACAGTTTATCCCCCGTTAGCTGGTAATCTAGCACATGCCGGAGCTTCTGTAGACCTTAC
AATCTTCTCTCTTCACCTAGCAGGTGTTTCCTCTATTCTGGCATCCATCAACTTTATCACAACAATTATTAATATAAAACCACCTGCAAT
CTCCCAGTATCAAACCCCATTATTCGTCTGGTCTATTCTTGTTACAACTGTACTTCTCCTGCTATCCCTACCAGTCCTGGCAGCTGGCAT
TACTATACTCCTCACAGACCGAAATCTTAATACAACTTTCTTTGACCCGGCTGGGGGAGGAGATCCCATTCTTTACCAACA

Scientific name: *Ophisurus serpens* **Linnaeus, 1758**
English name: Serpent eel
<u>Classification</u>
Class: Actinopterygii
Order: Anguilliformes
Family: Ophichthidae

Standard length: 715 mm
Fin formula: Dorsal to Anal fin ray-400, P1-16, P2-Absent
Identification: Colour uniform light or dark to various patterns of spots, stripes, or bars; usually darker dorsally than ventrally. Body snake-like or worm-like, more or less rounded in cross section. Throat swollen. Eye usually small and just above mouth. Snout pointed. Anterior nostril tubular, near tip of snout. Posterior nostril low on head, on lip, or opening inside of mouth. Mouth moderate to large, terminal or inferior. Teeth variable in form, from fang-like to conical to molariform to villiform.

DNA Barcode: MK340605

MK340605 (mtDNA COI)
GGCACTGCTCTTAGCCTATTAATTCGAGCAGAGCTTAGTCAACCCGGGGCCCTCCTTGGTGATGACCAAATTTATA
ATGTCATCGTCACAGCGCATGCCTTCGTAATAATTTTCTTTATAGTAATGCCAGTTATAATTGGGGGCTTTGGTAA
CTGGCTTGTTCCTATAATAATTGGAGCCCCAGACATAGCATTTCCACGAATAAATAATATAAGCTTTTGGCTTTTA
CCTCCGTCATTTCTCCTTCTACTCACCTCCTCAATAGTTGAAGCAGGCGCGGGAACAGGATGGACTGTATATCCTC
CACTTGCTGGAAACTTAGCCCATGCTGGAGCCTCAGTTGATCTAACAATCTTCTCCCTTCATCTTGCTGGAGTTTCA
TCTATTTTAGGTGCTATTAATTTTATCACTACAATTATTAATATAAAACCCCCAGCGATTAATCAATATCATACACC
ATTATTTGTATGGTCAGTCTTAGTTACTGCCGTACTTCTTCTTCTATCTTTACCAGTTCTTGCTGCTGGAATTACAAT
ATTACTTACAGATCGTAATCTTAACACTACATTCTTTGATCCTGCAGGTGGGGGGGACCCTATCCTTTATCAACA

Scientific name: *Gymnothorax favagineus* **Bloch & Schneider, 1801**
English name: Laced moray, Honeycomb moray
<u>Classification</u>
Class: Actinopterygii
Order: Anguilliformes
Family: Muraenidae

Identification: Colour grey to pale brown with black spots on the head, body and fins. The spots become relatively smaller as the fish grows. Small to very large eels. Body elongate. Dorsal profile of head above and behind eye raised. Eye well developed. Snout short to elongate. Mouth large, gape usually extending behind posterior margin of eye. Posterior nostril high on head, above or before eye, a simple pore or in a tube. Dorsal and anal fins variously developed, continuous with caudal fin around tail tip. Pectoral and pelvic fins absent.

Remarks: A rare sighting from coral habitat of St. martin’s island. This species has been recorded during the underwater scuba diving.

Scientific name: *Trachinocephalus myops* **Forster, 1801**
English name: Blunt-nose lizardfish
Classification
Class: Actinopterygii
Order: Aulopiformes
Family: Synodontidae

Standard length: 82 mm
Fin formula: D-11, P1-15, P2-9, A-11, and C-21
Identification: Body colour greenish-brown above, belly silvery, with alternating pale blue and yellow stripes; an oblique black spot at upper end of gill opening; fins pale yellow. Interorbital deeply concave; snout very short, equal to eye diameter; eye close to anterior end of upper jaw; anal fin base distinctly longer than dorsal fin base; pectoral fin rather small.

DNA Barcode: MK340735, MK340736

MK340735 (mtDNA COI)
GGCACGGCTTTAAGCCTTTTGATTCGAGCTGAGCTTAGCCAGCCCGGGGCCCTTCTAGGAGACGACCAGATTTA
CAATGTAATCGTCACGGCCCATGCCTTCGTAATAATCTTTTTTATAGTAATACCAATCATGATCGGGGGCTTCGG
CAACTGGCTTATTCCTTTAATGATCGGTGCCCCGGACATGGCTTTTCCCCGAATAAACAACATAAGCTTTTGGCT
TCTGCCTCCATCTTTTCTTCTTCTCCTGGCTTCGTCTGGCGTAGAAGCTGGCGCAGGCACCGGGTGGACAGTTTA
CCCGCCCTTGGCGGGTAACCTAGCCCATGCAGGTGCTTCCGTAGATCTAACTATTTTTTCCCTCCATCTAGCCGG
GATCTCATCTATTCTTGGCGCCATCAACTTTATCACAACCATCATTAACATAAAACCCCCTTCGATTACTCAGTAT
CAGACTCCTTTGTTTGTCTGGGCCGTCTTGATTACTGCCGTACTTCTTTTGCTTTCTCTTCCCGTCCTGGCGGCAG
GAATCACTATGCTTCTAACCGACCGCAACTTGAACACCACATTTTTTGACCCTGCAGGCGGGGGAGACCCTATC
TTGTACCAGCA

MK340736 (mtDNA COI)
GGCACGGCTTTAAGCCTTTTGATTCGAGCTGAGCTGAGCCAGCCCGGGGCCCTTCTAGGAGACGACCAGATTT
ACAATGTAATCGTCACGGCCCATGCCTTCGTAATAATCTTTTTTATAGTAATACCAATCATGATCGGGGGCTTCG
GCAACTGGCTTATTCCTTTAATGATCGGTGCCCCGGACATGGCTTTTCCCCGAATGAACAACATAAGCTTTTGG
CTTCTGCCTCCATCTTTTCTTCTTCTCCTGGCTTCGTCTGGCGTAGAAGCTGGCGCAGGTACCGGGTGGACAGTT
TACCCGCCCTTGGCGGGTAACCTAGCCCATGCAGGTGCTTCCGTAGATCTAACTATTTTTTCCCTCCATCTAGCC
GGGATCTCATCTATTCTTGGCGCCATCAACTTTATCACAACCATCATTAACATAAAACCCCCTTCGATTACTCAGT
ATCAGACTCCTTTGTTTGTCTGGGCCGTCTTGATTACTGCCGTACTTCTTTTGCTTTCTCTTCCCGTCCTGGCGGC
AGGAATCACTATGCTTCTAACCGACCGCAACTTGAACACCACATTTTTTGACCCTGCAGGCGGGGGAGACCCTA
TCTTGTACCAGCA

Scientific name: *Saurida micropectoralis* **Shindo & Yamada, 1972**
English name: Shortfin lizardfish
Classification
Class: Actinopterygii
Order: Aulopiformes
Family: Synodontidae

Standard length: 163 mm

Fin formula: D-13, P1-15, P2-6, A-10, C-32

Identification: Body elongated, cylindrical. Back and upper sides brown, lower sides and belly white. Nine to 10 faint blotches along the lateral line, sometimes with traces of very indistinct cross-bars on the back. Upper edges of pectoral and caudal fins occasionally with faint black dots. The upper portion of the inner side of the pectoral fins dark.

DNA Barcode: MK335881, MK335882, MK340700, MK340701

Remarks: New distributional record from Bangladesh.

MK335881 (mtDNA 16s)
TACCCAGAATGGAGGTCCCGCCTGCCCTGTGACTCAAGAGTTTAACGGCCGCGGTATCTTGACCGTGCGAAGG
TAGCGCAATCACTTGTCCTTTAAATGAGGACCTGTATGAATGGCATAACGAGGGCTCAACTGTCTCCCCTCCCT
AGTCAGTGAAATTGATCTCCCCGTGCAGAAGCGGGGATACACCCATAAGACGAGAAGACCCTATGGAGCTTT
AGTCATTAAGCAGCTTGCAACCAAACAAACCCCCCCAAGGGCTACAAACAACGCATTACTTCCTGCTGAAATGT
CTTCGGTTGGGGCGACCGTGGGATAAAAAAAACCTCCCATGAGGACCGGGAAAACCTTCCCAGAACCAAGGG
CTACCGCCCTAAGCAACAGAAACTCTGACCTAAATGATCCAGCCTAGCAGCTGATCAACGGACCGAGTTACCC
TAGGGATAACAGCGCAATCCCCTCCTAGAGCCCCCATCGACGAGAGGGTTTACGACCTCGATGTTGGATCAGG
ACATCCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGATCTGAGT

MK340701 (mtDNA COI)
GGCACTGCCCTAAGCCTATTAATTCGTGCCGAACTAAGCCAACCAGGAGCCCTCCTAGGGGAC
GACCAGATCTACAATGTAATTGTTACCGCACACGCCTTCGTAATAATTTTCTTTATAGTAATA
CCAATTATGATCGGTGGATTCGGAAACTGGCTCATTCCCCTCATGATCGGGGCCCCCGACATG
GCATTTCCCCGAATAAACAACATAAGCTTTTGGCTTCTCCCTCCCTCTTTCCTCCTCCTTCTT
GCCTCCTCTGGGGTAGAAGCCGGGGCCGGAACTGGATGGACAGTCTACCCACCCCTAGCAGGC
AACCTTGCCCACGCCGGGGCATCTGTCGACCTAACTATTTTTTCACTTCACCTTGCAGGGATT
TCCTCCATCCTGGGGGCCATTAACTTTATTACCACAATCATTAATATGAAACCTCCCGCTATT
TCACAATATCAGACCCCACTATTTGTATGGGCAGTCTTAATTACCGCCGTCCTCCTCCTCCTC
TCCCTCCCCGTCCTTGCAGCTGGAATTACTATACTCCTAACAGATCGAAACCTCAACACTACCT
TCTTCGACCCCGCGGGAGGGGGGGACCCAATCCTTTACCAACA

MK340700 (mtDNA COI)
GGCACTGCCCTAAGCCTATTAATTCGTGCCGAACTAAGCCAACCAGGAGCCCTCCTAGGGGACGACCAGATCT
ACAATGTAATTGTTACCGCACACGCCTTCGTAATAATTTTCTTTATAGTAATACCAATTATGATCGGTGGATTCG
GAAACTGGCTCATTCCCCTCATGATCGGGGCCCCCGACATGGCATTTCCCCGAATAAACAACATAAGCTTTTGG
CTTCTCCCTCCCTCTTTCCTCCTCCTTCTTGCCTCCTCTGGGGTAGAAGCCGGGGCCGGAACTGGATGGACAGT
CTACCCACCCCTAGCAGGCAACCTTGCCCACGCCGGGGCATCTGTCGACCTAACTATTTTTTCACTTCACCTTGC
AGGGATTTCCTCCATCCTGGGGGCCATTAACTTTATTACCACAATCATTAATATGAAACCTCCCGCTATTTCACA
ATATCAGACCCCACTATTTGTATGGGCGGTCTTAATTACCGCCGTCCTCCTCCTCCTCTCCCTCCCCGTCCTTGCA
GCTGGAATTACTATACTCCTAACAGATCGAAACCTCAACACTACCTTCTTCGACCCCGCGGGAGGGGGGGACC
CAATCCTTTACCAACA

MK335882 (mtDNA 16s)
CCGATTTAGGAGGTCCCGCCTGCCCTGTGACTCAAGAGTTTAACGGCCGCGGTATCTTGACCGTGCGAAGGTA
GCGCAATCACTTGTCCTTTAAATGAGGACCTGTATGAATGGCATAACGAGGGCTCAACTGTCTCCCCTCCCTAG
TCAGTGAAATTGATCTCCCCGTGCAGAAGCGGGGATACACCCATAAGACGAGAAGACCCTATGGAGCTTTAGT
CATTAAGCAGCCTGCAACCAAACAAACCCCCCCAAGGGCTACAAACAACGCATTACTTCCTGCTGAAATGTCTT
CGGTTGGGGCGACCGTGGGATAAAAAAAACCTCCCATGAGGACCGGGAAAACCTTCCCAGAACCAAGGGCTA
CCGCCCTAAGCAACAGAAACTCTGACCTAAATGATCCAGCCTAGCAGCTGATCAACGGACCGAGTTACCCTAG
GGATAACAGCGCAATCCCCTCCTAGAGCCCCCATCGACGAGAGGGTTTACGACCTCGATGTTGGATCAGGACA
TCCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGATCTGAGTTCCAGAAC

Scientific name: *Synodus variegates* **Lacepède, 1803**
English name: Variegated lizardfish
<u>Classification</u>
Class: Actinopterygii
Order: Aulopiformes
Family: Synodontidae

Standard length: 163 mm

Fin formula: D-12, P1-12, P2-8, A-8, C-20-24

Identification: Colour of body brown to red markings dorsally on body, silvery white ventrally; a longitudinal series of reddish blotches along lateral midline. Body sub-cylindrical, moderately elongate. Teeth on jaws not exposed when mouth closed; palatine teeth arranged in a single band on each side of roof of mouth. Nasal flap on anterior nostril short and triangular; cheek fully scaled posteriorly. Outermost ray of pelvic fin distinctly shorter than innermost ray.

DNA Barcode: MK335889, MK340725

Remarks: New distributional record from Bangladesh.

MK335889 (mtDNA 16s)

AGGTCCCGCCTGCCCTGTGACTAAATGTTTAACGGCCGCGGTATCTTGACCGTGCGAAGGTAGCGCAATCACTTGT
CCTTTAAATGGGGACCTGTATGAATGGCACAACGAGGGCTTAACTGTCTCCCCCCTCCTGTCAGTGAAACTGATCTC
CCCGTGAAGAAGCGGGGATTCCACTACCAGACGAGAAGACCCTATGGAGCTTAAAACAAAAGAGGGCCTATATAA
ACCAAGGGCAGATAAACACAGCAGTTGTTTAGTTCCCTCCGTAGTTTTTGGTTGGGGCGACCGTGGAGAAACAAAA
AACCCCCATGCAGAACAGGATTACTAGAACCTAAACCCAGAGCCACAGCTCTAAGTATCAAAATATTTGACAGACG
ATCCGGCCCCCGGCCGATCAACGGACCTAGTTACCCTAGGGATAACAGCGCAATCTCCTCCCAGAGCCCATATCGA
CGAGGGGGTTTACGACCTCGATGTTGGATCAGGACATCCAAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAA
CGATTAAAGTCCTACGTGAT

MK340725 (mtDNA COI)

GGCACGGCCCTCAGCCTTTTAATTCGCGCGGAACTAAGCCAGCCCGGGGCTCTTTTAGGCGATGATCAAATTTACAA
CGTAATTGTTACAGCCCACGCATTTGTAATGATTTTTTTTATAGTAATACCTATTATGATTGGGGGGTTCGGAAACTG
GCTTATTCCTTTGATAATTGGCGCCCCGGACATGGCTTTTCCCCGAATAAATAATATAAGTTTCTGGCTACTTCCGCC
ATCATTCCTTTTACTTTTAGCATCTTCTGGTGTTGAAGCTGGTGCGGGGACTGGTTGGACTGTCTACCCCCCCTTAGC
AGGAAACCTGGCCCACGCCGGGGCTTCAGTAGACCTGACAATTTTTTCCTTGCACTTGGCAGGCATTTCTTCTATCTT
AGGAGCAATCAATTTTATTACAACTATTATCAACATAAAGCCCCCTTCAATTTCACAATACCAGACCCCGCTTTTCGT
ATGGGCTGTTCTAATTACAGCTGTCCTTCTTCTTTTATCTTTGCCCGTACTGGCAGCCGGAATTACAATACTTCTGACT
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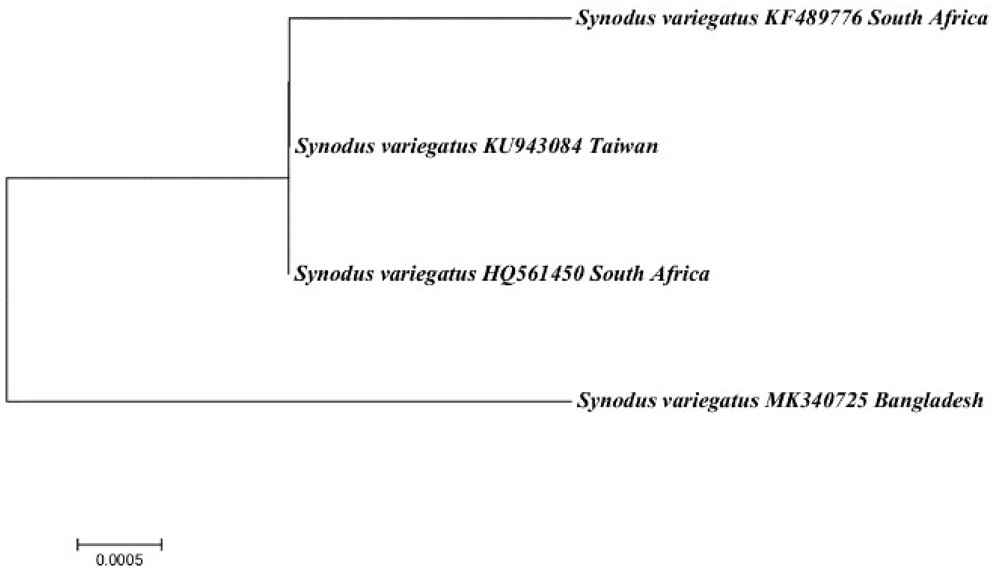

Figure 11: Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene with other sequences rerported from different countries. Bootstrap support of >70% are used with 1000 replications.

Scientific name: *Cheilopogon furcatus* **Mitchill, 1815**
English name: Spotfin flyingfish
Classification
Class: Actinopterygii
Order: Beloniformes
Family: Exocoetidae

Standard length: 222 mm
Fin formula: D-13, P1-15, P2-6, A-10,C-32
Identification: Colour of back iridescent blue. Belly silvery, Dorsal fin lightly or not pigmented: pectoral fins relatively dark snout with metalic margin. The central portion crossed by a pale curved stripe: tail dusky. Body elongate, thick, somewhat flattened ventrally. Teeth in jaws conical. Pectoral fins strikingly long, reach to or near end of dorsal fin. Pelvic fins large, reaching well beyond anal-fin origin. Scales are large.
DNA Barcode: MK335846, MK335847, MK340601, MK340602
Remarks: New distributional record from Bangladesh.

MK335846 (mtDNA 16s)
AGGTCCCGCCTGCCCTGTGACAAAAAGTTTAACGGCCGCGGTATCTTGACCGTGCGAAGGTAGCGCAATCA
CTTGTTTCTTAAATGGAGACCTGTATGAATGGCATAACGAGGGCCAACCTGTCTCCTTCTCCCAGTCAATGA
AATTGATCTCCCCGTGCAGAAGCGGGGATAAGCACATAAGACGAGAAGACCCTTTGGAGCTTTAGACTGCA
AGCAGACCATGCTAATTAGACCTGATTAAAGGAACTAAGCCAATTGGACATCTGCCCTAATGTCTTCGGTTG
GGGCGACCACGGGGAAACACAAAACCCCCATGAGGAGCAGGAGAACTTTTCTCCCAGAACTAAGACCGAC
AGGTCTAAGTACCAGAAATTCTGACCAAAAGATCCGGCCAAGCCGATCAACGGACCAAGTTACCCTAGGGA
TAACAGCGCAATCCCCTTTTAGAGCCCATATCGACAAGGGGGTTTACGACCTCGATGTTGGATCAGGACAT
CCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGAT

MK340601 (mtDNA COI)

GGGACAGCCCTAAGCCTTCTTATTCGAGCAGAACTAAGCCAACCAGGCTCTCTTCTTGGAGACGACCAAATT
TATAACGTAATTGTTACAGCACATGCCTTTGTAATAATTTTCTTTATAGTAATGCCAATTATAATTGGTGGCTT
TGGAAACTGGCTCGTACCCCTTATGATCGGAGCCCCCGACATGGCATTCCCTCGAATGAATAATATGAGCTT
TTGGCTTCTTCCACCCTCCTTCCTTCTACTCCTAGCCTCTTCAGGAGTCGAAGCTGGGGCCGGGACAGGATG
GACAGTGTACCCCCCTCTAGCAGGAAACCTAGCCCACGCTGGAGCATCTGTTGACCTAACAATTTTTTCACT
CCATCTAGCAGGAATTTCATCAATTCTCGGGGCTATTAACTTTATTACAACAATTATTAATATAAAACCTCCT
GCAATTTCACAGTACCAAACCCCACTTTTCGTATGGGCAGTTCTTATTACAGCAGTTCTTCTGCTTCTCTCTCT
TCCCGTTCTTGCAGCAGGAATTACTATACTTCTTACAGACCGAAATTTAAACACAACATTCTTTGACCCTGCC
GGAGGAGGTGACCCAATTCTTTACCAACA

MK340602 (mtDNA COI)

GGGACAGCCCTAAGCCTTCTTATTCGAGCAGAATTAAGCCAACCAGGCTCTCTTCTTGGAGACGACCAAATT
TATAACGTAATTGTTACAGCACATGCCTTTGTAATAATTTTCTTTATAGTAATGCCAATTATAATTGGTGGTTT
TGGAAACTGGCTCGTACCCCTTATGATCGGAGCCCCCGACATGGCATTCCCTCGAATGAACAATATGAGCTT
TTGGCTTCTTCCACCCTCCTTCCTTCTACTCCTAGCCTCTTCAGGAGTCGAAGCTGGGGCCGGGACAGGATG
GACAGTGTACCCCCCTCTAGCAGGAAACCTAGCCCACGCTGGAGCATCTGTTGACCTAACAATTTTTTCACT
CCATCTAGCAGGAATTTCATCAATTCTCGGGGCTATTAACTTTATTACAACAATTATTAATATAAAACCTCCT
GCAATTTCACAGTACCAAACCCCACTTTTCGTATGGGCAGTTCTTATTACAGCAGTTCTTCTGCTTCTCTCTCT
TCCCGTTCTTGCAGCAGGAATTACTATACTTCTTACAGACCGAAATTTAAACACAACATTCTTTGACCCTGCC
GGAGGAGGTGACCCAATTCTTTACCAACA

MK335847 (mtDNA 16s)

AGGTCCCGCCTGCCCTGTGACAAAAAGTTTAACGGCCGCGGTATCTTGACCGTGCGAAGGTAGCGCAATCA
CTTGTTTCTTAAATGGAGACCTGTATGAATGGCATAACGAGGGCCAACCTGTCTCCTTCTCCCAGTCAATGA
AATTGATCTCCCCGTGCAGAAGCGGGGATAAGCACATAAGACGAGAAGACCCTTTGGAGCTTTAGACTGCA
AGCAGACCATGCTAATTAGACCTGATCAAAGGAACTAAGCCAATTGGACATCTGCCCTAATGTCTTCGGTTG
GGGCGACCACGGGGAAACACAAAACCCCCATGAGGAGCAGGAGAACTTTTCTCCCAGAACTAAGACCGAC
AGGTCTAAGTACCAGAAATTCTGACCAAAAGATCCGGCCAAGCCGATCAACGGACCAAGTTACCCTAGGGA
TAACAGCGCAATCCCCTTTTAGAGCCCATATCGACAAGGGGGTTTACGACCTCGATGTTGGATCAGGACAT
CCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGAT

Scientific name: *Ablennes hians* **Valenciennes, 1846**
English name: Flat needlefish
<u>Classification</u>
Class: Actinopterygii
Order: Beloniformes
Family: Belonidae

Standard length: 676 mm
Fin formula: D-25, P1-13, P2-6, A-27, C-20-24
Identification: Body colour dark bluish above, silvery white below; 12 black bars or vertically elongated blotches on sides. Body strongly compressed; elongate jaws form a relatively short beak, with numerous needle-like teeth; fins without spines; dorsal and anal fins with long concave front lobes; dorsal fin with large, dark rear lobe; pectorals concave; tail base compressed, without a keel; tail fin strongly concave.

DNA Barcode: MK340570, MK340571

MK340570 (mtDNA COI)
GGCACTGCCTTAAGCCTCCTTATTCGAGCGGAACTAAGCCAACCTGGCTCCCTTTTAGGTGATGATCAAATTTA
TAATGTTATCGTCACAGCACATGCTTTTGTAATAATTTTCTTTATAGTAATACCAATTATAATTGGAGGCTTTGG
AAACTGGTTGGTACCACTAATAATCGGAGCCCCTGATATAGCATTCCCCCGAATAAATAACATAAGCTTCTGG
CTCTTGCCCCCCTCATTTCTTCTCCTTTTGGCTTCATCTGGAGTCGAAGCAGGTGCAGGAACCGGGTGGACTGT
TTACCCTCCTTTAGCCGGAAATCTAGCTCATGCTGGAGCATCCGTAGACCTAACAATTTTTTCTTTACATTTAGC
AGGTATTTCATCAATCCTTGGGGCTATTAACTTTATCACCACAATTATTAATATGAAACCCCCTGCAATCTCACA
ATACCAAACCCCTCTCTTCGTATGGGCCGTTTTAATTACTGCCGTCCTTCTTCTCCTTTCCCTCCCTGTTTTAGCT
GCTGGCATTACTATGCTCTTAACAGATCGAAATTTAAACACCACCTTCTTTGACCCTGCTGGAGGCGGAGATC
CCATCCTTTACCAACA

MK340571 (mtDNA COI)

GGCACTGCCTTAAGCCTCCTTATTCGAGCGGAACTAAGCCAACCTGGCTCCCTTTTAGGTGATGATCAAATTTA
TAATGTTATCGTCACAGCACATGCTTTTGTAATAATTTTCTTTATAGTAATACCAATTATAATTGGAGGCTTTGG
AAACTGGTTGGTACCACTAATAATCGGAGCCCCTGATATAGCATTCCCCCGAATAAATAACATAAGCTTCTGG
CTCTTGCCCCCCTCATTTCTTCTCCTTTTGGCTTCATCTGGAGTCGAAGCAGGTGCAGGAACCGGGTGGACTGT
TTACCCTCCTTTAGCCGGAAATCTAGCTCATGCTGGAGCATCCGTAGACCTAACAATTTTTTCTTTACATTTAGC
AGGTATTTCATCAATCCTTGGGGCTATTAACTTTATCACCACAATTATTAATATGAAACCCCCTGCAATCTCACA
ATACCAAACCCCTCTCTTCGTATGGGCCGTTTTAATTACTGCCGTCCTTCTTCTCCTTTCCCTCCCTGTTTTAGCT
GCTGGCATTACTATGCTCTTAACAGATCGAAATTTAAACACCACCTTCTTTGACCCTGCTGGAGGCGGAGATC
CCATCCTTTACCAACA

Scientific name: *Sargocentron rubrum* **Forsskål, 1775**
English name: Redcoat
Classification
Class: Actinopterygii
    Order: Beryciformes
        Family: Holocentridae

Standard length: 124 mm
Fin formula: D-XI/13, P1-14, P2-I/7, A-IV/9, C-V+IV/19-20
Identification: Colour of body brownish red and silvery white stripes of about equal width; a triangular streak of brownish red on cheek from eye to corner of preopercle; spinous dorsal fin red with white-tipped spines and a large quadrangular whitish blotch on each membrane; an elongate brown spot beneath soft portion of dorsal fin and a roundish blotch above base of soft portion of anal fin; upper and lower edges of caudal fin with red to brownish red band, with a very narrow bluish white margin. Body moderately deep; dorsal profile of head convex; snout short and blunt; corner of preopercle with a sharp spine; nasal fossa without spinules.

DNA Barcode: MK340697, MK340698, MK340699

MK340699 (mtDNA COI)
GGAACGGCCCTTAGCCTTCTTATTCGAGCTGAACTTAGTCAACCCGGAGCCCTTCTGGGGGACGATCAAATTTA
TAATGTCATTGTTACAGCGCACGCGTTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGCTTTGG
GAACTGGCTAATCCCCCTAATAATCGGAGCTCCTGACATAGCATTCCCTCGAATAAATAACATAAGCTTTTGGC
TGCTACCTCCCTCATTCCTTCTTCTGCTAGCTTCTTCAGGAGTAGAAGCCGGTGCCGGAACAGGGTGGACAGTT
TACCCACCCCTTGCAGGTAATTTAGCCCACGCAGGGGCTTCTGTTGATCTTACTATTTTCTCACTCCATTTAGCC
GGTATTTCCTCAATCCTAGGGGCCATTAATTTTATTACAACTATCATTAATATGAAACCCCCTGCCATCTCCCAAT
ATCAAACCCCTCTTTTCGTATGGGCTGTCCTAATTACAGCTGTCCTTCTTCTCCTGTCCCTACCTGTACTTGCAGC
AGGTATTACTATGCTGCTAACAGACCGAAATCTAAACACAACATTCTTCGACCCAGCAGGAGGTGGAGACCCT
ATTCTATATCAACA

MK340698 (mtDNA COI)
GGAACGGCCCTTAGCCTTCTTATTCGAGCTGAACTTAGTCAACCCGGAGCCCTTCTGGGGGACGATCAAATTTA
TAATGTCATTGTTACAGCGCACGCGTTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGCTTTGG
GAACTGGCTAATCCCCCTAATAATCGGAGCTCCTGACATAGCATTCCCTCGAATAAATAACATAAGCTTTTGGC
TGCTACCTCCCTCATTCCTTCTTCTGCTAGCTTCTTCAGGAGTAGAAGCCGGTGCCGGAACAGGGTGGACAGTT
TACCCACCCCTTGCAGGTAATTTAGCCCACGCAGGGGCTTCTGTTGATCTTACTATTTTCTCACTCCATTTAGCC
GGTATTTCCTCAATCCTAGGGGCCATTAATTTTATTACAACTATCATTAATATGAAACCCCCTGCCATCTCCCAAT
ATCAGACCCCTCTTTTCGTATGGGCTGTCCTAATTACAGCTGTCCTTCTTCTCCTGTCCCTACCTGTACTTGCAGC
AGGTATTACTATGCTGCTAACAGACCGAAATCTAAACACAACATTCTTCGACCCAGCAGGAGGTGGAGACCCT
ATTCTATATCAACA

MK340697 (mtDNA COI)
GGAACGGCCCTTAGCCTTCTTATTCGAGCTGAACTTAGTCAACCCGGAGCCCTTCTGGGGGACGATCAAATTTA
TAATGTCATTGTTACAGCGCACGCGTTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGCTTTGG
GAACTGGCTAATCCCCCTAATAATCGGAGCTCCTGACATAGCATTCCCTCGAATAAATAACATAAGCTTTTGGC
TGCTACCTCCCTCATTCCTTCTTCTGCTAGCTTCTTCAGGAGTAGAAGCCGGTGCCGGAACAGGGTGGACAGTT
TACCCACCCCTTGCAGGTAATTTAGCCCACGCAGGGGCTTCTGTTGATCTTACTATTTTCTCACTCCATTTAGCC
GGTATTTCCTCAATCCTAGGGGCCATTAATTTTATTACAACTATCATTAATATGAAACCCCCTGCCATCTCCCAAT
ATCAGACCCCTCTTTTCGTATGGGCTGTCCTAATTACAGCTGTCCTTCTTCTCCTGTCCCTACCTGTACTTGCAGC
AGGTATTACTATGCTGCTAACAGACCGAAATCTAAACACAACATTCTTCGACCCAGCAGGAGGTGGAGACCCT
ATTCTATATCAACA

Scientific name: *Myripristis hexagona* **Lacepède, 1802**
English name: Doubletooth soldierfish
Classification
Class: Actinopterygii
Order: Beryciformes
Family: Holocentridae

Standard length: 144 mm
Fin formula: D-X+I/15, P1-16, P2-I/7, A-IV/14, C-III/21
Identification: Colour of scales of body silvery to white, the edges dark red to reddish brown; a board red band from upper end of gill opening to axil of pectoral fin, enclosing opercular membrane which is darker red or reddish brown; iris red, sometimes with a blackish blotch above and below pupil; spinous dorsal fin light red and whitish basally, broadly bright red distally; soft dorsal, anal, and caudal fins pale red, the distal part of the lobes of these fins more red than the proximal part. Body moderately deep; corner of preopercle without a sharp spine; lower jaw prominently projecting. Numerous small scales in ventral part of axil of pectoral fins.
DNA Barcode: MK340664, MK335869
Remarks: New distributional record from Bangladesh.

MK340664 (mtDNA COI)

GGCACCGCTCTAAGCCTTTTAATTCGGGCTGAACTGAGCCAACCCGGAGCTCTTCTGGGCGACGACCAGATT
TATAACGTAATCGTTACGGCACACGCATTTGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGCTT
CGGAAACTGGCTCATCCCTCTAATGATCGGCGCCCCTGACATGGCATTCCCCCGAATGAACAATATAAGCTTC
TGGCTACTCCCACCTTCCTTCCTACTCCTTCTGGCCTCCTCTGGGGTAGAAGCCGGGGCTGGAACAGGATGGA
CTGTTTACCCACCCCTAGCAGGAAACCTAGCCCACGCAGGAGCTTCCGTTGATCTAACCATCTTCTCACTTCAC
CTAGCAGGTATCTCCTCAATTCTAGGGGCCATCAACTTCATCACAACAATTATCAACATGAAACCTCCAGCTAT
CTCTCAGTACCAAACACCTCTGTTTGTCTGGGCTGTCCTAATTACAGCTGTCCTTCTTCTCCTATCCCTTCCGGT
TCTTGCTGCTGGCATTACTATGCTTCTAACCGACCGAAACCTAAACACTACCTTCTTCGACCCAGCTGGAGGT
GGAGATCCAATCCTTTATCAACA

MK335869 (mtDNA COI)

GGCACCGCTCTAAGCCTTTTAATTCGGGCTGAACTGAGCCAACCCGGAGCTCTTCTGGGCGACGACCAGATT
TATAACGTAATCGTTACGGCACACGCATTTGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGCTT
CGGAAACTGGCTCATCCCTCTAATGATCGGCGCCCCTGACATGGCATTCCCCCGAATGAACAATATAAGCTTC
TGGCTACTCCCACCTTCCTTCCTACTCCTTCTGGCCTCCTCTGGGGTAGAAGCCGGGGCTGGAACAGGATGGA
CTGTTTACCCACCCCTAGCAGGAAACCTAGCCCACGCAGGAGCTTCCGTTGATCTAACCATCTTCTCACTTCAC
CTAGCAGGTATCTCCTCAATTCTAGGGGCCATCAACTTCATCACAACAATTATCAACATGAAACCTCCAGCTAT
CTCTCAGTACCAAACACCTCTGTTTGTCTGGGCTGTCCTAATTACAGCTGTCCTTCTTCTCCTATCCCTTCCGGT
TCTTGCTGCTGGCATTACTATGCTTCTAACCGACCGAAACCTAAACACTACCTTCTTCGACCCAGCTGGAGGT
GGAGATCCAATCCTTTATCAACA

Scientific name: *Acanthurus xanthopterus* **Valenciennes, 1835**
English name: Yellowfin Surgeon Fish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Acanthuridae

Standard length: 245 mm
Fin formula: D-IX/26, P1-17, P2-I/5, A-III/25, C-20
Identification: Body colour purplish or blue grey with irregular dark grey lines; a dull yellow area behind and in front of eye and a lesser extension posterior to lower part of eye; outer 1/3 of pectoral fin yellow, extreme distal part hyaline; dorsal and anal fins yellowish grey basally, dull yellow distally; caudal fin base whitish; caudal fin purplish or bluish-grey, fin lunate and spine small. Body deep or more elongated. Teeth fixed, denticulate on all of margin, with expanded incurved tips. Caudal fin deeply emarginated to lunate. Caudal peduncle with 1 folding spine.

DNA Barcode: MK340579

MK340579 (mtDNA COI)
GGAACGGCTCTGAGCCTCCTAATCCGAGCAGAATTAAGCCAACCAGGCGCCCTCTTAGGGGATGACCAAATTTATA
ATGTAATTGTTACAGCACACGCGTTCGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGTGGGTTCGGAAACT
GGTTAATTCCACTAATGATTGGAGCCCCTGATATAGCATTCCCACGAATGAACAATATGAGTTTTTGGCTACTACCCC
CATCTTTCCTACTCTTACTTGCATCCTCTGCAGTAGAATCCGGTGCTGGTACTGGATGGACAGTCTACCCTCCTCTAGC
TGGTAACCTTGCACATGCAGGAGCATCCGTAGACCTAACTATTTTCTCCCTTCACCTCGCAGGAATTTCCTCAATTCTT
GGAGCTATTAATTTTATTACAACAATTATTAATATAAAACCTCCTGCTACTTCTCAATATCAAACCCCTTTATTTGTATG
GGCAGTATTAATTACTGCCGTCTTACTGCTTCTTTCACTTCCTGTTCTTGCTGCTGGTATTACAATATTA

Scientific name: *Acanthurus mata* **Cuvier, 1829**
English name: Elongate surgeonfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Acanthuridae

Standard length: 149 mm
Fin formula: D-IX/25, P1-19, P2-I/5, A-III/24, C-16-20
Identification: Color of body gray to brown with lengthwise blue lines on head and body; a small blackish spot at upper end of gill opening, preceded by a yellow band that continues in front of eye as a double band. Body deep. Teeth fixed, denticulate on all of margin, with expanded incurved tips. Caudal fin deeply emarginate. Caudal peduncle with 1 folding spine.

Scientific name: *Lepidamia kalosoma* **Bleeker, 1852**
English name: Pinstripe cardinalfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Apogonidae

Standard length: 89 mm
Fin formula: D1-VII, D2-I/9, P1-14, P2-I/5, A-II/8, C-18-22
Identification: Body brownish dorsally with small black spots; fins yellowish with dark spots. Body flabby; eyes large; head and body with long pointed spines; no downward pointed spine below eye; no barbels on chin. Pectoral fins broad. Caudal fin rounded.
DNA Barcode: MK340634
Remarks: New distributional record from Bangladesh.

MK340634 (mtDNA COI)
GGGACAGCCCTTAGCCTCCTCATCCGAGCAGAACTAAGTCAACCCGGAGCTCTTCTTGGCGATGACCAAATTTA
CAATGTGATTGTTACGGCACACGCATTTGTAATGATTTTCTTTATAGTAATGCCAATCATGATTGGAGGCTTCGG
GAACTGGCTGATCCCACTTATGATTGGGGCCCCCGACATAGCATTCCCTCGAATAAACAACATAAGCTTCTGGC
TCCTTCCCCCTTCATTCCTCCTTCTCCTCGCCTCCTCAGGCGTAGAAGCTGGAGCCGGAACCGGGTGGACCGTTT
ATCCCCCCCTCGCAGGCAACCTCGCCCACGCAGGGGCCTCAGTTGATTTAACAATTTTCTCCCTTCATCTGGCCG
GTATCTCATCAATTCTAGGTGCTATCAATTTTATCACCACAATCATTAATATGAAACCTCCAGCCATTACCCAATA
TCAAACCCCCCTATTTGTCTGGGCAGTCCTAATTACTGCTGTTCTTCTCCTACTCTCCCTCCCTGTTCTAGCCGCTG
GCATCACAATGCTGCTTACAGATCGAAATCTTAACACAACCTTCTTCGATCCTGCAGGAGGTGGAGATCCCATTC
TCTATCAACA

Scientific name: *Ostorhinchus cookie* **MacLeay, 1881**
English name: Cook's cardinalfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Apogonidae

Standard length: 63 mm
Fin formula: D1-VII, D2-I/9, P1-14, P2-I/5, A-II/8, C-18-20
Identification: Colour of head and body pale with six longitudinal dark brown stripes with various widths; 3rd stripe short and extends from dorsal margin of eye to, or slightly beyond, a vertical through origin of second dorsal fin; a dusky rounded spot at caudal-fin base; fins sub-translucent or a little tinged with red. Body oblong, moderately deep and compressed; lateral line well developed, extending posteriorly to caudal-fin base. Snout moderately pointed. Posterior margin of pre-opercle serrated. No enlarged caninoid teeth on jaws. Base of anal fin sub-equal to base of second dorsal fin in length; caudal fin emarginate.

DNA Barcode: MK340670, MK335872

Remarks: New distributional record from Bangladesh.

MK340670 (mtDNA COI)
GGGACTGCATTAAGTCTCCTTATTCGAGCCGAACTAAGTCAACCCGGAGCCCTTCTCGGCGACGACCAG
ATTTACAATGTTATTGTTACGGCACATGCCTTCGTAATAATTTTCTTTATAGTAATGCCAATTATAATCGG
AGGCTTTGGGAACTGGTTAATTCCCCTAATGATTGGTGCTCCTGACATGGCATTCCCCCGAATAAATAAC
ATAAGCTTCTGGCTTCTACCCCCCTCCTTCCTACTCCTCCTTGCTTCCTCTGGAGTTGAGGCCGGAGCCGG
TACAGGATGGACCGTATACCCCCCTCTTGCAGGCAACCTCGCCCATGCGGGAGCTTCTGTGGACCTGAC
AATTTTTTCCCTTCACTTGGCAGGTGTCTCATCAATTCTAGGAGCAATTAATTTTATTACCACTATTATTAA
CATAAAACCCCCTGCTATTACTCAGTATCAAACTCCCTTGTTTGTCTGGGCAGTACTAATTACTGCGGTCC
TTCTCCTTCTTTCCCTTCCAGTCTTAGCAGCCGGGATCACAATGCTTCTTACAGATCGTAATTTAAATACA
ACCTTCTTTGACCCAGCGGGGGGAGGGGACCCCATTCTTTACCAGCA

MK335872 (mtDNA 16s)

AGGTCCCGCCTGCCCAGTGACTATCTGTTCAACGGCCGCGGTACTCTGACCGTGCGAAGGTAGCGCAA
TCACTTGTCTCTTAAATGGGGACCTGTATGAATGGCATAACGAGGGCTAAACTGTCTCCTTTTTCAAGTC
AATGAAATTGATCTTCCCGTGCAGAAGCGGGAATACTAACATAAGACGAGAAGACCCTATGGAGCTTA
AGACACCAAAGCAGGGCATGTTAAAAATTCCCATATAAGGAGATGAACCTAGTGGCCGCTGCCCTACT
GTCTTTGGTTGGGGCGACCGCGGAGAAGAAAAAAACCCCCGTGTGGAACAGGGATAACCCCCCTTAA
ACCCAGAGTGACAACTCTAACAAACAGAACTTCTGACCAATTTAAGATCCGGCAAAGCCGATCAACGG
ACCGAGTTACCCTAGGGATAACAGCGCAATCCCCTTCTAGAGCCCATATCGACAAGGGGGTTTACGAC
CTCGATGTTGGATCAGGACATCCTATTGGCGCAGCCGCTACTAAGGGTTCGTTTGTTCAACGATTAAAG
TCCTACGTGAT

Scientific name: *Apogonichthyoides pseudotaeniatus* **Gon, 1986**
English name: Doublebar cardinalfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Apogonidae

Standard length: 64 mm
Fin formula: D1-VII, D2-I/9, P1-14, P2-I/5, A-II/8, C-16-22
Identification: Silver color with two distinct black vertical stripes from the dorsal fins down over the body, also on the pectoral fin.

Remarks: New distributional record from Bangladesh.

Scientific name: *Istiblennius dussumieri* **Valenciennes, 1836**
English name: Streaky rockskipper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Blenniidae

Standard length: 9 mm
Fin formula: D-XIII/21, P1-14, P2-I/4, A-II/23, C-12-14
Identification: Colour of body dusky gray with a series of 7 double, brownish orange bars; small dark spots scattered on body in females; outer part of median fins broadly dark in males. Body elongate. Nape lacking cirri. Supraorbital tentacle variable, with up to five branches on each side. Single blade-like occipital crest present in adult males. Nasal with short cirri. Canine teeth absent on dentary. Several caudal-fin rays branched. Lateral line ending below 4th to 10th dorsal spines.
DNA Barcode: MK340623, MK340624, MK335853, MK335854
Remarks: New distributional record from Bangladesh.

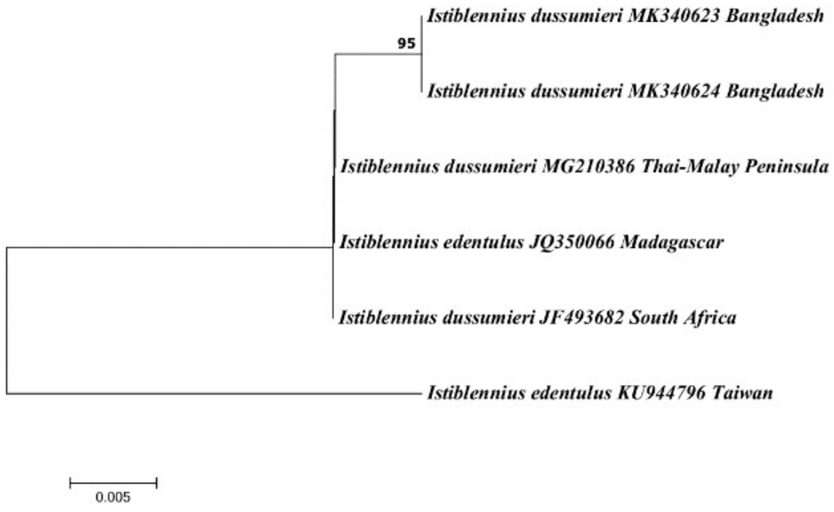

Figure 12: Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene with other sequences rerported from different countries. Bootstrap support of >70% is used with 1000 replications.

MK340623 (mtDNA COI)
GGTACAGCCCTTAGCCTCCTCATTCGGGCAGAACTAAGCCAGCCGGGAGCACTCCTTGGCGACGACCAAATCT
ATAACGTAATTGTTACGGCCCACGCCTTCGTAATAATCTTCTTTATAGTAATACCAATTATAATTGGCGGTTTCG
GCAACTGGCTTATCCCTCTTATAATTGGGGCCCCTGACATGGCCTTCCCACGAATAAACAACATGAGCTTCTGG
CTCCTCCCCCCTTCCTTTCTTCTCCTCCTTGCCTCTTCCGGGGTGGAAGCCGGAGCTGGGACAGGGTGGACAGT
GTATCCACCTTTATCTGGCAACCTAGCTCACGCAGGCGCATCAGTAGATCTAACCATTTTTTCACTTCATTTAGC
AGGTGTGTCTTCAATCCTGGGAGCTATTAACTTTATTACAACTATCATTAATATAAAACCCCCTGCAATCTCTCA
GTACCAGACGCCTTTATTTGTGTGGGCAGTATTAATTACAGCGGTTCTTCTTCTCCTCTCCCTCCCCGTTTTGGC
CGCCGGTATTACAATACTCCTTACAGACCGAAACCTAAACACAACATTCTTTGATCCTGCCGGCGGGGGTGAC
CCGATCCTTTACCAGCA

MK340624 (mtDNA COI)
GGTACAGCCCTTAGCCTCCTCATTCGGGCAGAACTAAGCCAGCCGGGAGCACTCCTTGGCGACGACCAAATCT
ATAACGTAATTGTTACGGCCCACGCCTTCGTAATAATCTTCTTTATAGTAATACCAATTATAATTGGCGGTTTCG
GCAACTGGCTTATCCCTCTTATAATTGGGGCCCCTGACATGGCCTTCCCACGAATAAACAACATGAGCTTCTGG
CTCCTCCCCCCTTCCTTTCTTCTCCTCCTTGCCTCTTCCGGGGTGGAAGCCGGAGCTGGGACAGGGTGGACAGT
GTATCCACCTTTATCTGGCAACCTAGCTCACGCAGGCGCATCAGTAGATCTAACCATTTTTTCACTTCATTTAGC
AGGTGTGTCTTCAATCCTGGGAGCTATTAACTTTATTACAACTATCATTAATATAAAACCCCCTGCAATCTCTCA
GTACCAGACGCCTTTATTTGTGTGGGCAGTATTAATTACAGCGGTTCTTCTTCTCCTCTCCCTCCCCGTTTTGGC
CGCCGGTATTACAATACTCCTTACAGACCGAAACCTAAACACAACATTCTTTGATCCTGCCGGCGGGGGTGAC
CCGATCCTTTACCAGCA

MK335853 (mtDNA 16s)
AGGTCCCGCCTGCCCTGTGACTAAAAGTTTAACGGCCGCGGTATTTTGACCGTGCAAAGGTAGCGCAATCACT
TGTCTCTTAAATGGAGACCTGTATGAATGGCATAACGAGGGCTTAACTGTCTCCCCCTCCTAGTCAGTGAAATT
GATTTTCCCGTGCAGAAGCGGGAATAACACCATAAGACGAGAAGACCCTGTGGAGCTTTAGACAATAAATAG
CACCTGTAAAGACTTGCCTACACATAAAAACAAAAGGTACCCCTATTTTGTATGTCTTCGGTTGGGGCGACCG
CGGGGGACACAAAACCCCCATGTGGAACAAGAACTTCCTCTTTAAATCCAGAGCTGCCGCTCTAAGAAGCAG
AATATCTGACCAAAATGACCCGGTAAATTTCCACCGATCAACGAAACTAGTTACCCCAGGGATAACAGCGCAA
TCCCCTCCCAGAGCCCATATCGACGAGGGGGTTTACGACCTCGATGTTGGATCAGGACATCCTAATGGTGCAG
TCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGAT

Scientific name: *Blenniella periophthalmus* **Valenciennes, 1836**
English name: Blue-dashed rockskipper
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Blenniidae

Identification: Body of males with 6-7 dusky bands with 1 or a pair of dark margined, pale, oblong spots on each band; dark spots on spinous dorsal, dusky lines on rayed dorsal. Females with spots on caudal peduncle; body sometimes with fine dark specks. Three colour-pattern types described for different localities.

Remarks: New distributional record from Bangladesh. This species has been recorded during the underwater scuba diving

Scientific name: *Caesio cuning* **Bloch, 1791**
English name: Redbelly yellowtail fusilier
Classification
Class: Actinopterygii
Order: Perciformes
Family: Caesionidae

Standard length: 109 mm
Fin formula: D-X/15, P1-19, P2-I/5, A-III/11, C-18-20
Identification: Colour of caudal fin, upper caudal peduncle and posterior portion of back yellow; upper body if not yellow, grayish blue; lower sides and belly white or pinkish; axil and upper base of pectoral fins black; dorsal fin yellow posteriorly and grayish blue anteriorly. Body fairly deep and compressed. A single postmaxillary process; small conical teeth in jaws. Scale rows above lateral line; dorsal and anal fins scaly.

DNA barcode: MK340588, MK340589, MK340590

MK340588 (mtDNA COI)

GGCACAGCATTAAGCCTACTTATTCGAGCGGAACTAAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGATTT
ACAATGTAATTGTAACAGCACATGCATTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATCGGAGGATTC
GGGAACTGGCTGATCCCGCTAATGATCGGAGCACCCGACATGGCATTCCCCCGAATGAATAACATGAGCTTTT
GGCTTCTCCCTCCATCATTCCTACTCTTACTCGCTTCCTCTGGAGTAGAGGCAGGGGCTGGAACTGGGTGGACA
GTGTACCCCCCGCTAGCAGGAAACCTCGCACACGCCGGAGCATCTGTTGACCTAACTATTTTCTCCCTCCACTT
GGCAGGTGTTTCCTCAATTCTAGGGGCTATCAACTTCATTACAACTATCATCAATATGAAACCTCCAGCCATCTC
CCAGTACCAAACACCACTATTCGTTTGGGCCGTTCTAATTACCGCTGTCCTACTTCTTCTTTCCCTACCAGTCCTG
GCTGCCGGAATTACAATGCTTCTTACAGACCGAAACCTAAATACAACCTTCTTCGACCCAGCCGGAGGGGGTG
ATCCCATCCTCTACCAGCA

MK340589 (mtDNA COI)
GGCACAGCATTAAGCCTACTTATTCGAGCGGAACTAAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGATTT
ACAATGTAATTGTAACAGCACATGCATTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATCGGAGGATTC
GGGAACTGGCTGATCCCGCTAATGATCGGAGCACCCGACATGGCATTCCCCCGAATGAATAACATGAGCTTTT
GGCTTCTCCCTCCATCATTCCTACTCTTACTCGCTTCCTCTGGAGTAGAGGCAGGGGCTGGAACTGGGTGGACA
GTGTACCCCCCGCTAGCAGGAAACCTCGCACACGCCGGAGCATCTGTTGACCTAACTATTTTCTCCCTCCACTT
GGCAGGTGTTTCCTCAATTCTAGGGGCTATCAACTTCATTACAACTATCATCAATATGAAACCTCCAGCCATCTC
CCAGTACCAAACACCACTATTCGTTTGGGCCGTTCTAATTACCGCTGTCCTACTTCTTCTTTCCCTACCAGTCCTG
GCTGCCGGAATTACAATGCTTCTTACAGACCGAAACCTAAATACAACCTTCTTCGACCCAGCCGGAGGGGGTG
ATCCCATCCTCTACCAGCA

MK340590 (mtDNA COI)
GGCACAGCATTAAGCCTACTTATTCGAGCGGAACTAAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGATT
TACAATGTAATTGTAACAGCACATGCATTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATCGGAGGATT
CGGGAACTGGCTGATCCCGCTAATGATCGGAGCACCCGACATGGCATTCCCCCGAATGAATAACATGAGCTT
TTGGCTTCTCCCTCCATCATTCCTACTCTTACTCGCTTCCTCTGGAGTAGAGGCAGGGGCTGGAACTGGGTGG
ACAGTGTACCCCCCGCTAGCAGGAAACCTCGCACACGCCGGAGCATCTGTTGACCTAACTATTTTCTCCCTCC
ACTTGGCAGGTGTTTCCTCAATTCTAGGGGCTATCAACTTCATTACAACCATCATCAATATGAAACCTCCAGCC
ATCTCCCAGTACCAAACACCACTATTCGTTTGGGCCGTTCTAATTACCGCTGTCCTACTTCTTCTTTCCCTACCA
GTCCTGGCTGCCGGAATTACAATGCTTCTTACAGACCGAAACCTAAATACAACCTTCTTCGACCCAGCCGGAG
GGGGTGATCCCATCCTCTACCAGCA

Scientific name: *Caranx sexfasciatus* **Quoy & Gaimard, 1825**
English name: Bigeye trevally
<u>Classification</u>
Class: Actinopterygii
    Order: Perciformes
        Family: Carangidae

Standard length: 117 mm
Fin formula: D1-VIII, D2-I/19, P1-20, P2-I/5, A-II+I/15, C-22
Identification: Colour of body blue green above, silvery below; a small, black spot on upper edge of opercle; tips of soft dorsal and anal fins white; caudal fin yellowish. Body oblong; upper and lower profiles, equal, nape, elevated; 32 to 34 strong scutes on lateral line; breast completely scaled.
DNA Barcode: MK340592, MK340593, MK340594, MK340595

MK340592 (mtDNA COI)
GGAACCGCTTTAAGCTTACTCATCCGAGCAGAACTTAGTCAACCTGGCGCCCTTTTAGGAGACGACCAAATTTA
TAACGTAATTGTTACGGCCCATGCCTTCGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGCTTCGG
AAACTGGCTTATCCCTTTAATGATCGGAGCCCCTGACATGGCATTTCCCCGAATAAATAATATGAGCTTCTGGCT
TCTCCCTCCTTCCTTCCTCCTACTTTTAGCCTCTTCAGGGGTAGAAGCTGGAGCTGGGACAGGTTGGACTGTATA
TCCCCCATTAGCTGGTAATCTTGCCCATGCCGGAGCATCAGTAGATCTAACTATTTTCTCCCTTCATCTAGCAGG
GGTTTCATCAATTCTGGGGGCTATTAACTTCATTACTACGATCATTAACATGAAACCGCCCGCAGTCTCAATATA
CCAAATCCCACTATTTGTTTGGGCCGTATTAATTACAGCTGTTCTTCTCCTTCTTTCCCTCCCAGTCTTAGCTGCTG
GAATTACAATACTTCTTACAGATCGAAACCTAAACACCGCCTTCTTCGACCCAGCAGGGGGAGGGGATCCAATT
CTTTATCAACA

MK340594(mtDNA COI)
GGAACCGCTTTAAGCTTACTCATCCGAGCAGAACTTAGTCAACCTGGCGCCCTTTTAGGAGACGACCAAATTTA
TAACGTAATTGTTACGGCCCATGCCTTCGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGCTTCG
GAAACTGGCTTATCCCTCTAATGATCGGAGCCCCTGACATGGCATTTCCCCGAATAAATAATATGAGCTTCTGG
CTTCTCCCTCCTTCCTTCCTCCTACTTTTAGCCTCTTCAGGGGTAGAAGCTGGAGCTGGGACAGGTTGGACTGT
ATACCCCCCATTAGCTGGTAATCTTGCCCATGCCGGAGCATCAGTAGATCTAACTATTTTCTCCCTTCATCTAGC
AGGGGTTTCATCAATTCTGGGGGCTATTAACTTCATTACTACGATCATTAACATGAAACCGCCCGCAGTCTCAA
TATACCAAATCCCACTATTTGTTTGGGCCGTATTAATTACAGCTGTTCTTCTCCTTCTTTCCCTCCCAGTCTTAGC
TGCTGGAATTACAATACTTCTTACAGATCGAAACCTAAACACCGCCTTCTTCGACCCAGCAGGGGGAGGGGAT
CCAATTCTTTATCAACA

MK340595(mtDNA COI)

GGAACCGCTTTAAGCTTACTCATCCGAGCAGAACTTAGTCAACCTGGCGCCCTTTTAGGAGACGACCAAATTT
ATAACGTAATTGTTACGGCCCATGCCTTCGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGCTTC
GGAAACTGGCTTATCCCTCTAATGATCGGAGCCCCTGACATGGCATTTCCCCGAATAAATAATATGAGCTTCTG
GCTTCTCCCTCCTTCCTTCCTCCTACTTTTAGCCTCTTCAGGGGTAGAAGCTGGAGCTGGGACAGGTTGGACTG
TATACCCCCCATTAGCTGGTAATCTTGCCCATGCCGGAGCATCAGTAGATCTAACTATTTTCTCCCTTCATCTAG
CAGGGGTTTCATCAATTCTGGGGGCTATTAACTTCATTACTACGATCATTAACATGAAACCGCCCGCAGTCTCA
ATATACCAAATCCCACTATTTGTTTGGGCCGTATTAATTACAGCTGTTCTTCTCCTTCTTTCCCTCCCAGTCTTAG
CTGCTGGAATTACAATACTTCTTACAGATCGAAACCTAAACACCGCCTTCTTCGACCCAGCAGGGGGAGGGGA
TCCAATTCTTTATCAACA

MK340593(mtDNA COI)

GGAACCGCTTTAAGCTTACTCATCCGAGCAGAACTTAGTCAACCTGGCGCCCTTTTAGGAGACGACCAAATTTA
TAACGTAATTGTTACGGCCCATGCCTTCGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGCTTCG
GAAACTGGCTTATCCCTCTAATGATCGGAGCCCCTGACATGGCATTTCCCCGAATAAATAATATGAGCTTCTGG
CTTCTCCCTCCTTCCTTCCTCCTACTTTTAGCCTCTTCAGGGGTAGAAGCTGGAGCTGGGACAGGTTGGACTGT
ATATCCCCCATTAGCTGGTAATCTTGCCCATGCCGGAGCATCAGTAGATCTAACTATTTTCTCCCTTCATCTAGC
AGGGGTTTCATCAATTCTGGGGGCTATTAACTTCATTACTACGATCATTAACATGAAACCGCCCGCAGTCTCAA
TATACCAAATCCCACTATTTGTTTGGGCCGTATTAATTACAGCTGTTCTTCTCCTTCTTTCCCTCCCAGTCTTAGC
TGCTGGAATTACAATACTTCTTACAGATCGAAACCTAAACACCGCCTTCTTCGACCCAGCAGGGGGAGGGGAT
CCAATTCTTTATCAACA

Scientific name: *Alectis indica* **Rüppell, 1830**
English name: Indian thread fish, Thread fin scades
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 236 mm
Fin formula: D-VI+I/19, P1-19, P2-I/5, A-II+I/18, C-20-22
Identification: Body colour silvery greenish or grayish dorsally, silvery white ventrally; dark bands on body in juveniles; anal fin yellowish. Body deeps, diamond shaped in juvenile, becoming more elongated with growth, strongly compressed; profile of forehead to nape somewhat angular. Anterior soft rays of dorsal and anal fins very long, filamentous in juveniles; pelvic fins elongated in juveniles. Body superficially naked, scales minute and embedded where present; straight part of lateral line with scutes (6-13) only posteriorly.

DNA Barcode: MK340580, MK340581

MK340580 (mtDNA COI)

GGCACAGCTTTAAGCTTACTCATTCGAGCGGAACTAAGCCAACCCGGCGCCCTTCTGGGGGACGACCAAATTTA
TAATGTTATTGTTACGGCCCACGCCTTCGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGTTTTGGA
AACTGGCTTATCCCTTTAATAATCGGGGCCCCCGATATAGCATTCCCCCGAATAAATAACATGAGCTTCTGGCTC
CTCCCCCCTTCTTTCCTCCTACTTTTAGCTTCTTCCGGGGTTGAAGCTGGGGCTGGGACCGGCTGGACAGTTTAC
CCTCCACTAGCCGGAAACCTCGCTCATGCTGGAGCATCAGTTGACTTAACCATTTTTTCTCTTCATCTAGCAGGA
GTTTCATCGATCCTAGGGGCTATCAATTTTATTACTACTATTATTAACATAAAACCTCCCGCAGTTTCAATGTACC
AAATTCCACTATTCGTCTGGGCTGTACTAATTACGGCCGTCCTTCTCCTCCTATCTCTTCCAGTCCTAGCCGCTGG

MK340581 (mtDNA COI)

GGCACAGCTTTAAGCTTACTCATTCGAGCGGAACTAAGCCAACCCGGCGCCCTTCTGGGGGACGACCAAATTTA
TAATGTTATTGTTACGGCCCACGCCTTCGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGTTTTGGA
AACTGGCTTATCCCTTTAATAATCGGGGCCCCCGATATAGCATTCCCCCGAATAAATAACATGAGCTTCTGGCTC
CTCCCCCCTTCTTTCCTCCTACTTTTAGCTTCTTCCGGGGTTGAAGCTGGGGCTGGGACCGGCTGGACAGTTTAC
CCTCCACTAGCCGGAAACCTCGCTCATGCTGGAGCATCAGTTGACTTAACCATTTTTTCTCTTCATCTAGCAGGA
GTTTCATCGATCCTAGGGGCTATCAATTTTATTACTACTATTATTAACATAAAACCTCCCGCAGTTTCAATGTACC
AAATTCCACTATTCGTCTGGGCTGTACTAATTACGGCCGTCCTTCTCCTCCTATCTCTTCCAGTCCTAGCCGCTGG
AATTACAATGCTCCTAACAGACCGAAACCTAAATACTGCCTTCTTTGACCCAGCAGGAGGCGGAGACCCTATCCT
TTACCAACA

Scientific name: *Megalaspis cordyla* **Linnaeus, 1758**
English name: Torpedo Scad
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Terapontidae

Standard length: 178 mm
Fin formula: D1-I+VI, D2-I/11+8(Finlets), P1-20, P2-I/5, A-II+I/9+7(Finlets), C-20-22
Identification: Colour of body dusky dorsally, silvery white ventrally; four dark brown horizontal stripes on body; spinous part of dorsal fin with black blotch dorsally on fin membranes between third and seventh spine; caudal fin with median rays pigmented; each caudal lobe with 1 transverse stripe, upper lobe with black tip. Body oblong, moderately compressed. Spinous part of dorsal fin strongly arched and deeply notched; penultimate spine about half length of ultimate spine. Caudal fin emarginated with rounded lobes.

DNA Barcode: MK340662

MK340662 (mtDNA COI)
GGGACAGCTTTAAGCCTCCTGATCCGAGCAGAACTTAGTCAACCTGGCGCCCTTTTAGGGGATGACCAAATTT
ATAACGTAATTGTTACGGCCCATGCCTTTGTAATAATTTTCTTTATAGTAATACCAATCATGATTGGAGGCTTCG
GAAACTGGCTTATCCCCTTAATGATCGGAGCCCCCGACATGGCATTCCCCCGAATAAATAATATGAGCTTCTGG
CTCCTCCCTCCTTCATTCCTTCTGCTTTTAGCCTCTTCAGGAGTAGAAGCTGGGGCTGGAACTGGTTGGACTGTA
TACCCTCCACTAGCTGGCAATCTCGCTCATGCCGGAGCATCAGTAGATCTAACTATCTTCTCCCTCCACTTAGCA
GGGGTCTCATCAATCCTTGGAGCTATTAATTTCATTACTACGATTATTAATATAAAACCGCCTGCAGTTTCAATA
TACCAAATTCCATTATTTGTCTGGGCCGTGCTGATTACAGCCGTCCTCCTCCTCTCTCTTCCAGTCTTAGCTG
CTGGGATCACGATACTTCTCACAGACCGAAACCTAAACACTGCCTTCTTTGATCCGGCAGGAGGTGGAGATCC
AATTCTTTATCAACA

Scientific name: *Alepes kleinii* **Bloch, 1793**
English name: Banded Scad
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 134 mm
Fin formula: D1-VIII, D2-I/23, P1-21, P2-I/5, A-II+I/20, C-20-22
Identification: Body silvery green dorsally, silvery white ventrally; a large black spot on upper margin of opercle; caudal fin yellowish especially in juvenile. Body oval, strongly compressed; ventral profile more convex than dorsal profile. Snout pointed; adipose eyelid well developed on posterior half of eye; upper jaw with a band of minute teeth; lower jaw with a single row of small conical teeth except 2 rows anteriorly. Straight part of lateral line entirely with scutes (35-45), longer than curved part.

DNA Barcode: MK340582, MK340583

MK340582 (mtDNA COI)

GGGACAGCTTTAAGCTTACTTATCCGAGCAGAACTTAGTCAACCTGGCGCCCTTTTAGGGGACGACCAAATTTATAACGTAA
TCGTTACGGCCCACGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGCTTCGGAAACTGGCTTATTCCC
CTAATGATCGGAGCCCCTGATATAGCATTCCCCCGAATAAATAATATGAGCTTCTGGCTTCTTCCCCCTTCTTTCCTTCTACTT
CTGGCTTCTTCAGGAGTTGAAGCCGGGGCTGGAACTGGTTGGACCGTTTACCCCCCTCTAGCCGGCAACTTAGCTCACGCTG
GGGCATCCGTAGATCTTACCATCTTCTCCTTGCATTTAGCCGGGGTCTCATCAATTCTAGGGGCTATTAACTTTATTACAACA
ATTATTAACATGAAACCTCCTGCGGTGTCAATATATCAAATTCCACTGTTCGTTTGGGCCGTCTTAATTACAGCCGTCCTTCTT
CTTCTATCCCTTCCGGTTTTAGCCGCTGGAATTACAATGCTCCTAACAGATCGAAACCTAAATACTGCCTTCTTCGACCCCGCT
GGAGGTGGAGATCCAATTCTTTATCAACA

MK340583 (mtDNA COI)

GGGACAGCTTTAAGCTTACTTATCCGAGCTGAACTTAGTCAACCTGGCGCCCTTTTAGGGGACGACCAAATTTATAACGTAA
TCGTTACGGCCCACGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGCTTCGGAAACTGGCTTATTCCC
CTAATGATCGGAGCCCCTGATATAGCATTCCCCCGAATAAATAATATGAGCTTCTGGCTTCTTCCCCCTTCTTTCCTTCTACTT
CTGGCTTCTTCAGGAGTTGAAGCCGGGGCTGGAACTGGTTGGACCGTTTACCCCCCTCTAGCCGGCAACTTAGCTCACGCTG
GGGCATCCGTAGATCTTACCATCTTCTCCTTGCATTTAGCCGGGGTCTCATCAATTCTAGGGGCTATTAACTTTATTACAACA
ATTATTAACATGAAACCTCCTGCGGTGTCAATATATCAAATTCCACTGTTCGTTTGGGCCGTCTTAATTACAGCCGTCCTTCTT
CTTCTATCCCTTCCGGTTTTAGCCGCTGGAATTACAATGCTCCTAACAGATCGAAACCTAAATACTGCCTTCTTCGACCCCGCT
GGAGGTGGAGATCCAATTCTTTATCAACA

Scientific name: *Scomberoides tol* **Cuvier, 1832**
English name: Needle scaled queenfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 362 mm
Fin formula: D-I+VII+I/20, P1-18, P2-I/5, A-II+I/18, C-27
Identification: Body colour silvery, the flanks with 4 to 8 vertically elongate blotches, most of them intersecting lateral line. Dorsal and anal fins uniformly pigmented. Dorsal profile of body more convex than ventral profile; cleft of mouth commences opposite to middle of eye; no scutes.

DNA Barcode: MK340711

MK340711 (mtDNA COI)
GGAACAGCCCTAAGCCTACTCATCCGAGCAGAACTAAGCCAACCCGGGGCCCTCCTCGGAGACGACCAAATCTATAA
CGTCATCGTTACAGCCCACGCCTTCGTAATAATCTTCTTTATAGTAATACCAATTATAATTGGGGGGTTCGGAAACTGG
CTCATTCCCCTAATAATTGGTGCCCCTGACATAGCTTTCCCTCGAATAAATAACATAAGCTTCTGGCTCCTTCCCCCTTC
CTTCCTTCTTCTCCTCGCCTCCTCAGGGGTTGAAGCCGGGGCAGGAACTGGTTGGACGGTCTACCCTCCTCTAGCAGG
GAACCTAGCCCATGCAGGAGCATCCGTAGACCTAACCATCTTCTCCCTCCACCTGGCCGGAATTTCCTCAATTCTAGG
GGCTATTAACTTCATCACAACTATTATTAACATAAAACCCCACGCCGTCTCCATGTACCAAATCCCTCTATTCGTCTGGG
CCGTCCTAATTACAGCAGTGCTTCTCCTTCTTTCTTTACCTGTTCTTGCCGCCGGCATTACAATACTTCTAACTGACCGA
AACCTAAACACCGCCTTCTTCGACCCTGCCGGAGGGGGTGACCCCATTCTCTACCAACA

Scientific name: *Scomberoides commersonnianus* **Lacepède, 1801**
English name: Talang queenfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 274 mm
Fin formula: D-I+VII+I/21, P1-18, P2-I/5, A-II+I/19, C-30
Identification: Body colour dusky green above and silvery below with 6 to 9 large oval blotches above on lateral line; 1st two blotches intersecting lateral line; colour of pectoral fin pale with dusky blotch; ventral fins white. Body compressed with blunt snout and depression over eyes; upper jaw extending well beyond eye; no scutes; posterior soft dorsal and anal with semi-detached finlets.

DNA Barcode: MK340708, MK340709

MK340709(mtDNA COI)
GGAACAGCCCTAAGCCTACTCATCCGAGCAGAACTAAGCCAACCCGGGGCCCTCCTCGGAGACGACCAAATCTATA
ACGTCATTGTTACGGCCCATGCCTTCGTAATAATCTTCTTTATAGTAATACCAATTATGATCGGAGGTTTCGGAAACT
GGCTCATTCCCCTAATAATTGGTGCTCCCGATATAGCTTTCCCTCGAATAAACAACATAAGCTTCTGGCTCCTACCCCC
TTCCTTTCTTCTCCTCCTTGCCTCCTCAGGAGTTGAAGCTGGAGCAGGAACTGGCTGGACAGTCTACCCTCCCCTAGC
AGGCAACCTAGCCCACGCAGGAGCATCCGTAGACCTAACCATCTTCTCCCTCCACCTAGCCGGAATTTCCTCAATTCT
AGGAGCCATCAACTTCATCACAACTATCATTAACATAAAACCCCATGCCGTTTCCATATACCAAATCCCCCTATTCGTT
TGGGCCGTCCTAATTACAGCAGTCCTTCTCCTTCTTTCTTTACCTGTTCTTGCCGCCGGCATTACAATACTTCTAACCGA
CCGAAACCTAAACACCGCCTTCTTCGACCCTGCTGGAGGAGGTGACCCTATTCTCTACCAGCA

MK340708 (mtDNA COI)

GGAACAGCCCTAAGCCTACTCATCCGAGCAGAACTAAGCCAACCCGGGGCCCTCCTCGGAGACGACCAAAT
CTATAACGTCATTGTTACGGCCCATGCCTTCGTAATAATCTTCTTTATAGTAATACCAATTATGATCGGAGGT
TTCGGAAACTGGCTCATTCCCCTAATAATTGGTGCTCCCGATATAGCTTTCCCTCGAATAAACAACATAAGCT
TCTGGCTCCTACCCCCTTCCTTTCTTCTCCTCCTTGCCTCCTCAGGAGTTGAAGCTGGAGCAGGAACTGGCTG
GACAGTCTACCCTCCCCTAGCAGGCAACCTAGCCCACGCAGGAGCATCCGTAGACCTAACCATCTTCTCCCT
CCACCTAGCCGGAATTTCCTCAATTCTAGGAGCCATCAATTTCATCACAACTATCATTAACATAAAACCCCAT
GCCGTTTCCATATACCAAATCCCCCTATTCGTTTGGGCCGTCCTAATTACAGCAGTCCTTCTCCTTCTTTCTTTA
CCTGTTCTTGCCGCCGGCATCACAATACTTCTAACCGACCGAAACCTAAACACCGCCTTCTTCGACCCTGCTG
GAGGAGGTGACCCCATTCTCTACCAGCA

Scientific name: *Scomberoides lysan* **Forsskål, 1775**
English name: Double spotted queenfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 92 mm
Fin formula: D-I+VII+I/20, P1-19, P2-I/5, A-II+I/18, C-20-22
Identification: Colour of body greenish gray dorsally, silvery white ventrally, with a double series of 6-8 dusky roundish blotches above and below lateral line in adults; distal part of dorsal fin lobe black; anal-fin lobe white in young, but often black in adult. Body elongate, strongly compressed. Hind tip of upper jaw reaching to or slightly beyond a vertical through posterior margin of. Body covered with small lanceolate scales; no scutes along lateral line.
DNA Barcode: MK340710

MK340710 (mtDNA COI)
GGAACAGCCCTAAGCCTACTCATCCGAGCAGAACTAAGCCAACCCGGGGCCCTCCTCGGAGACGACCAAATCTATAA
TGTTATTGTTACGGCCCACGCCTTCGTAATAATCTTCTTTATAGTAATGCCAATCATGATCGGAGGATTCGGAAACTG
GCTTATCCCCCTAATAATTGGTGCCCCCGACATAGCTTTCCCTCGAATAAATAACATAAGCTTCTGGCTCCTCCCCCCTT
CATTCCTCCTCCTCCTCGCCTCCTCAGGAGTCGAAGCTGGGGCGGGAACTGGATGGACAGTTTACCCTCCACTAGCAG
GAAACCTAGCCCACGCAGGAGCATCCGTAGACCTAACCATCTTCTCCCTCCATCTAGCCGGAATTTCCTCAATTCTAG
GGGCTATTAACTTTATCACAACTATCATTAACATGAAACCCCATGCCGTCTCCATGTATCAAATCCCCCTATTCGTATG
GGCCGTCCTCATCACAGCAGTACTTCTCCTTCTCTCCCTACCTGTTCTTGCTGCCGGCATTACAATGCTTCTAACCGATC
GAAACCTAAACACCGCTTTCTTTGACCCCGCTGGAGGAGGTGACCCTATTCTCTACCAACA

Scientific name: *Ulua mentalis* **Cuvier, 1833**
English name: Longrakered trevally
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 238 mm
Fin formula: D1-VII+I, D2-I/21, P1-20, P2-I/5, A-II+I/17, C-20-24
Identification: Colour of body olive green above and silvery white below; dusky patch present behind corner of mouth; colour of lower jaw white. First dorsal fin hyaline, other fins greenish with darker anterior margins. Body deep, oval and strongly compressed. Head profile strongly arched above eyes. Single row of minute teeth in jaws. Pectoral fins falcate, extending to middle of anal fin base. Breast naked. Lateral line moderately arched joins lateral line straight under 8th to 11th soft dorsal rays.

DNA Barcode: MK340738

MK340738(mtDNA COI)
GGCACAGCTTTAAGCCTGCTTATTCGAGCAGAACTAAGCCAACCTGGCGCCCTTTTAGGAGACGACCAAATTTATAAT
GTTATTGTTACGGCCCACGCCTTTGTAATAATTTTCTTTATAGTAATACCAATCATGATTGGAGGCTTCGGAAATTGGC
TAATTCCACTAATGATTGGAGCCCCTGACATAGCATTCCCCCGAATGAACAATATGAGCTTTTGGCTTCTTCCACCTTC
TTTCCTGCTACTTTTAGCCTCTTCGGGGGTTGAAGCTGGGGCCGGAACTGGTTGGACAGTTTACCCACCACTGGCTG
GAAACCTTGCTCACGCCGGAGCATCCGTTGATTTAACAATCTTTTCCCTTCACTTAGCAGGGGTCTCATCGATTCTAG
GAGCAATTAACTTTATTACCACCATTATCAACATGAAGCCTCCTGCAGTGTCAATATACCAAATCCCCCTGTTTGTTTG
GGCCGTGCTAATTACAGCTGTCCTTCTCCTTTTATCCCTGCCAGTCCTAGCCGCTGGAATTACAATACTCCTAACAGAC
CGAAACCTAAACACTGCCTTCTTTGACCCCGCAGGAGGTGGAGACCCCATTCTTTACCAGCA

Scientific name: *Caranx heberi* **Bennett, 1830**
English name: Blacktip trevally
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 265 mm
Fin formula: D1-VIII, D2-I/20, P1-21, P2-I/5, A-II+I/16, C-22-24
Identification: Colour of body yellow-greenish silvery-bronze dorsally, silvery white ventrally; no black opercular spot; all fins yellowish; upper lobe of caudal fin black distally in juveniles and young adults. Body oblong, compressed; dorsal profile strongly convex, ventral profile slightly convex. Adipose eyelid moderately developed on posterior half of eye. Breast usually naked ventrally with a small patch of prepelvic scales, rarely scaled completely; straight part of lateral line almost entirely with scutes.

DNA Barcode: MK340591, MK335844
Remarks: New distributional record from Bangladesh.

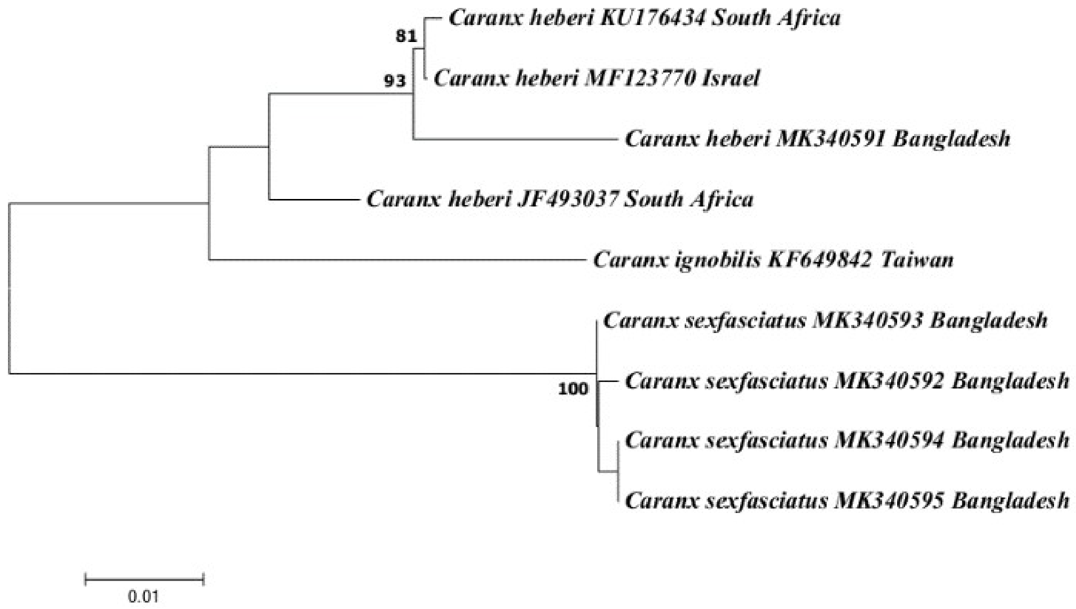

Figure 13: Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene with other sequences rerported from different countries. Bootstrap support of >70% are used with 1000 replications.

MK340591 (mtDNA COI)

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GGAACAGCTTTAAGCTTACTCATCCGAGCAGAACTTAGTCAACCTGGCGCTCTTTTAGGAGATGACCAAATTTATA
ACGTAATTGTTACCGCCCATGCCTTTGTAATAATTTTCTTTATAGTAATGCCAATCATGATCGGAGGCTTCGGAAAC
TGGCTTATTCCTCTAATGATCGGAGCCCCTGACATGGCATTCCCCCGAATGAATAATATGAGCTTCTGGCTTCTCCC
TCCCTCCTTCCTACTACTTCTAGCTTCTTCAGGGGTAGAAGCCGGGGCTGGAACAGGTTGGACTGTGTATCCTCCAT
TAGCTGGCAATCTCGCCCATGCCGGAGCATCAGTAGATCTAACTATTTTCTCCCTCCATCTAGCAGGAGTCTCATCA
ATCCTGGGAGCCATCAACTTTATCACTACAATTATTAATATGAAACCACCCGCAGTTTCAATGTACCAGATTCCACT
ATTTGTTTGGGCCGTACTAATCACGGCTGTCCTTCTCCTTCTCTCCCTTCCAGTCCTAGCTGCTGGAATTACAATACT
CCTCACAGATCGAAACCTAAACACCGCTTTCTTTGACCCGGCGGGGGGAGGGGATCCAATCCTTTACCAACA
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Scientific name: *Gnathanodon speciosus* **Forsskål, 1775**
English name: Golden trevally
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 155 mm
Fin formula: D1-I+VI+I, D2-I/9, P1-22, P2-I/5, A-II+I/16, C-20-22
Identification: Colour of body silvery yellow with 7-11 black bands, usually alternating broad and narrow in juveniles and young adults; the first band oblique through eye. All fins yellow, caudal fin tips black. Body oblong, somewhat deep. Both jaws without teeth in adults, a few feeble teeth on lower jaw in young; lips fleshy and remarkably thick. Breast completely scaled; straight part of lateral line with scutes (17-26) posteriorly.

DNA Barcode: MK340622

MK340622 (mtDNA COI)
GGAACAGCTTTAAGTCTACTTATCCGAGCAGAACTTAGTCAACCTGGCGCTCTTCTAGGAGACGACCAAATTTATA
ACGTAATTGTTACGGCTCATGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGCTTCGGAAAC
TGGCTTATCCCTCTAATAATCGGAGCCCCTGACATAGCATTCCCCCGAATAAATAATATGAGCTTTTGGCTTCTTCC
CCCTTCTTTCCTTCTACTCTTAGCCTCTTCAGGAGTTGAGGCCGGGGCCGGAACTGGTTGGACTGTCTATCCTCCCC
TAGCTGGTAACCTAGCCCACGCCGGAGCATCAGTAGATTTAACCATCTTTTCCCTCCACCTGGCAGGTGTCTCATCA
ATTCTAGGAGCCATTAATTTTATTACCACAATTATTAATATAAAACCACCCGCAGTTTCAATATACCAAATCCCATTA
TTCGTTTGGGCTGTACTAATTACAGCCGTTCTTCTTCTTCTATCTCTTCCAGTTCTAGCTGCTGGCATTACGATGCTA
TTAACGGACCGAAACCTAAACACCGCCTTCTTCGACCCTGCGGGGGGTGGAGATCCAATCCTTTATCAACA

Scientific name: *Seriolina nigrofasciata* **Rüppell, 1829**
English name: Golden trevally
Classification
Class: Actinopterygii
Order: Perciformes
Family: Carangidae

Standard length: 101 mm
Fin formula: D1-VII, D2-I/31, P1-20, P2-I/5, A-II/17, C-18-20
Identification: Colour of body dark brown, paler below, with 5-7 black oblique bands dorso-laterally; tips of dorsal and anal fin lobes whitish. Body elongate and slightly compressed. Hind tip of upper jaw broadly rounded, reaching to a vertical through posterior margin of eye; teeth on both jaws minute, forming a broad band. Gill rakers on first gill arch consisting mostly of rudiments. Caudal peduncle with fleshy lateral keel and dorsal and ventral grooves.

DNA Barcode: MK340712

MK340712 (mtDNA COI)
GGCACAGCCCTAAGTCTGCTTATCCGAGCAGAACTAAGTCAACCGGGGGCTCTCCTGGGAGATGATCAAATTTAT
AACGTAATTGTTACAGCGCATGCGTTTGTAATAATTTTCTTTATAGTAATGCCAATTATAATCGGAGGCTTTGGAAA
CTGGCTTATCCCCTTAATGATCGGGGCCCCTGACATAGCATTTCCTCGAATAAACAATATGAGCTTTTGGCTTCTTC
CCCCCTCATTCCTCCTGCTTTTAGCATCTTCAGGCGTCGAAGCCGGGGCTGGTACGGGTTGGACAGTTTACCCACC
CCTGGCCGGAAACCTCGCCCATGCTGGGGCATCCGTAGACTTAACTATCTTCTCCCTTCATTTAGCAGGGATTTCCT
CTATTCTAGGGGCTATTAACTTTATCACAACCATCATCAACATGAAACCCCATGCCGTCTCTATGTACCAGATCCCT
CTGTTCGTTTGGGCCGTCCTAATTACGGCTGTACTCTTACTTCTCTCTCTCCCGGTATTAGCAGCTGGTATTACGAT
GCTTCTTACAGACCGAAATTTAAACACTGCCTTCTTCGACCCAGCAGGAGGAGGAGACCCCATTCTCTACCAGCA

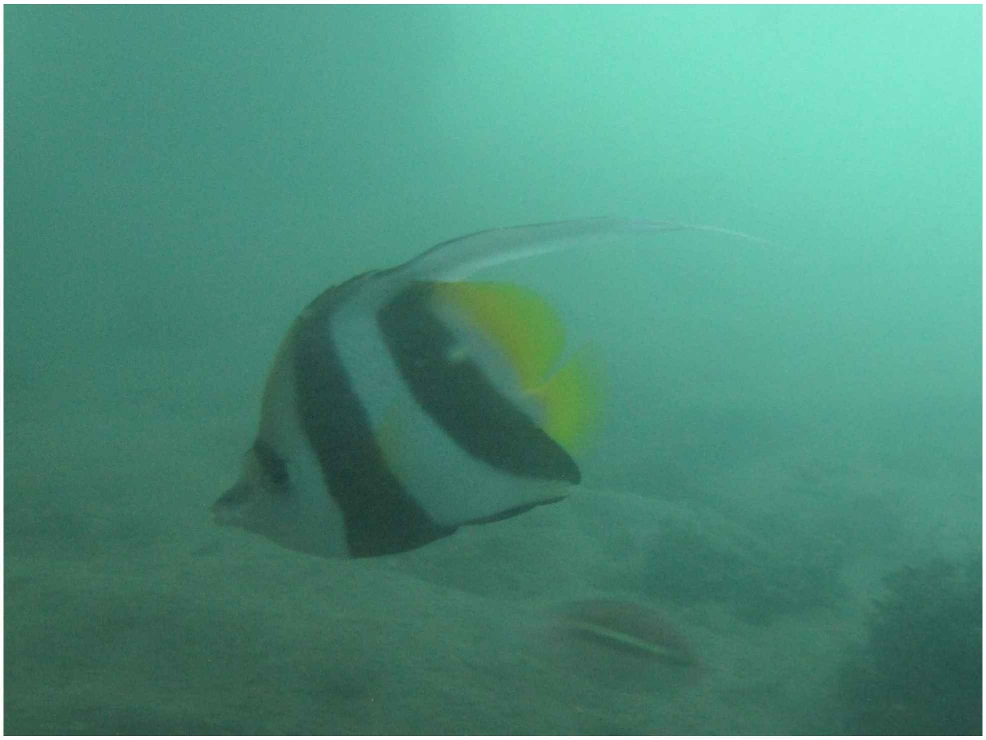
Scientific name: *Chaetodon decussatus* **Cuvier, 1829**
English name: Indian vagabond butterflyfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Chaetodontidae

Standard length: 97 mm
Fin formula: D-XIII/25, P1-15, P2-I/5, A-III/21, C-17-19
Identification: Colour of body ground mostly white, with 2 sets of diagonal blackish lines; entire posterior part of body, encompassing soft portions of dorsal and anal fin, blackish; head with a black bar from high on nape through eye; caudal fin yellow with a black bar in the middle, a clear posterior border, and a blackish submarginal band. Snout moderate to short; predorsal contour nearly straight. Lateral line incomplete. Caudal fin truncates to slightly round.

DNA Barcode: MK340600

MK340600 (mtDNA COI)
GGAACTGCCCTAAGTCTGCTCATTCGAGCAGAGCTCAGCCAACCAGGCTCCCTCCTGGGCGACGACCAGATCTATA
ATGTAATTGTTACAGCGCATGCATTCGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGGTTCGGAAACT
GGCTGATTCCTCTAATGATCGGAGCCCCAGATATGGCCTTCCCTCGGATGAACAATATGAGCTTTTGGCTCCTGCCC
CCCTCCTTTTTCCTACTCCTTGCCTCTTCTGGTGTAGAGTCCGGGGCTGGTACTGGATGGACGGTTTACCCCCCGCTA
GCTGGCAACCTAGCACACGCCGGAGCATCCGTTGATCTAACCATCTTCTCCCTCCACCTCGCAGGGGTTTCCTCCATC
CTTGGGGCAATTAATTTCATCACAACAATTCTCAACATGAAACCCCCTGCCATGTCTCAGTACCAAACCCCTCTTTTCG
TGTGGTCTGTTTTAATTACAGCCGTCCTGCTTCTCCTATCCCTACCTGTTCTTGCAGCCGGGATTACAATACTCCTTAC
AGATCGAAACCTCAATACAACCTTTTTTGACCCCGCAGGAGGAGGCGACCCTATTCTGTACCAACA

Scientific name: *Heniochus acuminatus* **Linnaeus, 1758**
English name: Pennant Coralfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Chaetodontidae



Identification: Colour white, with 2 broad, oblique, black bands on sides, the first continuous with black pelvic fins and the second from middle of spinous portion of dorsal fin to posterior half, but not extending anteriorly to longest soft ray of anal fin; soft dorsal and caudal fins yellow; snout and interorbital largely blackish. Body very deep; snout moderate, pointed. Lateral line complete. Fourth dorsal-fin spine greatly elongate, filamentous, often exceeding length of body. Caudal fin truncate to slightly round.

Remarks: This species has been recorded during the underwater scuba diving.

Scientific name: *Chaetodon octofasciatus* **Bloch, 1787**
English name: Eightband butterflyfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Chaetodontidae

Identification: Colour creamy yellow with eight black vertical stripes, including an eyeband, 5 central body stripes, and the other 2 stripes crossing dorsal and anal fins; pelvic fins yellow. Body rounded, almost circular; snout short, blunt; predorsal contour straight. Lateral line incomplete. Dorsal and anal fins strongly rounded, caudal fin truncate to slightly round.

Remarks: This species has been captured during the under water scuba diving

Scientific name: *Drepane longimana* **Bloch & Schneider, 1801**
English name: Sicklefish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Drepaneidae

Standard length: 73 mm
Fin formula: D-IX/21, P1-16, P2-I/5, A-III/18, C-16-18
Identification: Colour of head and body silvery with 4-10 vertical dark bars usually visible on dorsal part of body from head to caudal-fin base. Body very deep, strongly compressed. Snout profile straight or concave; mouth terminal and protrusible, forming a downward-pointing tube when protruded. Pectoral fins long, falciform, reaching caudal peduncle.

DNA Barcode: MK340610, MK340611

MK340610 (mtDNA COI)
GGCACGGCCCTGAGCCTCCTAATCCGAGCAGAACTGAGCCAACCCGGCGCCCTCCTTGGAGATGACCAAATCTACAATGTA
ATCGTTACCGCACACGCATTCGTAATAATTTTCTTTATAGTAATACCAATTATGATCGGAGGCTTTGGAAACTGGCTAATTCC
CTTAATAATCGGCGCCCCCGACATAGCATTCCCCCGTATAAATAACATAAGCTTCTGGCTACTTCCCCCCTCCTTCCTCCTTCT
CCTCGCCTCCTCTGGCGTAGAGGCCGGGGCAGGAACTGGATGGACGGTCTACCCCCCACTGGCCGGCAACTTAGCACACGC
CGGGGCATCCGTTGACCTGACAATCTTCTCCCTCCACCTAGCAGGTGTTTCCTCAATCCTAGGGGCTATCAACTTCATCACAA
CCATTATTAATATAAAACCACCCGCCATCTCCCAGTACCAAACACCCCTATTCGTGTGGGCAGTCCTAATTACCGCTGTCCTTC
TCCTCCTCTCGCTTCCGGTTCTGGCCGCCGGCATTACAATATTACTCACGGACCGAAATTTAAATACCACCTTCTTTGACCCG
GCAGGGGGAGGTGACCCAATCCTTTACCAACA

MK340611 (mtDNA COI)
GGCACGGCCCTGAGCCTCCTAATCCGAGCAGAACTGAGCCAACCCGGCGCCCTCCTTGGAGATGACCAAATCTACAATGTA
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CTTAATAATCGGCGCCCCCGACATAGCATTCCCCCGTATAAATAACATAAGCTTCTGGCTACTTCCCCCCTCCTTCCTCCTTCT
CCTCGCCTCCTCTGGCGTAGAGGCCGGGGCAGGAACTGGATGGACGGTCTACCCCCCACTGGCCGGCAACTTAGCACACGC
CGGGGCATCCGTTGACCTGACAATCTTCTCCCTCCACCTAGCAGGTGTTTCCTCAATCCTAGGGGCTATCAACTTCATCACAA
CCATTATTAATATAAAACCACCCGCCATCTCCCAGTACCAAACACCCCTATTCGTGTGGGCAGTCCTAATTACCGCTGTCCTTC
TCCTCCTCTCGCTTCCGGTTCTGGCCGCCGGCATTACAATATTACTCACGGACCGAAATTTAAATACCACCTTCTTTGACCCG
GCAGGGGGAGGTGACCCAATCCTTTACCAACA

Scientific name: *Echeneis naucrates***Linnaeus, 1758**
English name: Sharksucker
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Echeneidae

Standard length: 407 mm
Fin formula: D-35, P1-22, P2-I/5, A-35, C-12-20
Identification: Colour of body gray to blackish, with a white-edged black stripe from tip of lower jaw to caudal fin base. Upper and lower margins of fins whitish in juveniles. Pectoral fins blackish. Pelvic fins grayish to whitish. Body elongate. Sucking disc large. Caudal fin lanceolate in young, middle rays elongate and filamentous; almost truncate in adults, with upper and lower lobes longer than middle rays. Pectoral fins pointed.
DNA Barcode: MK340612

MK340612(mtDNA COI)
GGAACCGCACTAAGCTTACTCATTCGGGCAGAACTTAGTCAACCAGGCTCATTATTAGGTGATGATCAGATTTA
TAATGTTATCGTCACAGCACATGCCTTTGTAATAATTTTCTTTATAGTTATACCAGTAATAATTGGAGGTTTTGGT
AATTGGTTAGTACCTCTTATAATTGGTGCACCAGACATAGCCTTCCCTCGAATAAATAATATAAGCTTCTGGCTA
CTGCCTCCTTCCTTCCTCCTACTGCTAACATCTTCAGGAGTAGAAGCAGGGGCAGGAACTGGTTGGACTGTTTA
TCCTCCTTTAGCCGGAAACCTTGCCCATGCAGGAGCATCTGTTGACCTAACTATCTTTTCACTTCATCTGGCAGG
AATTTCCTCAATTCTTGGAGCAATTAATTTTATTACAACAATCATTAATATGAAACCTGCAGCTGCTTCTATATAT
CAACTCCCATTATTTGTATGGGCCGTATTAATTACAGCAGTTCTTCTTCTCCTATCCCTCCCTGTTCTAGCTGCTG
GGATTACAATACTACTAACAGACCGTAATCTTAATACCGCCTTCTTTGATCCTGCAGGAGGGGGAGATCCCATC
CTTTATCAACA

Scientific name: *Platax teira* **Forsskål, 1775**
English name: Spotbelly batfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Ephippidae

Standard length: 156 mm
Fin formula: D-V/35, P1-18, P2-I/5, A-III/26, C-20-22
Identification: Colour of body yellowish silver with 3 vertical black bands; pelvic fin yellow; a black blotch laterally on belly. Body orbicular, strongly compressed. Snout short, contour of frontal almost vertical in large adults. Five pores on each side of lower jaw. Tricuspid teeth on jaws; middle cusp slightly larger than lateral cusps; a few teeth on vomer but palatines toothless.

DNA Barcode: MK340675, MK340676

MK340675 (mtDNA COI)
GGCACAGCACTAAGCCTGCTTATCCGAGCAGAGCTAAACCAACCAGGCGCTCTCCTTGGAGACGACCAGATTTATA
ATGTAATTGTTACAGCACATGCGTTCGTAATAATTTTCTTTATAGTCATGCCAGTAATGATCGGGGGCTTTGGAAAT
TGGCTAATCCCACTAATAATCGGCGCCCCAGACATGGCTTTCCCTCGAATGAATAACATAAGCTTCTGGCTCCTTCCC
CCCTCATTTCTCCTGCTCCTCGCCTCTTCCGGAGTAGAAGCTGGTGCTGGAACTGGCTGGACTGTCTACCCCCCACTA
GCCAGCAACCTGGCACATGCAGGCGCATCTGTCGACCTGACTATTTTCTCCCTACACTTAGCAGGCATCTCCTCAATT
CTAGGGGCTATTAACTTTATCACAACAATTATTAACATAAAACCCCCTGCCATTTCCCAATATCAGACCCCTCTGTTC
GTTTGGGCCGTTCTAATTACGGCCGTCCTCTTGCTCCTTTCACTTCCCGTCCTTGCCGCGGGCATTACTATGCTACTTA
CAGATCGAAACCTAAACACCACCTTTTTCGACCCGGCAGGAGGAGGAGACCCAATTCTTTATCAACA

MK340676 (mtDNA COI)
GGCACAGCACTAAGCCTGCTTATCCGAGCAGAGCTAAACCAACCAGGCGCTCTCCTTGGAGACGACCAGATTT
ATAATGTAATTGTTACAGCACATGCGTTCGTAATAATTTTCTTTATAGTCATGCCAGTAATGATCGGGGGCTTT
GGAAATTGGCTAATCCCACTAATAATCGGCGCCCCAGACATGGCTTTCCCTCGAATGAATAACATAAGCTTCTG
GCTCCTTCCCCCCTCATTTCTCCTGCTCCTCGCCTCTTCCGGAGTAAAAGCTGGTGCTGGAACTGGCTGGACTG
TCTACCCCCCACTAGCCAGCAACCTGGCACATGCAGGCGCATCTGTCGACCTGACTATTTTCTCCCTACACTTA
GCAGGCATCTCCTCAATTCTAGGGGCTATTAACTTTATCACAACAATTATTAACATAAAACCCCCTGCCATTTCC
CAATATCAGACCCCTCTGTTCGTTTGGGCCGTTCTAATTACGGCCGTCCTCTTGCTCCTTTCACTTCCCGTCCTTG
CCGCGGGCATTACTATGCTACTTACAGATCGAAACCTAAACACCACCTTTTTCGACCCGGCAGGAGGAGGAGA
CCCAATTCTTTATCAACA

Scientific name: *Cryptocentrus maudae* Fowler**, 1937**
English name: Maude's shrimpgoby
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Gobiidae

Standard length: 137 mm
Fin formula: D1-VI, D2-I/11, P1- 18, P2-I/5, A-I/10, C-19
Identification: Colour of head and body blackish brown; anterodorsal part of eye, interorbital space, snout and anterior tip of lower jaw pale or pale brown; several pale or pale brown saddles on head and body, in addition to numerous minute pale spots; anal fin with 5-6 diagonal black lines. Body elongate, compressed. Head slightly compressed; jaws subequal, not reaching to a vertical through posterior margin of eye; gill opening reaching anteriorly around a vertical through posterior margin of preopercle. Pelvic fins united medially; frenum present. Scales minute, cycloid; head, breast and pectoralfin base naked. Sensory canals and pores present on head; distinct transverse sensory-papillae rows on cheek; a pair of short longitudinal sensory papillae rows just behind chin.

DNA Barcode: MK293942, MK293944
Remarks: New distributional record from Bangladesh.

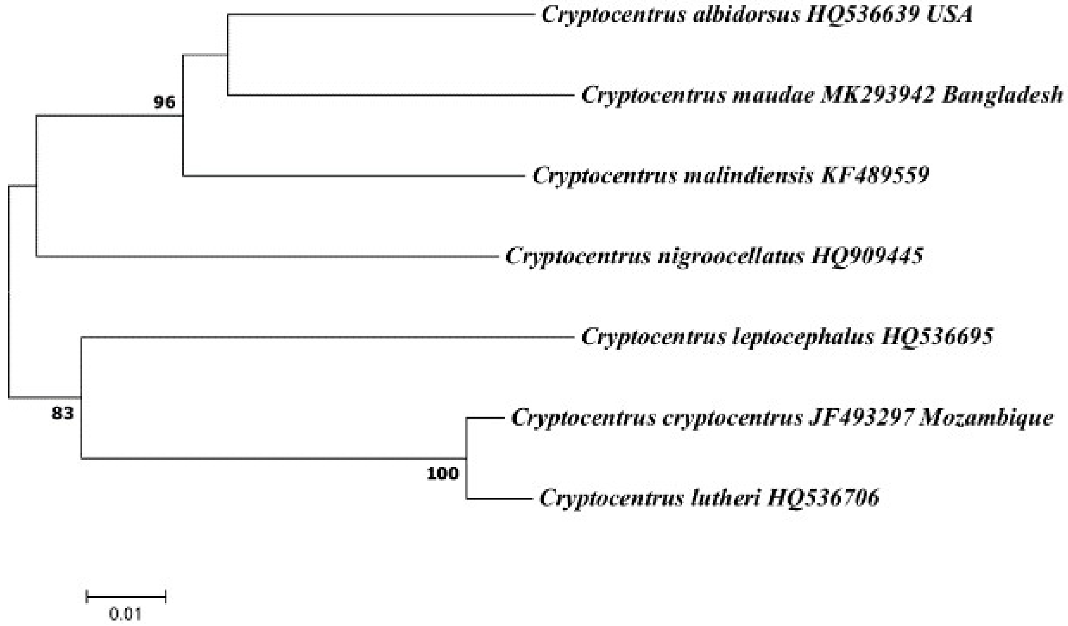

Figure 14: Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene with other sequences rerported from different countries. Bootstrap support of >70% are used with 1000 replications.

MK293944 (mtDNA 16s)

GGGCATCTGGATCTATGGAGGTCCCGCCTGCCCTGTGACTGAAAGTTTAACGGCCGCGGTATTTTGACCGTGC
GAAGGTAGCGTAATCACTTGTCTTTTAAATAAAGACCTGTATGAATGGCATAACGAGGGCTAAGCTGTCTCCT
TTTTCCAGTCAATGAAATTGATCTGCCCGTGCAGAAGCGGGCATACCCACATAAGACGAGAAGACCCTATGG
AGCTTAAGACACCAGAATAGACCACGTCAACAACCCCCAAATCACCAGGAATAAACCAAATGGCCTCTATTCC
CCTGTCTTTGGTTGGGGCGACCGCGGAGTAATAAGTAACCCCCACGTGGAATGGGCTCCCACCCCTAAAGCC
AGGGCCACAGCCCTAGCGAACAGAAAATCTGACCATTAAGATCCGGCAACGCCGATCAACGGACCCAGTTAC
CCTAGGGATAACAGCGCAATCCCCTTCTAGAGCCCATATCGACAAGGGGGTTTACGACCTCGATGTTGGATCA
GGACATCCTAATGGTGCAGCCGCTATTAAGGGTTC

Scientific name: *Valenciennea muralis* **Valenciennes, 1837**
English name: Mural Goby
Classification
Class: Actinopterygii
Order: Perciformes
Family: Gobiidae

Standard length: 89 mm
Fin formula: D1-VI, D2-I/13, P1- 19, P2-I/5, A-I/12, C-16-20
Identification: Colour of head and body pale gray or pale beige, with 4-5 longitudinal narrow pink or dusky stripes; lips yellowish; black spot at distal part of first dorsal fin just behind third spine. Body moderately elongate, compressed. Head sub-cylindrical; lower jaw not projecting anteriorly beyond upper jaw; gill opening relatively narrow, restricted to pectoralfin base. Third spine of first dorsal fin slightly elongate, forming pointed fin; pelvic fins separated; frenum absent; caudal fin rounded. Scales small ctenoid, excepting those on belly and prepelvic region, if present, cycloid; head and pectoral-fin base naked. Sensory canals and pores present on head; longitudinal pattern of sensory-papillae rows on cheek.

DNA Barcode: MK340745, MK340746, MK335891
Remarks: New distributional record from Bangladesh.

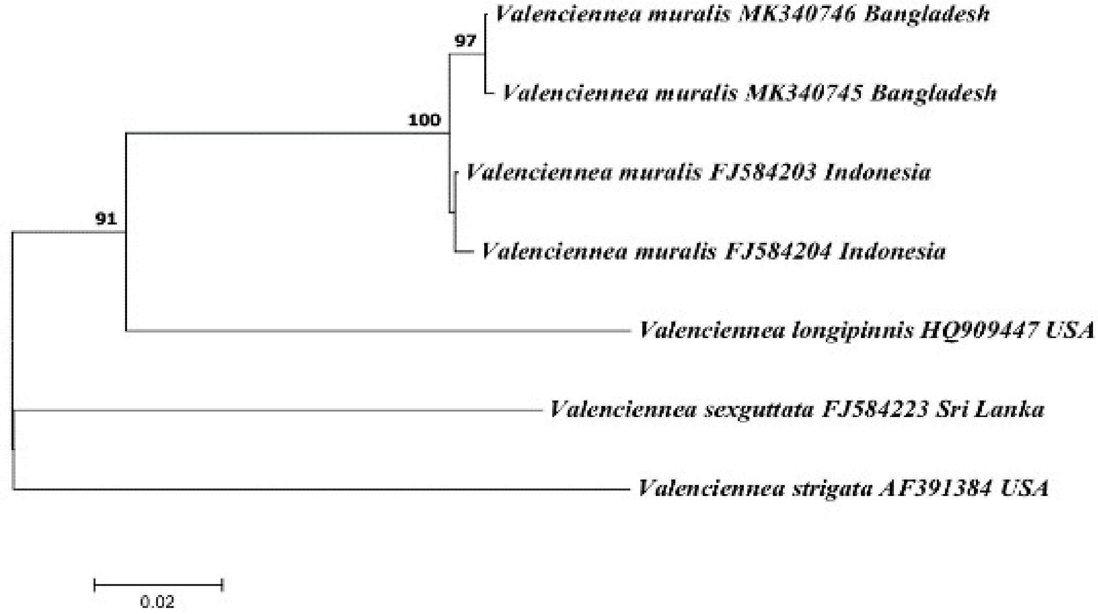

Figure 15: Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene with other sequences rerported from different countries. Bootstrap support of >70% are used with 1000 replications.

MK340745 (mtDNA COI)

GGCACTGCACTAAGTCTTCTCATTCGAGCCGAGCTAAGCCAACCTGGGGCACTGCTCGGTGACGACCAGAT
TTACAACGTAATTGTTACCGCCCACGCATTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGC
TTTGGAAACTGGCTAATTCCTCTAATGATTGGAGCCCCAGACATGGCTTTCCCTCGAATAAACAACATGAGC
TTCTGGCTACTCCCTCCCTCTTTCCTTCTACTATTAGCTTCCTCCGGAGTTGAAGCAGGGGCAGGAACAGGAT
GGACTGTTTATCCCCCTCTAGCGGGAAACCTGGCCCACGCCGGAGCTTCCGTAGATTTAACAATTTTTTCCCT
TCATTTAGCAGGAATTTCGTCAATCCTAGGAGCAATTAACTTTATTACAACCATCCTAAATATAAAACCCCCT
GCTATTTCGCAGTACCAAACCCCACTATTTGTGTGGGCAGTACTAATTACAGCCGTCCTGCTTCTTCTTTCAC
TCCCAGTACTTGCCGCAGGCATTACAATGCTTCTTACAGACCGAAACCTAAACACCACATTCTTTGACCCTGC
AGGAGGAGGGGACCCAATCCTCTATCAACA

MK340746 (mtDNA COI)

GGCACTGCACTAAGTCTTCTCATTCGAGCCGAGCTAAGCCAACCTGGGGCACTGCTCGGTGACGACCAGAT
TTACAACGTAATTGTTACCGCCCACGCATTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGC
TTTGGAAACTGGCTAATTCCTCTAATGATTGGAGCCCCAGACATGGCTTTCCCTCGAATAAACAACATGAG
CTTCTGGCTACTCCCTCCCTCTTTCCTTCTACTATTAGCTTCCTCCGGAGTTGAAGCAGGGGCAGGAACAGG
ATGGACTGTATATCCCCCTCTAGCGGGAAACCTGGCCCACGCCGGAGCTTCCGTAGATTTAACAATTTTTTC
CCTTCATTTAGCAGGAATTTCGTCAATCCTAGGAGCAATTAACTTTATTACAACCATCCTAAATATAAAACCC
CCTGCTATTTCGCAGTACCAAACCCCACTATTTGTGTGGGCAGTACTAATTACAGCCGTCCTGCTTCTTCTTT
CACTCCCAGTACTTGCCGCAGGCATTACAATGCTTCTTACAGACCGAAACCTAAACACCACATTCTTTGACC
CTGCAGGAGGAGGGGACCCAATCCTCTATCAACA

Scientific name: *Amblyeleotris downingi* **Randall, 1994**
English name: Downing's shrimpgoby
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Gobiidae

Standard length: 98 mm
Fin formula: D1-VI, D2-I/16, P-20, P2-I/5, A-I/17, C-18-20
Identification: Four faint broad dark brown bars on body, as well as a weak similar-coloured short vertical line may be at middle of each interspace; dorsal part of operculum tinged with dark brown; a dusky spot above dorsal end of gill opening; a faint dusky spot on first dorsal fin. Body elongate and compressed. Head slightly compressed; lower jaw slightly protruding beyond upper jaw; gill opening extending anteriorly beyond a vertical line through posterior margin of preopercle. Pelvic fins united medially; frenum present. Scales ctenoid posteriorly, cycloid anteriorly; head naked. Sensory canals and pores present on head; a series of short transverse rows of sensory papillae below eye; a pair of sensory papillae just behind chin.
DNA barcode: MK340584

Remarks: New distributional record from Bangladesh.

MK340584 (mtDNA COI)
GGCACAGCACTTAGCCTGCTAATCCGAGCCGAACTCTCCCAACCCGGCGCCCTACTGGGGGACGATCAGATTTACA
ATGTCATTGTAACCGCCCACGCATTTGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGGTTTGGAAACT
GGCTAATCCCACTTATGATCGGGGCCCCCGACATAGCCTTCCCTCGAATAAATAATATGAGCTTTTGGCTACTACCC
CCTTCTTTCCTCCTACTCTTGGCATCCTCTGGAGTTGAAGCCGGAGCTGGAACAGGTTGGACTGTCTACCCCCCACTT
GCAGGCAACCTGGCACATGCCGGAGCCTCCGTTGATCTAACCATCTTCTCCCTCCACCTGGCAGGAATTTCATCAAT
TCTTGGGGCAATCAACTTCATCACAACCATCCTAAATATGAAACCCCCAGCCATCTCACAATACCAAACCCCCCTATT
TGTGTGGGCTGTGCTAATCACAGCCGTACTCCTTCTTCTCTCCCTGCCCGTTCTTGCTGCCGGCATCACAATGCTCCT
AACAGACCGAAACCTTAATACAACCTTCTTCGACCCCGCAGGAGGAGGGGACCCAATCCTTTATCAACA

Scientific name: *Istigobius ornatus Ruppell*, **1830**
English name: Ornate goby
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Gobiidae

Standard length: 80 mm
Fin formula: D1-VI, D2-I/10, P-19, P2-I/5, A-I/9, C-16-18
Identification: Color of head and body pale gray, with numerous small black dots or horizontally-elongate blotches; distal tip of first dorsal fin tinged with yellow. Body moderately elongate and compressed. Head subcylindrical or slightly depressed; snout rounded, slightly projecting anteriorly beyond upper jaw; Upper part of pectoral fin with some filamentous free rays; pelvic fins united medially; frenum present. Scales on head and body ctenoid, except for occipital region, breast and pectoral-fin base with cycloid scales; head naked. Sensory canals and pores present on head.

DNA Barcode: MK335855, MK335856
Remarks: New distributional record from Bangladesh.

Scientific name: *Cryptocentrus cyanotaenia***Bleeker, 1853**
English name: Lagoon shrimpgoby
Classification
Class: Actinopterygii
Order: Perciformes
Family: Gobiidae

Standard length: 96 mm
Fin formula: D1-VI, D2-I/10, P-18, P2-I/5, A-I/10, C-20-22
Identification: Color numerous short diagonal blue lines on head; alternative yellow and red lines on anal fin. Body elongate, compressed. Head slightly compressed; jaws subequal, large, extending beyond a vertical through posterior margin of eye. Pelvic fins united medially; frenum present. Scales cycloid; head breast and pectoral-fin base naked. Sensory canals and pores present on head; distinct transverse sensory papillae rows on cheek; a pair of short longitudinal sensory papillae rows just behind chin.
DNA Barcode: MK560526, MK561627
Remarks: New distributional record from Bangladesh.

Scientific name: *Opistognathus variabilis* **Smith-Vaniz, 2009**
English name: Variable jawfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Opistognathidae

Standard length: 84 mm
Fin formula: D-XI/15, P1-19, P2-I/5, A-III/15, C-17-20
Identification: Colour of body mottled with various shades of brown. Usually a single black stripe (well-developed in fish with elongate jaws but only slightly in those with relatively short jaws) at the inner lining of upper jaw and adjacent membranes; lateral-line ends below verticals between segmented dorsal-fin rays 3-6 (typically fourth or fifth). Small-sized, moderately elongate fishes. Head bulbous. Eye relatively large, oriented dorsolaterally. Mouth large, posterior margin of maxilla extending well beyond eye.
DNA Barcode: MK340669
Remarks: New distributional record from Bangladesh.

MK340669 (mtDNA COI)

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GGCACCGCCCTTAGCCTTCTTATCCGAGCAGAACTTAGCCAACCTGGAGCGCTCCTTGGTGACGACCAGATCTATAA
TGTAATTGTTACGGCACACGCCTTTGTAATAATTTTCTTCATAGTAATACCAATTATGATTGGAGGCTTTGGCAACTG
GCTAATCCCTCTAATGATCGGGGCCCCTGACATGGCATTCCCTCGAATAAATAACATGAGTTTTTGGCTCTTACCTCC
CTCCTTCCTTCTTCTCCTAGCATCTTCCGGAGTAGAAGCTGGTGCCGGTACAGGTTGGACTGTCTACCCACCCCTCTCA
GGAAACTTAGCCCATGCCGGAGCCTCTGTTGATCTAACTATTTTCTCCCTCCACCTAGCAGGTGTATCCTCAATTCTCG
GAGCTATTAATTTTATTACAACAATTATTAACATGAAACCCCCTGCTATCTCCCAGTACCAAACGCCCCTGTTCGTATG
GGCTGTTCTAATTACAGCTGTCCTGCTTCTCCTCTCTCTTCCAGTCCTCGCAGCCGGTATTACAATGCTACTTACAGAT
CGAAATCTAAACACCACCTTCTTTGACCCGGCAGGGGGAGGAGACCCAATTCTTTACCAACA
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Scientific name: *Pomadasys maculatus* **Bloch, 1793**
English name: Silver grunt
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Haemulidae

Standard length: 126 mm
Fin formula: D-XII/14, P1-17, P2-I/5, A-III/7, C-18-20
Identification: Body colour silvery white, nape and back with series of incomplete variable cross bars on upper half of body; spinous dorsal fin large with black blotch; caudal fin dusky distally. Body compressed; head and dorsal profile convex; mouth small and slightly oblique; narrow bands of small pointed teeth in the jaws. Dorsal and anal fin spines strong; caudal fin emarginated. Scales ctenoid, moderate; present on head excluding snout. Lateral line slightly arched.

DNA Barcode: MK340692, MK340693

MK340692 (mtDNA COI)
GGCACAGCCCTAAGCCTGCTCATCCGAGCAGAACTCAGCCAACCGGGCGCACTCCTCGGAGACGACCAGATTTAT
AACGTAATCGTTACTGCACATGCCTTCGTAATAATTTTCTTTATAGTAATGCCTATTCTAATTGGCGGTTTCGGAAAC
TGGCTCGTGCCCTTAATGATTGGAGCACCCGATATGGCATTCCCTCGGATGAACAACATGAGTTTTTGGCTGCTTC
CCCCCTCTTTCCTCCTTCTACTTGCCTCTTCAGGGGTTGAAGCTGGGGCCGGGACCGGATGGACAGTTTACCCACCT
CTGGCCGGAAACCTCGCTCACGCAGGAGCATCAGTCGACCTAACCATCTTCTCCCTTCACTTGGCTGGTGTTTCCTC
AATCCTTGGGGCAATTAACTTCATTACAACAATTATTAACATGAAACCCCCTGCAATCTCCCAATACCAAACTCCTCT
CTTCGTTTGGTCTGTACTAGTAACTGCCGTCTTACTACTACTTTCCCTCCCAGTCCTAGCCGCTGGCATTACAATGCT
TCTGACAGACCGAAACCTAAATACTACCTTCTTCGACCCCGCCGGAGGAGGAGACCCAATCCTGTATCAACA

MK340693 (mtDNA COI)

GGCACAGCCCTAAGCCTGCTCATCCGAGCAGAACTCAGCCAACCGGGCGCACTCCTCGGAGACGACCAGATTT
ATAACGTAATCGTTACTGCACATGCCTTCGTAATAATTTTCTTTATAGTAATGCCTATTCTAATTGGCGGTTTCGG
AAACTGGCTCGTGCCCTTAATGATTGGAGCACCCGATATGGCATTCCCTCGGATGAACAACATGAGTTTTTGGC
TGCTTCCCCCCTCTTTCCTCCTTCTACTTGCCTCTTCAGGGGTTGAAGCTGGGGCTGGGACCGGATGGACAGTTT
ACCCACCTCTGGCCGGAAACCTCGCTCACGCAGGAGCATCAGTCGACCTAACCATCTTCTCCCTTCACTTGGCTG
GTGTTTCCTCAATCCTTGGGGCAATTAACTTCATTACAACAATTATTAACATGAAACCCCCTGCAATCTCCCAATA
CCAAACTCCTCTCTTCGTTTGGTCTGTACTAGTAACTGCCGTCTTACTACTACTTTCCCTCCCAGTCCTAGCCGCT
GGCATTACAATGCTTCTGACAGACCGAAACCTAAATACTACCTTCTTCGACCCCGCCGGAGGAGGAGACCCAAT
CCTGTATCAACA

Scientific name: *Pomadasys guoraca* **Cuvier, 1829**
English name: Silver grunt
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Haemulidae

Standard length: 122 mm
Fin formula: D-XII/14, P1-17, P2-I/5, A-III/7, C-17-20
Identification: Body silvery, slightly darker on back. Fins yellowish brown. Young with large dusky blotch on operculum. Body elongate and compressed. Mouth small, lips fairly thick; maxilla (upper jaw) reaching to front edge of eye. Teeth in villiform bands, the outer series slightly enlarged. Anal fin second spine conspicuously larger than third spine. Scales moderate, ctenoid.
DNA Barcode: MK340689, MK340690, MK340691
Remarks: New distributional record from Bangladesh.

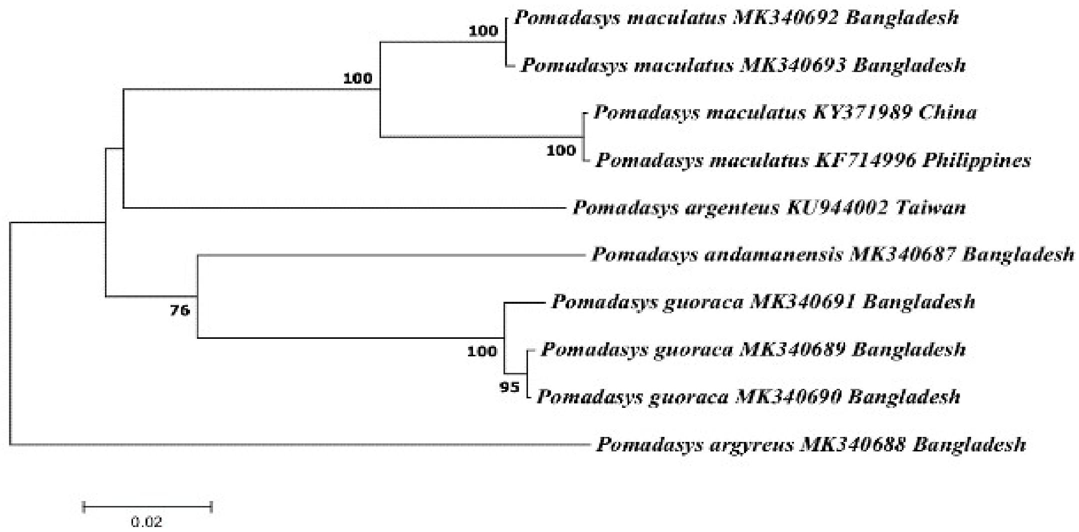

Figure 16: Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene with other sequences rerported from different countries. Bootstrap support of >70% are used with 1000 replications.

MK340689 (mtDNA COI)
AAGTGCAGTAGAGGTCCCGCCTGCCCTGTGACTATATGTTTAACGGCCGCGGTATTTTGACCGTGCGAAGGT
AGCGCAATCACTTGTCCTTTAAATAGGGACCGGTATGAATGGCACAACGAGGGCTTAACTGTCTCCTTTTTCA
AGTCAATGAAATTGATCCCCCCGTGCAGAAGCGGGGATAACCCCATAAGACGAGAAGACCCTGTGGAGCTT
TAGACGCCAGGACAGATCACGTTAAGCACACCTAAATACAGGGCCAAACCAAATGACACCTGCCCCTATGTC
TTCGGTTGGGGCGACCATGGGGTAAAACAAACCCCCCACGCGGAATAGGAGCACTTTCCTCCTAGAAATCCA
GAGCCTCCGCTCTAGTTAGCAGAACTTCTGACCTACAGACCCGGCAAGACCGATCAACGGACCAAGTTACCC
CAGGGATAACAGCGCAATCCTCTTTTAGAGCCCATATCGACAAGAGGGTTTACGACCTCGATGTTGGATCAG
GACATCCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGATCTGAGTTCC
AGACCG

MK340690 (mtDNA COI)
ATGACGGAAGGGCCCGCCTGCCCTGTGACTATATGTTTAACGGCCGCGGTATTTTGACCGTGCGAAGGTAGC
GCAATCACTTGTCCTTTAAATAGGGACCGGTATGAATGGCACAACGAGGGCTTAACTGTCTCCTTTTTCAAGTC
AATGAAATTGATCCCCCCGTGCAGAAGCGGGGATAACCCCATAAGACGAGAAGACCCTGTGGAGCTTTAGAC
GCCAGGACAGATCACGTTAAGCACACCTAAATACAGGGCCAAACCAAATGACACCTGCCCCTATGTCTTCGGT
TGGGGCGACCATGGGGTAAAACAAACCCCCCACGCGGAATAGGAGCACTTTCCTCCTAGAAATCCAGAGCCT
CCGCTCTAGTTAGCAGAACTTCTGACCTACAGACCCGGCAAGACCGATCAACGGACCAAGTTACCCCAGGGAT
AACAGCGCAATCCTCTTTTAGAGCCCATATCGACAAGAGGGTTTACGACCTCGATGTTGGATCAGGACATCCT
AATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGATCTGAGTTCAGACACGGA
AA

MK340691 (mtDNA COI)
GTAGAGGTCCCGCCTGCCCTGTGACTATATGTTTAACGGCCGCGGTATTTTGACCGTGCGAAGGTAGCGCAAT
CACTTGTCCTTTAAATAGGGACCGGTATGAATGGCACAACGAGGGCTTAACTGTCTCCTTTTTCAAGTCAATGA
AATTGATCCCCCCGTGCAGAAGCGGGGATAACCCCATAAGACGAGAAGACCCTGTGGAGCTTTAGACGCCAG
GACAGATCACGTTAAGCACACCTAAATACAGGGCCAAACCAAATGACACCTGCCCCTATGTCTTCGGTTGGGG
CGACCATGGGGTAAAACAAACCCCCCACGCGGAATAGGAGCACTTTCCTCCTAGAAATCCAGAGCCTCCGCTC
TAGTTAGCAGAACTTCTGACCTACAGACCCGGCAAGACCGATCAACGGACCAAGTTACCCCAGGGATAACAG
CGCAATCCTCTTTTAGAGCCCATATCGACAAGAGGGTTTACGACCTCGATGTTGGATCAGGACATCCTAATGG
TGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTA

Scientific name: *Pomadasys argyreus* **Valenciennes, 1833**
English name: Silver grunt
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Haemulidae

Standard length: 71mm
Fin formula: D-XII/13, P1-16, P2-I/5, A-III/7, C-17-22
Identification: Colour of body silver-mauve above and white below; plain or scattered charcoal scale spots on back and upper sides; Spots only on body, absent on head and snout; snout is dark brown; operculum charcoal or purplish. Body ovate; head profile almost straight. Mouth small; lips not thickened.

DNA Barcode: MK340688

MK340688 (mtDNA COI)
GCACAGCCCTAAGCCTGCTTATCCGAGCAGAACTTAGCCAGCCAGGCGCCCTCCTGGGAGATGACCAGATTTATA
ATGTAATCGTCACTGCCCATGCTTTCGTAATAATTTTCTTCATAGTTATGCCTATCCTAATTGGGGGTTTTGGTAACT
GGCTGGTCCCCCTAATAATTGGGGCCCCCGACATGGCCTTCCCTCGAATAAATAATATAAGCTTCTGGCTCCTTCC
ACCTTCTTTCCTTCTTCTCCTTGCCTCATCAGGTGTTGAAGCTGGGGCAGGGACCGGATGGACAGTCTACCCCCCTC
TAGCTGGAAACCTAGCCCACGCAGGGGCATCAGTCGACCTGACAATTTTCTCACTTCACCTCGCAGGTGTTTCCTC
AATCCTTGGAGCTATTAACTTTATCACAACAATTATTAACATAAAACCCCCTGCTATCTCTCAATACCAAACCCCTCT
ATTCGTTTGGTCCGTCCTAGTGACCGCCGTCCTCCTCCTGCTTTCCCTCCCAGTTCTGGCCGCGGGCATTACAATAC
TGCTTACCGACCGTAATTTAAATACCACCTTCTTCGACCCTGCCGGAGGGGGCGACCCAATCCTATACCAGCA

Scientific name: *Pomadasys andamanensis* **McKay & Satapoomin, 1994**
English name: Grunt
Classification
Class: Actinopterygii
Order: Perciformes
Family: Haemulidae

Standard length: 93 mm
Fin formula: D-XII/13, P1-18, P2-I/5, A-III/8, C-18-20
Morphologycal characteristics: Silvery white with 4 horizontal black or dark brown stripes on dorsal half of body; anal fin with a dark brown streak or blotch covering anterior two-thirds of soft-rayed portion. Body deep, compressed. Snout round, dorsal profile of head straight. Mouth small, terminal, without fleshy lips; 2 pores and a median pit on chin. Scales ctenoid.

DNA Barcode: MK340687
Remarks: New distributional record from Bangladesh.

MK340687 (mtDNA COI)
ACGACTGAAGGTCCGCCTGCCCTGTGACTATATGTTTAACGGCCGCGGTATCTTGACCGTGCGAAGGTAGCGCA
ATCACTTGTCCTTTAAATAGGGACCGGTATGAATGGCATAACGAGGGCTTAACTGTCTCCTTTTTCAAGTCAATG
AAATTGATCCCCCCGTGCAGAAGCGGGGATAACCCCATAAGACGAGAAGACCCTGTGGAGCTTTAGACACCAG
GGCAGATCACGTTAAGCACACCTAAATACAGGGCCAAACCAAATGACACCTGCCCCTATGTCTTCGGTTGGGGC
GACCGTGGGGTAAAACAAACCCCCCATGCGGAACGAGAGCACTTTCCTCCCAAAAATCCAGAGCCTCCGCTCTA
GTTAGCAGAACTTCTGACCTACAGACCCGGCAAAGCCGATCAACGGACCAAGTTACCCCAGGGATAACAGCGCA
ATCCTCTTTTAGAGTCCATATCGACAAGAGGGTTTACGACCTCGATGTTGGATCAGGACATCCTAATGGTGCAGC
CGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGATCTGAGTTTCAGACCGGAAACGTGAACACAC
CCTTCTTTGCCCCTGCCGAACTACAAAACCCAATTCTTTACCAACTCTTATTCTGATCTCCTCTCCTTCGCATATACT
AAAGTCCC

Scientific name: *Diagramma pictum***Thunberg, 1792**
English name: Yellow-spotted slatey
<u>Classification:</u>
Class: Actinopterygii
  Order: Perciformes
    Family: Haemulidae

Standard length: 105 mm
Fin formula: D-X/23, P1-17, P2-I/5, A-III/7, C-17-20
Identification: Colour varying much by size; large adult silvery grey, with or without dusky spots; sub-adult pale grey with numerous bright yellow or dusky spots or lines on head, body and fins; juvenile with broad longitudinal black bands on body. Body deep and compressed. Profile of snout steep; lips fleshy; chin with six pores; lower jaw without longitudinal groove at midline.

DNA Barcode: MK340608, MK340609

MK340608 (mtDNA COI)

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GGAACGGCCCTAAGCCTGCTCATCCGGGCAGAGTTAAGCCAACCCGGCGCGCTCCTAGGAGACGACCAGATTTAC
AATGTTATCGTTACGGCGCATGCGTTCGTAATAATCTTCTTTATAGTTATACCTATCCTAATTGGAGGGTTCGGAAAC
TGGCTAGTCCCGCTAATAATCGGAGCACCTGACATGGCATTCCCCCGAATGAACAATATGAGTTTCTGGCTTCTCCC
TCCGTCCTTCCTTCTCCTCCTTGCCTCCTCAGGCGTAGAAGCCGGGGCAGGGACTGGTTGGACAGTCTACCCCCCGT
TGGCCGGAAATTTAGCGCACGCAGGTGCATCTGTAGACCTCACGATCTTCTCCCTACATCTGGCCGGTATCTCATCA
ATTCTCGGGGCGATTAATTTTATTACAACAATCATTAACATGAAACCCCCTGCAATTTCACAATATCAGACCCCTCTG
TTTGTCTGGTCAGTACTAGTAACCGCTGTTCTCCTACTCCTTTCCCTTCCGGTCCTTGCTGCTGGGATTACTATGCTCC
TCACAGATCGAAACCTCAACACCACTTTCTTTGATCCTGCGGGGGGAGGAGACCCAATTCTTTACCAACA
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MK340609 (mtDNA COI)

GGAACGGCCCTAAGCCTGCTCATCCGGGCAGAGTTAAGCCAACCCGGCGCGCTCCTAGGAGACGACCAGATTTA
CAATGTTATCGTTACGGCGCATGCGTTCGTAATAATCTTCTTTATAGTTATACCTATCCTAATTGGAGGGTTCGGA
AACTGGCTAGTCCCGCTAATAATCGGAGCACCTGACATGGCATTCCCCCGAATGAACAATATGAGTTTCTGGCTT
CTCCCTCCGTCCTTCCTTCTCCTCCTTGCCTCCTCAGGCGTAGAAGCCGGGGCAGGGACTGGTTGGACAGTCTACC
CCCCATTGGCCGGAAATTTAGCGCACGCAGGTGCATCTGTAGACCTCACGATCTTCTCCCTACATCTGGCCGGTA
TCTCATCAATTCTCGGGGCGATTAATTTTATTACAACAATCATTAACATGAAACCCCCTGCAATTTCACAATATCAG
ACCCCTCTGTTTGTCTGGTCAGTACTAGTAACCGCTGTTCTCCTACTCCTTTCCCTTCCGGTCCTTGCTGCTGGGAT
TACTATGCTCCTCACAGATCGAAACCTCAACACCACTTTCTTTGATCCTGCGGGGGGAGGAGACCCAATTCTTTAC
CAACA

Scientific name: *Plectorhinchus macrospilus* **Satapoomin & Randall, 2000**
English name: Largespot sweetlips
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Haemulidae

Standard length: 300 mm
Fin formula: D-XII/21, P1-17, P2-I/5, A-III/8, C-18=20
Identification: Colour whitish to grayish ground colour on most parts of body; yellowish on soft portions of median fins, contrasting with many large mostly larger or equal to orbit diameter), irregularly rounded black spots on body, nape, and soft portions of median fins, and smaller black spots on head. Body oblong, compressed. Dorsal profile of head strongly convex. Mouth small; lips fleshy, moderately thick; chin with 6 pores and no median pit. Dorsal fin slightly notched. Caudal fin truncate. Scales ctenoid; front of snout, lips an chin naked.

DNA barcode: MK561628, MK335874

Remarks: New distributional record from Bangladesh.

MK561628 (mtDNA 16s)
GTCTTCGTCCGGAGGTCCCGCCTGCCCCGTGACCAAAGGTTTAACGGCCGCGGTATTTTGACCGTGCAAAGG
TAGCGCAATCACTTGTCTCTTAAATGGGGACCCGTATGAATGGCATAACGAGGGCTTAGCTGTCTCCTTTTTC
AAGTCAATGAAATTGATCTCCCCGTGCAGAAGCGGGGATAACCACATAAGACGAGAAGACCCTATGGAGCT
TTAGACACCAAGACAGACTATGTTAAACACCCCAAATCAAAGGACCAAACTAAATGGAAACCTGTCCTAATG
TCTTCGGTTGGGGCGACCGCGGGGAAACACAAAACCCCCACGTGGAAAGGGAGCACAACCCTCCTACAGCC
AAGAGCTTCCGCTCTACTAAACAGAACTTCTGACCTTAAGATCCGGCAAAGCCGATCAACGGACCAAGTTAC
CCTAGGGATAACAGCGCAATCCCCTTCTAGAGCCCATATCGACAAGGGGGTTTACGACCTCGATGTTGGATC
AGGACATCCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTC

MK335874 (mtDNA 16s)
GTCTTCGTCCGGAGGTCCCGCCTGCCCCGTGACCAAAGGTTTAACGGCCGCGGTATTTTGACCGTGCAAAGG
TAGCGCAATCACTTGTCTCTTAAATGGGGACCCGTATGAATGGCATAACGAGGGCTTAGCTGTCTCCTTTTTC
AAGTCAATGAAATTGATCTCCCCGTGCAGAAGCGGGGATAACCACATAAGACGAGAAGACCCTATGGAGCT
TTAGACACCAAGACAGACTATGTTAAACACCCCAAATCAAAGGACCAAACTAAATGGAAACCTGTCCTAATG
TCTTCGGTTGGGGCGACCGCGGGGAAACACAAAACCCCCACGTGGAAAGGGAGCACAACCCTCCTACAGCC
AAGAGCTTCCGCTCTACTAAACAGAACTTCTGACCTTAAGATCCGGCAAAGCCGATCAACGGACCAAGTTAC
CCTAGGGATAACAGCGCAATCCCCTTCTAGAGCCCATATCGACAAGGGGGTTTACGACCTCGATGTTGGATC
AGGACATCCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCAACGATTAAAGTCCTACGTGATCTGAGTT
CC

Scientific name: *Kyphosus cinerascens* **Forsskål, 1775**
English name: Blue sea chub
<u>Classification:</u>
Class: Actinopterygii
    Order: Perciformes
        Family: Kyphosidae

Standard length: 186 mm
Fin formula: D-XI/12, P1-19, P2-I/5, A-III/11, C-20
Identification: Dorsal fin spines somewhat short, weak; longest dorsal spine; anterior part of dorsal fin and anal fin soft-rayed portions well elevated with growth, longest dorsal and anal soft rays clearly longer than longest dorsal spine; base of spinous portion of dorsal fin equal to or a little longer than that of soft-rayed portion.

DNA Barcode: MK340627

MK340627 (mtDNA COI)
GGCACAGCCCTAAGCCTTCTCATTCGAGCAGAACTAAGCCAACCAGGCGCCCTCCTAGGGGACGACCAAATTTATA
ATGTCATTGTTACAGCACATGCCTTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGGTTTGGGAACT
GGCTTGTCCCACTTATGATCGGTGCCCCAGATATGGCATTCCCTCGAATAAATAATATGAGCTTCTGGCTCCTCCCCC
CTTCCTTCCTGCTACTTCTCGCCTCCTCCGGAGTAGAAGCTGGGGCCGGAACCGGTTGGACTGTCTACCCACCTCTCG
CTGGGAACCTAGCCCACGCAGGAGCCTCCGTTGATCTCACAATCTTCTCCCTGCACTTAGCAGGTGTCTCCTCAATTC
TTGGGGCAATTAATTTTATCACAACCATTATTAACATGAAACCCCCAGCTATTTCCCAGTATCAGACACCACTATTTGT
ATGGGCAGTACTGATCACTGCCGTCCTCCTTCTTCTCTCCCTACCCGTCCTTGCTGCTGGCATTACTATGCTCCTAACA
GACCGAAATCTTAACACCACCTTCTTCGACCCTGCAGGAGGAGGTGACCCCATCCTCTACCAACA

Scientific name: *Thalassoma lunare***Linnaeus, 1758**
English name: Moon wrasse
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Labridae

Standard length: 149 mm
Fin formula: D-VIII/13, P1-14, P2-I/5, A-III/11, C-15-17
Identification: Colour of initial phase green with vertical red lines on scales; head green with many irregular rose pink bands; a blue-edged rose pink band in each lobe of caudal fin, the broad central and posterior part of fin yellow; pectoral fins blue with a broad pink band in upper central part. Terminal males similar but more blue overall. Juveniles olive green on upper half of body, blue-white below; a large black spot in middle of dorsal fin and a large diffuse blackish spot at caudal-fin base. Body moderately slender. Dorsal profile of head slightly convex; mouth small, 2 prominent canines anteriorly in each jaw. Lateral line abruptly curved below posterior portion of dorsal-fin base; head naked except for a patch of small scales on upper end of opercle; scales on thorax about half the size of those on body. Caudal fin varying from truncate in young to highly lunate with upper and lower corners produced into filaments in large adults.

DNA Barcode: MK340733, MK340734, MK340735

MK340733 (mtDNA COI)
GGGACAGCCCTGAGCCTGCTCTTTCGAGCAGAATTAAGCCAGCCCGGCGCCCTCCTTGGAGACGACCAAATTTAT
AACGGCTTCGTCACAGCCCATGCATTCGTCATAATTTTCTTTATAGTAATACCAATTATGATTGGCGGATTCGGAA
ACTGGCTTATTCCCCTAATGATTGGCGCCCCCGATATGGCCTTCCCTCGTATGAACAATATGAGCTTTTGGCTTCT
TCCCCCTTCATTCCTTCTCCTTCTCGCTTCTTCTGGTGTTGAAGCGGGGGCCGGGACCGGATGGACAGTCTACCCA
CCCCTAGCAGGCAACCTTGCCCACGCTGGCGCATCCGTTGATCTAACCATCTTCTCCCTACATCTGGCAGGTATTT
CATCAATTTTAGGTGCAATTAACTTCATTACAACTATCATTAACATGAAACCCCCAGCCATCTCTCAATACCAAAC
GCCTCTTTTCGTATGGGCCGTTCTAATTACAGCAGTCCTTCTTCTGCTCTCTCTTCCAGTACTTGCTGCCGGCATTA
CAATGCTCCTGACGGACCGAAATCTAAACACTACCTTCTTTGACCCAGCTGGAGGAGGGGACCCAATTCTTTATC
AACA

MK340734 (mtDNA COI)

GGGACAGCCCTGAGCCTGCTCATTCGAGCAGAATTAAGCCAGCCCGGCGCCCTCCTTGGAGACGACCAAATT
TATAACGTCATCGTCACAGCCCATGCATTCGTCATAATTTTCTTTATAGTAATACCAATTATGATTGGCGGATT
CGGAAACTGGCTTATTCCCCTAATGATTGGCGCCCCCGATATGGCCTTCCCTCGTATGAACAATATGAGCTTTT
GGCTTCTTCCCCCTTCATTCCTTCTCCTTCTCGCTTCTTCTGGTGTTGAAGCGGGGGCCGGGACCGGATGGACA
GTCTACCCACCCCTAGCAGGCAACCTTGCCCACGCTGGCGCATCCGTTGATCTAACCATCTTCTCCCTACATCT
GGCAGGTATTTCATCAATTTTAGGTGCAATTAACTTCATTACAACTATCATTAACATGAAACCCCCAGCCATCT
CTCAATACCAAACGCCTCTTTTCGTATGGGCCGTTCTAATTACAGCAGTCCTCCTTCTGCTCTCTCTTCCAGTGC
TTGCTGCCGGCATTACAATGCTCCTGACGGACCGAAATCTAAACACTACCTTCTTTGACCCAGCTGGAGGAGG
GGACCCAATTCTTTATCAACA

Scientific name: *Halichoeres nigrescens* **Bloch & Schneider, 1801**
English name: Bubblefin wrasse
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Labridae

Standard length: 108 mm
Fin formula: D-IX/12, P1-14, P2-I/5, A-III/12, C-16-18
Identification: Colour irregular green and pink stripes and 6 groups of 7-10 small black spots in a midlateral row on body which may coalesce into and indistinct dark stripe; a short vertical black line behind eye preceded by a blue line and followed by a dusky pink bar; a small triangular black spot at upper base of pectoral fins. Body slightly elongate, compressed. Dorsal-fin origin slightly posterior to upper end of gill opening. Scales on nape extending to or slightly anterior to a vertical at rear edge of eyes; rest of head naked. Lateral line complete. Caudal fin rounded.

DNA barcode: MK840723

MK840723 (mtDNA COI)
GGTACAGCTCTAAGCCTACTTATTCGAGCCGAACTTAGTCAACCGGGCTCTCTCTTAGGAGACGACCAAATTTATAA
TGTTATCGTAACAGCACACGCCTTTGTAATAATCTTTTTTATGGTAATACCCATTATGATTGGGGGCTTTGGGAACTG
GCTTATTCCCCTAATAATTGGCGCTCCAGACATAGCATTCCCCCGAATAAATAATATAAGCTTTTGGCTACTCCCCCC
TTCCTTTCTCTTACTCCTTTCTTCTTCGGCTGTAGAAGCGGGAGCCGGGACAGGATGGACAGTTTATCCTCCCTTAGC
TGGAAATTTGGCCCATGCAGGAGCATCCGTCGACCTAACCATTTTCTCCCTTCACCTGGCAGGTATTTCTTCAATCCT
AGGGGCTATTAATTTTATTACCACTATTATTAACATGAAACCAGCGGCGACTTCAATGTACCAAATTCCTCTGTTCGT
TTGGGCTGTACTAATCACTGCCGTTCTCCTTCTCCTTTCACTCCCTGTCTTAGCTGCTGGCATTACAATGCTCTTGACA
GATCGAAATCTAAACACCGCCTTCTTTGACCCAGCAGGAGGAGGAGACCCCATTCTGTACCAGCA

Scientific name: *Cheilinus chlorourus* **Bloch, 1791**
English name: Floral Wrasse
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Labridae

Standard length: 90 mm
Fin formula: D-X/9, P1-15, P2-I/5, A-III/8, C-16-18
Identification: Colour variable, greenish brown to deep reddish brown, usually flecked with white; each scale on side usually with a blue or brown spot; median fins reddish brown with whitish dots; a blackish spot basally on first 1 or 2 membranes of dorsal fin; head with orange-red spots, some joining to form line radiating from eye. Body moderately deep; dorsal profile of head convex in front of dorsal fin, then straight to tip of snout. Jaws prominent, anterior tip of lower jaw even with anterior tip of upper jaw. Lateral line interrupted below posterior portion of dorsal-fin base. Scales reaching well onto bases of dorsal and anal fins. Caudal fin rounded in small fishes, in large individuals the upper and lower rays form elongate lobes. Lateral line almost entirely with scutes.

DNA Barcode: MK335845

Scientific name: *Bodianus neilli* **Day, 1867**
English name: Bay of Bengal hogfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Labridae

Identification: Colour of body pale brownish orange shading to white posterior to a diagonal from font of abdomen to soft portion of dorsal fin; short brownish red streaks at base of pectoral fins and in soft portion of dorsal and anal fins; small brownish red spots at front of dorsal fin; caudal fin light brownish orange, the upper and lower margins narrowly brownish red. Body moderately deep; dorsal profile of head nearly straight, snout pointed; 4 strong canines situated anteriorly in each jaw; a large, curved canine present on each side of rear of upper jaw. Lateral line complete and smoothly curved; sheath of scales extending onto dorsal and anal fins. Caudal fin truncate to slightly double emarginate.

Remarks: New distributional record from Bangladesh. This species has been recorded during the underwater scuba diving.

Scientific name: *Lactarius lactarius* **Bloch & Schneider, 1801**
English name: False trevally
Classification
Class: Actinopterygii
Order: Perciformes
Family: Lactariidae

Standard length: 113 mm
Fin formula: D1-VIII, D2-22, P1-I/13, P2-I/5, A-III/26, C- 22-24
Identification: Body colour silvery-grey above and silvery-white below; a dusky spot on upper part of operclum; fins pale yellow; margin of dorsal and caudal fins dusky. Head large; mouth oblique, the lower jaw prominent; two small canine teeth in front of each jaw; ventral fins below the level of pectoral fin base; soft portions of dorsal and anal fins covered with scales.

DNA Barcode: MK340629

MK340629 (mtDNA COI

GGCACAGCCCTAAGCCTGCTTATCCGGGCAGAACTAAGCCAACCTGGCGCTCTCTTAGGGGACGACCAGATCTAC
AATGTAATTGTTACAGCACACGCCTTTGTAATAATTTTCTTCATAGTAATACCAATCATGATTGGAGGATTTGGGAA
CTGGCTCATCCCCCTAATAATCGGCGCCCCTGACATAGCATTCCCTCGAATGAATAACATAAGCTTCTGGCTTCTCC
CTCCATCCTTCCTCCTGCTCCTCTCCTCCTCAAGTGTTGAAGCTGGGGCTGGTACCGGATGGACAGTTTACCCTCCT
CTAGCCGGCAACCTTGCCCATGCAGGAGCCTCCGTAGACCTGACTATTTTCTCCCTCCATCTTGCTGGAGTTTCTTC
AATTCTTGGTGCTATCAATTTTATTACCACCATTATTAATATGAAACCTGTCGCTGTTTCAATGTATCAAATCCCCCT
ATTCGTATGGGCCGTCCTAATTACGGCCGTCCTTCTTCTTCTTTCCCTTCCCGTCCTAGCTGCTGGCATTACAATGCT
CTTAACCGACCGAAACTTAAACACTACCTTCTTCGACCCAGCGGGGGGAGGAGACCCAATTCTTTACCAGCA

Scientific name: *Gazza dentex* **Valenciennes, 1835**
English name: Ovoid toothpony
<u>Classification</u>
Class: Actinopterygii
    Order: Perciformes
        Family: Leiognathidae

Standard length: 88 mm
Fin formula: D-VIII/16, P1-17, P2-I/5, A-III/14, C-20-22
Identification: Colour of body bluish silver dorsally, brilliant silvery-white ventrally; anal fin yellowish distally; caudal fin yellowish with faintly black margin. Body oval, compressed, somewhat elongated. Mouth protruding forwards, not downwards, with distinct canine teeth on both jaws; a long narrow anterodorsal extension of subocular silvery region, proximal contact only with orbit. Pelvic-fin tips not reaching to origin of anal fin when appressed. Scaled area of anterior dorsolateral surface of body extending anteriorly beyond a vertical through posterior tip of sensory canal on temporal; breast completely naked.

DNA Barcode: MK340619, MK340620, MK340621
Remarks: New distributional record from Bangladesh.

MK340619 (mtDNA COI)
GGGACAGCCCTAAGCTTGCTCATCCGAGCAGAGCTGAGCCAGCCCGGTGCGCTCCTGGGAGATGACCACA
TCTATAATGTTATCGTCACCGCACATGCATTTGTAATAATTTTCTTCATGGTTATACCCATCATAATCGGCGG
CTTCGGCAATTGGCTCATTCCTCTAATAATTGGAGCCCCTGACATGGCATTCCCCCGAATAAATAACATAAG
CTTTTGGCTTCTTCCCCCATCATTCCTGCTCCTCTTAGCATCTTCCGGCATCGAAGCCGGGGCAGGCACAGG
GTGGACTGTTTACCCCCCTTTAGCGGGGAATCTCGCCCATGCAGGCGCCTCCGTTGACCTGACAATCTTCTC
ACTTCACCTGGCCGGGATCTCCTCAATTTTAGGGGCTATCAACTTCATTACAACAATTATTAACATAAAGCCC
CCAGCCATCTCACAATTTCAAACCCCCCTATTCGTCTGGGCCGTTCTTATTACAGCTGTCCTCCTTCTTCTATC
ACTACCTGTTCTAGCAGCAGGCATTACAATGCTTCTAACAGATCGAAACTTAAACACTACTTTCTTTGACCCA
GCAGGAGGGGGAGACCCAATCCTATACCAACA

MK340621 (mtDNA COI)
GGGACAGCCCTAAGCTTGCTCATCCGAGCAGAGCTGAGCCAGCCCGGTGCGCTCCTGGGAGATGACCACAT
CTATAATGTTATCGTCACCGCACATGCATTTGTAATAATTTTCTTCATGGTTATACCCATCATAATCGGCGGCT
TCGGCAATTGGCTCATTCCTCTAATAATTGGAGCCCCTGACATGGCATTCCCCCGAATAAATAACATAAGCTT
TTGGCTTCTTCCCCCATCATTCCTGCTCCTCTTAGCATCTTCCGGCATCGAAGCCGGGGCAGGCACAGGGTG
GACTGTTTACCCCCCTTTAGCGGGGAATCTCGCCCATGCAGGCGCCTCCGTTGACCTGACAATCTTCTCACTT
CACCTGGCCGGGATCTCCTCAATTTTAGGGGCTATCAACTTCATTACAACAATTATTAACATAAAGCCCCCAG
CCATCTCACAATTTCAAACCCCCCTATTCGTCTGGGCCGTTCTTATTACAGCTGTCCTCCTTCTTCTATCACTAC
CTGTTCTAGCAGCAGGCATTACAATGCTTCTAACAGATCGAAACTTAAACACTACTTTCTTTGACCCAGCAGG
AGGGGGAGACCCAATCCTATACCAACA

MK340620 (mtDNA COI)
GGGACAGCCCTAAGCTTGCTCATCCGAGCAGAGCTGAGCCAGCCCGGTGCGCTCCTGGGAGATGACCACAT
CTATAATGTTATCGTCACCGCACATGCATTTGTAATAATTTTCTTCATGGTTATACCCATCATAATCGGCGGCT
TCGGCAATTGGCTCATTCCTCTAATAATTGGAGCCCCTGACATGGCATTCCCCCGAATAAATAACATAAGCTT
TTGGCTTCTTCCCCCATCATTCCTGCTCCTCTTAGCATCTTCCGGCATCGAAGCCGGGGCAGGCACAGGGTGG
ACTGTTTACCCCCCTTTAGCGGGGAATCTCGCCCATGCAGGCGCCTCCGTTGACCTGACAATCTTCTCACTTCA
CCTGGCCGGGATCTCCTCAATTTTAGGGGCTATCAACTTCATTACAACAATTATTAACATAAAGCCCCCAGCC
ATCTCACAATTTCAAACCCCCCTATTCGTCTGGGCCGTTCTTATTACAGCTGTCCTCCTTCTTCTATCACTACCT
GTTCTAGCAGCAGGCATTACAATGCTTCTAACAGATCGAAACTTAAACACTACTTTCTTTGACCCAGCAGGAG
GGGGAGACCCAATCCTATACCAACA

Scientific name: *Leiognathus daura* **Cuvier, 1829**
English name: Goldstripe ponyfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Leiognathidae

Standard length: 66 mm
Fin formula: D-VIII/16, P1-20, P2-I/5, A-III/14, C-24
Identification: Colour of body bluish or greenish silver dorsally, brilliant silvery-white ventrally; a broad yellow or golden band usually over lateral line; no dark marking on nape; distal half of spinous portion of dorsal fin jetblack: anal fin yellow or orange. Body deep, rhomboid, compressed. Mouth protruding downwards, with small slender teeth on both jaws; ventral profile of lower jaw slightly concave or almost straight; lower margin of eye located below level of mouth gape. Cheek and breast completely naked.

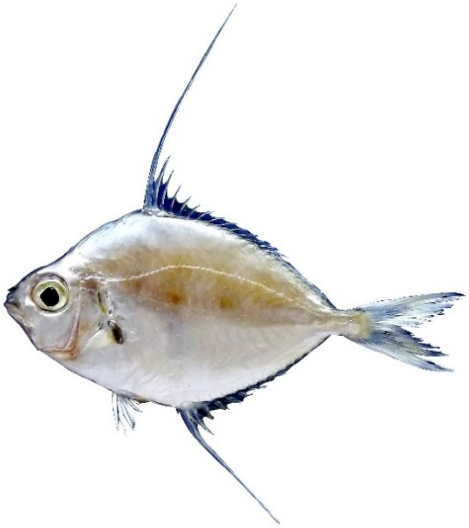
DNA Barcode: MK340630, MK340631, MK340632, MK335857, MK335858, MK335859
Remarks: New distributional record from Bangladesh.

MK340630 (mtDNA COI)
GGGACTGCTTTAAGCTTGCTTATCCGAGCAGAACTAAGTCAACCTGGCGCCCTTTTAGGTGACGATCACATCTATAA
TGTTATTGTTACCGCACATGCATTCGTAATAATTTTCTTTATAGTCATGCCAATCATAATTGGAGGCTTTGGCAACTG
GCTCATTCCCCTGATAATTGGCGCCCCTGACATAGCATTCCCACGAATAAACAACATAAGCTTCTGGCTTCTTCCCCC
ATCATTTCTGCTTCTTTTAGCATCCTCTGGCATTGAAGCCGGCGCAGGCACAGGATGGACAGTTTATCCACCTTTAGC
AGGCAATCTTGCCCATGCAGGAGCATCTGTTGACTTAACAATCTTTTCTCTCCACTTAGCCGGAATTTCCTCAATTCTA
GGGGCAATTAACTTTATTACCACAATCATTAACATAAAACCCCCAGCAATTACACAATTCCAGACCCCCTTATTTGTTT
GGGCAGTACTAATTACAGCAGTCTTACTTCTTCTTTCCCTCCCCGTCCTTGCAGCAGGAATTACTATACTACTCACTGA
CCGTAACCTTAACACCACCTTCTTTGATCCTGCAGGAGGAGGGGACCCAATTTTATACCAACA

MK340631 (mtDNA COI)
GGGACTGCTTTAAGCTTGCTTATCCGAGCAGAACTAAGTCAACCTGGCGCCCTTTTAGGTGACGATCACATCT
ATAATGTTATTGTTACCGCACATGCATTCGTAATAATTTTCTTTATAGTCATGCCAATCATAATTGGAGGCTTT
GGCAACTGGCTCATTCCCCTGATAATTGGCGCCCCTGACATAGCATTCCCACGAATAAACAACATAAGCTTCT
GGCTTCTTCCCCCATCATTTCTGCTTCTTTTAGCATCCTCTGGCATTGAAGCCGGCGCAGGCACAGGATGGAC
AGTTTATCCACCTTTAGCAGGCAATCTTGCCCATGCAGGAGCATCTGTTGACTTAACAATCTTTTCTCTCCACT
TAGCCGGAATTTCCTCAATTCTAGGGGCAATTAACTTTATTACCACAATCATTAACATAAAACCCCCAGCAATT
ACACAATTCCAGACCCCCTTATTTGTTTGGGCAGTACTAATTACAGCAGTCTTACTTCTTCTTTCCCTCCCCGTC
CTTGCAGCAGGAATTACTATACTACTCACTGACCGTAACCTTAACACCACCTTCTTTGATCCTGCAGGAGGAG
GGGACCCAATTTTATACCAACA

MK340632 9mtDNA COI)
GGAACTGCTTTAAGCTTGCTTATCCGAGCAGAACTAAGTCAACCTGGCGCCCTTTTAGGTGACGATCACATCT
ATAATGTTATTGTTACCGCACATGCATTCGTAATAATTTTCTTTATAGTCATGCCAATCATAATTGGAGGCTTT
GGCAACTGGCTCATTCCCCTGATAATTGGCGCCCCTGACATAGCATTCCCACGAATAAACAACATAAGCTTCT
GGCTTCTTCCCCCATCATTTCTGCTTCTTTTAGCATCCTCTGGCATTGAAGCCGGCGCAGGCACAGGATGGAC
AGTTTATCCACCTTTAGCAGGCAATCTTGCCCATGCAGGAGCATCTGTTGACTTAACAATCTTTTCTCTCCACT
TAGCCGGAATTTCCTCAATTCTAGGGGCAATTAACTTTATTACCACAATCATTAACATAAAACCCCCAGCAATT
ACACAATTCCAGACCCCCTTATTTGTTTGGGCAGTACTAATTACAGCAGTCTTACTTCTTCTTTCCCTCCCCGTC
CTTGCAGCAGGAATTACTATACTACTCACTGACCGTAACCTTAACACCACCTTCTTTGATCCTGCAGGAGGAG
GGGACCCAATTTTATACCAACA

Scientific name: *Leiognathus longispinis* **Valenciennes, 1835**
English name: Smithurst's ponyfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Leiognathidae



Standard length: 91 mm
Fin formula: D-VII/17, P1-19, P2-I/5, A-III/14, C-20-22
Identification: Colour of body blue-grayish silver dorsally, brilliant silvery-white ventrally; dorsolateral body with 5 or 6 dark vertical bands in juveniles; usually yellow blotches laterally on body. Body extremely deep, compressed. Mouth protruding downwards, with small slender teeth on both jaws; profile of lower jaw slightly concave; supraorbital ridge smooth or weakly serrated. Second dorsal and anal fin spines distinctly elongated, filamentous; retrorse spines of dorsal and anal fin pterygiophores strong and exposed. Cheek, breast, and belly completely naked.

DNA Barcode: MK340633, MK335860
Remarks: New distributional record from Bangladesh.

MK340633 (mtDNA COI)
GGAACAGCCCTAAGTCTTCTTATCCGGGCAGAACTAAGCCAACCTGGGGCCCTCCTTGGAGATGACCACATTT
ACAATGTTATCGTTACCGCACATGCATTCGTAATAATTTTTTTTATGGTTATACCCATTATAATTGGAGGCTTTG
GCAACTGGCTTATCCCGCTAATGATTGGGGCCCCCGACATAGCATTCCCACGTATAAACAACATAAGCTTCTG
GCTCCTGCCCCCCTCATTCTTGCTTCTCCTGGCATCTTCAGGCATCGAAGCTGGCGCAGGTACTGGCTGGACA
GTATACCCCCCTCTAGCAGGCAACCTTGCCCATGCAGGTGCTTCCGTAGACCTAACCATCTTCTCACTCCACCT
CGCCGGAATCTCATCAATCCTGGGGGCTATTAACTTCATTACAACAATTATTAACATAAAACCCCCAGCCATCT
CACAATTTCAAACCCCCCTATTCGTTTGGGCTGTCCTAATTACAGCAGTACTTCTTCTTCTTTCCCTCCCAGTTCT
CGCAGCGGGTATCACAATGCTACTAACAGACCGTAACCTAAACACCACATTCTTTGATCCTGCAGGAGGGGG
AGACCCAATTTTATACCAACA

MK335860(mtDNA COI)

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GGAACAGCCCTAAGTCTTCTTATCCGGGCAGAACTAAGCCAACCTGGGGCCCTCCTTGGAGATGACCACATTT
ACAATGTTATCGTTACCGCACATGCATTCGTAATAATTTTTTTTATGGTTATACCCATTATAATTGGAGGCTTTG
GCAACTGGCTTATCCCGCTAATGATTGGGGCCCCCGACATAGCATTCCCACGTATAAACAACATAAGCTTCTG
GCTCCTGCCCCCCTCATTCTTGCTTCTCCTGGCATCTTCAGGCATCGAAGCTGGCGCAGGTACTGGCTGGACA
GTATACCCCCCTCTAGCAGGCAACCTTGCCCATGCAGGTGCTTCCGTAGACCTAACCATCTTCTCACTCCACCT
CGCCGGAATCTCATCAATCCTGGGGGCTATTAACTTCATTACAACAATTATTAACATAAAACCCCCAGCCATCT
CACAATTTCAAACCCCCCTATTCGTTTGGGCTGTCCTAATTACAGCAGTACTTCTTCTTCTTTCCCTCCCAGTTCT
CGCAGCGGGTATCACAATGCTACTAACAGACCGTAACCTAAACACCACATTCTTTGATCCTGCAGGAGGGGG
AGACCCAATTTTATACCAACA
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Scientific name: *Equulites leuciscus* **Günther, 1860**
English name: Whipfin ponyfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Leiognathidae

Standard length: 102 mm
Fin formula: D-VIII/16, P1-17, P2-I/5, A-III/14, C-20-25
Identification: Color of body brownish silver dorsally, brilliant silvery-white ventrally; irregular oblique dark lines dorsolaterally on body. Body oblong, somewhat elongate, compressed; dorsal and ventral profiles similarly convex. Mouth protruding downwards, with small slender teeth on both jaws. Cheek naked; breast completely scaled laterally with narrow naked area ventrally. Second dorsal fin spine distinctly elongated, filamentous.

DNA Barcode: MK560527
Remarks: New distributional record from Bangladesh.

Scientific name: *Lethrinus crocineus* **Smith, 1959**
English name: Yellowtail emperor
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Lethrinidae

Standard length: 92 mm
Fin formula: D-X/9, P1-13, P2-I/5, A-III/8, C-17-19
Identification: Colour of body tan or yellowish, the base of scales sometimes black; head brown; fins pale or yellowish, the edge of the dorsal fin reddish or yellowish. Body fairly deep, dorsal profile near eye nearly straight; snout moderately short; snout angle relative to upper jaw; interorbital space convex; posterior nostril an oblong longitudinal opening, closer to orbit than to anterior nostril or about halfway between orbit and anterior nostril; eye situated close or relatively removed from dorsal profile. Dorsal fin with 10 spines and 9 soft rays, the fourth dorsal spine usually the longest; anal fin with 3 spines and 8 soft rays, the first or second soft ray usually the longest. Inner surface of pectoral fin densely covered with scales; posterior angle of operculum fully scaled or sometimes with a wide scaleless area.

DNA Barcode: MK340636, MK340637, MK340638, MK340639

MK340636 (mtDNA COI)
GGGACAGCCCTAAGCCTACTCATTCGGGCCGAACTTAGTCAACCCGGAGCCCTCCTGGGAGACGACCAAATT
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GGCAACTGGCTTATCCCCCTAATGATTGGCGCCCCCGACATGGCATTCCCACGCATGAATAACATGAGCTTTT
GGCTTCTACCCCCTTCGTTCCTCCTCCTACTTGCGTCCTCAGGTGTAGAAGCTGGGGCTGGCACCGGATGGAC
AGTTTACCCTCCACTAGCAGGCAACCTTGCCCACGCTGGTGCATCTGTCGACTTAACAATCTTTTCCCTTCATC
TAGCAGGGGTCTCCTCAATTCTAGGGGCTATCAACTTCATCACAACAATTATTAACATGAAGCCTCCGGCTAT
TTCTCAGTATCAAACACCCCTATTTGTATGGGCCGTTCTAATTACCGCCGTACTACTTCTCCTATCCCTACCAGT
TCTTGCAGCTGGCATCACAATGCTGTTGACGGACCGAAACCTAAACACCACCTTCTTTGACCCCGCAGGGGG
AGGGGACCCAATCCTCTATCAGCA

MK340637 (mtDNA COI)
GGGACAGCCCTAAGCCTACTCATTCGGGCCGAACTTAGTCAACCCGGAGCCCTCCTGGGAGACGACCAAATT
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GGCTTCTACCCCCTTCGTTCCTCCTCCTACTTGCGTCCTCAGGTGTAGAAGCTGGAGCTGGCACCGGATGGAC
CGTTTACCCTCCACTAGCAGGCAACCTTGCCCACGCTGGTGCATCTGTCGACTTAACAATCTTTTCCCTTCATCT
AGCAGGGGTCTCCTCAATTCTAGGGGCTATCAACTTCATTACAACAATTATTAACATGAAGCCTCCGGCTATTT
CTCAGTATCAAACACCCCTATTTGTATGGGCCGTTCTAATTACCGCCGTACTACTTCTCCTATCCCTACCAGTTC
TTGCAGCTGGCATCACAATGCTGTTGACGGACCGAAACCTAAACACCACCTTCTTTGACCCCGCAGGGGGAG
GGGACCCAATCCTCTATCAGCA

MK340638 (mtDNA COI)
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TATAATGTTATTGTTACAGCACATGCTTTCGTAATAATTTTCTTTATGGTAATGCCTATTATGATTGGAGGTTTC
GGCAACTGGCTTATCCCCCTAATGATTGGCGCCCCCGACATGGCATTCCCACGCATGAATAACATGAGCTTTT
GGCTTCTACCCCCTTCGTTTCTCCTCCTACTTGCGTCCTCAGGTGTAGAAGCTGGAGCTGGCACCGGATGGAC
AGTTTACCCTCCACTAGCAGGCAACCTTGCCCACGCTGGTGCATCTGTCGACTTAACAATCTTTTCCCTTCATC
TAGCAGGGGTCTCCTCAATTCTAGGGGCTATCAACTTCATCACAACAATTATTAACATGAAGCCTCCGGCTAT
TTCTCAGTATCAAACACCCCTATTTGTATGGGCCGTTCTAATTACCGCCGTACTACTTCTCCTATCCCTACCAGT
TCTTGCAGCTGGCATCACAATGCTGTTGACGGACCGAAACCTAAACACCACCTTCTTTGACCCCGCAGGGGG
AGGGGACCCAATCCTCTATCAGCA

Scientific name: *Lutjanus fulvus* **Forster, 1801**
English name: Blacktail snapper
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae

Standard length: 104 mm
Fin formula: D-X/13, P1-16, P2-I/5, A-III/8, C-17
Identification: Colour of dorsal side is whitish or pale yellow and ventral side yellowish. Upper side of the eye with yellow margin. Dorsal and caudal fins are black with a narrow white border. Pectoral, pelvic and anal fins are yellow in colour. Body large, elongated and laterally compressed. Dorsal profile of head steeply sloped. Preopercular notch and knob moderately developed. Mouth large, terminal and pointed. Head moderate in comparison with body. Scale ctenoid, scale rows on back rising obliquely above lateral line. Teeth canine present along the upper jaw. Jaws medium and equal. Nostril rounded. Barble absent. Lateral line single, complete and curved. Eye dorsal in position. Caudal fin emarginated. Fourth dorsal spine is the longest.

DNA Barcode: MK340642, MK335865
Remarks: New distributional record from Bangladesh.

MK340642 (mtDNA COI)
GGCACGGCCCTAAGCCTGCTCATTCGAGCAGAACTAAGCCAGCCAGGAGCCCTTCTTGGAGACGACCAGATTTATAA
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GCTAATCCCCCTAATAATCGGAGCCCCTGATATGGCATTCCCCCGAATAAATAACATGAGCTTTTGGCTGCTTCCTCC
GTCGTTCCTTCTGCTCCTAGCCTCCTCAGGAGTAGAAGCCGGTGCTGGAACTGGGTGGACCGTCTATCCTCCCCTGGC
AGGAAACCTCGCACACGCCGGAGCATCTGTTGATCTGACTATTTTCTCCCTACATCTGGCAGGTGTATCCTCAATCCT
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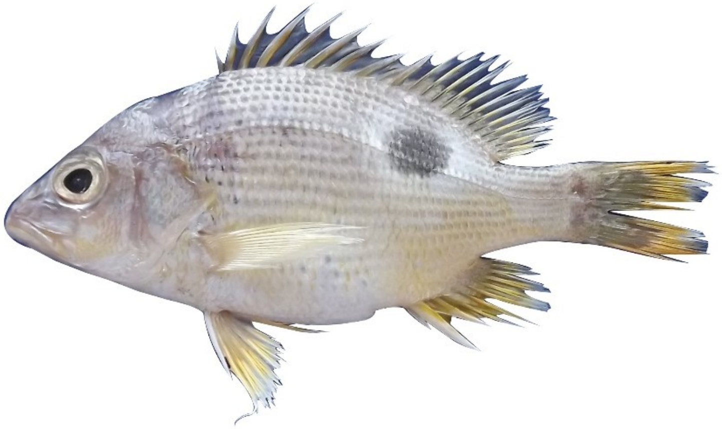
TGGGCCGTCCTAATTACCGCTGTCCTACTTCTTCTCTCCCTCCCAGTCCTAGCCGCCGGAATTACAATGCTTCTTACAG
ACCGAAACCTAAATACTACCTTCTTCGACCCTGCAGGAGGAGGAGATCCTATTCTTTACCAACA

Scientific name: *Lutjanus johnii* **Bloch, 1792**
English name: Red snapper
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae



Standard length: 126 mm
Fin formula: D-X/14, P1-18, P2-I/5, A-III/8, C-20
Identification: Colour generally yellow with a bronze to silvery sheen, grading to silvery white on belly; a round black spot, larger than eye, on back, mainly above lateral line. Body moderately deep. Caudal fin truncate or slightly emarginate. Scale rows on back parallel to lateral line.

DNA Barcode: MK340643, MK340644

MK340643 (mtDNA COI)
CATGCGTTCGTAATAATTTTCTTTATAGTAATACCAATCATGATCGGCGGGTTTGGAAACTGGCTAGTACCCTTAATAATTGGGG
CCCCAGACATAGCATTCCCCCGAATAAATAATATGAGCTTTTGGCTCCTTCCCCCATCATTCCTGCTACTCCTGGCTTCCTCAGGC
GTAGAAGCTGGTGCCGGAACCGGATGGACAGTTTATCCTCCCCTAGCAGGAAACCTAGCACATGCAGGAGCATCTGTTGACCTA
ACTATCTTTTCCCTCCATCTAGCAGGTGTTTCTTCAATTCTAGGGGCCATCAATTTTATTACAACAATTATTAATATAAAACCCCCT
GCCATCTCTCAATATCAAACACCCCTATTTGTTTGGGCCGTCCTAATCACCGCTGTCCTGCTCCTCCTATCCCTTCCTGTCCTGGCC
GCCGGAATCACAATACTTCTCACAGATCGAAATCTTAATACCACCTTCTTTGACCCACCAGGCGGAGGAGACCCCATCCTCTATC
AACA

MK340643 (mtDNA COI)
GGCACAGCCCTAAGCCTGCTCATTCGAGCAGAACTCAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGATTTACAATGTTATT
GTTACAGCGCATGCGTTCGTAATAATTTTCTTTATAGTAATACCAATCATGATCGGCGGGTTTGGAAACTGGCTAGTACCCTTAA
TAATTGGGGCCCCAGACATAGCATTCCCCCGAATAAATAATATGAGCTTTTGGCTCCTTCCCCCATCATTCCTGCTACTCCTGGCT
TCCTCAGGCGTAGAAGCTGGTGCCGGAACCGGATGGACAGTCTATCCTCCCCTAGCAGGAAACCTAGCACATGCAGGAGCATCT
GTTGACCTAACTATCTTTTCCCTCCATCTAGCAGGTGTTTCTTCAATTCTAGGGGCCATCAATTTTATTACAACAATTATTAATATA
AAACCCCCTGCCATCTCTCAATATCAAACACCCCTATTTGTTTGGGCCGTCCTAATCACCGCTGTCCTGCTCCTCCTATCCCTTCCT
GTCCTGGCCGCCGGAATCACAATACTTCTCACAGATCGAAATCTTAATACCACCTTCTTTGACCCAGCAGGCGGAGGAGACCCCA
TCCTCTATCAACA

Species Name: *Lutjanus madras* **Valenciennes, 1831**
English name: Indian snapper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae

Standard length: 127mm
Fin formula: D-X/13, P1-16, P2-I/5, A-III/8, C-17-20
Identification: Body yellowish or brownish in colour. Fine straight yellow lines on lower half of the body, and similar lines running obliquely above the lateral line. Dorsal fin black or grey colour with yellowish tip. Pectoral yellow and pelvic fin whitish. Anal and caudal fin yellow to dark yellow in colour. Body elongated, laterally compressed. Dorsal profile more convex than ventral. Dorsal profile of head moderately to gently sloped. Preopercular notch and knob poorly developed. Mouth large, oblique and terminal. Head moderate in comparison with body. Scale ctenoid, scale rows on back rising obliquely above lateral line. Teeth canine and present along the upper jaw. Jaws large and equal. Nostril rounded. Barble absent. Lateral line single, complete and curved. Eye slightly dorsal in position. Caudal fin emarginated not forked. Fourth dorsal spine is the longest.

DNA Barcode: MK340655, MK340656, MK340657

MK340655 (mtDNA COI)
GGCACGGCCCTAAGCTTGCTCATTCGAGCAGAATTAAGCCAACCCGGCGCTCTTCTTGGAGACGACCAGATTTATA
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TGGCTAATCCCACTAATGATCGGGGCTCCTGACATGGCATTCCCCCGAATGAATAACATGAGCTTTTGGCTCCTCCC
CCCATCATTCCTGCTACTCCTAGCCTCCTCAGGGGTTGAAGCCGGAGCTGGAACTGGATGGACAGTCTACCCCCCT
CTAGCAGGAAACCTTGCACACGCAGGGGCATCTGTTGACCTAACTATCTTTTCCCTTCACCTAGCAGGTGTTTCTTC
AATTCTGGGGGCCATCAATTTCATTACAACAATTATTAATATGAAACCCCCTGCCATTTCTCAGTACCAAACGCCCC
TGTTCGTCTGGGCCGTTCTAATTACCGCTGTCCTACTTCTTCTTTCCCTCCCTGTTTTAGCGGCGGGAATTACAATGC
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MK340656 (mtDNA COI)
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CTGGCTAATCCCACTAATGATCGGAGCTCCTGACATGGCATTCCCCCGAATGAATAACATGAGCTTTTGGCTCCTC
CCCCCATCATTCCTGCTACTCCTAGCCTCCTCAGGGGTTGAAGCCGGAGCTGGAACTGGATGGACAGTCTACCCCC
CTCTAGCAGGAAACCTTGCACACGCAGGGGCATCTGTTGACCTAACTATCTTTTCCCTTCACCTAGCAGGTGTTTCT
TCAATTCTGGGGGCCATCAATTTCATTACAACAATTATTAATATGAAACCCCCTGCCATTTCTCAGTACCAAACGCC
CCTGTTCGTCTGGGCCGTTCTAATTACCGCTGTCCTACTTCTTCTTTCCCTCCCTGTTTTAGCGGCGGGAATTACAAT
GCTTCTTACAGATCGAAACCTAAATACCACTTTCTTTGACCCAGCAGGAGGAGGGGACCCCATCCTCTACCAACA

MK340657 (mtDNA COI)
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CTGGCTAATCCCACTAATGATCGGGGCTCCTGACATGGCATTCCCCCGAATGAATAACATGAGCTTTTGGCTCCTC
CCCCCATCATTCCTGCTACTCCTAGCCTCCTCAGGGGTTGAAGCCGGAGCTGGAACTGGATGGACAGTCTACCCC
CCTCTAGCAGGAAACCTTGCACACGCAGGGGCATCTGTTGACCTAACTATCTTTTCCCTTCACCTAGCAGGTGTTT
CTTCAATTCTGGGGGCCATCAATTTCATTACAACAATTATTAATATGAAACCCCCTGCCATTTCTCAGTACCAAACG
CCCCTGTTCGTCTGGGCCGTTCTAATTACCGCTGTCCTACTTCTTCTTTCCCTCCCTGTTTTAGCGGCGGGAATTAC
AATGCTTCTTACAGATCGAAACCTAAATACCACTTTCTTTGACCCAGCAGGAGGAGGGGACCCCATCCTCTACCAA
CA

Scientific name: *Lutjanus lemniscatus* **Valenciennes, 1828**
English name: Ribboned snapper
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae

Standard length: 163 mm
Fin formula: D-X/14, P1-16, P2-I/5, A-III/8, C-17-20
Identification: Colour of back and upper sides gray-brown or olive; sides gray, brown or reddish; juveniles with a broad black horizontal band from snout tip to caudal-fin base. Body moderately deep. Preopercular notch and knob poorly developed. Caudal fin truncate or slightly emarginate. Scale rows on back rising obliquely above lateral line.

DNA Barcode: MK340645, MK340646, MK340647, MK340648

MK340645 (mtDNA COI)
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TCCTCAGGGGTAGAAGCCGGCGCTGGAACTGGGTGGACAGTGTACCCCCCTCTAGCAGGAAACCTTGCGCACGCAGGAGCATC
TGTTGACCTAACTATCTTCTCCCTTCATCTGGCAGGTGTTTCTTCAATTCTGGGGGCCATTAATTTTATTACAACAATTATTAATAT
GAAACCCCCTGCTATCTCTCAATACCAAACACCTCTGTTCGTCTGGGCCGTTCTAATTACCGCGGTCCTGCTTCTTCTCTCTCTCCC
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ATCCTCTACCAACA

MK340646 (mtDNA COI)
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TCCTGCTGCTACTAGCCTCCTCAGGGGTAGAAGCCGGCGCTGGAACTGGGTGGACAGTGTACCCCCCTCTAGCAGGAA
ACCTTGCGCACGCAGGAGCATCTGTTGACCTAACTATCTTCTCCCTTCATCTGGCAGGTGTTTCTTCAATTCTGGGGGCC
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MK340647 (mtDNA COI)
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MK340648 (mtDNA COI)
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CTAATTACCGCTGTGCTACTTCTTCTCTCTCTCCCCGTCCTAGCTGCCGGAATTACAATGCTTCTCACAGATCGAAACCTA
AACACCACCTTCTTTGACCCCGCAGGAGGAGGAGATCCTATTCTTTACCAACA

Scientific name: *Lutjanus lunulatus* **Park, 1797**
English name: Lunartail snapper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae

Standard length: 164 mm
Fin formula: D-X/14, P1-17, P2-I/5, A-III/8, C-16-18
Identification: Dorsal side is reddish, upper part of ventral side is reddish pink, and lower part is yellowish. Dorsal fin greyish with a reddish colour margins at the anterior part. Pectoral, pelvic and anal fins are yellow in colour. Caudal fin reddish with a black lunar shape marking. Body large, elongated and laterally compressed. Dorsal profile of head steeply sloped. Preopercular notch and knob poorly developed. Mouth large, oblique shape and mouth position terminal. Head large in comparison with body. Scale ctenoid, scale rows on back rising obliquely above lateral line. Teeth canine present along the both upper and lower jaw. Vomerine teeth also present and small. Jaws medium and equal. Nostril rounded. Barble absent. Lateral line single, complete and curved. Eye dorsal in position. Caudal fin emarginated. Fourth dorsal spine is the longest.

DNA Barcode: MK340649, MK340650, MK340651

MK340649 (mtDNA COI)
GGCACGGCCCTAAGCCTGCTCATTCGAGCAGAGCTAAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGA
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GGATGGACAGTGTACCCCCCTCTAGCAGGGAACCTCGCACACGCAGGGGCATCTGTTGACCTTACCATCTT
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CCCCCTGCCATCTCTCAATACCAAACACCTCTGTTCGTCTGGGCCGTTCTAATTACCGCTGTGCTACTTCTTC
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CCCCGCAGGAGGAGGAGATCCTATTCTTTACCAACA

MK340651 (mtDNA COI

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GATGGACAGTGTACCCCCCTCTAGCAGGGAACCTCGCACACGCAGGGGCATCTGTTGACCTTACCATCTTT
TCCCTCCATCTAGCAGGTGTTTCTTCAATTCTAGGGGCCATCAATTTTATTACAACAATTATCAACATGAAAC
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MK340650 (mtDNA COI

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TCCCTCCATCTAGCAGGTGTTTCTTCAATTCTAGGGGCCATCAATTTTATTACAACAATTATCAACATGAAAC
CCCCTGCCATCTCTCAATACCAAACACCTCTGTTCGTCTGGGCCGTTCTAATTACCGCTGTGCTACTTCTTCT
CTCTCTCCCCGTCCTAGCTGCCGGAATCACAATGCTTCTCACAGATCGAAACCTAAACACCACCTTCTTTGAC
CCAGCTGGAGGAGGGGACCCAATTCTTTATCAACA

Scientific name: *Lutjanus lutjanus* **Bloch, 1790**
English name: Big eye snapper, rosy snapper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae

Standard length: 120 mm
Fin formula: D-XI/12, P1-17, P2-I/5, A-III/8, C-17-19
Identification: Dorsal side of the body is golden brown in colour and ventral side is silvery white. A yellow stripe running along middle of the body that reach nearly to the eye. Dorsal fin is yellow in colour, pectoral fin yellowish, ventral fin orange in colour and caudal fin is pale yellow. Body elongated, laterally compressed. Dorsal side of the head gently sloped. Size moderate, dorsal profile convex. Head moderate in size. Mouth is terminal, superior and mouth protractile. Nostril rounded. Ctenoid scale present along the body. Large canine teeth present along the upper jaw, vomerine teeth also present. Lateral line present, complete and slightly curved. Eye slightly dorsal in position and large.

DNA Barcode: MK340652, MK340653, MK340654

MK340654 (mtDNA COI)
GGTACGGCCCTAAGCTTGCTCATTCGAGCAGAATTAAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGA
TTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTATAGTAATGCCAATTATGATCGGAG
GGTTTGGAAACTGGCTAATCCCACTAATAATCGGGGCCCCTGACATGGCATTTCCTCGAATGAATAACAT
GAGTTTTTGGCTTCTCCCCCCATCATTCCTACTACTACTCGCCTCCTCAGGCGTAGAAGCCGGAGCTGGGA
CTGGATGGACAGTGTACCCCCCTCTAGCAGGAAATCTTGCACACGCAGGAGCATCTGTTGACCTAACTAT
TTTCTCCCTTCACCTGGCAGGTGTTTCTTCAATTCTAGGGGCCATCAATTTTATTACAACGATTATTAATAT
GAAACCCCCTGCTATCTCTCAATATCAGACACCTCTATTCGTTTGGGCCGTTCTAATTACCGCTGTCCTACT
CCTTCTTTCCCTCCCTGTCCTAGCTGCCGGAATTACAATGCTTCTCACAGATCGAAACCTAAATACCACCTT
CTTTGACCCAGCAGGAGGAGGAGACCCCATCCTCTACCAGCA

MK340653 (mtDNA COI)

GGTACGGCCCTAAGCTTGCTCATTCGAGCAGAATTAAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGA
TTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATCTTTTTTATAGTAATGCCAATTATGATCGGAG
GGTTTGGAAACTGGCTAATCCCACTAATAATCGGGGCCCCTGACATGGCATTTCCTCGAATGAATAACAT
GAGTTTTTGGCTTCTCCCCCCATCATTCCTGCTACTACTCGCCTCCTCAGGCGTAGAAGCCGGAGCTGGGA
CTGGATGGACAGTGTACCCCCCTCTAGCAGGAAATCTTGCACACGCAGGAGCATCTGTTGACCTAACTAT
TTTCTCCCTTCACCTGGCAGGTGTTTCTTCAATTCTAGGGGCCATCAATTTTATTACAACGATTATTAATAT
GAAACCCCCTGCTATTTCTCAATATCAGACACCTCTATTCGTTTGGGCCGTTCTAATTACCGCTGTCCTGCT
CCTTCTTTCCCTCCCTGTCCTAGCTGCCGGAATTACAATGCTTCTCACAGATCGAAACCTAAATACCACCTT
CTTTGACCCAGCAGGAGGAGGAGACCCCATCCTCTACCAGCA

MK340652 (mtDNA COI)

GGTACGGCCCTAAGCTTGCTCATTCGAGCAGAATTAAGCCAACCAGGAGCTCTTCTTGGAGACGACCAGA
TTTATAATGTAATTGTTACAGCACATGCTTTTGTAATAATTTTTTTTATAGTAATGCCAATTATGATCGGAG
GGTTTGGAAACTGGCTAATCCCACTAATAATCGGGGCCCCTGACATGGCATTTCCTCGAATGAATAACAT
GAGTTTTTGGCTTCTCCCCCCATCATTCCTACTACTACTCGCCTCCTCAGGCGTAGAAGCCGGAGCTGGGA
CTGGATGGACAGTGTACCCCCCTCTAGCAGGAAATCTTGCACACGCAGGAGCATCTGTTGACCTAACTAT
TTTCTCCCTTCACCTGGCAGGTGTTTCTTCAATTCTAGGGGCCATCAATTTTATTACAACGATTATTAATAT
GAAACCCCCTGCTATTTCTCAATATCAGACACCTCTATTCGTTTGGGCCGTTCTAATTACCGCTGTCCTGCT
CCTTCTTTCCCTCCCTGTCCTAGCTGCCGGAATTACAATGCTTCTCACAGATCGAAACCTAAATACCACCTT
CTTTGACCCAGCAGGAGGAGGAGACCCCATCCTCTACCAGCA

Species Name: *Lutjanus rivulatus* **Cuvier, 1828**
English name: Blubberlip snapper
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae

Standard length: 236 mm
Fin formula: D-X/16, P1-17, P2-I/5, A-III/8, C-17-19
Identification: Dorsal side is brownish and ventral side blackish. Head with numerous blue and yellow wavy line. Body with 5 brown transverse bars. A chalky white spot present just below the anterior part of the dorsal soft ray. Dorsal fin black with a black lower margin. Pectoral and pelvic fin blackish. Anal fin is also black with a lower white margin and caudal fin dark in colour. Body large, elongated and laterally compressed. Dorsal profile of head steeply sloped. Preopercular notch and knob moderately developed. Mouth large, oblique and terminal. Lip large and fleshy. Head moderate in comparison with body. Scale ctenoid, scale rows on back rising obliquely above lateral line. Teeth canine and present along the upper jaw. Jaws large and equal. Nostril rounded. Lateral line single, complete and curved. Eye dorsal in position. Caudal fin truncated.

DNA Barcode: MK340658, MK340659, MK340660

MK340658 (mtDNA COI)
GGCACGGCCTTAAGCCTGCTTATCCGAGCAGAGCTTAGCCAACCAGGAGCTCTTCTTGGAGACGACCAAAT
TTATAATGTAATTGTTACAGCACATGCGTTTGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGA
TTTGGAAACTGGCTGATCCCATTAATAATTGGTGCCCCTGATATAGCATTCCCCCGAATAAACAATATAAGC
TTTTGGCTTCTACCCCCATCATTCCTGCTACTCCTAGCCTCTTCAGGAGTAGAAGCCGGTGCCGGGACTGGG
TGGACAGTTTATCCTCCCCTGGCAGGAAACCTGGCACATGCAGGAGCATCTGTTGACCTCACTATTTTCTCC
TTACATCTAGCAGGTGTTTCTTCAATTCTAGGAGCTATCAATTTCATCACAACAATCATCAACATAAAACCCC
CTGCTATTTCCCAATACCAAACACCCCTATTCGTCTGGGCCGTCCTAATCACTGCCGTTCTACTTCTTCTCTCC
CTCCCAGTTCTGGCTGCCGGAATTACAATGCTTCTCACAGATCGAAATCTAAACACCACCTTCTTCGACCCA
GCAGGAGGGGGTGATCCCATCCTCTACCAACA

MK340659 (mtDNA COI)
GGCACGGCCTTAAGCCTGCTTATCCGAGCAGAGCTTAGCCAACCAGGAGCTCTTCTTGGAGACGACCAAAT
TTATAATGTAATTGTTACAGCACATGCGTTTGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGA
TTTGGAAACTGGCTGATCCCATTAATAATTGGTGCCCCTGACATAGCATTCCCCCGAATGAACAATATAAGC
TTTTGGCTTCTACCCCCATCATTCCTGCTACTCCTAGCCTCTTCAGGAGTAGAAGCCGGTGCCGGGACTGGG
TGGACAGTTTATCCTCCCCTGGCAGGAAACCTGGCACATGCAGGAGCATCTGTTGACCTCACTATTTTCTCC
TTACATCTAGCAGGTGTTTCTTCAATTCTAGGAGCTATCAATTTCATCACAACAATCATCAACATAAAACCCC
CTGCTATTTCCCAATACCAAACACCCCTATTCGTCTGGGCCGTCCTAATCACTGCCGTTCTACTTCTTCTCTCC
CTCCCAGTTCTGGCTGCCGGAATTACAATGCTTCTCACAGATCGAAATCTAAACACCACCTTCTTCGACCCA
GCAGGAGGGGGTGATCCCATCCTCTACCAACA

MK340659 (mtDNA COI)
GGCACGGCCTTAAGCCTGCTTATCCGAGCAGAGCTTAGCCAACCAGGAGCTCTTCTTGGAGACGACCAAAT
TTATAATGTAATTGTTACAGCACATGCGTTTGTAATAATTTTCTTTATAGTAATGCCAATCATGATTGGAGGA
TTTGGAAACTGGCTGATCCCATTAATAATTGGTGCCCCTGATATAGCATTCCCCCGAATGAACAATATAAGC
TTTTGGCTTCTACCCCCATCATTCCTGCTACTCCTAGCCTCTTCAGGAGTAGAAGCCGGTGCCGGGACTGGG
TGGACAGTTTATCCTCCCCTGGCAGGAAACCTGGCACATGCAGGAGCATCTGTTGACCTCACTATTTTCTCC
TTACATCTAGCAGGTGTTTCTTCAATTCTAGGAGCTATCAATTTCATCACAACAATCATCAACATAAAACCCC
CTGCTATTTCCCAATACCAAACACCCCTATTCGTCTGGGCCGTCCTAATCACTGCCGTTCTACTTCTTCTCTCC
CTCCCAGTTCTGGCTGCCGGAATTACAATGCTTCTCACAGATCGAAATCTAAACACCACCTTCTTCGACCCA
GCAGGAGGGGGTGATCCCATCCTCTACCAACA

Species Name: *Lutjanus erythropterus* **Bloch, 1790**
English name: Crimson snapper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Lutjanidae

Standard length: 124 mm
Fin formula: D-XI/14, P1-17, P2-I/5, A-III/9, C-19-22
Identification: Body reddish or brownish in colour. Head region contain a brownish band that extend to the base of the dorsal fin. Dorsal fin grey colour with a brown anterior margin. Pectoral fin brownish. Pelvic and anal fin grey colour. Caudal fin brown and caudal peduncle contain a large black mark surrounded by creamy white border. Body large, elongated and laterally compressed. Body relatively deep. Dorsal profile of head steeply sloped. Preopercular notch and knob poorly developed. Mouth large, terminal and pointed. Head large in comparison with body. Scale ctenoid, scale rows on back rising obliquely above lateral line. Teeth canine and present along the upper jaw. Vomerine teeth also present. Jaws medium and equal. Nostril rounded. Barble absent. Lateral line single, complete and curved. Eye dorsal in position. Dorsal fin single, large and spine present. Caudal fin truncate. Fifth dorsal spine is the longest.

Species Name: *Lutjanus russellii* **Bleeker, 1849**
English name: Russell's snapper
<u>Classification</u>
Class: Actinopterygii
    Order: Perciformes
        Family: Lutjanidae

Standard length: 103 mm
Fin formula: D-X/14, P1-16, P2-I/5, A-III/8, C-17-20
Identification: Colour of back and upper side brownish; lower sides and belly pink to whitish with a silvery sheen; a black spot, sometimes faint, is on the lateral line below the anterior portions of the soft dorsal fin; adults from the Indian Ocean usually with 7 or 8 narrow golden brown stripes on sides; juveniles from the western Pacific whitish with 4 black stripes on sides and with a round black spot on upper back. Body moderately deep. Anterodorsal profile of head steeply to moderately sloped; preorbital width about equal to, or slightly less than eye diameter; preopercular notch and knob poorly developed. Posterior profile of dorsal and anal fins rounded; caudal fin truncate. Scale rows on back rising obliquely above lateral line.

DNA Barcode: MK340661

MK340661 (mtDNA)
GGCACGGTCCTAAGCCTGCTCATTCGAGCAGAGCTTAGTCAACCAGGAGCTCTTCTTGGAGACGACCAGATTTATAA
TGTAATTGTTACAGCACATGCTTTTGTAATAATTTTCTTTATAGTAATACCAATCATGATTGGAGGGTTCGGGAACTG
GCTAATCCCATTAATGATCGGAGCCCCTGACATGGCATTCCCCCGAATGAACAACATGAGTTTTTGGCTCCTCCCACC
ATCCTTCCTACTGCTATTAGCTTCTTCAGGAGTAGAAGCCGGAGCCGGGACTGGATGGACAGTTTATCCCCCTCTAGC
AGGAAACCTTGCACACGCAGGGGCATCTGTTGACCTGACCATCTTCTCCCTTCACCTAGCAGGTGTTTCTTCAATTCT
AGGGGCTATCAATTTCATTACAACAATCATTAACATGAAACCCCCCGCTATCTCTCAGTACCAAACACCTCTATTTGTC
TGGGCCGTCCTAATTACCGCTGTCCTGCTCCTTCTTTCTCTTCCAGTACTAGCTGCCGGAATTACAATACTTCTCACAG
ATCGAAACCTAAATACTACCTTCTTTGACCCAGCAGGAGGAGGAGACCCCATTCTTTACCAACA

Species Name: *Mene maculata***Bloch & Schneider, 1801**
English name: Moonfish
<u>Classification</u>
Class: Actinopterygii
    Order: Perciformes
        Family: Menidae

Standard length: 147 mm
Fin formula: D-IV/42, P1-16, P2-I/5, A-32, C-20-24
Identification: Body dark blue above, silvery whitebelow; 3 rows of dark spots immediately above and below lateral line; dorsal and caudal fins dusky. Mouth protrudes upwards; first two rays of ventral fin fused and elongate; scales small, deciduous.

DNA Barcode: MK340663

MK340663 (mtDNA COI)
GGGGCCGCCCTAAGTCTACTCATCCGAGCAGAACTTAACCAACCTGGCACTCTCCTGGGAGACGACCAAATCTATA
ATGTAATTGTTACGGCACACGCCTTTGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGCTTCGGAAACT
GGCTGATCCCCCTAATAGTTGGAGCCCCCGACATAGCATTCCCTCGAATAAACAACATGAGCTTCTGGCTTCTCCCTC
CCTCGTTCCTTCTCCTACTGGCCTCCTCAGGAGTAGAAGCCGGTGCCGGAACGGGATGGACCGTATACCCGCCTCTT
GCCGGGAATTTAGCCCACGCCGGAGCATCTGTTGACCTCACAATTTTCTCACTTCACTTGGCCGGGGTCTCTTCAATT
CTTGGGGCAATTAATTTTATTACTACGATTATCAACATGAAACCACCTACTGTCTCAATGTACCAAATTCCTTTATTTG
TTTGGGCAGTCCTAATTACAGCCGTCCTTCTCCTCCTTTCCCTCCCGGTCCTAGCTGCCGGAATTACAATGCTGTTAAC
AGACCGAAACCTGAACACCGCTTTCTTTGACCCTGCTGGAGGAGGAGACCCAATCCTCTACCAGCA

Species Name: *Upeneus guttatus***Day, 1868**
English name: Two-tone goatfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Mullidae

Standard length: 64 mm
Fin formula: D1-VII, D2-9, P1-14, P2-I/5, A-I/7, C-16-18
Identification: Colour of body silvery pink with bright vermilion spots or blotches; barbels yellow; bright red bars on both dorsal fins; faint reddish bars on pelvic fins; upper lobe of caudal fin with 5 red oblique bars, the lower lobe with a red wide band from center of caudal fin base to inner hind margin and 5 red oblique bars. Body elongate, cylindrical. Chin with 2 slender barbels, usually just reaching to posterior margin of preopercle. Mouth small; small conical blunt teeth in a narrow band on jaws. Scales present on side of snout.

DNA Barcode: MK340739

MK340739 (mtDNA COI)
GGAACTGCTTTAAGCCTCCTCATCCGTGCCGAACTAGCCCAACCTGGGGCTCTCCTGGGCGACGACCAGATTTATAAT
GTAATCGTTACAGCCCACGCCTTTGTAATAATTTTCTTCATGGTAATGCCTATCATGATTGGAGGATTCGGCAACTGG
CTCATTCCTCTGATGATCGGTGCACCAGACATGGCCTTCCCTCGTATGAACAATATGAGCTTCTGGCTACTCCCTCCTT
CTTTCCTCCTTCTACTTGCCTCCTCAGGCGTCGAAGCAGGGGCTGGAACAGGCTGGACTGTTTACCCTCCTTTAGCAG
GCAACCTTGCACATGCCGGGGCCTCTGTTGACCTCACTATCTTCTCCCTGCATCTGGCAGGGATCTCCTCTATCCTGG
GGGCCATTAATTTTATTACAACAATTATCAACATGAAACCTCCAGCAATTTCACAATATCAAACACCTCTATTCGTTTG
GGCTGTCCTGATTACAGCCGTCCTACTCCTTCTTTCCCTGCCAGTCCTTGCTGCCGGGATTACCATGCTGCTTACAGAT
CGAAACCTAAATACAACCTTCTTCGACCCAGCTGGGGGCGGGGATCCCATCCTTTATCAACA

Species Name: *Upeneus sulphureus* **Cuvier, 1829**
English name: Sulpher goatfish

Classification
Class: Actinopterygii
Order: Perciformes
Family: Mullidae

Standard length: 105 mm
Fin formula: D1-VIII, D2-9, P1-17, P2-I/5, A-I/7, C-22-24
Identification: Body colour grayish bronze; head reddish; lower sides and belly pale with two yellowish horizontal stripes on sides ; tip of first dorsal fin black ; no bars on caudal and anal fins. Body elongate and slightly com pressed; dorsal prole of head convex. One pair of short and thin barbels. Scales ctenoid; pre-orbital scales absent.

DNA Barcode: MK340740, MK340741, MK340742, MK340743

MK340740 (mtDNA COI)
GGAACCGCTTTAAGCCTTCTTATTCGTGCTGAACTATCTCAACCTGGGGCCCTCCTAGGTGATGATCAAATTTATAACGTAATTG
TTACGGCGCACCCCTTTGTAATAATTTTCTTCATGGTAATGCCAATCATGATCGGGGGATTCGGTAACTGGCTAATCCCACTAAT
GATTGGTGCGCCCGACATGGCCTTCCCTCAAATGAATAACATGAGCTTCTGGCTCCTACCCCCTTCTTTCCTCCTGCTACTTGCCT
CTTCAGGCGTTGAAGCCGGGGCAGGGACAGGTTGGACTGTTTACCCTCCTTTAGCAGGTAACCTTGCACACGCCGGGGCCTCA
GTTGACCTTACCATCTTCTCTCTCCATCTGGCAGGTATTTCTTCTATTCTAGGGGCTATTAACTTCATTACCACGATTATTAATATG
AAACCTCCTGCAATTTCACAGTATCAAACACCTTTATTTGTGTGGGCCGTACTAATTACAGCTGTCCTTCTCCTTCTGTCCCTACC
AGTCCTAGCTGCAGGCATCACAATGCTGCTAACAGATCGAAACCTCAATACAACCTTCTTCGACCCAGCAGGTGGAGGAGACCC
AATCCTTTATCAACA

MK340741 (mtDNA COI)
GGAACCGCTTTAAGCCTTCTTATTCGTGCTGAACTATCTCAACCTGGGGCCCTCCTAGGTGATGATCAAATT
TATAACGTAATTGTTACGGCGCACGCCTTTGTAATAATTTTCTTCATGGTAATGCCAATCATGATCGGGGGA
TTCGGTAACTGGCTAATCCCACTAATGATTGGTGCGCCCGACATGGCCTTCCCTCGAATGAATAACATGAGC
TTCTGGCTCCTACCCCCTTCTTTCCTCCTGCTACTTGCCTCTTCAGGCGTTGAAGCCGGAGCAGGGACAGGT
TGGACTGTTTACCCTCCTTTAGCAGGTAACCTTGCACACGCCGGGGCCTCAGTTGACCTTACCATCTTCTCTC
TCCATCTGGCAGGTATTTCTTCTATTCTAGGGGCTATTAACTTCATTACCACGATTATTAATATGAAACCTCC
TGCAATTTCACAGTATCAAACACCTTTATTTGTGTGGGCCGTACTAATTACAGCTGTCCTTCTCCTTCTGTCC
CTACCAGTCCTAGCTGCAGGCATCACAATGCTGCTAACAGATCGAAACCTCAATACAACCTTCTTCGACCCA
GCAGGTGGAGGAGACCCAATCCTTTATCAACA

MK340742 (mtDNA COI)
GGAACCGCTTTAAGCCTTCTTATTCGTGCTGAACTATCTCAACCTGGGGCCCTCCTAGGTGATGATCAAATT
TATAACGTAATTGTTACGGCGCACGCCTTTGTAATAATTTTCTTCATGGTAATGCCAATCATGATCGGGGGA
TTCGGTAACTGGCTAATCCCGCTAATGATTGGTGCGCCCGACATGGCCTTCCCTCGAATGAATAACATGAG
CTTCTGGCTCCTACCCCCTTCTTTCCTCCTGCTACTTGCCTCTTCAGGCGTTGAAGCCGGGGCAGGGACAGG
TTGGACTGTTTACCCTCCTTTAGCAGGTAACCTTGCACACGCCGGGGCCTCAGTTGACCTTACCATCTTCTCT
CTCCATCTGGCAGGTATTTCTTCTATTCTAGGGGCTATTAACTTCATTACCACGATTATTAATATGAAACCTC
CTGCAATTTCACAGTATCAAACACCTTTATTTGTGTGGGCCGTACTAATTACAGCTGTCCTTCTCCTTCTGTC
CCTACCAGTCCTAGCTGCAGGCATCACAATGCTGCTAACAGATCGAAACCTCAATACAACCTTCTTCGACCC
AGCAGGTGGAGGAGACCCAATCCTTTATCAACA

MK340743 (mtDNA COI)
GGAACCGCTTTAAGCCTTCTTATTCGTGCTGAACTATCTCAACCTGGGGCCCTCCTAGGTGATGATCAAATT
TATAACGTAATTGTTACGGCACACGCCTTTGTAATAATTTTCTTCATGGTAATGCCAATCATGATCGGGGGA
TTCGGTAACTGGCTAATCCCGCTAATGATTGGTGCGCCCGACATGGCCTTCCCTCGAATGAATAACATGAG
CTTCTGGCTCCTACCCCCTTCTTTCCTCCTGCTACTTGCCTCTTCAGGCGTTGAAGCCGGGGCAGGGACAGG
TTGGACTGTTTACCCTCCTTTAGCAGGTAACCTTGCACACGCCGGGGCCTCAGTTGACCTTACCATCTTCTCT
CTCCATCTGGCAGGTATTTCTTCTATTCTAGGGGCTATTAACTTCATTACCACGATTATTAATATGAAACCTC
CTGCAATTTCACAGTATCAAACACCTTTATTTGTGTGGGCCGTACTAATTACAGCTGTCCTTCTCCTTCTGTC
CCTACCAGTCCTAGCTGCAGGCATCACAATGCTGCTAACAGATCGAAACCTCAATACAACCTTCTTCGACCC
AGCAGGTGGAGGAGACCCAATCCTTTATCAACA

Species Name: *Upeneus tragula* Richardson, 1846
English name: Freckled goatfish
Classification
Class: Actinopterygii
Order: Perciformes
Family: Mullidae

Standard length: 103 mm
Fin formula: D1-VIII, D2-9, P1-13, P2-I/5, A-I/6, C-16-18
Identification: Highly variable in colour, from red, to irregular dots and blotches on body; a dark reddish brown to blackish stripe from front of snout to base of caudal fin; head and body above stripe brownish to greenish gray, flecked with small dark reddish brown or blackish spots; upper lobe of caudal fin with 4-6 blackish cross bands, and lower lobe with 5-7; outer third to half of first dorsal fin with a large dark red to black blotch containing 2 to several small yellow spots; second dorsal fin with 3 dark reddish or blackish bands; barbels usually yellow. Body elongate. Chin with 2 slender barbels, usually not reaching rear margin of preopercle. Mouth small; villiform teeth in a narrow band in jaws. Scales present on side of snout.

DNA Barcode: MK340744

MK340744 (mtDNA COI)
GGAACTGCTTTAAGCCTCCTCATTCGTGCCGAACTAGCCCAACCTGGGGCTCTCCTGGGCGACGACCAGATTTA
TAATGTAATCGTCACAGCCCACGCCTTTGTAATGATTTTCTTCATGGTAATGCCTATCATGATCGGAGGATTTGG
CAACTGGCTTATCCCTCTAATGATTGGTGCACCAGACATGGCCTTCCCTCGTATGAACAATATGAGCTTCTGGCT
ACTCCCCCCTTCTTTCCTCCTACTACTCGCCTCCTCAGGCGTTGAAGCAGGGGCTGGGACAGGTTGGACTGTTTA
CCCTCCTTTAGCAGGCAACCTTGCACACGCCGGGGCCTCTGTTGATCTCACTATTTTCTCCCTACACCTAGCGGG
GATTTCCTCTATTCTAGGGGCCATCAATTTTATTACAACAATTATCAACATGAAACCTCCAGCAATTTCACAATAT
CAGACACCTCTATTCGTCTGGGCTGTGCTAATTACGGCTGTCCTTCTCCTTCTTTCCCTACCAGTTCTTGCTGCGG
GGATTACTATGCTGCTTACAGATCGAAATCTGAATACTACCTTCTTCGACCCAGCAGGTGGAGGGGACCCCATC
CTTTACCAACA

Species Name: *Parupeneus indicus***Shaw, 1803**
English name: Indian goatfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Mullidae

Standard length: 218 mm
Fin formula: D1-VIII, D2-9, P1-16, P2-I/5, A-I/7, C-16-20
Identification: Colour of body brownish-white above and silvery white below; a horizontally elongate yellow spot on middle of back centered on lateral line; a black spot posteriorly on caudal peduncle; upper part of head with light blue lines; fins hyaline. Barbels extending slightly behind hind margin of preoperculum.
DNA Barcode: MK340674, MK335873
Remarks: New distributional record from Bangladesh.

MK340674(mtDNA COI)

GGAACTGCTTTAAGCCTTCTTATTCGTGCCGAGCTCAGCCAACCCGGCGCTCTTTTAGGTGACGACCAAATT
TATAATGTAATTGTTACAGCACATGCCTTTGTAATAATTTTCTTTATGGTAATGCCAATTATGATTGGAGGG
TTCGGTAACTGGCTTATTCCACTCATGATCGGGGCACCCGACATGGCTTTCCCTCGAATGAACAACATGAG
CTTCTGGCTACTCCCTCCCTCTTTCCTGCTTCTTCTTGCCTCTTCAGGTGTTGAAGCTGGGGCCGGAACTGGT
TGGACGGTCTACCCTCCACTTGCAGGTAATCTAGCACATGCCGGAGCATCTGTTGACCTAACTATCTTCTCC
CTCCACCTTGCAGGTATTTCTTCAATCCTGGGAGCTATTAATTTTATTACTACAATTATTAATATGAAACCCC
CTGCAATTTCACAATACCAGACACCTCTGTTCGTCTGGGCTGTGTTAATTACAGCCGTGCTACTCCTTCTGTC
ACTTCCAGTCCTTGCCGCTGGCATTACAATGCTACTCACGGACCGAAACCTAAATACAACTTTCTTCGACCC
GGCAGGCGGGGGAGACCCAATCCTTTACCAACA

Species Name: *Scolopsis vosmeri***Bloch, 1792**
English name: Whitecheek monocle bream
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Nemipteridae

Standard length: 108 mm
Fin formula: D-X/9, P1-18, P2-I/5, A-III/7, C-17-19
Identification: Colour: head and body brownish, paler ventrally; distinct, broad white vertical bar on head. Body deep. Suborbital with a large backwardly-pointed spine; no antrorse spine just below eye; external edge of maxilla smooth; lower limb of preopercle scaled. Pelvic fin reaching to or beyond anus when appressed; caudal fin forked.

DNA Barcode: MK340705, MK340706, MK340707

MK340705 (mtDNA COI)
GGGACGGCATTAAGCCTGCTCATTCGAGCTGAACTAAGTCAGCCAGGCGCTCTCTTAGGAGACGACCAAA
TTTATAATGTGATTGTCACGGCCCATGCTTTCGTGATAATTTTCTTTATGGTTATACCAATTATAATTGGAGG
GTTCGGAAACTGGCTAATTCCACTTATGATTGGTGCGCCAGACATGGCATTTCCTCGTATGAACAATATGA
GTTTTTGGCTACTTCCTCCATCATTCCTTCTACTTTTAGCTTCTTCAGGAGTTGAAGCAGGGGCTGGAACAG
GTTGGACAGTGTACCCCCCTCTTGCTGGAAACTTAGCACATGCTGGAGCGTCAGTCGATTTAACCATCTTCT
CGCTGCATCTGGCAGGAATTTCTTCAATCCTAGGAGCTATTAATTTTATTACAACAATTATTAACATGAAACC
TCCAGCTATTTCACAATACCAGACACCCCTCTTTGTATGGGCCGTCCTCATCACTGCTGTTCTTCTTCTTCTCT
CCCTCCCTGTTCTTGCTGCCGGAATTACAATACTCCTTACAGACCGAAACTTGAACACAACCTTTTTTGACCC
TGCAGGAGGAGGAGACCCAATTCTTTACCAACA

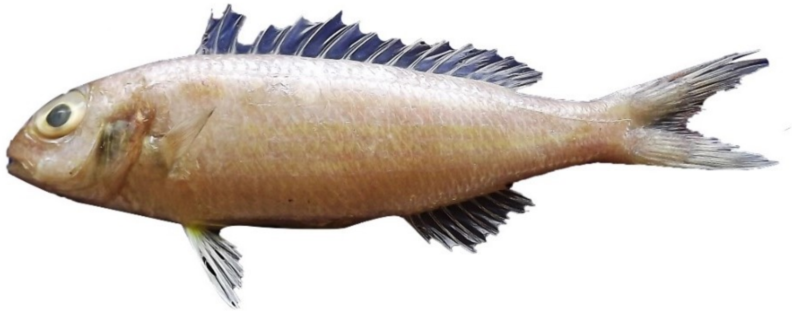
MK340706 (mtDNA COI)
GGGACGGCATTAAGCCTGCTCATTCGAGCTGAACTAAGTCAGCCAGGCGCTCTCTTAGGAGACGACC
AAATTTATAATGTGATTGTCACGGCCCATGCTTTCGTGATAATTTTCTTTATGGTTATACCAATTATAAT
TGGAGGGTTCGGAAACTGGCTAATTCCACTTATGATTGGTGCGCCAGACATGGCATTTCCTCGTATGA
ACAATATGAGTTTTTGGCTACTTCCTCCATCATTCCTTCTACTTTTAGCTTCTTCAGGAGTTGAAGCAGG
GGCTGGAACAGGTTGGACAGTGTACCCCCCTCTTGCTGGAAACTTAGCACATGCTGGAGCGTCAGTC
GATTTAACCATCTTCTCGCTGCATCTGGCAGGAATTTCTTCAATCCTAGGAGCTATTAATTTTATTACAA
CAATTATTAACATGAAACCTCCAGCTATTTCACAATACCAGACACCCCTCTTTGTATGGGCCGTCCTCA
TCACTGCTGTTCTTCTTCTTCTCTCCCTCCCTGTTCTTGCTGCCGGAATTACAATACTCCTTACAGACCGA
AACTTGAACACAACCTTTTTTGACCCTGCAGGAGGAGGAGACCCAATTCTTTACCAACA

MK340707 (mtDNA COI)
GGGACGGCATTAAGCCTGCTCATTCGAGCTGAACTAAGTCAGCCAGGCGCTCTCTTAGGAGACGACC
AAATTTATAATGTGATTGTCACGGCCCATGCTTTCGTGATAATTTTCTTTATGGTTATACCAATTATAAT
TGGAGGGTTCGGAAACTGGCTAATTCCACTTATGATTGGTGCGCCAGACATGGCATTTCCTCGTATGA
ACAATATGAGTTTTTGGCTACTTCCTCCATCATTCCTTCTACTTTTAGCTTCTTCAGGAGTTGAAGCAGG
GGCTGGAACAGGTTGGACAGTGTACCCCCCTCTTGCTGGAAACTTAGCACATGCTGGAGCGTCAGTC
GATTTAACCATCTTCTCGCTGCATCTGGCAGGAATTTCTTCAATCCTAGGAGCTATTAATTTTATTACAA
CAATTATTAACATGAAACCTCCAGCTATTTCACAATACCAGACACCCCTCTTTGTATGGGCCGTCCTCAT
CACTGCTGTTCTTCTTCTTCTCTCCCTCCCTGTTCTTGCTGCCGGAATTACAATACTCCTTACAGACCGAA
ACTTGAACACAACCTTTTTTGACCCTGCAGGAGGAGGAGACCCAATTCTTTACCAACA

Species Name: *Nemipterus peronii* **Valenciennes, 1830**
English name: Notched threadfin bream

Classification

Class: Actinopterygii
Order: Perciformes
Family: Nemipteridae



Standard length: 44 mm
Fin formula: D-X/9, P1-17, P2-I/5, A-III/7, C-18-20
Identification: Colour of upper part of body pinkish with 7 or 8 indistinct darker pink saddles reaching to or just below lateral line; lower part of body silvery, with faint golden lines following each scale row. A diffuse pale reddish spot below and just posterior to origin of lateral line. Anal fin pale whitish pink. Caudal fin pinkish. Pelvic fins whitish and pectoral fin translucent. Body slender. Snout length almost equal to eye diameter. Lower margin of eye just above a line from tip of snout to upper base of pectoral fin. A line drawn up from the hind margin of suborbital reaching the dorsal profile. Dorsal fin spines elongate. Pectoral fins short, not reaching to level of anus. Pelvic fins more or less long, reaching to level of anus. Caudal fin deeply forked.
DNA Barcode: MK340666, MK340667

MK340666 (mtDNA COI)

GGAACCGCCCTAAGCCTCCTAATTCGAGCTGAGCTAAGCCAGCCAGGCGCTCTCTTGGGAGACGACCAGATTTACAACGTCATCG
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TCGGCGCCCCTGACATGGCATTCCCTCGTATGAACAACATGAGCTTTTGGCTTCTTCCCCCCTCATTCCTTCTTCTCCTTGCCTCCTC
AGGCATTGAAGCAGGTGCAGGAACAGGTTGGACAGTTTACCCACCCCTTGCAGGCAATCTAGCACATGCAGGAGCATCTGTAGA
CCTAACCATCTTTTCCCTTCACCTAGCAGGGATCTCTTCAATCTTAGGAGCTATCAATTTCATTACCACAATCATTAATATGAAGCCT
CCTGCTATTTCACAATATCAAACACCGCTGTTCGTTTGGGCAGTACTAATCACAGCTGTTCTTCTCCTCCTCTCTCTTCCAGTTTTAG
CAGCAGGTATTACAATATTACTAACTGACCGAAACTTGAACACAACTTTCTTTGATCCTGCGGGAGGGGGAGATCCAATTCTCTAC
CAACA

MK340666 (mtDNA COI)

GGAACCGCCCTAAGCCTCCTAATTCGAGCTGAGCTAAGCCAGCCAGGCGCTCTCTTGGGAGACGACCAGATTTACAACGTCATCG
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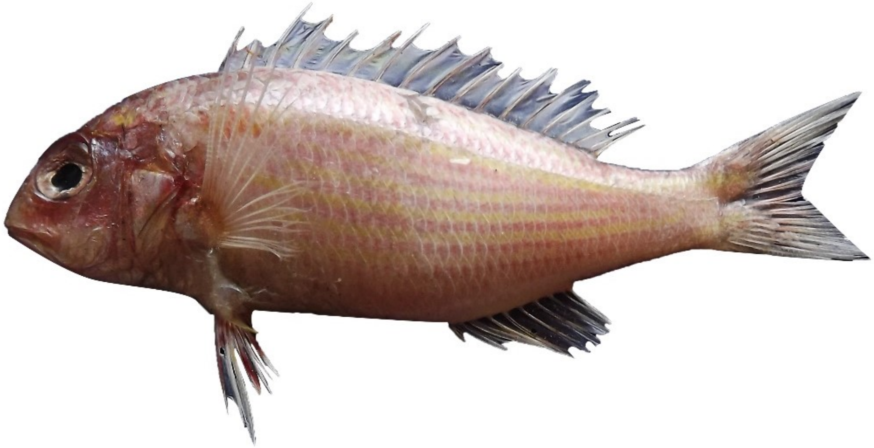
TCGGCGCCCCTGACATGGCATTCCCTCGTATGAACAACATGAGCTTTTGGCTTCTTCCCCCCTCATTCCTTCTTCTCCTTGCCTCCTC
AGGCATTGAAGCAGGTGCAGGAACAGGTTGGACAGTTTACCCACCCCTTGCAGGCAATCTAGCACATGCAGGAGCATCTGTAGA
CCTAACCATCTTTTCCCTTCACCTAGCAGGGATCTCTTCAATCTTAGGAGCTATCAATTTCATTACTACAATCATTAATATGAAGCCT
CCTGCTATTTCACAATATCAAACACCGCTGTTCGTTTGGGCAGTACTAATCACAGCTGTTCTTCTCCTCCTCTCTCTTCCAGTTTTAG
CAGCAGGTATTACAATATTACTAACTGACCGAAACTTGAACACAACTTTCTTTGATCCTGCGGGAGGGGGAGATCCAATTCTCTAC
CAACA

Species Name: *Nemipterus japonicas* **Bloch, 1791**
English name: Japanese threadfin bream
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Nemipteridae



Standard length: 97 mm
Fin formula: D-X/9, P1-17, P2-I/5, A-III/7, C-22
Identification: Colour of upper part of body pinkish, pale on sides to silvery-white on ventral surface. Sides with 11 to 12 longitudinal pale golden yellow stripes extending from posterior of head to base of caudal fin. A conspicuous yellow or orange blotch present on upper margin of opercle. Dorsal fin with a yellow band near base. Anal fin whitish with broken pale lemon coloured bands. Body somewhat deep. Snout length equal to or longer than eye diameter. Lower margin of eye above a line from tip of snout to upper base of pectoral fin. First two dorsal spines separated by a membrane, not produced into a long filament, and shorter than the following spines. Caudal fin forked, upper lobe slightly longer than lower and produced into a short or moderately long filament. Pectoral fins very long, reaching to or beyond level of anus. Pelvic fins reaching to or just beyond level of anal fin origin.

DNA Barcode: MK340665

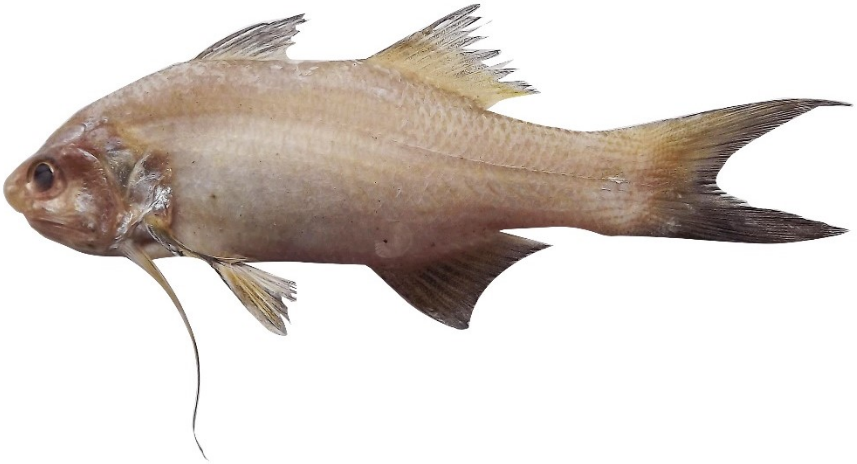
MK340665 (mtDNA COI)
GGGACTGCTCTAAGTCTGCTTATTCGGGCAGAACTTAGCCAACCAGGTGCCCTCTTAGGTGACGACCAGATTTATA
ATGTTATTGTTACGGCTCACGCTTTCGTAATAATCTTTTTTATAGTAATACCAATCATGATCGGAGGGTTCGGAAACT
GGCTGGTACCACTAATGATTGGTGCCCCTGATATAGCATTCCCTCGAATAAATAATATGAGCTTCTGGCTTCTGCCC
CCCTCATTCCTTCTTCTTCTCGCTTCATCAGGCATTGAAGCAGGTGCGGGAACCGGCTGGACAGTTTATCCTCCCCTT
GCAGGCAACCTAGCACATGCAGGAGCGTCTGTTGACCTCACTATTTTTTCCCTTCACTTGGCAGGGATTTCTTCAATT
TTAGGGGCCATTAATTTTATTACAACTATTATTAACATAAAACCTCCTGCTATCTCCCAATATCAAACGCCTCTCTTCG
TTTGGGCAGTACTAATTACAGCTGTTCTTCTCCTTCTCTCCCTTCCCGTCTTAGCAGCCGGTATTACTATACTTCTTAC
TGACCGAAACCTAAACACAACCTTCTTTGACCCTGCAGGTGGAGGAGACCCCATTCTTTACCAACA

Species Name: *Parapercis clathrata* **Ogilby, 1910**
English name: Latticed sandperch
Classification
Class: Actinopterygii
Order: Perciformes
Family: Pinguipedidae

Identification: Colour of body light brown dorsally with rows of small dark spots, whitish ventrally with a lower series of 9 or 10 elliptical brown or brown and red spots, with blackish centers; single black spot with white margin above gill opening in males; caudal fin with a white or yellow spots. Body cylindrical. Three pairs of canine teeth on lower jaw anteriorly. Palatine teeth absent. Middle dorsal spines longest. Membrane from spinous dorsal connected to 1st soft ray opposite tip of last spine.

Remarks: New distributional record from Bangladesh. This species has been recorded during the underwater scuba diving.

Species Name: *Filimanus similis* **Feltes, 1991**
English name: Indian sevenfinger threadfin
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Polynemidae



Standard length: 102 mm
Fin formula: D1-VIII, D2-I/13, P1-14+6/7 filaments, P2-I/5, A-III/12, C-22-24
Identification: Colour of upper sides of head and trunk with brown tinge, becoming golden on lower sides. Posterior margins of first, second dorsal, anal, and caudal fins blackish, remaining parts yellowish. Pectoral fin mostly black; pectoral filament base white, becoming yellowish-white on posterior tips. Pelvic-fin base white, other parts yellowish. Body moderately elongate, compressed. Snout pointed; occipital profile nearly straight. Lip on lower jaw well-developed, dentary teeth restricted to dorsal surface. Longest pectoral filament usually reaching anal fin origin. Lateral line simple, extending from upper end of gill opening to mid-distal margin of caudal-fin membrane.

DNA Barcode: MK340618, MK335852

MK340618 (mtDNA COI)
GGGACAGCCCTAAGCCTACTGATTCGTACAGAACTAAGCCAACCCGGCGCACTTCTGGGCGACGACCAAATTTATA
ATGTTATCGTTACAGCACACGCCTTTGTAATAATTTTCTTTATAGTAATGCCCATCATGATTGGTGGCTTTGGAAATT
GGCTTGTTCCGCTTATGATCGGTGCCCCAGATATAGCATTTCCCCGGATAAACAACATGAGTTTTTGGCTACTGCCCC
CTTCTTTCCTTCTTCTTCTGGCCTCTTCCGGAATCGAGGCTGGGGCCGGCACAGGGTGGACTGTCTACCCCCCACTAG
CGGGCAATCTTGCGCACGCAGGAGCATCAGTTGACCTAACCATCTTCTCCCTTCACCTGGCGGGGGTCTCGTCTATC
TTAGGTGCAATCAATTTTATTACAACTGTGCTAAATATGAAGCCCCCTGCCGCCTCAATATACCAACTCCCCCTGTTT
GTGTGGGCAGTTTTAATTACAGCTGTTCTTCTTCTCTTATCCCTTCCTGTACTAGCCGCTGGTATTACCATACTACTTA
CAGACCGAAACTTAAATACCTCATTCTTTGACCCTACTGGGGGAGGGGACCCAATCCTCTACCAACA

Species Name: *Pomacentrus tripunctatus* **Cuvier, 1830**
English name: Three-spot damsel
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family:Pomacentridae

Standard length: 71 mm
Fin formula: D-XIII/14, P1-17, P2-I/5, A-II/14, C-18-19
Identification: Colour of adults are brownish with darker scale margins. They have a large dark spot on the upper caudal peduncle. Juveniles are lighter in colour and have a large, blue-margined black spot on the dorsal fin. Small size.

DNA Barcode: MK335876

Species Name: *Chromis cinerascens* **Cuvier, 1830**
English name: Green chromis
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Pomacentridae

Standard length: 70 mm
Fin formula: D-XIII/11, P1-19, P2-I/5, A-II/11, C-20-22
Identification: Colour of head and body gray or dark gray brown dorsally, paler and tinged with gold ventrally; pelvic and anal fins whitish. Body deep and compressed. Posterior margin of preopercle smooth. Suborbital scaled, with entire ventral edge. Teeth on jaws conical, muliserial; teeth of outermost row larger than those of inner rows. Caudal fin forked; some conspicuous projecting spine like rays at upper and lower edges of caudal-fin base.

DNA Barcode: MK340603, MK335848

MK340603 (mtDNA COI)
GCACAGCACTAAGCCTGCTCATTCGAGCGGAACTTAGCCAACCAGGCGCTCTCCTCGGAGACGACCAAATTTATAACG
TCATCGTCACGGCGCACGCCTTTGTAATAATTTTCTTTATAGTAATACCAATCATGATCGGAGGATTCGGAAACTGGCT
TATCCCCCTCATGATTGGGGCCCCCGACATGGCATTTCCTCGAATAAACAATATGAGCTTCTGGCTCCTCCCTCCCTCAT
TTCTCCTCCTGCTTGCCTCCTCTGGCGTTGAGGCAGGGGCAGGCACAGGATGGACCGTATACCCCCCCTTATCAGGAA
ATTTAGCACATGCGGGGGCCTCCGTAGATTTAACCATTTTTTCCCTACACCTCGCAGGTATTTCCTCGATTCTAGGGGCT
ATCAACTTTATTACTACTATCATTAACATAAAACCCCCTGCCATCTCCCAATATCAAACCCCTCTATTCGTGTGGGCTGTA
CTCATCACCGCCGTCCTCCTCCTCCTCTCCCTCCCAGTTTTAGCCGCCGGCATCACCATACTCCTCACCGATCGTAACTTA
AACACCACATTCTTTGACCCTGCCGGGGGAGGGGACCCAATCCTTTACCAACA

Scientific name: *Pomacanthus annularis* **Bloch, 1787**
English name: Blue ringed angelfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family:Pomacentridae

Standard length: 207 mm
Fin formula: D-XIII/22, P1-19, P2-I/5, A-III/21, C-17
Identification: Body yellowish brown with seven brilliant blue curved lines radiating from pectoral fin to soft dorsal fin; two blue horizontal lines on opercie, the superior one crossing, eye and the inferior One below it. Base of pecoral with transverse lines; blue ring above opercle margin n ar lateral line; caudal,and pectoral fins yellow; pelvic fins grey. Body compessed; rostro dorsal profile straight to ape; pre-opercle spine strong.
DNA Barcode: MK340679

MK340679 (mtDNA COI)
GGCACCGCCCTGAGCCTACTCATTCGAGCTGAACTTAGCCAACCCGGCGCTTTACTGGGCGATGACCAGATCTACAAT
GTTATCGTTACAGCCCATGCCTTTGTAATAATTTTCTTTATGGTCATGCCAATCATGATCGGCGGCTTTGGCAACTGGC
TTATTCCCCTAATAATTGGTGCACCAGACATGGCATTCCCTCGAATAAACAACATAAGCTTCTGGCTCTTGCCTCCATCT
TTTCTACTTCTCCTAGCCTCCTCAGCCGTAGAAGCTGGGGCAGGGACCGGATGGACAGTCTACCCACCCTTGTCAAGC
AATCTAGCCCATGCTGGAGCTTCTGTAGACCTAACAATCTTTTCCCTCCATTTAGCAGGAATTTCTTCAATTCTCGGGG
CCATCAACTTCATTACAACCATTATTAATATAAAACCCATTGCTATTACCCAATACCAAACACCTCTATTCGTATGGTCA
GTCCTTATCACAGCCGTTCTTCTTCTCCTTTCCCTTCCTGTTCTGGCTGCCGGCATCACAATGCTGCTTACAGACCGAAA
CCTGAATACCACCTTCTTTGACCCTGCAGGAGGAGGGGACCCAATTCTATACCAACA

Scientific name: *Abudefduf sordidus* **Forsskål, 1775**
English name: Black-spot sergeant
Classification
Class: Actinopterygii
Order: Perciformes
Family: Pomacentridae

Standard length: 102 mm
Fin formula: D-XIII/13, P1-18, P2-I/5, A-II/15, C-17-19
Identification: Body yellowish-white, lighter below with 5-6 dark grey bars on sides; a black spot at tip of caudal fin base; all fins dusky. Body deep and compressed. Posterior margin of preopercle smooth. Suborbital scaled, with entire ventral margin. Teeth on jaws uniserial, incisor-like. Caudal fin forked; no conspicuous projecting spine-like rays at upper and lower edges of caudal-fin base.

DNA Barcode: MK340576

MK340576 (mtDNA COI)

GGCACAGCTTTAAGCCTTCCTATTCGAGCAGAACTTAGCCAACCAGGCGCTCTCCTCGGAGACGACCAAATTTATAAC
GTAATTGTTACGGCACACGCCTTTGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGGTTTGGAAACTGGC
TAATTCCCCTTATGATCGGTGCCCCCGACATGGCTTTCCCCCGAATAAATAACATGAGCTTCTGGCTCCTCCCTCCCTCA
TTCCTACTTTTACTCGCCTCTTCCGGAGTTGAAGCAGGTGCAGGAACAGGTTGGACTGTTTACCCTCCCCTATCTGGCA
ACTTAGCCCATGCAGGAGCCTCTGTTGACCTGACTATTTTCTCCCTCCACCTGGCAGGTGTCTCCTCAATTTTAGGTGC
CATCAACTTTATTACTACGATCATTAACATGAAACCCCCTGCTATTTCCCAATATCAAACCCCCCTCTTCGTATGGGCCG
TGCTAATTACTGCCGTTCTTCTCCTTCTGTCCCTCCCTGTCCTAGCCGCTGGAATTACAATGCTTTTAACCGACCGAAAC
TTAAACACCACATTCTTTGACCCTGCCGGAGGAGGGGACCCAATTCTTTACCAACA

Scientific name: *Abudefduf septemfasciatus* **Cuvier, 1830**
English name: Seven-bar damsel
Classification
Class: Actinopterygii
Order: Perciformes
Family:Pomacentridae

Standard length: 102 mm
Fin formula: D-XIII/13, P1-18, P2-I/5, A-II/15, C-18-19
Identification: Whitish body with six dark bands, each wider than the spaces between. There is a seventh band on the head that has spots below. A small black spot is present on the upper pectoral fin base; anal and caudal fins dusky; pectoral fins yellowish with basal triangular black spot. Margin of opercle smooth; caudal fin forked, lobes rounded; soft dorsal.

DNA Barcode: MK340573

MK340573 myDNA COI)
GGCACAGCCCTAAGCCTTCTTATTCGAGCAGAACTTAGCCAACCAGGCGCTCTCCTCGGAGACGACCAAATCTACAAC
GTAATTGTTACGGCGCATGCCTTTGTAATAATTTTCTTTATAGTAATACCAATTATAATCGGAGGGTTTGGAAACTGG
CTAATCCCCCTAATGATCGGTGCCCCCGATATGGCATTCCCCCGAATGAATAATATGAGCTTCTGGCTTCTCCCTCCAT
CATTTTTACTTCTTCTTGCCTCCTCAGGAGTTGAAGCAGGTGCAGGGACAGGCTGGACTGTTTATCCACCACTGTCAG
GCAACTTAGCTCACGCAGGAGCTTCTGTTGACTTAACTATTTTCTCCCTCCACCTGGCAGGTGTATCCTCAATTTTAGG
AGCCATTAATTTTATTACTACCATCATTAACATGAAACCTCCTGCTATTTCTCAATACCAGACCCCTCTTTTCGTATGGG
CTGTACTTATCACGGCCGTGCTTCTTCTTCTATCTCTCCCTGTTTTGGCCGCCGGAATTACAATACTTCTAACTGACCGA
AACTTAAATACCACGTTCTTCGACCCAGCTGGGGGAGGAGATCCTATTCTTTACCAACA

Scientific name: *Stegastes apicalis* **De Vis, 1885**
English name: Australian Gregory
Classification
Class: Actinopterygii
Order: Perciformes
Family: Pomacentridae

Standard length: 105 mm
Fin formula: D-XIII/14, P1-20, P2-I/5, A-II/13, C-16-20
Identification: Body colour is generally dark brown with yellow or reddish suffusion on antero-dorsal part ofhead and body. The scales have blackish streaks near margin, giving an overall appearance of narrow transverse bands; a few small blue spots is scattered on head, breast and posteriorly on the sides. The spinous dorsal fin is reddish brown with orange submarginal band while outer edge of soft rays orange. A black spot is on the distal part of membrane between 2nd and 3rd dorsal spine. The tip of the upper caudal lobe is orange; the anterior edge of pelvic and anal fins is blue.
DNA Barcode: MK340724, MK335888
Remarks: New distributional record from Bangladesh.

MK340724 (mtDNA COI)

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GGGACAGCTTTAAGCCTTCCAATTCGGGCAGAACTAAGTCAACCAGGCGCCCTCCTCGGAGACGACCAAATTTAT
AATGTTATTGTTACAGCACACGCCTTTGTAATAATTTTCTTTATAGTAATACCAATCATAATTGGAGGGTTTGGAAA
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CCCCTTCATTTCTTCTTCTACTCGCCTCCTCAGGCGTAGAAGCAGGTGCAGGAACAGGATGGACTGTATACCCTCC
ACTATCCGGCAACCTAGCCCACGCAGGGGCCTCCGTTGATTTGACCATTTTCTCCCTTCACTTAGCAGGTATTTCTT
CTATTCTAGGGGCCATTAACTTTATTACCACAATTATTAACATAAAACCACCTGCTATCTCCCAATACCAGACCCCT
CTCTTTGTATGGGCCGTTCTTATTACTGCTGTCCTACTTCTCCTGTCTCTTCCAGTACTAGCCGCCGGAATTACCATG
CTTCTAACCGACCGAAACCTAAACACCACCTTCTTTGACCCCGCAGGGGGAGGAGACCCCATTCTCTACCAGCA
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Scientific name: *Johnius amblycephalus***Bleeker, 1855**
English name: Bearded croaker
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Sciaenidae

Standard length: 129 mm
Fin formula: D-X+I/25, P1-18, P2-I/5, A-II/7, C-18
Identification: Colour of body black or dark brown dorsally, whitish or cream yellow ventrally; prolonged spinous portion of dorsal fin black distally. Body moderately elongate. A stiff, blunt barbel on chin. Teeth differentiated into large and small in upper jaw, villiform teeth only in lower jaw. Second to fifth dorsal-fin spines prolonged. Scales on head and body cycloid; small scales covering soft rayed portions of dorsal and anal fins.
DNA Barcode: MK340625

MK340625 (mtDNA COI)
GGCTCCGCCCTCAGTCTCCTAGTTCGAGCAGAACTTAGCCAACCCGGCTCCCTGCTTGGAAACGATCAAATTTATAA
CGTAATCGTTACAGCCCATGCGTTCGTCATAATTTTTTTTATAGTTATACCAACCATGATTGGAGGCTTTGGAAACTG
GCTTGTACCCCTTATGCTCGGAGCCCCTGACATAGCATTCCCTCGAATAAACAACATAAGCTTTTGGCTCTTACCCCC
TTCACTCCTTCTACTTCTAACCTCCTCAGCAGTTGAAGCGGGGGCTGGAACTGGATGGACAGTTTATCCGCCCCTTG
CCGGAAACCTCGCACACGCCGGAGCTTCCGTCGACTTAGCCATCTTCTCTTTACATCTCGCAGGTATCTCTTCAATCC
TGGGCGCAATTAACTTCATTACAACAATTATTAACATAAAAGCCCCCGCCATTTCTCTTTATCAAGTGCCCTTATTTG
TATGGTCCGTCCTAATCACAGCAGTACTCCTTCTCCTTTCCCTCCCTGTATTAGCCGCCGGTATTACAATGCTACTAAC
AGACCGTAACCTTAACACAACATTCTTCGACCCCGCAGGCGGAGGTGATCCCATTCTCTACCAACA

Scientific name: *Protonibea diacanthus* **Lacepède, 1802**
English name: Spotted croaker
Classification
Class: Actinopterygii
Order: Perciformes
Family:Sciaenidae

Standard length: 215 mm
Fin formula: D-X+I/24, P1-20, P2-I/5, A-II/7, C-18-20
Identification: Colour of body with 3-5 poorly defined grayish vertical bands; numerous small black spots scattered on dorsal body and dorsal and caudal fins. Pectoral, pelvic and anal fins blackish. Body moderately elongate. Three pairs of pores on ventral surface of lower jaw, first pair united by a groove. Teeth differentiated into large and small in upper jaw, but without outstanding canines. Cycloid scales on snout and below orbit and ctenoid scales on remainder. No barbels on chin.

DNA Barcode: MK340694, MK340695

MK340694 (mtDNA COI)
GGCACAGCCCTAAGCCTCTTAATCCGGGCGGAGCTAAGCCAACCCGGCTCCCTCCTCGGAGACGATCAAATC
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GGAAACTGGCTTGTGCCCTTAATAATTGGCGCCCCTGACATGGCATTCCCCCGAATGAACAATATGAGCTTCT
GGCTTCTCCCCCCTTCCTTTCTTTTACTCCTAACTTCCTCAGGGGTTGAAGCGGGAGCCGGAACCGGGTGGAC
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TCGCGGGGGTATCCTCCATTCTAGGGGCTATCAACTTTATCACAACGATTATTAACATAAAACCCCCTGCTATT
TCCCAATACCAGACACCACTATTTGTCTGGGCCGTCCTAATTACAGCCGTCCTCCTGCTACTCTCACTTCCCGTC
CTAGCCGCTGGCATTACAATGCTTTTGACAGACCGCAACCTAAATACAACCTTCTTCGACCCCGCAGGAGGAG
GTGACCCTATCCTCTACCAACA

MK340694 (mtDNA COI)
GGCACAGCCCTAAGCCTCTTAATCCGGGCGGAGCTAAGCCAACCCGGCTCCCTCCTCGGAGACGATCAAATC
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GGAAACTGGCTTGTGCCCTTAATAATTGGCGCCCCTGACATGGCATTCCCCCGAATGAACAATATGAGCTTCT
GGCTTCTCCCCCCTTCCTTTCTTTTACTCCTAACTTCCTCAGGGGTTGAAGCGGGAGCCGGAACCGGATGGAC
AGTATATCCCCCACTTGCCGGAAACCTCGCACACGCAGGGGCCTCCGTCGACTTAGCCATCTTCTCCCTCCACC
TCGCGGGGGTATCCTCCATTCTAGGGGCTATCAACTTTATCACAACGATTATTAACATAAAACCCCCTGCTATC
TCCCAATACCAGACACCACTATTTGTCTGGGCCGTCCTAATTACAGCCGTCCTCCTGCTACTCTCACTTCCCGTC
CTAGCCGCTGGCATTACAATGCTTTTGACAGACCGCAACCTAAATACAACCTTCTTCGACCCCGCAGGAGGAG
GTGACCCTATCCTCTACCAACA

Scientific name: *Otolithes ruber* **Bloch & Schneider, 1801**
English name: Tiger toothed croaker
Classification
Class: Actinopterygii
Order: Perciformes
Family: Sciaenidae

Standard length: 175 mm
Fin formula: D-X+I/30, P1-17, P2-I/5, A-II/7, C-18
Identification: Body colour silvery, anal, pectoral and ventral fins yellowish. Body elongate and slender, mouth large and terminal; lower jaw slightly projecting; inter-orbital space flat; pre-opercular scarcely denticulated; opercle with two flat spines; no pores or barbels on chin; a pair of very large canines in front of both jaws; caudal fin rhomboid.

DNA Barcode: MK340671

MK340671 (mtDNA COI)

GGCACGGCCTTAAGCCTCCTAATCCGAGCAGAGCTGAGTCAACCTGGCTCCCTCCTCGGAGACGATCAAATTTTTAA
CGTGATTGTTACAGCCCATGCTTTTGTAATAATTTTCTTTATAGTAATACCGGTTATGATTGGAGGATTCGGAAATTG
GTTAGTACCCTTAATAATTGGGGCCCCCGACATAGCATTTCCCCGAATAAATAATATAAGCTTCTGGCTCCTCCCCCC
TTCCTTCCTTCTACTCCTCACCTCCTCAGGGGTTGAGGCAGGGGCCGGGACGGGTTGGACAGTTTATCCTCCGCTCG
CGGGTAATCTCGCACACGCAGGGGCCTCTGTCGACTTAGCCATCTTCTCCCTACACCTTGCAGGAGTTTCCTCAATCT
TAGGGGCCATTAACTTTATTACAACAATTATTAATATAAAACCACCTGCAATCTCCCAATACCAAACACCTTTATTTG
TATGGGCTGTTTTAATTACAGCAGTACTCCTTCTACTTTCACTTCCGGTCCTAGCTGCGGGCATCACAATACTCCTGA
CAGACCGTAACCTTAATACAACCTTTTTTGACCCGGCAGGTGGAGGGGACCCTATTCTATACCAACA

Scientific name: *Otolithoides pama* **Hamilton, 1822**
English name: Bronze croaker
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family:Sciaenidae

Standard length: 228 mm
Fin formula: D-X+I/41, P1-16, P2-I/5, A-II/7, C-16-18
Identification: Colour of body brown along back and white beneath; fin yellowish. Body elongated; head ovoid; rounded snout. Size of eye small; mouth large terminal. Dorsa fin weakly notched and dorsal fin rather weak. Body size medium Scales small cycloid on head and breast, elsewhere weakly ctenoid.

DNA Barcode: MK340672

MK340672 (mtDNA COI)
GGCACAGCCTTAAGCCTCCTAATCCGGGCGGAACTCAGCCAACCCGGCTCACTCCTAGGAGATGACCAAATTTTTA
ATGTAATTGTTACAGCACATGCCTTCGTCATAATCTTCTTTATAGTAATACCTGTAATAATTGGAGGATTTGGGAACT
GGCTTGTACCTCTAATAATTGGAGCCCCTGACATAGCATTTCCCCGAATAAACAACATAAGCTTCTGGCTCCTTCCTC
CTTCTTTTTTACTACTCCTGACCTCTTCAGGGGTAGAGGCAGGTGCTGGAACAGGATGGACCGTTTATCCCCCTCTT
GCTGGAAATCTCGCACACGCAGGAGCTTCTGTGGACCTAGCCATTTTTTCCCTCCACCTGGCAGGTGTTTCATCAAT
TCTTGGGGCCATCAACTTTATTACAACTATTATTAATATAAAACCCCCAGCCATCTCCCAATACCAAACACCTCTGTT
CGTATGGGCCGTTCTTATTACAGCAGTCCTCCTACTTCTCTCGCTACCAGTATTAGCTGCTGGTATTACAATACTTTT
AACAGACCGTAACCTAAATACAACTTTCTTCGACCCTGCAGGAGGGGGAGACCCAATTCTCTATCAACA

Scientific name: *Chrysochir aureus* **Richardson, 1846**
English name: Reeve's croaker
Classification
Class: Actinopterygii
Order: Perciformes
Family:Sciaenidae

Standard length: 157 mm
Fin formula: D-X+I/27, P1-18, P2-I/5, A-II/7, C-18
Identification: Colour of body metallic blue above, shading to silvery below. Pectoral fins yellow, other fins greyish. A small species with an acute snout and large, nearly horizontal and inferior mouth. Teeth villiform jaws, in upper jaw the outer row enlarged with two pairs of canines at tip; in lower jaw teeth in inner row slightly enlarged.
DNA Barcode: MK340604, MK335850

MK340604 (mtDNA COI)
GGCACAGCCTTAAGCCTCCTAATCCGGGCGGAACTCAGCCAACCCGGCTCACTCCTAGGAGATGACCAAATTTTTAA
TGTAATTGTTACAGCACATGCCTTCGTCATAATCTTCTTTATAGTAATACCTGTAATAATTGGAGGATTTGGGAACTG
GCTTGTACCTCTAATAATTGGAGCCCCTGACATAGCATTTCCCCGAATAAACAACATAAGCTTCTGGCTCCTTCCTCCT
TCTTTTTTACTACTCCTGACCTCTTCAGGGGTAGAGGCAGGTGCTGGAACAGGATGGACCGTTTATCCCCCTCTTGCT
GGAAATCTCGCACACGCAGGAGCTTCTGTGGACCTAGCCATTTTTTCCCTCCACCTGGCAGGTGTTTCATCAATTCTT
GGGGCCATCAACTTTATTACAACTATTATTAATATAAAACCCCCAGCCATCTCCCAATACCAAACACCTCTGTTCGTAT
GGGCCGTTCTTATTACAGCAGTCCTCCTACTTCTCTCGCTACCAGTATTAGCTGCTGGTATTACAATACTTTTAACAGA
CCGTAACCTAAATACAACTTTCTTCGACCCTGCAGGAGGGGGAGACCCAATTCTCTATCAACA

MK335850 (mtDNA COI)
GGCACTGCCTTGAGCCTTCTAATCCGAGCAGAGCTCAGTCAACCCGGCCCCCTCCTCGGGGACGACCAAATCTATA
ATGTAATCGTTACAGCCCATGCCTTCGTCATGATTTTCTTTATAGTAATGCCGGTAATGATCGGCGGGTTTGGAAAC
TGGCTTGTGCCCCTAATGATTGGTGCCCCTGACATGGCATTCCCCCGAATGAACAATATAAGCTTCTGGCTTCTTCC
CCCTTCCTTTCTTCTACTCTTGACCTCTTCAGCGGTAGAGGCAGGCGCCGGGACAGGCTGGACAGTTTACCCCCCAC
TTGCCGGAAACCTTGCACACGCAGGGGCCTCCGTTGACTTAGCCATCTTCTCTTTACACCTCGCAGGTGTATCCTCC
ATCCTAGGGGCTATCAACTTCATTACAACCATCATTAATATAAAGCCCCCCGCCATCTCCCAATATCAAACACCCCTA
TTTGTTTGGGCCGTCCTAATCACAGCCGTCCTTTTACTACTATCCCTCCCGGTTTTAGCCGCTGGCATTACAATGCTT
TTAACAGACCGAAACCTGAACACAACCTTTTTTGACCCCGCAGGAGGAGGAGACCCTATCCTCTACCAACA

Scientific name: *Pterotolithus maculatus* **Cuvier, 1830**
English name: Spotted croaker
Classification
Class: Actinopterygii
Order: Perciformes
Family:Sciaenidae

Standard length: 353 mm
Fin formula: D-IX+I/31, P1-20, P2-I/5, A-II/10, C-16-20
Identification: Colour of body greyish above, silvery on flanks and belly, upper part of body and dorsal fin with numerous black patches. Body size large and slender species, with head profile low and only slightly curved; mouth large and strongly oblique, lower jaw projecting. Caudal fin rhomboid. Scales cycloid and in very irregular rows; lateral line scales reaching to tip of caudal fin.

DNA Barcode: MK340696

MK340696 (mtDNA COI)
GGCACAGCCTTGAGCCTCCTAATCCGAGCAGAACTGAGTCAACCCGGCTCCCTTCTCGGCGATGATCAGATTTTTAA
TGTAATTGTCACAGCCCATGCCTTCGTCATAATTTTCTTTATAGTAATACCCGTCATGATCGGGGGGTTCGGAAACTG
GCTGGTACCCTTAATAATTGGCGCTCCAGACATGGCATTCCCCCGAATGAACAATATAAGCTTCTGGCTTCTCCCACC
CTCTTTTCTTCTACTCCTAACTTCTTCAGGCGTAGAGGCAGGGGCCGGGACAGGATGGACCGTTTACCCTCCGCTCG
CTAGCAACCTAGCACATGCAGGGGCATCCGTCGATTTAGCCATCTTCTCCCTCCACCTTGCTGGTGTTTCCTCAATTC
TTGGGGCCATCAACTTTATTACAACAATCGTTAATATAAAACCCCCCGCCATCTCCCAGTACCAAACACCCTTATTCG
TGTGGGCTGTTTTAATTACAGCAGTCCTCCTGCTACTTTCACTCCCTGTCCTAGCCGCCGGCATCACAATACTCCTTAC
TGACCGCAACCTTAACACAACCTTCTTTGATCCCGCGGGCGGAGGAGATCCTATTTTGTACCAACA

Scientific name: *Rastrelliger kanagurta* **Cuvier, 1816**
English name: Indian mackerel

<u>Classification</u>

Class: Actinopterygii
Order: Perciformes
Family: Scombridae

Standard length: 119 mm
Fin formula: D1-XI, D2-12+5 (finlents), P1-19, P2-I/5, A-I/12+5(finlents), C-22-24
Identification: Colour of head and body bluish green dorsally, silvery white ventrally. One or two rows of small, dark spots dorsolaterally on body. First dorsal, caudal and pectoral fins yellowish. Body slightly deep, compressed. Head longer than body depth. Maxilla covered by lacrimal bone. Adipose eyelid well developed. Caudal fin base with 2 small lateral keels. Two dorsal fins widely separated. Anal fin spine rudimentary. Five or six dorsal and anal finlets. Pectoral fins short; a small single flap between pelvic fins. Body covered with small scales.

Scientific name: *Epinephelus erythrurus* **Valenciennes, 1828**
English name: Cloudy grouper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Serranidae

Standard length: 114 mm
Fin formula: D-XI/16, P1-18, P2-I/5, A-III/8, C-18
Identification: Head and body dark brown or greenish brown, marbled with irregular pale spots and blotches; 1 or 2 faint dark streaks running posteriorly from eye; no dark spots on head, body or fins. A small serranid with robust body. Teeth in narrow bands. Pectoral fins rather short, about equal to postorbital part of head. Pelvic fins not reaching to anus. Caudal fin rounded. Scales on head cycloid, on body ctenoid.
DNA Barcode: MK340613, MK340614, MK340615, MK340616

MK340613 (mtDNA COI)
GGAACAGCTCTCAGCCTGCTTATTCGAGCCGAGCTTAGCCAACCAGGGGCTCTACTAGGTGACGATCAGATCTATA
ATGTAATTGTTACAGCACACGCTTTTGTAATAATCTTTTTTATAGTAATACCAATCATGATTGGTGGCTTTGGAAACT
GGCTCATCCCGCTAATAATTGGTGCCCCAGACATAGCATTCCCTCGAATAAATAATATGAGCTTCTGGCTTCTCCCC
CCATCCTTCTTACTTCTTCTCGCTTCTTCTGGAGTAGAAGCCGGTGCTGGTACCGGCTGGACGGTCTATCCACCCCTA
GCCGGAAACCTAGCCCATGCAGGTGCATCTGTAGACTTAACTATCTTCTCATTACATTTAGCAGGAATCTCATCAAT
TCTAGGTGCAATCAATTTTATCACAACTATTATTAATATGAAACCCCCAGCTATCTCCCAATACCAAACACCTTTATTT
GTATGGGCGGTGCTAATTACAGCAGTGCTCCTGCTCCTCTCCCTTCCTGTTCTCGCCGCCGGCATCACAATACTACTT
ACAGATCGCAACCTTAACACCACTTTCTTTGACCCCGCTGGAGGAGGAGACCCAATTCTTTACCAACA

MK340614 (mtDNA COI)
GGAACAGCTCTCAGCCTGCTTATTCGAGCCGAGCTTAGCCAACCAGGGGCTCTACTAGGTGACGATCAGATCTATA
ATGTAATTGTTACAGCACACGCTTTTGTAATAATCTTTTTTATAGTAATACCAATCATGATTGGTGGCTTTGGAAACT
GGCTCATCCCGCTAATAATTGGTGCCCCAGACATAGCATTCCCTCGAATAAATAATATGAGCTTCTGGCTTCTCCCC
CCATCCTTCTTACTTCTTCTCGCTTCTTCTGGAGTAGAAGCCGGTGCTGGTACCGGCTGGACGGTCTATCCACCCCT
AGCCGGAAACCTAGCCCATGCAGGTGCATCTGTAGACTTAACTATCTTCTCATTACATTTAGCAGGAATCTCATCAA
TTCTAGGTGCAATCAATTTTATCACAACTATTATTAATATGAAACCCCCAGCTATCTCCCAATACCAAACACCTTTAT
TTGTATGGGCGGTGCTAATTACAGCAGTGCTCCTGCTCCTCTCCCTTCCTGTTCTCGCCGCCGGCATCACAATACTA
CTTACAGATCGCAACCTTAACACCACTTTCTTTGACCCCGCTGGAGGAGGAGACCCAATTCTTTACCAACA

MK340615 (mtDNA COI)
GGAACAGCTCTCAGCCTGCTTATTCGAGCCGAGCTTAGCCAACCAGGGGCTCTACTAGGTGACGATCAGATCTATA
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GGCTCATCCCGCTAATAATTGGTGCCCCAGACATAGCATTCCCTCGAATAAATAATATGAGCTTCTGGCTTCTCCCC
CCATCCTTCTTACTTCTTCTCGCTTCTTCTGGAGTAGAAGCCGGTGCTGGTACCGGCTGGACGGTCTATCCACCCCT
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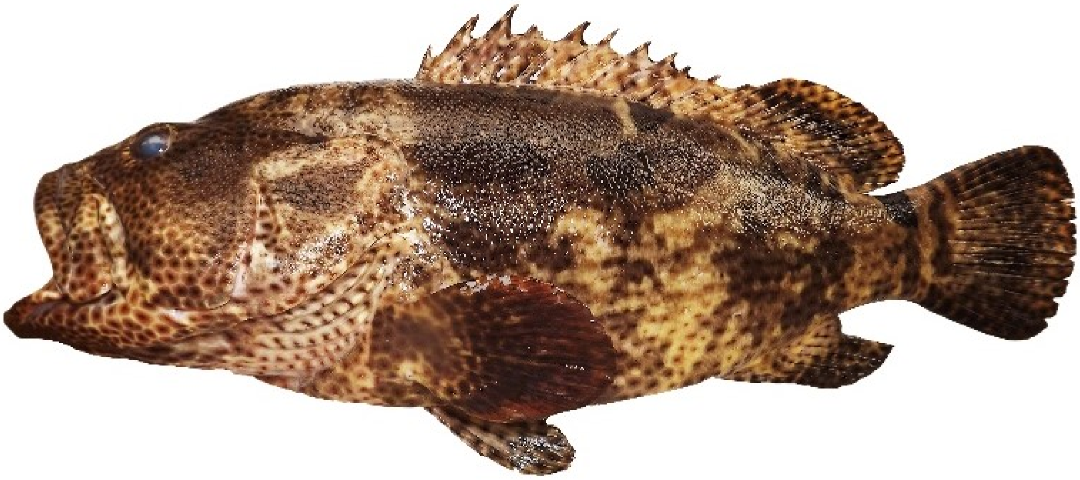
TTCTAGGTGCAATCAATTTTATCACAACTATTATTAATATGAAACCCCCAGCTATCTCCCAATACCAAACACCTTTAT
TTGTATGGGCGGTGCTAATTACAGCAGTGCTCCTGCTCCTCTCCCTTCCTGTTCTCGCCGCCGGCATCACAATACTA
CTTACAGATCGCAACCTTAACACCACTTTCTTTGACCCCGCTGGAGGAGGAGACCCAATTCTTTACCAACA

MK340616 (mtDNA COI)
GGAACAGCTCTCAGCCTGCTTATTCGAGCCGAGCTTAGCCAACCAGGGGCTCTACTAGGTGACGATCAGATCTA
TAATGTAATTGTTACAGCACACGCTTTTGTAATAATCTTTTTTATAGTAATACCAATCATGATTGGTGGCTTTGGA
AACTGGCTCATCCCGCTAATAATTGGTGCCCCAGACATAGCATTCCCTCGAATAAATAATATGAGCTTCTGGCTT
CTCCCCCCATCCTTCTTACTTCTTCTCGCTTCTTCTGGAGTAGAAGCCGGTGCTGGTACCGGCTGGACGGTCTATC
CACCCCTAGCCGGAAACCTAGCCCATGCAGGTGCATCTGTAGACTTAACTATCTTCTCATTACATTTAGCAGGAA
TCTCATCAATTCTAGGTGCAATCAATTTTATCACAACTATTATTAATATGAAACCCCCAGCTATCTCCCAATACCA
AACACCTTTATTTGTATGGGCGGTGCTAATTACAGCAGTGCTCCTGCTCCTCTCCCTTCCTGTTCTCGCCGCCGGC
ATCACAATACTACTTACAGATCGCAACCTTAACACCACTTTCTTTGACCCCGCTGGAGGAGGAGACCCAATTCTT
TACCAACA

Scientific name: *Epinephelus fuscoguttatus* **Forsskal, 1775**
English name: Brown-marbled grouper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Serranidae



Standard length: 375 mm
Fin formula: D-X+I/15, P1-19, P2-I/5, A-III/8, C-19-24
Identification: Pale yellowish brown colour with five vertical series of irregular dark brown blotches; head, body and fins with numerous close-set, small brown spots; caudal peduncle with small black saddle dorsally. Body moderately deep; flat or slightly concave interorbital area; adults dorsal head profile indented at eyes and distinctly convex from there to origin of dorsal fin; rounded preopercle, finely serrate. Triangular posterior nostrils. 3-4 rows of teeth on midlateral part of lower jaw. Nostrils are close together. Scales cycloid.
DNA Barcode: MK340617, MK335851

MK340617 (mtDNA COI)
GGAACAGCCCTCAGCCTGCTAATTCGAGCTGAGCTTAGCCAACCAGGGGCTTTACTAGGTGACGACCAGATCTATAA
TGTAATTGTTACAGCACATGCTTTTGTAATAATCTTTTTTATAGTAATACCAATTATAATTGGTGGCTTTGGAAACTGG
CTTATTCCACTTATAATTGGCGCCCCAGACATAGCATTCCCTCGAATGAATAATATAAGCTTCTGGCTTCTTCCTCCAT
CCTTCCTGCTCCTTCTTGCTTCTTCTGGAGTAGAAGCCGGTGCTGGTACTGGTTGGACGGTTTACCCACCCTTAGCTG
GAAACTTAGCCCATGCAGGTGCATCCGTAGACTTAACCATCTTCTCACTACATTTAGCAGGTATTTCATCAATTCTAG
GTGCAATTAACTTTATTACAACCATTATTAATATAAAACCCCCTGCTATCTCTCAATACCAAACACCTTTATTTGTATGG
GCTGTATTAATTACAGCCGTGCTTCTACTCCTCTCTCTTCCCGTTCTTGCCGCTGGCATTACAATATTACTCACAGATCG
CAACCTTAACACTACTTTCTTTGACCCAGCCGGAGGGGGAGACCCTATTCTTTACCAACA

Scientific name: *Cephalopholis boenak* **Bloch, 1790**
English name: Brown-banded rockcod
Classification
Class: Actinopterygii
Order: Perciformes
Family: Serranidae

Standard length: 121 mm
Fin formula: D-IX/15, P1-16, P2-I/5, A-III/8, C-18-20
Identification: Colour brown with slightly irregular reddish brown bars on body; fins dark brown; distal margin of caudal fin bluish white; inside of the mouth orange. Small sized grouper with a stout body; mouth oblique; teeth fine, in bands in jaws with a pair of canine teeth, anteriorly in jaws; minute teeth. Pelvic fins usually not reaching, anus; caudal fin rounded.

DNA Barcode: MK340596

MK340596 (mtDNA COI)
GGGACAGCACTTAGCCTACTAATCCGAGCTGAACTAAGCCAACCAGGTGCTTTACTGGGCGACGATCAAATTTATAA
TGTTATCGTTACAGCACATGCTTTCGTAATAATTTTCTTTATAGTAATACCAATCATGATTGGAGGTTTCGGAAACTGG
CTTATTCCGCTGATAATTGGTGCTCCGGACATAGCCTTCCCTCGAATAAATAACATAAGCTTTTGGCTACTACCTCCAT
CTTTCTTACTCCTGCTAGCTTCATCTGGGGTAGAAGCAGGTGCTGGAACTGGTTGGACAGTCTACCCTCCCCTGGCTG
GTAATTTAGCCCATGCAGGCGCTTCCGTTGACTTAACAATCTTTTCACTACATTTAGCAGGTATTTCTTCAATTCTAGG
GGCAATCAACTTTATTACAACCATCATTAACATGAAACCTCCTGCCATCTCCCAATACCAGACACCTCTATTTGTATGG
GCCGTACTAATTACAGCGGTACTCCTGCTTCTTTCCCTTCCAGTTCTCGCTGCAGGTATTACAATACTTCTAACTGATC
GAAACCTAAACACCACCTTCTTTGACCCAGCTGGAGGAGGGGACCCAATTCTTTATCAACA

Scientific name: *Cephalopholis Formosa* **Shaw, 1812**
English name: Bluelined grouper
Classification
Class: Actinopterygii
Order: Perciformes
Family: Serranidae

Standard length: 161 mm
Fin formula: D-IX/17, P1-18, P2-I/5, A-III/8, C-18-20
Identification: Colour dark brown to yellowish brown, with irregular dark blue lines on head, body and fins; snout, lips, and ventral part of head and chest with small dark blue spots. Caudal fin rounded; pectoral fins short. Snout largely scaled; maxilla partially scaled; scales on abdomen ctenoid.

DNA Barcode: MK340597, MK340598, MK340599

MK340597 (mtDNA COI)
GGGACAGCACTTAGCCTGCTAATCCGAGCTGAATTGAGCCAACCAGGTGCTCTACTGGGCGATGATCAAATTTAT
AATGTTATCGTTACAGCACATGCTTTCGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGTGGTTTCGGAAA
CTGGCTTATTCCACTGATAATTGGTGCCCCCGACATAGCTTTCCCCCGGATAAACAACATGAGCTTTTGGCTCCTG
CCTCCATCTTTCTTGCTCCTGCTAGCCTCATCTGGGGTAGAAGCAGGTGCGGGTACTGGCTGGACAGTCTACCCTC
CCCTAGCCGGTAACCTAGCCCATGCAGGTGCTTCTGTTGATTTAACAATCTTTTCACTGCATTTAGCAGGTATTTCA
TCAATTCTAGGAGCAATTAACTTTATCACAACCATCATTAACATAAAACCTCCAGCCATCTCCCAGTATCAAACACC
CCTATTTGTATGGGCTGTATTAATTACAGCTGTTCTCCTCCTTCTTTCCCTCCCTGTTCTCGCTGCAGGTATTACAAT
GCTTCTAACTGATCGAAACCTGAACACCACCTTCTTTGACCCAGCTGGTGGAGGAGACCCAATTCTTTACCAGCA

MK340598 (mtDNA COI)
GGGACAGCACTTAGCCTGCTAATCCGAGCTGAATTGAGCCAACCAGGTGCTCTACTGGGCGATGATCAAATTTA
TAATGTTATCGTTACAGCACATGCTTTCGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGTGGTTTCGGA
AACTGGCTTATTCCACTGATAATTGGTGCCCCCGACATAGCTTTCCCCCGGATAAACAACATGAGCTTTTGGCTC
CTGCCTCCATCTTTCTTGCTCCTGCTAGCCTCATCTGGGGTAGAAGCAGGTGCGGGTACTGGCTGGACAGTCTAC
CCTCCCCTAGCCGGTAACCTAGCCCATGCAGGTGCTTCTGTTGATTTAACAATCTTTTCACTGCATTTAGCAGGTA
TTTCATCAATTCTAGGAGCAATTAACTTTATCACAACCATCATTAACATAAAACCTCCAGCCATCTCCCAGTATCA
AACACCCCTATTTGTATGGGCTGTATTAATTACAGCTGTTCTCCTCCTTCTTTCCCTCCCTGTTCTCGCTGCAGGTA
TTACAATGCTTCTAACTGATCGAAACCTGAACACCACCTTCTTTGACCCAGCTGGTGGAGGAGACCCAATTCTTT
ACCAGCA

MK340598 (mtDNA COI)
GGACAGCACTTAGCCTGCTAATCCGAGCTGAATTGAGCCAACCAGGTGCTCTACTGGGCGATGATCAAATTTAT
AATGTTATCGTTACAGCACATGCTTTCGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGTGGTTTCGGAA
ACTGGCTTATTCCACTGATAATTGGTGCCCCCGACATAGCTTTCCCCCGGATAAACAACATGAGCTTTTGGCTCC
TGCCTCCATCTTTCTTGCTCCTGCTAGCCTCATCTGGGGTAGAAGCAGGTGCGGGTACTGGCTGGACAGTCTACC
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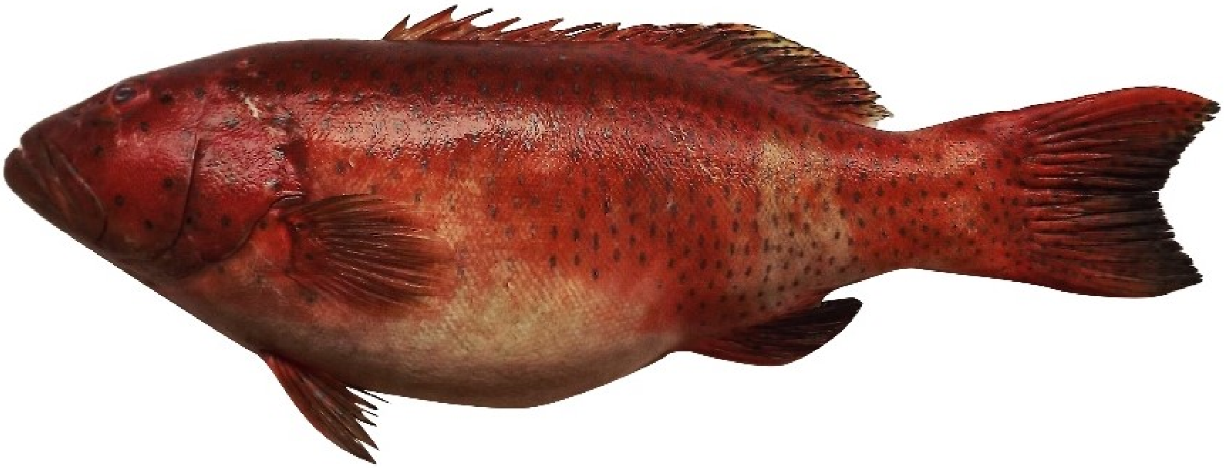
TTCATCAATTCTAGGAGCAATTAACTTTATCACAACCATTATTAACATAAAACCTCCAGCCATCTCCCAGTATCAA
ACACCCCTATTTGTATGGGCTGTATTAATTACAGCTGTTCTCCTCCTTCTTTCCCTCCCTGTTCTCGCTGCAGGTAT
TACAATGCTTCTAACTGATCGAAACCTGAACACCACCTTCTTTGACCCAGCTGGTGGAGGTGATCCCATCCTCTA
CCAACA

Scientific name: *Plectropomus pessuliferus* **Fowler, 1904**
English name: Roving coral grouper
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Serranidae



Standard length: 454 mm
Fin formula: D-VIII/11, P1-16, P2-I/5, A-II/8, C-16-22
Identification: Colour of body and fins brown to orange-red, with numerous small dark-edged blue spots; some spots on lateral surface of body vertically elongate in adults; spots few or absent on ventral part of body; spots on fins more bluish. Body elongate; Ventral margin of preopercle with 3 large spines. Opercle with 3 flat spines, upper and lower spines covered by skin. Anal-fin spines weak; first and second spines covered by skin. Caudal fin emarginated.

DNA Barcode: MK340678, MK335875
Remarks: New distributional record from Bangladesh.

MK340678 (mtDNA COI)
GGGACCGCTTTAAGCCTACTTATTCGGGCGGAGCTTAGTCAACCCGGTGCTCTTTTAGGAGACGACCAAATC
TATAACGTGATTGTTACCGCACACGCATTTGTAATAATCTTTTTTATAGTAATACCAATCATAATCGGAGGCT
TCGGAAATTGGCTTATTCCTCTAATAATCGGCGCCCCAGATATAGCATTCCCTCGAATAAACAATATAAGTTT
CTGGCTTCTACCTCCTTCTTTCCTCCTCCTTCTAGCCTCATCAGGCGTTGAAGCAGGTGCTGGGACAGGGTGG
ACAGTTTATCCCCCTCTAGCAGGAAACCTAGCCCATGCGGGTGCATCCGTAGATTTAACAATCTTCTCACTTC
ACTTAGCAGGTATTTCATCAATTCTTGGAGCAATCAACTTTATTACTACCATCATTAACATGAAACCCCCTGCT
ATCTCTCAATACCAGACCCCTCTATTCGTATGGGCAGTCCTAATTACTGCAGTTCTTCTTCTCCTATCACTACC
TGTTCTGGCTGCTGGAATTACAATACTATTAACCGACCGAAACCTCAACACTACCTTCTTTGACCCTGCTGGA
GGAGGAGACCCAATCCTCTACCAGCA

Scientific name: *Cromileptes altivelis* **Fowler, 1904**
English name: Roving coral grouper
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Serranidae

Identification: Colour white to light greenish brown with scattered round black spots on head, body, and fins, with body spots generally larger than those on head and fins; about 9 large roundish dusky blotches, with some extending partly into base of dorsal and anal fins. Body moderately deep. Small eyes. Small in size. Concave dorsal profile of head; anterior part of the head as compared to the elevated postorbital part; absence of canine teeth, except for a very small pair at the front of the upper jaw. Slit-like posterior nostril. Rounded caudal fin.

Remarks: This species has been recorded during the underwater scuba diving.

Scientific name: *Siganus javus* **Linnaeus, 1766**
English name: Java rabbit rish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Siganidae

Standard length: 111 mm
Fin formula: D-I+XIII/10, P1-18, P2-II/3, A-VII/9, C-16
Identification: Colour dark bronze on dorsal half, becoming paler ventrally; many blue spots on head and dorsal half of body; silvery blue undulating lines on ventral half of body. Body relatively deep, its depth. Soft parts of dorsal and anal fins moderately high, longest anal-fin ray sub-equal to longest anal-fin spine. Caudal fin slightly concave.

DNA Barcode: MK340716

MK340716 (mtDNA COI)

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GGGACAGCCTTAAGCCTACTAATTCGAGCAGAACTCAGCCAACCAGGCGCCCTCCTTGGGGATGACCAGATTTAT
AACGTCATTGTTACCGCCCATGCATTCGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGGTTTGGAA
ACTGGCTAATTCCCCTAATGATTGGAGCTCCTGACATGGCATTCCCACGAATGAACAATATGAGCTTCTGGCTTCT
CCCACCTTCTTTCCTGCTTCTCCTAGCCTCCTCTGGGGTAGAAGCCGGGGCTGGAACCGGATGGACAGTCTATCCC
CCCTTAGCTGGTAACTTAGCACACGCTGGTGCATCAGTCGACCTAACCATCTTCTCCCTTCATTTAGCAGGAATCTC
CTCAATTCTTGGGGCTATCAACTTCATTACAACCATTATTAACATGAAACCTCCCGCTATCTCCCAATACCAAACTC
CGCTATTCGTGTGGGCCGTCCTAATTACAGCTGTCCTTCTACTCCTTTCTCTTCCCGTTCTGGCTGCCGGAATTACA
ATGCTTCTCACAGACCGAAATCTAAATACAACATTCTTTGATCCGGCAGGAGGGGGTGACCCAATTCTGTATCAA
CA
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Scientific name: *Siganus canaliculatus* **Park, 1797**
English name: White-spotted rabbitfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Siganidae

Standard length: 111 mm
Fin formula: D-I+XIII/10, P1-16, P2-II/3, A-VII/9, C-18-20
Identification: Body colour silvery gray above and silvery below; nape and upper surface of head olive green; head and body with pearly white round or oval spots, some are elongate; a black patch below origin of lateral line; soft dorsal and anal fins are slightly dusky. Body elongate; spines slender and pungent; caudal fin emarginated in juveniles, becoming forked with increasing size; midline of thorax between pelvic ridges scaleless.

DNA Barcode: MK340713, MK340714, MK340715

MK340713 (mtDNA COI)
GGTACAGCTTTAAGCCTACAAATTCGAGCAGAACTTAGCCAACCAGGCGCTCTTCTAGGAGATGACCAAATT
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CGGAAACTGGCTAATCCCCCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACATGAGCTT
CTGGCTCCTTCCTCCATCCTTCCTTCTTCTTCTGGCCTCCTCTGGAGTAGAAGCAGGGGCAGGAACTGGTTGG
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GAGGTGACCCAATCCTCTACCAACA

MK340714 (mtDNA COI)
GGTACAGCTTTAAGCCTACAAATTCGAGCAGAACTTAGCCAACCAGGCGCTCTTCTAGGAGATGACCAAAT
TTATAATGTTATTGTTACTGCCCATGCATTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATTGGAGGGT
TCGGAAACTGGCTAATCCCCCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAATAACATGAGC
TTCTGGCTCCTTCCTCCATCCTTCCTTCTTCTTCTGGCCTCCTCTGGAGTAGAAGCAGGGGCAGGAACTGGTT
GGACAGTTTACCCCCCGTTAGCCGGGAATCTAGCACACGCCGGTGCATCCGTAGACCTGACTATTTTCTCCC
TGCATTTAGCCGGTATTTCCTCAATTCTCGGGGCTATTAATTTCATCACAACTATTATCAACATGAAACCTCCC
GCTATCTCCCAGTATCAGACTCCTCTGTTCGTATGGGCTGTCCTAATTACAGCTGTCCTTCTTCTTCTATCCCT
TCCTGTTCTGGCTGCTGGAATTACAATGCTCTTAACAGACCGAAACCTAAATACCACATTCTTTGACCCGGCA
GGAGGAGGTGACCCAATCCTCTACCAACA

MK340715 (mtDNA COI)
GGTACAGCTTTAAGCCTACAAATTCGAGCAGAACTTAGCCAACCAGGCGCTCTTCTAGGAGATGACCAAAT
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TTCGGAAACTGGCTAATCCCCCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACATGAG
CTTCTGGCTCCTTCCTCCATCCTTCCTTCTTCTTCTGGCCTCCTCTGGAGTAGAAGCAGGGGCAGGAACTGGT
TGGACAGTTTACCCCCCGCTAGCCGGGAACCTAGCACACGCCGGTGCATCCGTAGACCTGACTATTTTCTCC
CTACATTTAGCCGGTATTTCCTCAATTCTCGGAGCTATTAATTTCATCACAACTATTATCAACATGAAACCTC
CCGCTATCTCCCAGTATCAGACTCCTCTGTTCGTATGGGCTGTCCTAATTACAGCTGTCCTTCTTCTTCTATCC
CTTCCTGTTCTGGCTGCTGGAATTACAATGCTCTTAACAGACCGAAACCTAAATACCACATTCTTTGACCCG
GCAGGAGGAGGTGACCCAATCCTCTACCAACA

Scientific name: ***Siganus vermiculatus*** **Valenciennes, 1835**
English name: Vermiculated spinefoot
Classification
Class: Actinopterygii
Order: Perciformes
Family: Siganidae

Standard length: 185 mm
Fin formula: D-I+XIII/10, P1-16, P2-II/3, A-VII/9, C-18
Identification: Body deep and ovate; dorsal profile of snout steep; spines are stout; caudal fin emarginate; cheeks with strong scales, midline of thorax scaly except pelvic ridges. Body bluish white with irregular vermiculate dark spotted with brown bands spreading onto base of caudal except ventrally spotted with brown; head with narrow brown bands; caudal fin with small brown spots; a row of brown spots above base of soft dorsal and anal fins; dorsal and anal fins dusky; iris golden yellow.

DNA Barcode: MK340717

MK340717 (mtDNA COI)
GGAACAGCTTTGAGCCTACAAATTCGAGCAGAACTCAGCCAACCAGGCGCCCTCCTTGGAGATGACCAGATT
TATAATGTCATTGTTACCGCCCATGCATTCGTAATAATTTTCTTTATAGTAATGCCAATCATGATCGGAGGGTT
CGGAAACTGGCTAATCCCCCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACATGAGCTTC
TGGCTCCTCCCACCCTCTTTCTTACTTCTCCTTGCCTCTTCCGGAGTAGAAGCCGGGGCAGGAACCGGATGGAC
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AGCTGGAATTTCCTCAATTCTTGGGGCTATTAATTTTATTACAACCATTATTAACATGAAACCTCCCGCTATTTC
CCAATATCAAACTCCACTATTCGTGTGGGCTGTCCTAATTACAGCTGTCCTTCTACTCCTTTCTCTACCCGTTCT
GGCTGCTGGAATTACAATGCTTCTCACAGATCGAAACCTAAACACGACATTCTTCGACCCGGCAGGGGGAGG
TGATCCAATTCTATACCAACA

Scientific name: *Sillago sihama* **Forsskål, 1775**
English name: Silver sillago
Classification
Class: Actinopterygii
Order: Perciformes
Family: Siganidae

Standard length: 123 mm
Fin formula: D1-XI, D2-I/20, P1-16, P2-I/5, A-II/21, C-18
Identification: Colour of body silvery, olive-gray above, and with indistinct, silvery yellow mid-lateral band; soft dorsal with rows of darker spots. Body cylindrical; snout pointed; upper profile of head slightly convex; pre opercular margin serrated; eye about half snout; small, backwardly directed spine on operculum; teeth in a broad, villiform.
DNA Barcode: MK340718, K340719

MK340718 (mtDNA COI)
GGCACAGCCCTAAGCCTGCTTATCCGGGCAGAACTTAGCCAACCTGGCGCTCTGCTTGGCGATGACCAAATTTACAATGTCAT
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GATGATCGGGGCCCCTGATATAGCATTTCCGCGAATGAACAATATGAGCTTCTGGCTTCTCCCTCCCTCTTTCTTACTTCTCTTA
GCCTCATCAGGTGTTGAGGCAGGGGCCGGCACAGGATGGACAGTTTACCCTCCTTTAGCGGGCAACTTGGCCCATGCAGGA
GCTTCCGTTGATCTGACTATTTTCTCACTACACTTGGCCGGAGTCTCATCAATTTTAGGAGCAATCAACTTTATCACAACGATCA
TTAACATGAAACCTCCTGCTACTTCTCAATACCAAACCCCACTGTTTGTCTGGTCCGTCCTGATTACGGCCGTTCTTCTTCTCCTT
TCACTCCCCGTACTCGCAGCAGGAATTACTATGCTTCTTACAGATCGAAATCTAAACACCACCTTCTTCGACCCAGCCGGAGGA
GGAGACCCAATCCTTTACCAGCA

MK340719
GCACTGCCCTAAGCCTGCTTATCCGGGCAGAACTCAGCCAACCTGGCGCCCTGCTTGGTGACGACCAAATCTATAATGTTATT
GTTACGGCACACGCCTTTGTAATAATTTTCTTTATAGTAATACCAATCCTGATTGGAGGCTTCGGGAACTGGCTAGTTCCCCTA
ATGATTGGAGCCCCTGATATGGCATTCCCTCGAATGAACAACATGAGCTTCTGGCTTCTCCCTCCTTCTTTCTTACTCCTTCTGG
CCTCTTCTGGTGTTGAAGCTGGTGCCGGGACTGGGTGGACTGTGTACCCTCCTCTAGCAGGAAACTTAGCCCACGCAGGGGC
TTCCGTAGACCTTACCATTTTCTCACTCCACCTAGCAGGGGTTTCCTCAATTCTTGGTGCAATTAACTTCATCACAACAATTATT
AATATGAAGCCCCCAGCAACTTCACAGTACCAAACCCCTCTGTTCGTTTGGTCTGTCCTAATTACGGCCGTTCTACTCCTCCTCT
CGCTACCCGTGCTTGCAGCGGGCATTACGATGCTACTTACGGACCGAAACCTAAATACCACCTTTTTCGACCCTGCAGGAGGT
GGGGACCCAATCCTTTACCAACA

Scientific name: *Acanthopagrus berda* **Forsskål, 1775**
English name: Picnic sea bream
Classification
Class: Actinopterygii
Order: Perciformes
Family: Sparidae

Standard length: 167 mm
Fin formula: D-XI/11, P1-15, P2-I/5, A-III/8, C-20
Identification: Body colour dusky grey above, silvery white below. Dorsal and anal fins with dusky margins; dorsal spines often silvery: pectoral fins yellow: pelvic, soft dorsal and anal fins blackish. Body fairly deep and compressed. Head large, rather pointed, its upper profile oblique often with a bulge above eyes; eyes moderate in size.

DNA Barcode: MK340577, MK340578

MK340577 (mtDNA COI)
GGACCGCTTTAAGCCTGCTCATTCGAGCCGAATTAAGCCAACCTGGCGCTCTTCTAGGAGACGACCAAATTTACAAT
GTAATTGTTACAGCACATGCATTTGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGCTTCGGGAATTGG
TTAGTACCACTTATGATTGGTGCCCCTGATATAGCATTCCCTCGTATAAATAATATAAGCTTCTGGCTTCTTCCCCCAT
CATTTCTCCTGCTGCTAGCTTCTTCTGGGGTTGAAGCTGGGGCTGGTACCGGGTGGACAGTTTATCCCCCACTGGCA
GGAAACCTAGCCCACGCAGGTGCATCAGTTGACCTAACCATCTTTTCTCTTCACCTAGCCGGAATTTCATCTATTCTT
GGGGCTATTAATTTTATCACTACTATTATTAATATGAAACCACCAGCTATCTCACAATATCAAACACCCCTGTTCGTAT
GGGCCGTTTTAATTACTGCCGTCCTACTCCTCCTATCTCTCCCAGTCCTTGCTGCCGGAATTACAATGCTCCTTACAGA
TCGTAATCTAAACACCACCTTCTTCGACCCAGCTGGAGGAGGGGATCCTATCCTCTATCAACA

MK340578 (mtDNA COI)
GGGACCGCTTTAAGCCTGCTCATTCGAGCCGAATTAAGCCAACCTGGCGCTCTTCTAGGAGACGACCAAATT
TACAATGTAATTGTTACAGCACATGCATTTGTAATAATTTTCTTTATAGTAATACCAATTATGATTGGAGGCTT
CGGGAATTGGTTAGTACCACTTATGATTGGTGCCCCTGATATAGCATTCCCTCGTATAAATAATATAAGCTTC
TGGCTTCTTCCCCCATCATTTCTCCTGCTGCTAGCTTCTTCTGGGGTTGAAGCTGGGGCTGGTACCGGGTGGA
CAGTTTATCCCCCACTGGCAGGAAACCTAGCCCACGCAGGTGCATCAGTTGACCTAACCATCTTTTCTCTTCA
CCTAGCCGGAATTTCATCTATTCTTGGGGCTATTAATTTTATCACTACTATTATTAACATGAAACCACCAGCTA
TCTCACAATATCAAACACCCCTGTTCGTATGGGCCGTTTTAATTACTGCCGTCCTACTCCTCCTATCTCTCCCA
GTCCTTGCTGCCGGAATTACAATGCTCCTTACAGATCGTAATCTAAACACCACCTTCTTCGACCCAGCTGGAG
GAGGGGATCCTATCCTCTATCAACA

Scientific name: *Sphyraena putnamae* **Jordan & Seale, 1905**
English name: Banded barracuda
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Sphyraenidae

Standard length: 670 mm
Fin formula: D1-V, D2-I/9, P1-14, P2-I/5, A-II/8, C-18-20
Identification: Colour of head and body dusky yellow green above, silvery below; 10 to 20 vertical dusky cross-bars of a serpentine pattern on back; fading below lateral line. All fins dusky, except pelvic fins. Body elongate, fusiform and slightly compressed; head large with long pointed snout. Edge of preoperculum smoothly round, no produced flap. Mouth large, the maxilla reaches to level of front edge of eye. Two widely separated dorsal fins. Caudal fin typically forked.

DNA Barcode: MK340720, MK340721, MK340722, MK340723, MK335884, MK335885, MK335886, MK335887

Remarks: New distributional record from Bangladesh.

MK340720 (mtDNA COI)
GGTACAGCTCTAAGCCTACTTATTCGAGCCGAACTTAGTCAACCGGGCTCTCTCTTAGGAGACGACCAAATTT
ATAATGTTATCGTAACAGCACACGCCTTTGTAATAATCTTTTTTATGGTAATACCCATTATGATTGGGGGCTTT
GGGAACTGGCTTATTCCCCTAATAATTGGCGCTCCAGACATAGCATTCCCCCGAATAAATAATATAAGCTTTT
GGCTACTCCCCCCTTCCTTTCTCTTACTCCTTTCTTCTTCGGCTGTAGAAGCGGGAGCCGGGACAGGATGGAC
AGTTTATCCTCCCTTAGCTGGAAATTTGGCCCATGCAGGAGCATCCGTCGACCTAACCATTTTCTCCCTTCACC
TGGCAGGTATTTCTTCAATCCTAGGGGCTATTAATTTTATTACCACTATTATTAACATGAAACCAGCGGCGACT
TCAATGTACCAAATTCCTCTGTTCGTTTGGGCTGTACTAATCACTGCCGTTCTCCTTCTCCTTTCACTCCCTGTC
TTAGCTGCTGGTATTACAATGCTCTTGACAGATCGAAATCTAAACACCGCCTTCTTTGACCCAGCAGGAGGAG
GAGACCCCATTCTGTACCAGCA

MK340721 (mtDNA COI)
GGTACAGCTCTAAGCCTACTTATTCGAGCCGAACTTAGTCAACCGGGCTCTCTCTTAGGAGACGACCAAA
TTTATAATGTTATCGTAACAGCACACGCCTTTGTAATAATCTTTTTTATGGTAATACCCATTATGATTGGGG
GCTTTGGGAACTGGCTTATTCCCCTAATAATTGGCGCTCCAGACATAGCATTCCCCCGAATAAATAATATA
AGCTTTTGGCTACTCCCCCCTTCCTTTCTCTTACTCCTTTCTTCTTCGGCTGTAGAAGCGGGAGCCGGGACA
GGATGGACAGTTTATCCTCCCTTAGCTGGAAATTTGGCCCATGCAGGAGCATCCGTCGACCTAACCATTTT
CTCCCTTCACCTGGCAGGTATTTCTTCAATCCTAGGGGCTATTAATTTTATTACCACTATTATTAACATGAA
ACCAGCGGCGACTTCAATGTACCAAATTCCTCTGTTCGTTTGGGCTGTACTAATCACTGCCGTTCTCCTTCT
CCTTTCACTCCCTGTCTTAGCTGCTGGTATTACAATGCTCTTGACAGATCGAAATCTAAACACCGCCTTCTT
TGACCCAGCAGGAGGAGGAGACCCCATTCTGTACCAACA

MK340722 (mtDNA COI)
GGTACAGCTCTAAGCCTACTTATTCGAGCCGAACTTAGTCAACCGGGCTCTCTCTTAGGAGACGACCAAA
TTTATAATGTTATCGTAACAGCACACGCCTTTGTAATAATCTTTTTTATGGTAATACCCATTATGATTGGGG
GCTTTGGGAACTGGCTTATTCCCCTAATAATTGGCGCTCCAGACATAGCATTCCCCCGAATAAATAATATA
AGCTTTTGGCTACTCCCCCCTTCCTTTCTCTTACTCCTTTCTTCTTCGGCTGTAGAAGCGGGAGCCGGGACA
GGATGGACAGTTTATCCTCCCTTAGCTGGAAATTTGGCCCATGCAGGAGCATCCGTCGACCTAACCATTTT
CTCCCTTCACCTGGCAGGTATTTCTTCAATCCTAGGGGCTATTAATTTTATTACCACTATTATTAACATGAA
ACCAGCGGCGACTTCAATGTACCAAATTCCTCTGTTCGTTTGGGCTGTACTAATCACTGCCGTTCTCCTTCT
CCTTTCACTCCCTGTCTTAGCTGCTGGTATTACAATGCTCTTGACAGATCGAAATCTAAACACCGCCTTCTT
TGACCCAGCAGGAGGAGGAGACCCCATTCTGTACCAACA

MK340723 (mtDNA COI)
GGTACAGCTCTAAGCCTACTTATTCGAGCCGAACTTAGTCAACCGGGCTCTCTCTTAGGAGACGACCAAA
TTTATAATGTTATCGTAACAGCACACGCCTTTGTAATAATCTTTTTTATGGTAATACCCATTATGATTGGGG
GCTTTGGGAACTGGCTTATTCCCCTAATAATTGGCGCTCCAGACATAGCATTCCCCCGAATAAATAATATA
AGCTTTTGGCTACTCCCCCCTTCCTTTCTCTTACTCCTTTCTTCTTCGGCTGTAGAAGCGGGAGCCGGGACA
GGATGGACAGTTTATCCTCCCTTAGCTGGAAATTTGGCCCATGCAGGAGCATCCGTCGACCTAACCATTTT
CTCCCTTCACCTGGCAGGTATTTCTTCAATCCTAGGGGCTATTAATTTTATTACCACTATTATTAACATGAA
ACCAGCGGCGACTTCAATGTACCAAATTCCTCTGTTCGTTTGGGCTGTACTAATCACTGCCGTTCTCCTTCT
CCTTTCACTCCCTGTCTTAGCTGCTGGCATTACAATGCTCTTGACAGATCGAAATCTAAACACCGCCTTCTT
TGACCCAGCAGGAGGAGGAGACCCCATTCTGTACCAGCA

Scientific name: *Pampus argenteus* **Euphrasen, 1788**
English name: Silver pomfret
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Stromateidae

Standard length: 71 mm
Fin formula: D-VIII/37, P1-27, P2-ABSENT, A-VI/36, C-18-20
Identification: Colour of head and body dark brownish silver dorsally, silvery white ventrally. Anal and caudal fins yellowish. Body oval, strongly compressed. Gill opening short, slit-like. Anterior dorosal and anal fins falcate. Caudal fin deeply forked, lower lobe often extended. Sensory canal area on temporal extending backward along lateral line.

DNA Barcode: MK340673

MK340673 (mtDNA COI)
GGCACAGCCCTAAGCTTACTTATTCGAGCTGAATTAAACCAACCAGGTGCCCTCCTTGGGGATGACCAAATTTATAAT
GTAATCGTTACAGCACATGCTTTCGTAATAATTTTCTTTATAGTAATGCCAGTCATAATCGGAGGGTTTGGAAACTGG
CTTGTTCCTATAATGATTGGAGCCCCAGATATAGCATTTCCCCGAATAAATAACATAAGCTTCTGGCTTCTTCCCCCAT
CTTTCCTACTGTTATTAGCTTCTTCCGGAGTTGAAGCTGGCGCTGGAACTGGGTGGACAGTTTACCCACCTCTAGCTG
GCAACCTGGCCCATGCTGGAGCATCCGTTGATTTAACTATTTTTTCCCTACATTTAGCAGGGGTTTCCTCAATTCTTGG
GGCTATTAACTTTATTACAACTATTATTAATATAAAACCTCCCGGAATTTCCCAATACCAGACACCCCTTTTCGTCTGG
GCTGTATTAATTACAGCCGTTCTTCTCCTTCTATCACTACCAGTTCTTGCTGCCGGAATCACTATGCTTCTGACAGATC
GAAATCTTAACACAACCTTCTTTGACCCTGCTGGAGGTGGAGATCCAATCCTCTATCAACA

Scientific name: *Terapon jarbua* **Forsskål, 1775**
English name: Three-striped tiger fish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Serranidae

Standard length: 94 mm
Fin formula: D-XI/10, P1-13, P2-I/5, A-III/8, C-18-20
Identification: Body colour silvery with 3 to 4 curved dark brown stripes; spinous dorsal fin with black blotch between 3rd and 6th spine; anterior and posterior tips of dorsal black; caudal fin with three horizontal stripes. Body slightly compressed; jaws with strong conical teeth in outer row; spinous part of dorsal fin strongly arched and deeply notched; 3 to 5 large spines at angle of preoperculum; lower spine very long.

DNA Barcode: MK340726, MK340727, MK340728

MK340726 (mtDNA COI)
GGCACAGCTCTGAGCCTGCTTATCCGAGCAGAATTAAGCCAACCCGGCGCTCTCCTAGGGGACGACCAAATCTA
CAATGTAATTGTTACGGCACACGCCTTTGTAATAATTTTCTTTATGGTTATACCAATCATGATTGGAGGCTTTGGC
AACTGGCTTATCCCCCTAATGATTGGCGCCCCTGATATGGCATTCCCTCGTATGAATAACATGAGCTTCTGGCTC
CTCCCTCCCTCTTTCCTTCTCCTGCTCGCCTCCTCTGGAGTAGAAGCCGGGGCCGGAACTGGTTGGACTGTTTAC
CCACCTCTCGCTGGCAACTTAGCCCATGCCGGAGCATCCGTAGACTTAACAATTTTCTCCCTCCATCTAGCCGGG
GTGTCCTCAATTTTAGGTGCTATCAACTTCATCACAACTATTATTAACATGAAACCTCCCGCTATCTCACAATATC
AAACCCCTCTATTTGTTTGGGCCGTGCTAATCACCGCCGTTCTCCTTCTCCTTTCCCTTCCAGTCCTCGCTGCCGG
GATCACAATGCTCCTGACAGACCGAAACTTAAACACTACCTTCTTTGACCCTGCCGGAGGAGGTGACCCCATCCT
GTATCAACA

MK340727 (mtDNA COI)
GGCACAGCTCTGAGCCTGCTTATCCGAGCAGAATTAAGCCAACCCGGCGCTCTCCTAGGGGACGACCAAATC
TACAATGTAATTGTTACGGCACACGCCTTTGTAATAATTTTCTTTATGGTTATACCAATCATGATTGGAGGCTT
TGGCAACTGGCTTATCCCCCTAATGATTGGCGCCCCTGATATGGCATTCCCTCGTATGAATAACATGAGCTTC
TGGCTCCTCCCTCCCTCTTTCCTTCTCCTGCTCGCCTCCTCTGGGGTAGAAGCCGGGGCCGGAACTGGTTGGA
CTGTTTACCCACCTCTCGCTGGCAACTTAGCCCATGCCGGAGCATCCGTAGACTTAACAATTTTCTCCCTCCAT
CTAGCCGGGGTGTCCTCAATTTTAGGTGCTATCAACTTCATCACAACTATTATTAACATGAAACCTCCTGCTAT
CTCACAATATCAAACCCCTCTATTTGTTTGGGCCGTGCTAATCACCGCCGTTCTCCTTCTCCTTTCCCTTCCAGT
CCTCGCTGCCGGGATCACAATGCTCCTGACAGACCGAAACTTAAACACTACCTTCTTTGACCCTGCCGGAGGA
GGTGACCCCATCCTGTATCAACA

MK340728 (mtDNA COI)
GGCACAGCTCTGAGCCTGCTTATCCGAGCAGAATTAAGCCAACCCGGCGCTCTCCTAGGGGACGACCAAATC
TACAATGTAATTGTTACGGCACACGCCTTTGTAATAATTTTCTTTATGGTTATACCAATCATGATTGGAGGCTT
TGGCAACTGGCTTATCCCCCTAATGATTGGCGCCCCTGATATGGCATTCCCTCGTATGAATAACATGAGCTTC
TGGCTCCTCCCTCCCTCTTTCCTTCTCCTGCTCGCCTCCTCTGGAGTAGAAGCCGGGGCCGGAACTGGTTGGA
CTGTTTACCCACCTCTCGCTGGCAACTTAGCCCATGCCGGAGCATCCGTAGACTTAACAATTTTCTCCCTCCAT
CTAGCCGGGGTGTCCTCAATTTTAGGTGCTATCAACTTCATCACAACTATTATTAACATGAAACCTCCCGCTAT
CTCACAATATCAAACCCCTCTATTTGTTTGGGCCGTACTAATCACCGCCGTTCTCCTTCTCCTTTCCCTTCCAGT
CCTCGCTGCCGGGATCACAATGCTCCTGACAGACCGAAACTTAAACACTACCTTCTTTGACCCTGCCGGAGGA
GGTGACCCCATCCTGTATCAACA

Scientific name: *Terapon theraps* **Cuvier, 1829**
English name: Large-scaled banded grunter
Classification
Class: Actinopterygii
Order: Perciformes
Family: Serranidae

Standard length: 122 mm
Fin formula: D-XII/10, P1-14, P2-I/5, A-III/8, C-18-20
Identification: Colour of body dusky dorsally, silvery white ventrally; 4 dark brown horizontal stripes on body; spinous part of dorsal fin with black blotch dorsally on fin membranes between third and seventh spine; caudal fin with median rays pigmented; each caudal lobe with 1 transverse stripe, upper lobe with black tip. Body oblong, moderately compressed. Spinous part of dorsal fin strongly arched and deeply notched; penultimate spine about half length of ultimate spine. Caudal fin emarginate with rounded lobes.
DNA Barcode: MK340729, MK340730

MK340729 (mtDNA COI)
GGCACAGCTTTAAGCCTACAAATTCGAGCAGAACTAAGCCAGCCTGGCGCTCTCCTCGGAGATGACC
AAATTTATAATGTAATTGTTACAGCCCATGCCTTTGTAATAATTTTCTTTATAGTAATGCCAATTATGA
TCGGAGGCTTTGGGAACTGGCTAATTCCACTAATGATCGGGGCCCCCGACATGGCATTCCCACGAAT
AAATAACATGAGCTTCTGGCTCCTCCCTCCCTCATTCCTTCTTCTCCTAGCTTCTTCAGGAGTCGAAGC
AGGTGCAGGAACCGGCTGGACTGTTTACCCCCCTCTTGCCGGTAACTTAGCCCACGCTGGAGCATCTG
TAGACCTAACCATCTTCTCCCTCCACCTAGCTGGGGTATCATCTATTCTTGGGGCAATTAATTTCATTA
CCACGATCATTAATATGAAACCACCCGCTATTTCTCAATATCAAACCCCTCTATTTGTTTGGGCTGTG
CTCATCACAGCAGTTTTACTTCTCCTCTCTCTTCCAGTCCTCGCCGCCGGAATTACAATGCTCCTTACG
GACCGAAATTTAAATACTACCTTCTTTGATCCAGCAGGCGGAGGGGATCCCATCCTCTACCAACA

MK340730 (mtDNA COI)
GGCACAGCTTTAAGCCTACAAATTCGAGCAGAACTAAGCCAGCCTGGCGCTCTCCTCGGAGATGACCAAATTTA
TAATGTAATTGTTACAGCCCATGCCTTTGTAATAATTTTCTTTATAGTAATGCCAATTATGATCGGAGGCTTTGGG
AACTGGCTAATTCCACTAATGATCGGGGCCCCCGACATGGCATTCCCACGAATGAATAACATGAGCTTCTGGCTC
CTCCCTCCCTCATTCCTTCTTCTCCTAGCTTCTTCAGGAGTCGAAGCAGGTGCAGGAACCGGCTGGACTGTTTATC
CCCCTCTTGCCGGTAACTTAGCCCACGCTGGAGCATCTGTAGACCTAACCATCTTCTCCCTCCATCTAGCTGGGGT
ATCATCTATTCTTGGGGCAATTAATTTCATTACCACGATCATTAATATGAAACCACCCGCTATTTCTCAATATCAA
ACCCCTCTATTTGTTTGGGCTGTGCTCATCACAGCAGTTTTACTTCTCCTCTCTCTTCCAGTCCTCGCCGCCGGAAT
TACAATGCTCCTTACGGACCGAAATTTAAATACTACCTTCTTTGATCCAGCAGGCGGAGGGGATCCCATCCTCTA
CCAACA

Scientific name: *Platycephalus indicus* **Linnaeus, 1758**
English name: Bartail flathead
<u>Classification</u>
Class: Actinopterygii
    Order: Scorpaeniformes
        Family: Platycephalidae

Standard length: 293 mm
Fin formula: D-IX, D2-13, P1-19, P2-I/5, A-13, C-16
Identification: Back colour light blown, lower ventral flanks and belly whitish or silvery; without dark blotches. Both dorsal fins and caudal fin dusky; other fins pale. Body elongate, snout pointed; upper profile of head slightly convex. Mouth large with Bony ridges; a small pre-opercular and two pre-ocular spines present; teeth villiform. Two dorsal fins. Body very depressed, mouth large with Bony ridges; a small pre-opercular and two pre-ocular spines present.

DNA Barcode: MK986641

Scientific name: *Pterois volitans* **Linnaeus, 1758**
English name: Red lionfish
<u>Classification</u>
Class: Actinopterygii
Order: Scorpaeniformes
Family: Scorpaenidae

Identification: Colour of body is white or cream coloured red to reddish-brown vertical stripes. The vertical stripes alternate from wide to very thin (with the thin stripes being more numerous) and sometimes merge along the flank to form a V-shape. It has greatly elongated dorsal-fin spines. The membranes of all fins are often spotted.

Remarks: This species has been recorded during the underwater scuba diving.

Scientific name: *Pterois russelii* **Bennett, 1831**
English name: Plaintail turkeyfish
Classification
Class: Actinopterygii
Order: Scorpaeniformes
Family: Scorpaenidae

Identification: Head and body with numerous reddish-brown bars of variable width, separated by narrow white bars; generally brownish pectoral fins without prominent dark bands; dorsal spines free of membrane except basally; enlarged and wing-like pectoral fins with rays free of membrane distally, unbranched rays.

Remarks: This species has been recorded during the underwater scuba diving.

DNA Barcode: MK560529
Scientific name: *Dactyloptena orientalis* **Cuvier, 1829**
English name: Oriental flying gurnard
Classification
Class: Actinopterygii
Order: Scorpaeniformes
Family: Dactylopteridae

Standard length: 181 mm
Fin formula: D1-I+I+VI, D2-8, P1-32, P2-I/4, A-6, C-13-15
Identification: usually yellowish brown above, lighter brown below; small orange spots over top of head and back; dusky, golden spots on pectoral fins (larger distally); 4 golden bands on caudal fin; a yellow band along upper part of spinous dorsal fin. Body moderately elongate, squarish in cross-section. Head broad, blunt, depressed anteriorly, with a prominent keeled spine extending posteriorly from the nape to below second spine of continuous spinous part of dorsal fin. Angle of preopercle with a long, prominent spine. Eyes large. Mouth small, subterminal, and protractile. Upper jaw largely obscured by bones surrounding eye. Minute teeth present on jaws. Base of pectoral fins horizontal, the fins divided into 2 sections, a short anterior part with 5 rays, and a long posterior section with 27 to 30 rays. Scales strong, each with a distinct ridge. Large scute-like scales posteriorly on caudal peduncle. Lateral line absent or greatly obscured.

DNA barcode: MK340606, MK340607

MK340606 (mtDNA COI)
GGCACTGCTTTAAGCCTCTTAATCCGTGCAGAATTAAGTCAACCAGGCGCCCTCTTAGGGGACGACCAAATTTATAATGTA
ATCGTTACTGCTCATGCTTTTGTGATGATTTTCTTTATAGTAATGCCAATTATGATCGGAGGGTTCGGAAACTGGCTAATCC
CCCTAATGATCGGGGCCCCCGACATGGCCTTCCCCCGAATGAACAACATAAGCTTCTGGCTTCTACCCCCCTCCTTCTTGCT
TCTACTAGCCTCTTCAGGGGTTGAGGCCGGAGCGGGGACAGGATGGACTGTATACCCACCCCTAGCCGGCAATCTGGCA
CATGCAGGAGCTTCCGTTGACCTCACCATCTTCTCCCTTCACCTAGCTGGTGTCTCTTCCATCCTAGGTGCCATCAATTTTAT
TACAACAATTATTAACATGAAGCCCCCAGCCATCTCCCAATACCAGACCCCTCTGTTTGTCTGGGCTGTCCTAGTAACGGCC
GTTCTGCTACTACTCTCACTGCCAGTTCTTGCCGCTGGTATCACAATACTTCTTACCGACCGAAATCTAAATACTACCTTCTT
TGACCCGGCAGGAGGGGGGGATCCTATCCTTTACCAACA

MK340607 (mtDNA COI)
GGCACTGCTTTAAGCCTCTTAATCCGTGCAGAATTAAGTCAACCAGGCGCCCTCTTAGGGGACGACCAAATTTATAATGTA
ATCGTTACTGCTCATGCTTTTGTGATGATTTTCTTTATAGTAATGCCAATTATGATTGGAGGGTTCGGAAACTGGCTAATCC
CCCTAATGATCGGGGCCCCCGACATGGCCTTCCCCCGAATGAACAACATAAGCTTCTGGCTTCTACCCCCCTCCTTCTTGCT
TCTACTAGCCTCTTCAGGGGTTGAGGCCGGAGCGGGGACAGGATGGACTGTATACCCACCCCTAGCCGGCAATCTGGCA
CATGCAGGAGCTTCCGTTGACCTCACCATCTTCTCCCTTCACCTAGCTGGTGTCTCTTCCATCCTAGGTGCCATCAATTTTAT
TACAACAATTATTAACATGAAGCCCCCAGCCATCTCCCAATACCAGACCCCTCTGTTTGTCTGGGCTGTCCTAGTAACGGC
CGTACTGCTACTACTCTCACTGCCAGTTCTTGCCGCTGGTATCACAATACTTCTTACCGACCGAAATCTAAATACTACCTTCT
TTGACCCGGCAGGAGGAGGAGATCCTATCCTTTACCAACA

Scientific name: *Minous monodactylus* **Bloch & Schneider, 1801**
English name: Grey stingfish
<u>Classification</u>
Class: Actinopterygii
Order: Scorpaeniformes
Family: Synanceiidae

Standard length: 79 mm
Fin formula: D-X/11, P1-10+1(curved detached ray), P2-I/5, A-II/9
Identification: Colour of dorsal part of body with pale bars and stripes; ventral surface usually pale, without markings. Anterior part of segmented dorsal fin with a large black area or spot, usually followed by oblique pale bars; inner side of pectoral fin and pectoral fin axil pale, without distinctive markings; lateral side of pectoral and pelvic fins and anal fin blackish distally. Caudal fin with 2 broad vertical bars.Head spines well developed. Body compressed, without scale. Mouth oblique, two preorbital spines. A tentacle in lower jaws. First dorsal spine minute, caudal rounded.

DNA Barcode: MK340610

MK340610 (mtDNA COI)
GGCACGGCCCTGAGCCTCCTAATCCGAGCAGAACTGAGCCAACCCGGCGCCCTCCTTGGAGATGACCAAATCTACA
ATGTAATCGTTACCGCACACGCATTCGTAATAATTTTCTTTATAGTAATACCAATTATGATCGGAGGCTTTGGAAAC
TGGCTAATTCCCTTAATAATCGGCGCCCCCGACATAGCATTCCCCCGTATAAATAACATAAGCTTCTGGCTACTTCCC
CCCTCCTTCCTCCTTCTCCTCGCCTCCTCTGGCGTAGAGGCCGGGGCAGGAACTGGATGGACGGTCTACCCCCCACT
GGCCGGCAACTTAGCACACGCCGGGGCATCCGTTGACCTGACAATCTTCTCCCTCCACCTAGCAGGTGTTTCCTCAA
TCCTAGGGGCTATCAACTTCATCACAACCATTATTAATATAAAACCACCCGCCATCTCCCAGTACCAAACACCCCTAT
TCGTGTGGGCAGTCCTAATTACCGCTGTCCTTCTCCTCCTCTCGCTTCCGGTTCTGGCCGCCGGCATTACAATATTAC
TCACGGACCGAAATTTAAATACCACCTTCTTTGACCCGGCAGGGGGAGGTGACCCAATCCTTTACCAACA

Scientific name: *Plotosus lineatus* **Thunberg, 1787**
English name: Striped Eel Catfish
<u>Classification</u>
Class: Actinopterygii
    Order: Siluriformes
        Family: Plotosidae

Identification: Colour of head and body brown, becoming cream or white ventrally; 2 to 3 narrow pale yellow longitudinal stripes on body, of which 2 extending onto head. Body somewhat elongate; anterior nostril situated dorsal to upper lip, opening directed anteriorly; nasal and maxillary barbels short, reaching to or slightly beyond posterior margin of eye; origin of dorsal procurrent caudal fin inserting vertical above pelvic-fin base.

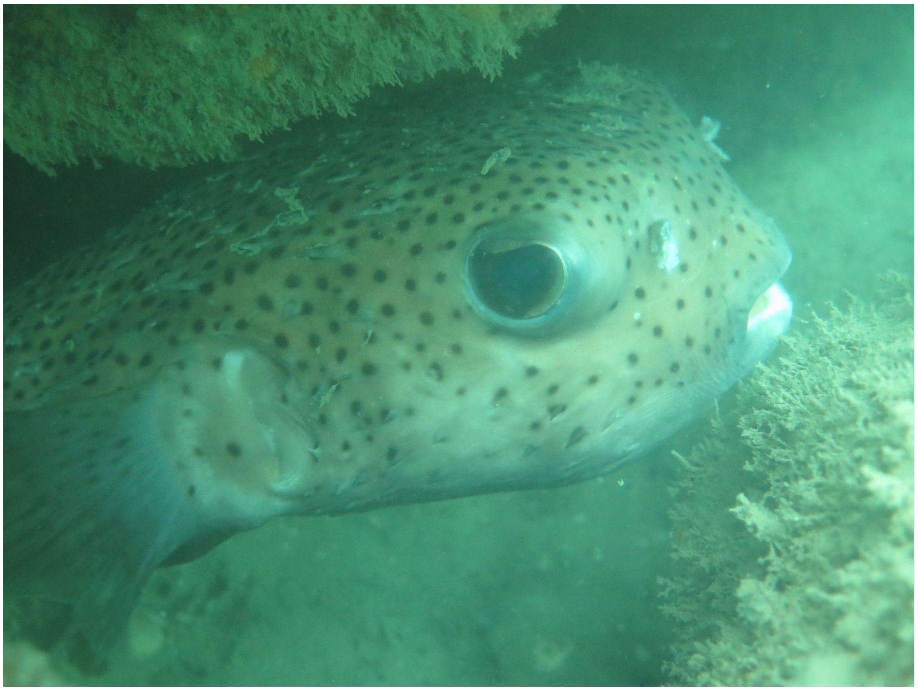
Remarks: This species has been recorded during the underwater scuba diving.

Scientific name: *Tetrosomus gibbosus Linnaeus*, **1758**
English name: Humpback turretfish
Classification
Class: Actinopterygii
Order: Tetraodontiformes
Family: Ostraciidae

Standard length: 49 mm
Fin formula: D-9,P1-10, P2-Absent, A-9, C-8
Identification: Colour of light brown to yellowish gray. Body triangular in cross section. Three sharp spines on longitudinal median ridge on back; 4 or 5 smaller spines on ventrolateral ridge. A small spine on ridge above eye.
DNA barcode: MK340731

MK340731 (mtDNA COI)
GGAACAGCCTTAAGCCTACTTATCCGAGCCGAACTAAGCCAGCCAGGCGCTCTTCTTGGAGACGATCAGATTTATA
ATGTAATCGTTACAGCACATGCATTCGTAATAATTTTCTTTATAGTAATACCAATCATGATTGGGGGGTTTGGAAAC
TGGCTGGTGCCCCTAATAATTGGGGCCCCTGATATAGCATTTCCCCGAATGAATAACATAAGCTTCTGGCTCCTCCC
TCCCTCCTTCCTCCTTCTCCTGGCCTCATCAGGGGTTGAAGCAGGCGCTGGAACTGGCTGGACAGTTTATCCCCCGT
TAGCAGGCAATCTAGCACATGCAGGAGCATCTGTTGATTTAACCATCTTTTCACTTCACCTAGCAGGGGTCTCCTCG
ATTTTAGGTGCTATTAATTTTATCACTACTATTATTAACATGAAGCCCCCTGCTATTTCTCAATATCAAACCCCTCTGT
TCGTATGGGCAGTTTTAATTACCGCCGTTCTTCTCCTTCTATCACTACCAGTTCTTGCTGCCGGTATTACAATGCTTCT
AACAGACCGAAATCTAAACACCACATTCTTTGACCCTGCAGGGGGAGGAGACCCCATTCTTTATCAACA

Scientific name: *Diodon hystrix* **Linnaeus, 1758**
English name: Spot-fin porcupinefish
Classification
Class: Actinopterygii
Order: Tetraodontiformes
Family: Diodontidae



Identification: Body brownish dorsally with small black spots; fins yellowish with dark spots. Body flabby; eyes large; head and body with long pointed spines; no downward pointed spine below eye; no barbels on chin. Pectoral fins broad. Caudal fin rounded.

Remarks: This species has been recorded during the underwater scuba diving.

Scientific name: *Balistoides viridescens Bloch* **& Schneider, 1801**
English name: Titan triggerfish
Classification
Class: Actinopterygii
Order: Tetraodontiformes
Family: Balistidae

Standard length: 440 mm
Fin formula: D1-III, D2-25, P1-14, P2-Absent, A-22, C-12-16
Identification: Color of body yellowish gray to brown, the centers o scales dark brown or greenish. Scales enlarged above the pectoralfin base and just behind the gill opening. A prominent groove before eye. Five or 6 rows of small anteriorly projecting spines on caudal peduncle.

DNA Barcode: MK560530

Remarks: New distributional record from Bangladesh.

Scientific name: *Chelonodontops patoca* **Hamilton, 1822**
English name: Milkspotted puffer
Classification
Class: Actinopterygii
Order: Tetraodontiformes
Family: Tetraodontidae

Standard length: 84 mm
Fin formula: D10, P1-16, P2-Absent, A-8, C-8
Identification: Color greenish-gray to brown on back with large round to ovate white spots, a broad yellow band running from chin to lower caudal-fin base. A patch of spinules on back from behind interorbital nearly to dorsal fin and another on throat and abdomen. Nasal organ in the form of a depression with slightly raised margin expanded before and behind into a pair of elongate flaps.

DNA Barcode: MK560528

Scientific name: *Sufflamen fraenatum***Latreille, 1804**
English name: Masked triggerfish
Classification
Class: Actinopterygii
Order: Tetraodontiformes
Family: Balistidae

Identification: Color of body gray to brown with lengthwise blue lines on head and body; a small blackish spot at upper end of gill opening, preceded by a yellow band that continues in front of eye as a double band. Body deep. Teeth fixed, denticulate on all of margin, with expanded incurved tips. Caudal fin deeply emarginate. Caudal peduncle with 1 folding spine.

Scientific name: *Hemiramphus far Forsskal*, **1775**
English name: Black-barred halfbeak
Classification
Class: Actinopterygii
Order: Beloniformes
Family: Hemiramphidae

Standard length: 191 mm
Fin formula: D1-13, P1-12, P2-6, A-10, C-17-19
Identification: Colour green or blue on the back and silvery white on the sides and ventrally; tip of lower jaw bright red or orange. Usually with 3 to 9, short dark vertical bars on sides of body. Body not ribbon-shaped; elongate with prolonged lower jaw and short triangular upper jaw; both upper and lower jaws elongate and armed with needle-sharp teeth. Nostrils in pit anterior to eyes. No spines in fins; dorsal and anal fins posterior in position; pelvic fins abdominal in position; pectoral fins usually short. Lateral line running down from pectoral-fin origin and then backwards along ventral margin of body. Scales moderately large, cycloid.

DNA Barcode: MK561619

Remarks: New distributional record from Bangladesh.

Scientific name: *Chlorurus rhakoura* **Randall & Anderson, 1997**
English name: Raggedfin Parrotfish
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Scaridae

Standard length: 314 mm
Fin formula: D1-IX/10, P1-14, P2-I/6, A-III/9, C-26
Identification: Color dark graybrown or deep blue, the scales of body with a dull blue-green cast and very dark purplish edges; margins of dorsal and anal fins bright blue; dental plates bluish white. Body moderately deep; adults with a large, bulbous, fleshy protuberance on forehead. Caudal fin with strongly inserted rays, giving the posterior margin a ragged appearance.

DNA Barcode: MK560524, MK561629

Remarks: New distributional record from Bangladesh.

Scientific name: *Heteromycteris oculus* **Alcock, 1889**
English name: Eyed sole
<u>Classification</u>
Class: Actinopterygii
Order: Pleuronectiformes
Family: Soleidae

Standard length: 59 mm
Fin formula: D1-95-100, P1-Absent, P2-5, A-67, C-10-14
Morphologycal characteristics: Body ovate and flat, snout hooq-like.Purplish brown with wavy anastomosing lighter lines, which surround irregular dark spots or ring. 8 large ocelli. Vertical fins with blakish spots and stripes.

DNA Barcode: MK560525

Scientific name: *Lobotes surinamensis* **Bloch, 1790**
English name: Tripletail
<u>Classification</u>
Class: Actinopterygii
Order: Perciformes
Family: Lobotidae

Standard length: 231 mm
Fin formula: D-XII/16, P1-16, P2-I/5, A-III/12, C-18-20
Identification: Color of body dark brown or greenish yellow above, silvery grey below; pectorals pale yellow, other fins darker than body; caudal fin with yellow margin. Rounded caudal fin that appear as single 3-lobed fin. A compressed, deep-bodied perch-like fish with the dorsal and anal fins rounded and symmetrical so that with the tail they appear to be a single three-lobed fin. Head dish-shaped, interorbital space narrow, upper profile concave; eye relatively small; mouth large, slightly oblique, upper jaw protractile. Bases of dorsal and anal fins scaled; pectoral fins shorter than pelvic fins.

DNA Barcode: MK560523

We obtained 366 sequences that derived from 366 morphologically confirmed individuals of 111 number of species. In additional 6 species failed to provide successful sequences and 8 species had been enlisted by scuba diving. All sequences and taxonomic files were submitted to BOLD system and GenBank accessible for all (annex 01 & 02). Among the successfully sequenced species, 111 were represented by one, two or more individuals. The average length of consensus sequences was over ≥450 bp showed no insertions, deletions, or stop except for few species, COI sequences of the same species clustered in mono-phyletic unit with very high bootstrap values (100%) (Fig. 7). The phylogenetic tree of newly recorded fish species from St. Martin’s Island given in figure 8.

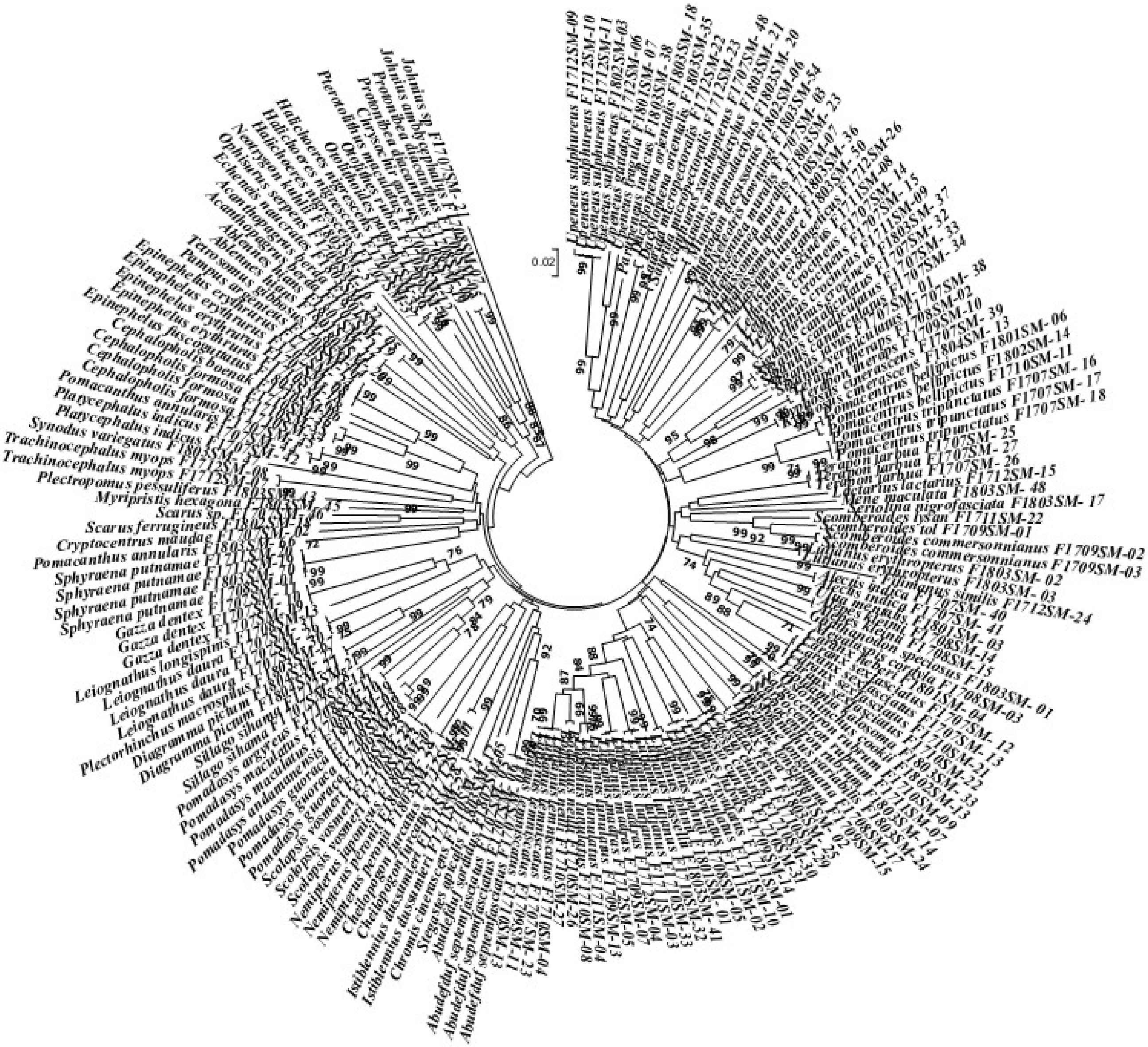


Figure 17. Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene sequences with all sequenced individuals. Bootstrap support of >70% are shown above branches. Scale represents genetic distance between species. Bootstrap replications 1000.

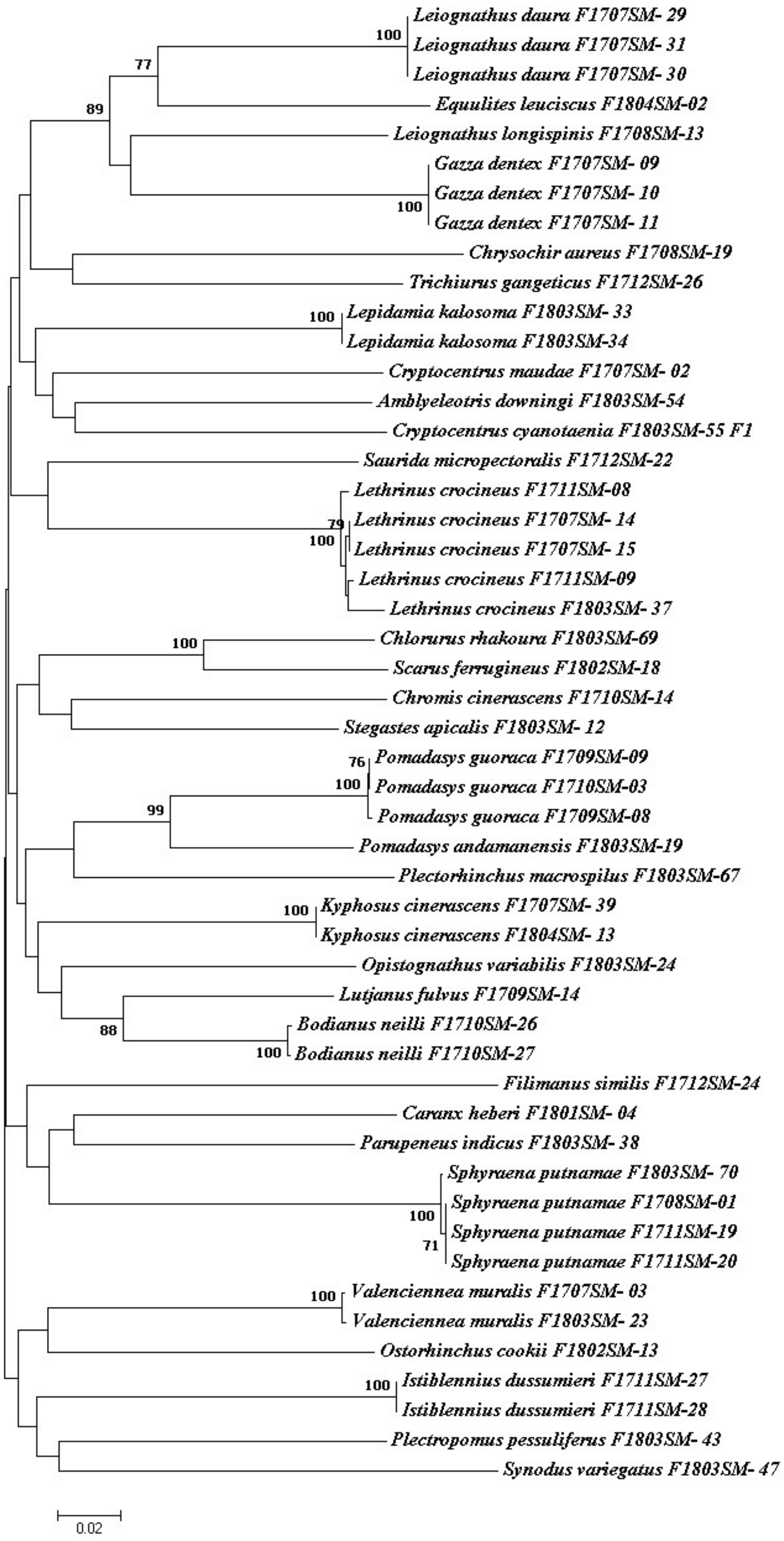


Figure 18. Neighbor-joining tree constructed using the Kimura 2-parameter model for COI gene sequences of **newly recorded individuals**. Bootstrap support of >70% are shown above branches. Scale represents genetic distance between species. Bootstrap replications 1000.

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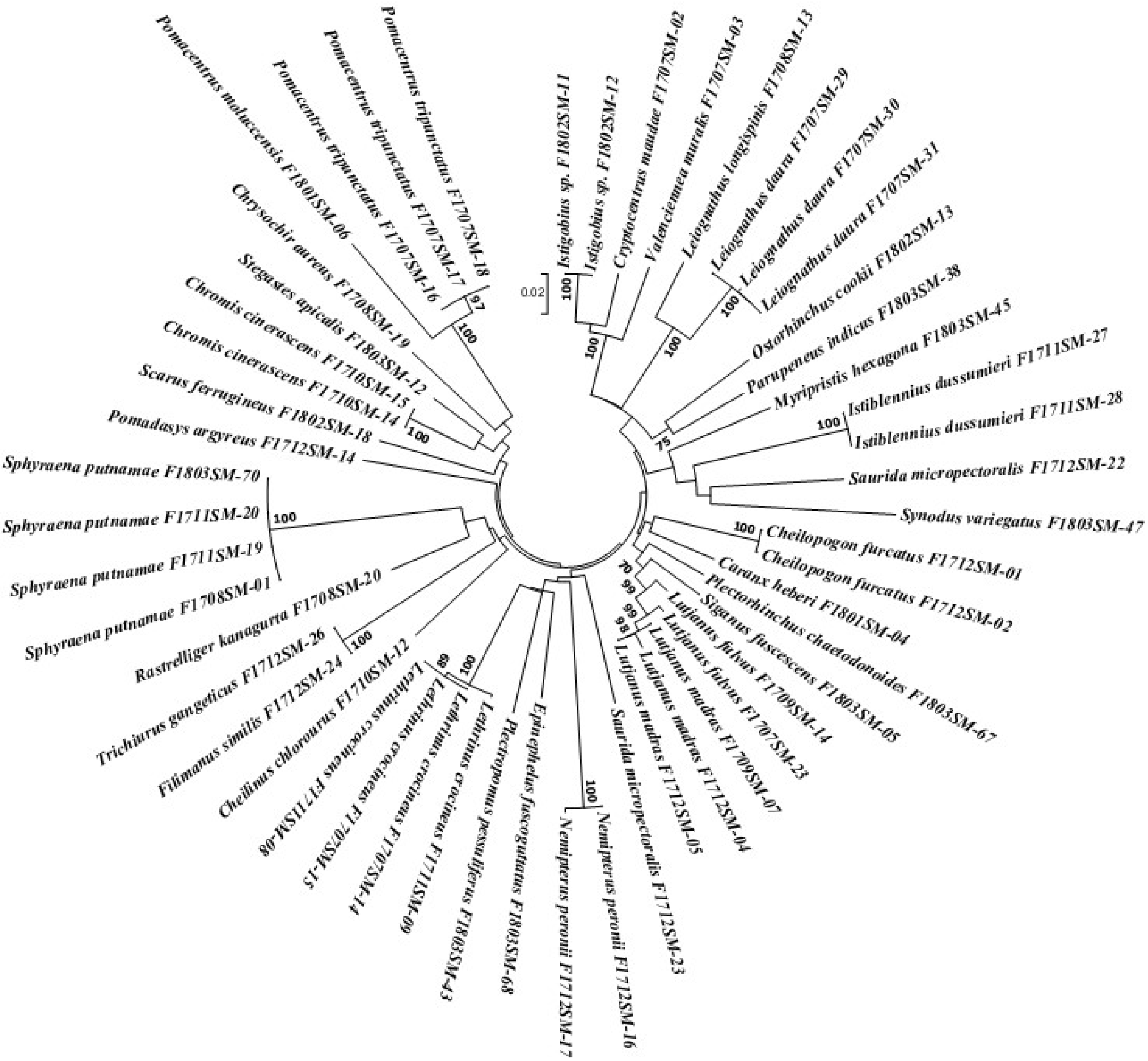
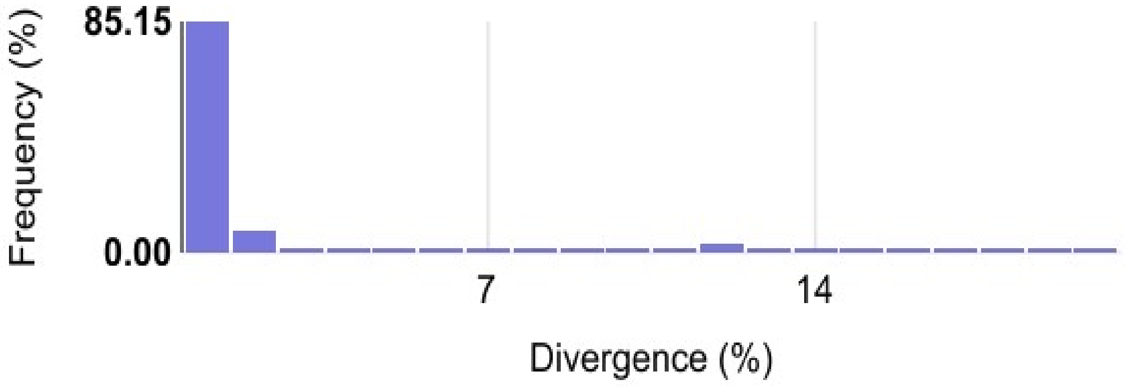


Figure 19. Neighbor-joining tree constructed using the Kimura 2-parameter model for !6S RRNA gene sequences with all sequenced individuals. Bootstrap support of >70% are shown above branches. Scale represents genetic distance between species. Bootstrap replications 1000.

Overall nucleotide frequencies for COI gene region of 182 successfully sequenced individuals mean value were A% (23.60±0.0949), T% (28.95±0.1372), C% (28.85±0.1563), G% (18.61±0.0720). Overall mean distance between sequences of COI gene was 0.2265±0.0120 for COI gene region. The distribution of sequence divergence within species 1.23±0.04% (mean value) followed by within genus 12.34±0.02%, within family 19.57±0.01% (Fig. 9).

Within Species



Within Genus

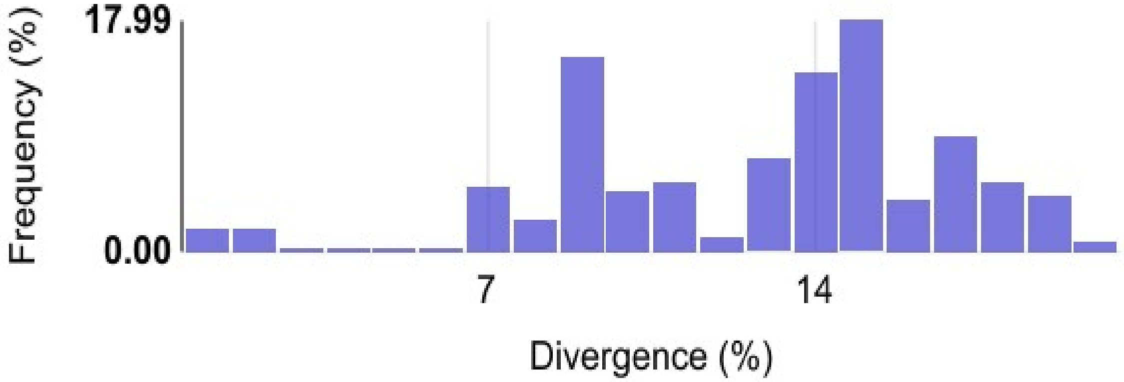


Figure 20. Sequence divergence between barcode sequences at the species, genus and family level, and also contrasts the distribution of within-species divergence to between-species divergence. Distance model: Kimura 2 Parameter, COI marker, Deletion method pairwise deletion, GPS alignment Kalign (Lassmann and Sonnhammer, 2005).

The within-species distribution is normalized to reduce bias in sampling at the species level. Normalized divergence mean within-Species dist. (%) 1.70±0.11 (Fig. 10).

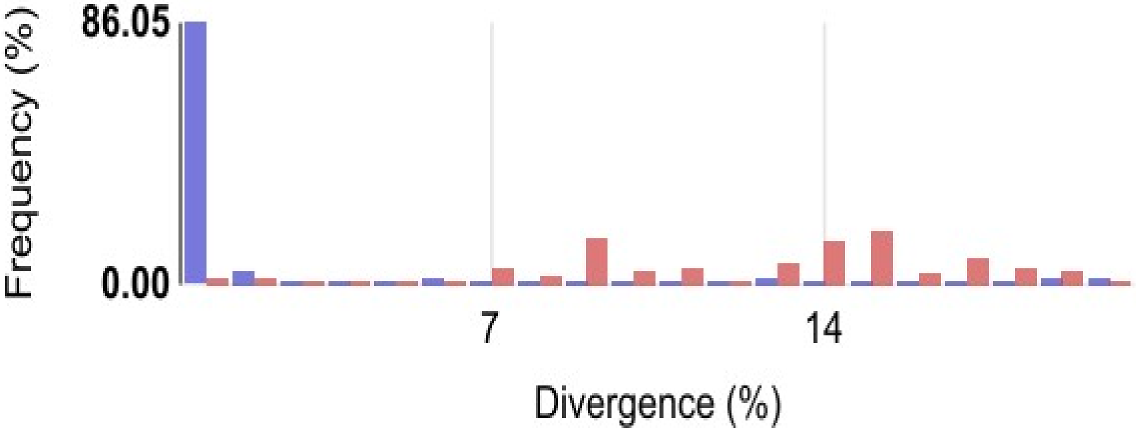
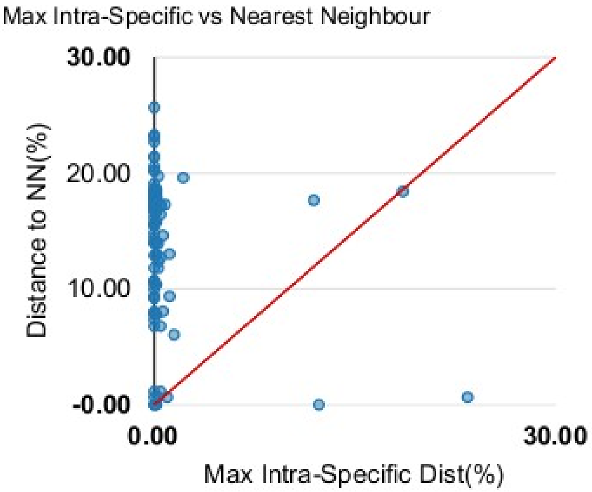
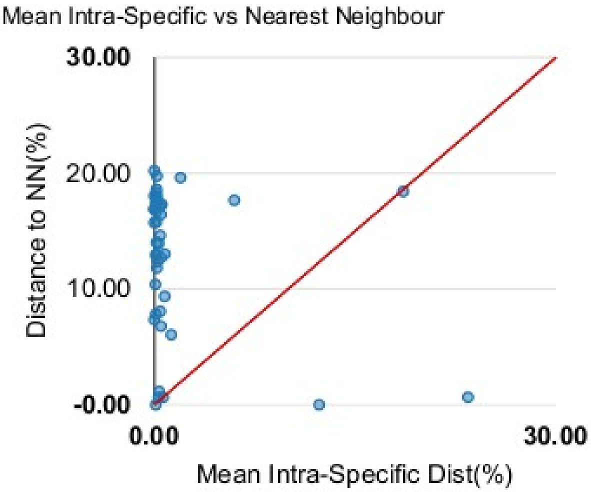


Figure 21. Normalized Divergence Histogram. The distribution of within-species divergence to between-species divergence. Histogram plots the distribution of normalized divergence for species (blue) against the genus divergences (red). Distance model: Kimura 2 Parameter, COI marker, Deletion method pairwise deletion, GPS alignment Kalign (Lassmann and Sonnhammer, 2005).

The Barcode Gap Analysis provides the distribution of distances within each species and the distance to the nearest neighbor of each species. Species are tested for the presence of the Barcode Gap. Three scatterplots are provided to confirm the existence and magnitude of the Barcode Gap. The first two scatterplots show the overlap of the max and mean intra-specific distances vs the inter-specific (nearest neighbour) distances. The third scatterplot plots the number of individuals in each species against their max intra-specific distances, as a test for sampling bias (Fig. 11).


Max Intra-Specific vs Nearest Neighbour


Mean Intra-Specific vs Nearest Neighbour

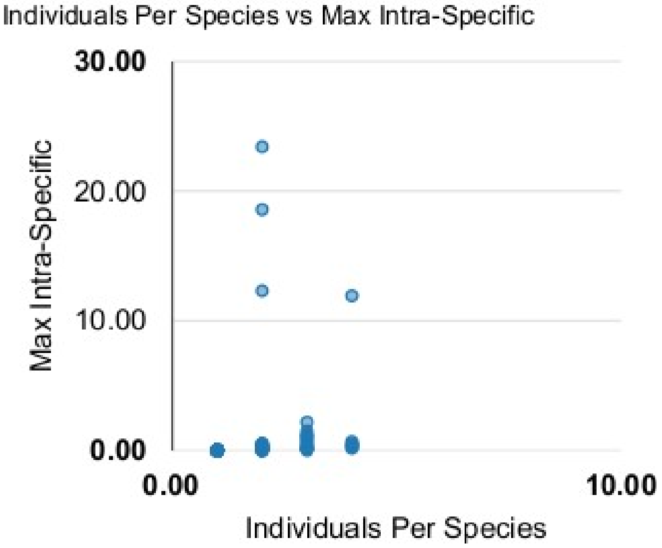


Figure 22. Scatterplots to confirm the existence and magnitude of barcode gap. Distance model: Kimura 2 Parameter, COI marker, Deletion method pairwise deletion, GPS alignment Kalign (Lassmann and Sonnhammer, 2005)

In the other hand, we sequenced 52 more sequences using 16s rRNA (16s large ribosomal) gene marker for ensuring of newly recorded species from st. martin's island additionally. Those sequences also submitted to NCBI GenBank accessible for all. The GenBank accession number for all 16s rRNA gene regions are MK335844 to MK293944.

The average length of consensus sequences was over ≥450 bp showed no insertions, deletions, or stop except for few species, 16s rRNA sequences of the same species clustered in mono-phyletic unit with very high bootstrap values (100%) (Fig.12).

St. Martin's island is only and unique ecosystem for Bangladesh, which supports a few of coral habitats of its surround periphery. That supports a large numbers of aquatic flora and faunal biodiversity. Although, the current project started as a rapid and intensive effort to collect fish samples and barcode as many species as possible from St. Martin`s Island, it took a shortage of time to validate and confirm the species profiles morphologically and genetically. Some inventoried taxa still lack species-level determination due to lack of data, but these will be resolved over time.

11.2: Results and Discussion on Study- 2: Population genetic structure of *S. lewini*

11. **Genetic diversity**: Sequences of all of the 33 individuals of BoB were obtained after sequencing. A total of 519 nucleotide long sequences of the D-loop region at the 5′ end were acquired after removing the confusing sequences near the primer ends. Most of the nucleotide substitutions were transitional in the studied sequences (Table 3). About 37% of the nucleotide substitutions were transversion. An indel was detected in all the sequences analyzed. Variations in the D-loop region defined 8 haplotypes with 9 polymorphic sites. The nucleotide diversity (π) were as low as 0.002 nucleotide differences per site. On the other hand, the haplotype diversity (h) were relatively high providing the values of 0.58 (Table 3).

12. **Population differentiation:** Estimates of F_{ST} between BoB and each of the compared populations were ranged from 0.308 to 0.530 with significant difference (*P*= 0.00) from random mixing, indicating a unique

population genetic structure (i.e. a single genetic stock) was established in the Bay of Bengal region. Exact test of population differentiation also showed significant differentiation between BoB and each of other populations investigated suggesting a non-panmictic BoB population.

Table 3: Genetic diversity of control region (d-loop) for BoB population.

Population	**Ni**	**Sb (ti+tv)**	**N_{id}**	**N_h**	**h**	**π**	**S**
BoB	**33**	**8 (5+3)**	**01**	**8**	**0.58**	**0.002**	**9**
[Number of individuals (Ni), number of substitution (Sb), Transition (ti), transversion (tv), number of indels (N_{id}), number of haplotype (N_h), haplotype diversity (*h*), nucleotide diversity (π), number of polymorphic site (S)							

Table 4: Pairwise F_{ST} and *P* values between the Bay of Bengal (BB) and other populations of *S. lewini* for mtDNA control region.

Population	**Bay of Bengal (BoB)**	
	F_{ST}	***P***
Bay of Bengal (BoB)	-	
Arabian Sea (AS)	0.376	0.00
Red Sea (RS)	0.320	0.00
Indo Pacific (IP)	0.398	0.00
Pacific Ocean (PO)	0.530	0.00
Indian Ocean (IO)	0.308	0.00
Atlantic Ocean (AO)	0.406	0.00

Haplotype network:

In the haplotype network, five haplotypes were singletons and unique (BD-05, 07, 24, 30, 38; Table: 6 and Fig. 23) for the BoB and three haplotypes include more than one individuals. All five haplotypes were novel, that is, not present in the global data set of Duncan *et al*. (2006) or in any of the regional data sets by Chapman *et al.* (2009), Nance et al. (2011), Castillo-Olguın *et al.* (2012) and Spaet *et al*. 2015. The most dominated haplotype of the BoB contained 21 individuals which is also the most dominated haplotype for both the Arabian Sea and Red Sea containing 150 and 81 haplotypes respectively. Within the rest two haplotypes, one was singleton and contained five individuals, and the other one was shared by the BoB and AS (Fig. 23). A lineage of BoB containing 4 unique haplotypes of BoB population and another unique haplotype indicates an evidence and support the result of *F*st i.e. BoB as a distinct population. The haplotype network also showed that AS and RS population is the closest group of BoB population.

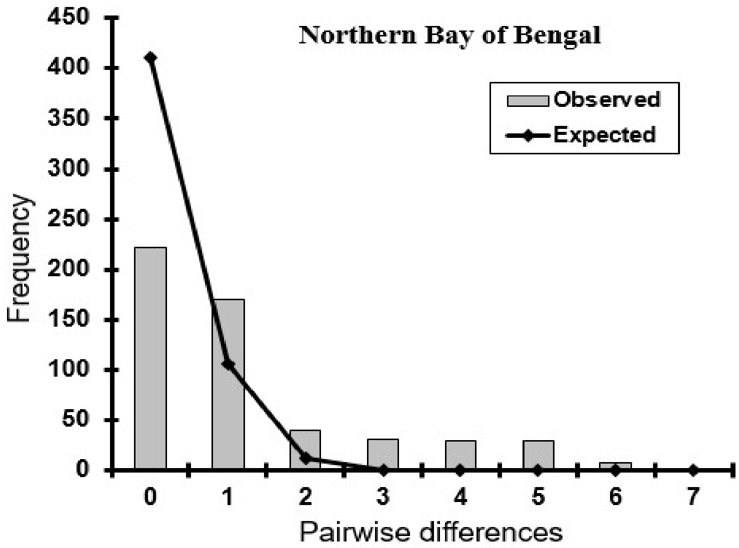


Figure 23: The observed pairwise difference and the expected mismatch distribution under the sudden expansion model for the haplotypes of d-loop region in *S. lewini*.

Demographic history:

In the neutrality tests, both Tajima's D and Fu's F_S statistics with the d-loop sequences showed significantly negative values ($D = -1.51$, $P = 0.05$; $F_S = -2.88$, $P < 0.05$) for the BoB population (Table 5), indicating a history of demographic expansion of these populations. Mismatch distributions of the d-loop sequences was unimodal for BoB population (Fig. 22) suggesting the history of demographic expansion for the Bay of Bengal population. The observed mismatch distributions did not deviate from the expected ones based on the sudden expansion model [P(SSDobs) > 0.05] (Table 5). Fitness between the observed and the expected mismatch distributions was also supported by the low Harpending's raggedness index (Hri = 0.006 – 0.035, P > 0.05). The times of demographic expansion for the populations were estimated as the mutational time τ in generation from the mismatch distribution. The τ values were found to be 0.234 for the BoB population. The τ values were then converted into the time in years since expansion according to the equation τ = 2ut and the divergence rates of 1.21%/MY (i.e. mutation rate 0.605%/MY) for the d-loop which resulted in the expansion time of approximately 558,926 years ago for the BoB populations.

Table 5. Tajimas's D andFu's F_S statistics, and mismatch distribution parameter estimates (τ, Θ_0, Θ_1) for BoB population.

Population	**Tajima's *D***		**Fu's F_S**		**Mismatch distribution**			**Goodness-of-fit tests**			
	D	P	F_S	P	τ	Θ_0	Θ_1	SSD	P	*Hri*	P
BoB	–1.51	0.05	–2.88	0.04	0.234	0.00	99999.99	0.169	0.00	0.07	1.00

τ (tau): date of onset of population expansion expressed in units of mutational time; ϑ_0&ϑ_1: mutational parameters of population size reflectingthe population sizes before and after the population expansion, respectively; SSD: sum of squared difference *Hri*: Harpending's reggedness index.

The τ values from the mismatch distribution analysis allow us to estimate the time of expansion of scalloped hammer headed Shark population of BoB, which would have been around 560,000 years ago during the second half of the Middle Pleistocene Series (0.126 - 0.78 million years ago; Gibbard and Head 2009). The Middle Pleistocene was characterized by a series of large glacial and interglacial changes with approximately 100,000 year intervals (Imbrie et al. 1992). Cyclic repetition of glaciation and deglaciation in the Middle Pleistocene possibly had a great impact on the demography of marine fishes in the region: displacement and eradication of populations occurred during glaciation whereas recolonization and expansion took place during deglaciation (Hewitt 2000; Lambeck *et al*. 2002; Liu *et al*. 2006a).

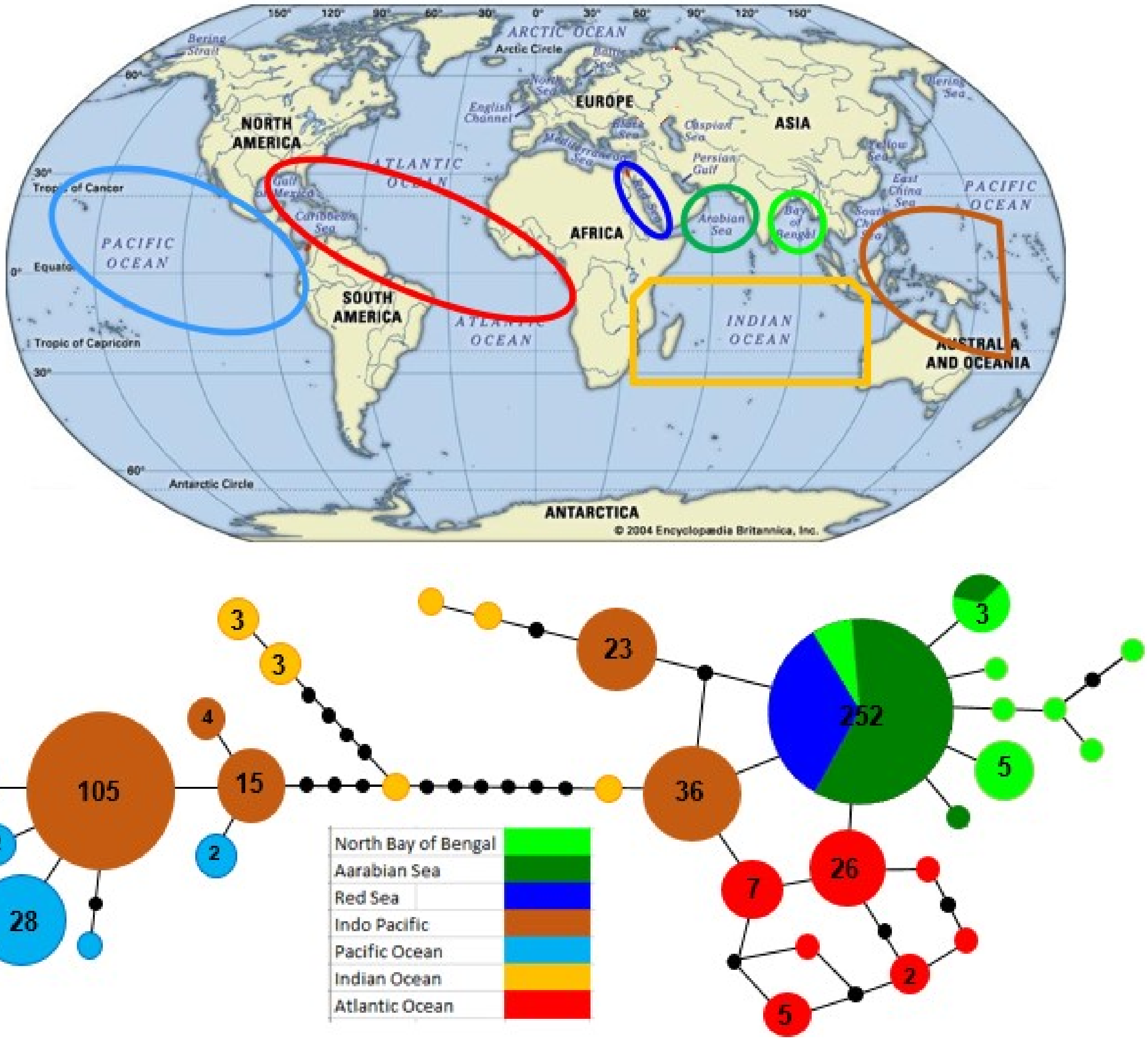


Figure 24. Haplotype network for *Sphyrna lewini* constructed by statistical parsimony in TCS 1.13 (Templeton *et al*. 1992; Clement *et al*. 2000).

Haplotypes are indicated by circles. The numbers given inside circle represent the number of individuals of that respective haplotype. Smallest circles represent the haplotype with single individual. Haplotype frequency corresponds to table 1. Ocean and sea basins are indicated by colours: Atlantic (red), Indian (orrange), Pacific (blue), Indo-Pacific (brown), Indian Ocean (Yellow), Red Sea (deep blue), Arabian Sea (deep green) and the Bay of Bengal (yellow-green). Each connecting line represents a single mutation. Black dots represent hypothetical missing ancestors. Haplotypes are connected only through ≤ 9 mutations, as indicated by the 95% connection confidence interval determined for this data set in TCS 1.13.

Table 6. Haplotype frequency of different populations

Haplotype ID (GenBank accession no.)	**North Bay of Bengal (BoB)**	**Arabian Sea Basin (AS)**	**Red Sea (RS)**	**Indo-Pacific (IP)**	**Pacific Ocean (PO)**	**Indian Ocean (IO)**	**Atlantic Ocean (AO)**	**Total**
SL1 (KR232953)	21	150	81					**252**
SL3 (KR232956)	02	01						**03**
SL5 (KR232955)		01						**01**
BD-02	05							**05**
BD-05	01							**01**
BD-07	01							**01**
BD-24	01							**01**
BD-30	01							**01**
BD-38	01							**01**
Hap1 (DQ438152)				105				**105**
Hap2 (DQ438153)					28			**28**
Hap3 (DQ438160)					1			**1**
Hap4 (DQ438170)					1			**1**
Hap5 (DQ438171)					2			**2**
Hap6 (DQ438157)					2			**2**
Hap7 (DQ438159)					1			**1**
Hap8 (DQ438158)				4				**4**
Hap9 (DQ438155)				15				**15**
Hap10 (DQ438150)							1	**1**
Hap11 (DQ438151)							1	**1**
Hap12 (DQ438154)							2	**2**
Hap13 (DQ438165)							1	**1**
Hap14 (DQ438166)							5	**5**
Hap15 (DQ438149)							26	**26**
Hap16 (DQ438164)							7	**7**
Hap17 (DQ438167)						1		**1**
Hap18 (DQ438168)						1		**1**
Hap19 (DQ438161)				36				**36**
Hap20 (DQ438169)						1		**1**
Hap21 (DQ438162)						1		**1**
Hap22 (DQ438163)						3		**3**
Hap23 (DQ438156)						3		**3**
Hap24 (DQ438172)				23				**23**
Total	**33**	**152**	**81**	**183**	**35**	**10**	**43**	**537**

11.3 Results and Discussion on Study-3: Assessing diversity of zooplankton through DNA metabarcoding

Although animals are among the best studied organisms, we still lack a full description of their diversity, especially for microscopic taxa. This is partly due to the time-consuming and costly nature of surveying animal diversity through morphological and molecular studies of individual taxa. Recent advances in DNA sequencing have provided a new tool for species detection from multiple DNA. A powerful alternative is the use of high-throughput environmental sequencing, providing molecular data from all organisms sampled. Next-generation sequencing (NGS) analyses that is increasingly applied to the field of fish biology. NGS technologies have permitted researchers to obtain large amounts of raw data in short periods of time. There have also been significant improvements in bioinformatics program to assemble the sequences and genes, thus facilitating the management of these large datasets. The combination of DNA sequencing and bioinformatics on fisheries research has improved our abilities to observe their biology, species identification, observing structure of an ecosystem, analyzing environmental samples, real biodiversity monitoring, management and conservation. Zooplankton is important as an energy messenger in the food chain of the ocean ecosystem. These zooplanktons live in diverse areas, such as the coastal seas, ranging from the surface to deep bottom layers of the ocean. Metabarcoding (large-scale taxonomic identification of complex samples via analysis of one or few orthologous DNA regions, called barcodes) is revolutionizing analysis of biodiversity of marine zooplankton assemblages. To discriminate species more variable genes are needed. A limited number of metabarcoding studies have used mitochondrial cytochrome oxidase I (COI), which ensures detection of species-level diversity, but may require group-specific primers and thus result in inconsistent amplification success rates. Analysis of species-level diversity and distribution of marine zooplankton using metabarcoding approaches will require development of reliable HTS protocols for more variable genes. The mitochondrial cytochrome oxidase I (COI) barcode region is one of the most commonly sequenced regions for analysis of specie s diversity among marine animals including zooplankton.

The zooplankton diversity has been assessed by analyzing using number of OTUs by community analysis and clustering programme MothurV1.39. A hundred repeated runs on distinct starting trees were carried out to select the tree with the best topology and 100 bootstrap replicates were performed using the same evolutionary model. Estimation error resulting from the level (order) of model complexity. The estimated number of zooplankton species using candidate models was compared with the observed numbers after optimal parameter estimation. A total of 332 OTUs found in 6 samples from two different sampling zone. Whereas 137 numbers of OTUs have ensuring 98% match NCBI reference database and output 67 number of OTUs identified up to species level under 9 numbers of phylum. Number of confirmed species given in table 3.

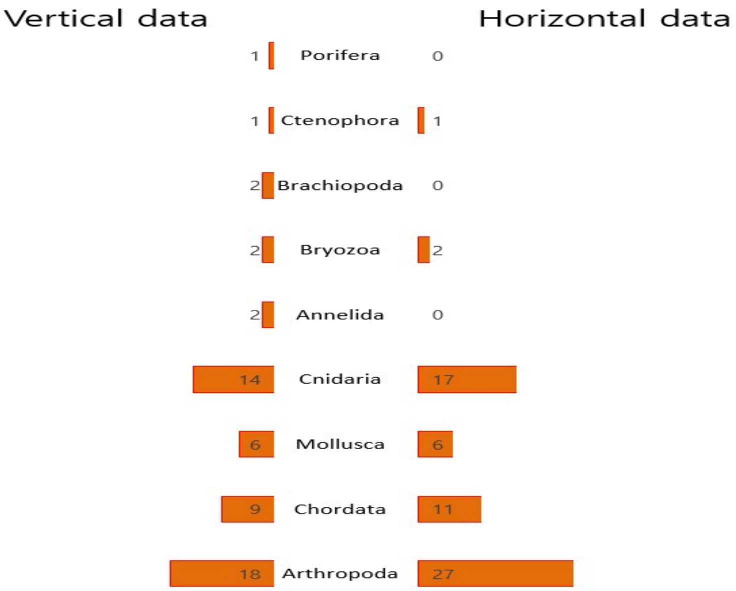


Figure 25. Species number from horizontal & vertical sample collected from two spots during the study time.

Table 7. Numbers of zooplankton species found by the metagenomics study from vertical and horizontal sampling

Phylum	**Vertical data**		**Horizontal data**	
	OTUs	**% of Reads**	**OTUs**	**% of Reads**
Arthropoda	18	32.73%	27	47.37%
Chordata	9	16.36%	11	19.30%
Mollusca	6	10.91%	6	10.53%
Cnidaria	14	25.45%	17	29.82%
Annelida	2	3.64%	0	0.00%
Bryozoa	2	3.64%	2	3.51%
Brachiopoda	2	3.64%	0	0.00%
Ctenophora	1	1.82%	1	1.75%
Porifera	1	1.82%	0	0.00%
Total	**55**		**64**	

Table 8. List of zooplankton species found by the metagenomics study through matching with GenBank reference data.

OUT ID	Organism	% Pairwise Identity	Query coverage	Taxonomy
Otu00202	*Parapenaeopsis sculptilis*	99.70%	100.00%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea; Penaeidae; Parapenaeopsis
Otu00226	*Portunus sanguinolentus*	99.70%	100.00%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Portunus
Otu01026	*Portunus pelagicus*	99.00%	100.00%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Portunus
Otu00465	*Euphausia pacifica*	100.00%	100.00%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Euphausiacea; Euphausiidae; Euphausia
Otu00078	*Amphibalanus rhizophorae*	98.40%	100.00%	Arthropoda; Crustacea; Maxillopoda; Cirripedia; Thoracica; Sessilia; Balanidae; Amphibalanus
Otu00039	*Canthocalanus pauper*	99.00%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Calanidae; Canthocalanus
Otu00179	*Centropages abdominalis*	100.00%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Centropagidae; Centropages
Otu00172	*Subeucalanus subcrassus*	100.00%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda;

				Calanoida; Eucalanidae; Subeucalanus
Otu03506	*Subeucalanus pileatus*	99.70%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Eucalanidae; Subeucalanus
Otu00020	*Paracalanus aculeatus*	100.00%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Paracalanidae; Paracalanus
Otu00504	*Paracalanus gracilis*	100.00%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Paracalanidae; Paracalanus
Otu01727	*Paracalanus indicus*	99.70%	99.36%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Paracalanidae; Paracalanus
Otu03472	*Labidocera acuta*	100.00%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Pontellidae; Labidocera
Otu00058	*Temora turbinata*	99.70%	100.00%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Temoridae; Temora
Otu00592	*Canthocalanus pauper*	92.90%	99.68%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Calanidae; Canthocalanus
Otu00382	*Matuta planipes*	92.60%	100.00%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Calappoidea; Matutidae; Matuta
Otu00939	*Lucifer hanseni*	85.60%	97.44%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Sergestoidea; Luciferidae; Lucifer

Otu00567	*Parapenaeus fissuroides*	81.90%	93.61%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea; Penaeidae; Parapenaeus
Otu00160	*Tortanus insularis*	81.80%	99.36%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Tortanidae; Tortanus
Otu00296	*Acetes indicus*	95.70%	81.85%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Sergestoidea; Sergestidae; Acetes
Otu00549	Uncultured zooplankton	96.80%	99.68%	environmental samples
Otu00480	Undinula vulgaris	91.20%	96.17%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Calanidae; Undinula
Otu00134	Savignium crenatum	90.40%	100.00%	Arthropoda; Crustacea; Maxillopoda; Cirripedia; Thoracica; Sessilia; Pyrgomatidae; Savignium
Otu00270	Uncultured zooplankton	90.40%	100.00%	environmental samples
Otu00423	Uncultured zooplankton	90.40%	90.10%	environmental samples
Otu00325	Darwiniella angularis	89.80%	100.00%	Arthropoda; Crustacea; Maxillopoda; Cirripedia; Thoracica; Sessilia; Pyrgomatidae; Darwiniella
Otu00212	Balanus trigonus	89.50%	98.40%	Arthropoda; Crustacea; Maxillopoda; Cirripedia; Thoracica; Sessilia; Balanidae; Balanus
Otu00121	Chiridius gracilis	88.80%	99.36%	Arthropoda; Crustacea; Maxillopoda; Copepoda; Calanoida; Aetideidae; Chiridius

Otu03500	Perisesarma guttatum	85.20%	97.76%	Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Grapsoidea; Sesarmidae; Perisesarma
Otu02698	*Thais malayensis*	98.40%	99.68%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Neogastropoda; Muricoidea; Muricidae; Thais
Otu00418	*Cerithidea cingulata*	92.00%	100.00%	Mollusca; Gastropoda; Caenogastropoda; Sorbeoconcha; Cerithioidea; Potamididae; Cerithidea
Otu01248	*Tricula hongshanensis*	91.30%	95.53%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Truncatelloidea; Pomatiopsidae; Triculinae; Tricula
Otu02690	*Stenothyra sp.*	90.10%	100.00%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Truncatelloidea; Stenothyridae
Otu01925	*Naticarius hebraeus*	86.00%	100.00%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Naticoidea; Naticidae; Naticarius
Otu00891	*Dendronotus frondosus*	85.30%	98.08%	Mollusca; Gastropoda; Heterobranchia; Euthyneura; Nudipleura; Nudibranchia; Dendronotina; Dendronotoidea; Dendronotidae; Dendronotus
Otu01896	*Trapezidae sp.*	84.90%	97.12%	Mollusca; Bivalvia; Heteroconchia; Euheterodonta; Veneroida; Arcticoidea; Trapezidae;

				Unclassified Trapezidae
Otu00824	*Fluminicola multifarious*	81.10%	99.36%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Truncatelloidea; Hydrobiidae; Fluminicola
Otu00737	*Antroselates spiralis*	80.60%	98.72%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Truncatelloidea; Hydrobiidae; Antroselates
Otu01672	*Echinolittorina sundaica*	80.50%	96.47%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Littorinoidea; Littorinidae; Echinolittorina
Otu00967	*Morula nodicostata*	79.30%	97.44%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Neogastropoda; Muricoidea; Muricidae; Morula
Otu03229	*Littorina obtusata*	78.90%	97.76%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Littorinoidea; Littorinidae; Littorina
Otu01925	*Naticarius hebraeus*	86.00%	100.00%	Mollusca; Gastropoda; Caenogastropoda; Hypsogastropoda; Littorinimorpha; Naticoidea; Naticidae; Naticarius
Otu00258	*Tenualosa ilisha*	100.00%	99.68%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupei; Clupeiformes; Clupeoidei; Clupeidae; Tenualosa
Otu00474	*Corica soborna*	100.00%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii;

				Teleostei; Clupei; Clupeiformes; Clupeoidei; Clupeidae; Corica
Otu00642	*Stolephorus waitei*	100.00%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupei; Clupeiformes; Clupeoidei; Engraulidae; Engraulinae; Stolephorus
Otu01041	*Coilia dussumieri*	100.00%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupei; Clupeiformes; Clupeoidei; Engraulidae; Coilinae; Coilia
Otu00175	*Exyrias puntang*	99.70%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Gobiaria; Gobiiformes; Gobioidei; Gobiidae; Gobiinae; Exyrias
Otu00705	*Stolephorus waitei*	98.90%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupei; Clupeiformes; Clupeoidei; Engraulidae; Engraulinae; Stolephorus
Otu00755	*Neophocaena phocaenoides*	98.40%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea; Odontoceti; Phocoenidae; Neophocaena
Otu01737	*Ostorhinchus aureus*	87.70%	99.04%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Gobiaria; Kurtiformes; Apogonoidei; Apogonidae; Apogoninae;

				Ostorhinchus
Otu00583	*Inimicus sinensis*	85.40%	94.89%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Eupercaria; Perciformes; Scorpaenoidei; Synanceiidae; Choridactylinae; Inimicus
Otu00168	*Parupeneus heptacanthus*	85.20%	98.72%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Syngnathiaria; Syngnathiformes; Mulloidea; Mullidae; Parupeneus
Otu00261	*Halichoeres nigrescens*	85.00%	98.41%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Eupercaria; Labriformes; Labridae; Halichoeres.
Otu00843	*Margrethia sp*	83.70%	99.68%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Stomiatii; Stomiiformes; Gonostomatidae; Margrethia
Otu00233	*Rhinogobius brunneus*	83.50%	99.04%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Gobiaria; Gobiiformes; Gobioidei; Gobiidae; Gobionellinae; Rhinogobius

Otu00691	*Gudusia chapra*	79.30%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupei; Clupeiformes; Clupeoidei; Clupeidae; Gudusia.
Otu01245	*Thalassoma lunare*	98.40%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Eupercaria; Labriformes; Labridae; Thalassoma.
Otu01246	*Sphyraena putnamae*	85.20%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Carangaria; Carangaria incertae sedis; Sphyraenidae; Sphyraena.
Otu01248	*Scolopsis vosmeri*	86.80%	100.00%	Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorphata; Eupercaria; Spariformes; Nemipteridae; Scolopsis.
Otu01375	*Favia pallida*	95.80%	100.00%	Cnidaria; Anthozoa; Hexacorallia; Scleractinia; Faviina; Mussidae; Faviinae; Favia.
Otu01379	*Favia sp.*	88.80%	100.00%	Cnidaria; Anthozoa; Hexacorallia; Scleractinia; Faviina; Mussidae; Faviinae.
Otu01381	*Favites abdita*	81.70%	98.00%	Cnidaria; Anthozoa; Hexacorallia; Scleractinia; Faviina; Merulinidae; Favites.
Otu01250	*Liriope tetraphylla*	95.80%	100.00%	Cnidaria; Hydrozoa; Trachylinae; Trachymedusae; Geryoniidae; Liriope
Otu01236	*Orthopyxis integra*	82.10%	93.27%	Cnidaria; Hydrozoa; Hydroidolina; Leptothecata; Campanulariidae; Orthopyxis

Otu00696	*Amphinema sp.*	100.00%	100.00%	Cnidaria; Hydrozoa; Hydroidolina; Anthoathecata; Filifera; Pandeidae; Amphinema
Otu02855	*Obelia sp.*	100.00%	100.00%	Cnidaria; Hydrozoa; Hydroidolina; Leptothecata; Campanulariidae; Obelia
Otu00048	*Clytia sp.*	99.40%	100.00%	Cnidaria; Hydrozoa; Hydroidolina; Leptothecata; Campanulariidae; Clytia
Otu00194	*Acromitus sp.*	97.40%	100.00%	Cnidaria; Scyphozoa; Rhizostomeae; Catostylidae; Acromitus
Otu02365	*Liriope tetraphylla*	95.80%	100.00%	Cnidaria; Hydrozoa; Trachylinae; Trachymedusae; Geryoniidae; Liriope
Otu00151	*Eucheilota maculata*	91.30%	99.68%	Cnidaria; Hydrozoa; Hydroidolina; Leptothecata; Campanulariidae; Eucheilota
Otu00340	*Turritopsis lata*	90.60%	100.00%	Cnidaria; Hydrozoa; Hydroidolina; Anthoathecata; Filifera; Oceaniidae; Turritopsis
Otu00509	*Coryne eximia*	90.20%	97.76%	Cnidaria; Hydrozoa; Hydroidolina; Anthoathecata; Capitata; Corynidae; Coryne
Otu00908	*Agalma elegans*	88.80%	99.68%	Cnidaria; Hydrozoa; Hydroidolina; Siphonophorae; Physonectae; Agalmatidae; Agalma
Otu00476	*Clytia hummelincki*	86.80%	99.36%	Cnidaria; Hydrozoa; Hydroidolina; Leptothecata; Campanulariidae; Clytia
Otu00285	*Cephea sp.*	83.70%	99.68%	Cnidaria; Scyphozoa; Rhizostomeae; Cepheidae; Cephea
Otu01236	*Orthopyxis integra*	82.10%	93.27%	Cnidaria; Hydrozoa; Hydroidolina; Leptothecata; Campanulariidae; Orthopyxis
Otu00211	*Apolemia rubriversa*	81.70%	97.76%	Cnidaria; Hydrozoa; Hydroidolina; Siphonophorae; Physonectae; Apolemiidae; Apolemia

Otu01513	*Eugorgia daniana*	76.50%	92.97%	Cnidaria; Anthozoa; Octocorallia; Alcyonacea; Holaxonia; Gorgoniidae; Eugorgia

Date& time	Site no	Location	Coordinate	Depth (m)	PSS	Temperature (◦C)	Conductivity (µS/cm)	Sound (m/s)	pH	Air Temp	DO	Flow meter	Time (min) of CTD
26.11.2017	01	Spot 01	Lat 20.6083 Lon 92.3482	8.07	28.82	29.03	44342	1537.1	6.13	30.4	5.8	Initial: 371931 Final: 389835	2.34
26.11.2017	02	Spot 02	Lat 20.5699 Lon 92.3454	12.27	28.60	29.16	44315	1537.4	6.12	30.9	5.9	Initial: 612200 Final: 629295	2.52
19.12.2017	01	Spot 01	Lat 20.6388 Lon 92.3169	1.5	28.76	26.05	44525	1530.4	6.15	31.2	7.9	Initial: 619363 Final: 633540	2.56
19.12.2017	02	Spot 02	Lat 20.5784	3.35	29.33	26.48	45312	1532.0	6.28	30.6	7.7	Initial: 633540	2.38

Otu01100	*Marphysa brevitentaculata*	82.30%	99.36%	Annelida; Polychaeta; Palpata; Aciculata; Eunicida; Eunicidae; Marphysa
Otu00690	*Marphysa viridis*	82.10%	99.68%	Annelida; Polychaeta; Palpata; Aciculata; Eunicida; Eunicidae; Marphysa

Table 9. Different water parameter on water quality, GPS locations, air temperature during meta barcoding sapling

			Lon 92.3414									Final: 643542	
28.01.2018	01	Spot 01	Lat 20.3643 Lon 92.2003	3.45	31.95	23.33	48957	1527.1	6.08	27.2	6.4	Initial: 644531 Final: 653241	3.19
28.01.2018	02	Spot 02	Lat 20.3348 Lon 92.2345	2.83	32.01	23.48	48957	1528.2	6.11	26.9	6.7	Initial: 653300 Final: 662413	2.59

Figure 26. Path mapping of fish DNA sampling and locations of zooplankton sampling during study time from St. martins island Bangladesh

Some observations on Biodiversity of SMI and Recommendations for Conservation

On coral reefs, the complex structure of scleractinian corals produces a diversity of habitat types that provide shelter, food and sites for reproduction for other reef organisms. St. Martin's Island is the only island in Bangladesh supporting coral reef-like ecosystem and coral associated floral and faunal diversity. Coral reefs support a high diversity of fishes that may ultimately depend on corals for their survival; however, the impact of long-term reef degradation on fish populations is unknown. The department of environment declared the St Martin's Island as “ecologically critical area (ECA)” in 1999.

Biodiversity of Bangladesh's only coral associated island is being lost day by day. There is increasing evidence that many organisms preferentially associate with particular coral species or coral morphologies at critical stages of their development which has been losted. High population density, huge illegal infrastructure is being built in an unplanned manner, destruction of mangrove plants and bushes, collection of sea shells and stones, unplanned development of tourism, visit by a huge number of tourists, and dumping of garbage are the main threats of the island. Rush of tourists and indiscriminate anchoring of boats are damaging the coral reefs, causing underwater pollution and changing the sediment dynamics of Saint Martin’s Island. As opposed to, many ecologists have expressed concern over the worldwide decline in coral cover due to global warming and associated coral bleaching, overfishing.

During the present study, internecine human intervention on coral reef destruction via indiscriminate anchoring of boats, fishing on coral reef habitat, throwing garbage to the water, etc. were observed frequently.The most damage has been caused by anchoring of hundreds of life boats that use very sharp metal anchors. Those boats carry passengers to roam around on dead coral reef in Cheradip which located an extension in the South side. While pulling up the anchors, the coral is broken into pieces. The fishermen also damage and disturb coral beds to save their nets, which get stuck during fishing. In contrast, collecting coral and mollusk for sale to tourists is also endangering shallow water coral species. Besides, garbage strewn on shore or dumped into the sea by hotels and tourists is another leading problem. However, recent research on hydrogeological investigations by different scholars identified that, the physical environment of the area is under severe ecological stress and the damages to coral species have now reached an alarming stage.The present research aslo conducted scuba diving for assessing of fish diversity, their ecology and abundance. Under water pollution through plastic bags, can, packets etc. were found on coral substrate. Another alrming observation was that the torned and entangled fishing nets covered the coral colony and siltration and subsequent sea weed growth caused coral bleaching beneath the net.

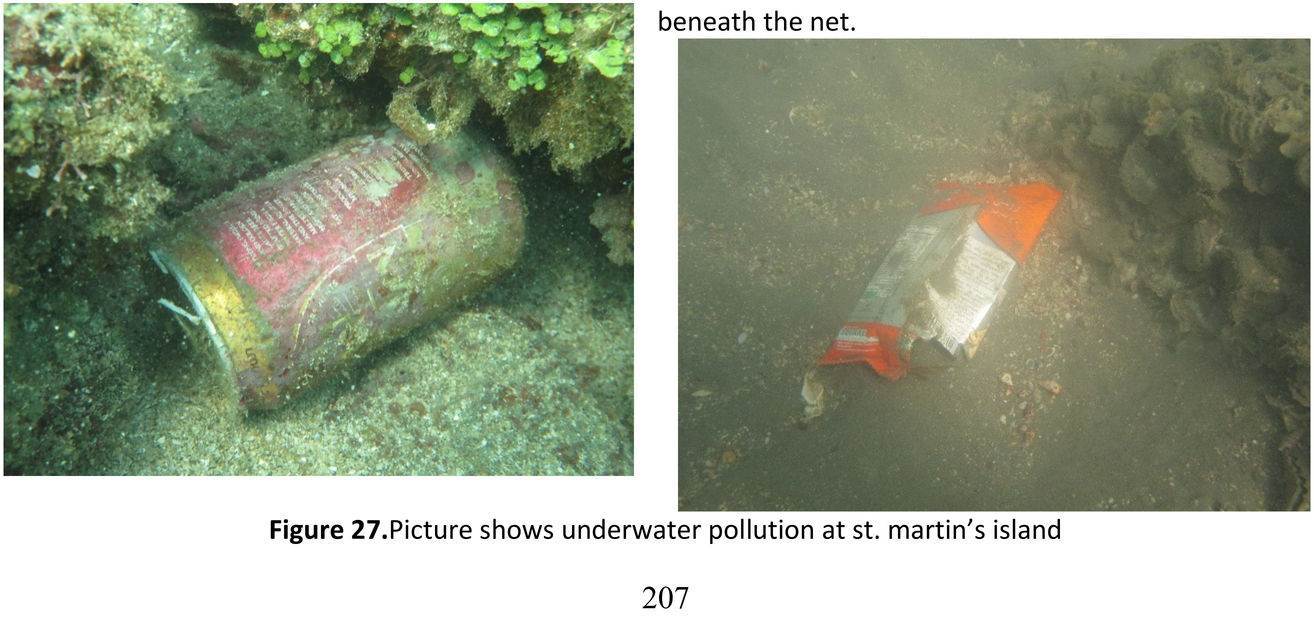


Figure 27. Picture shows underwater pollution at st. martin’s island

Figure 28. Picture shows coral associated fishing on coral bed (left) and collection of mollusk shell under the coral reef during low tide at st. martin’s island

Government should take steps to save the marine biodiversity of this island especially strong monitoring by local police is needed. It is needed to formulate sustainable strategic plan for the management of this lonely coral island in order to protect its internal biodiversity and the livelihood of the local communities. For the conservation of biodiversity in the St. Martin’s Island the following rules, regulations, policies and management strategies need to establish:

- Improve monitoring of reef fisheries and develop viable alternative livelihoods for those who are exclusively dependent on reef resources
- Strengthen surveillance, infrastructure and capacity building for resource management
- Cheradip situated in the south of the island which contains a little number of scleractinian corals till now. There should be prohibition of visiting tourists
- Restrict tourists to hangout every where in the island
- Every tourist will have to pay tour tax that will be used on the island's bio-diversity conservation purpose
- Initiate project to rehabilitate and conserve the coral reefs of this island through community based coral reef rehabilitation and monitoring
- Establish central information system for the conservation of biodiversity under marine research center/institute.
- Strengthen the research work to conserve the marine aquatic life via in-situ conservation of endangered species especially coral associated organism viz. sea Turtle, sea Snake, Gropers etc.
- Undertake awareness raising activities to highlight the importance of reef ecosystem among tourist
- Develop clear government policy statement with an updated strategic plan of this island on the future conservation, management and protection objectives of marine resources for St. Martin’s Island
- Involve local business man and non-government stakeholders to minimize the costal pollution
- Should established sustainable and controlled tourism mechanism

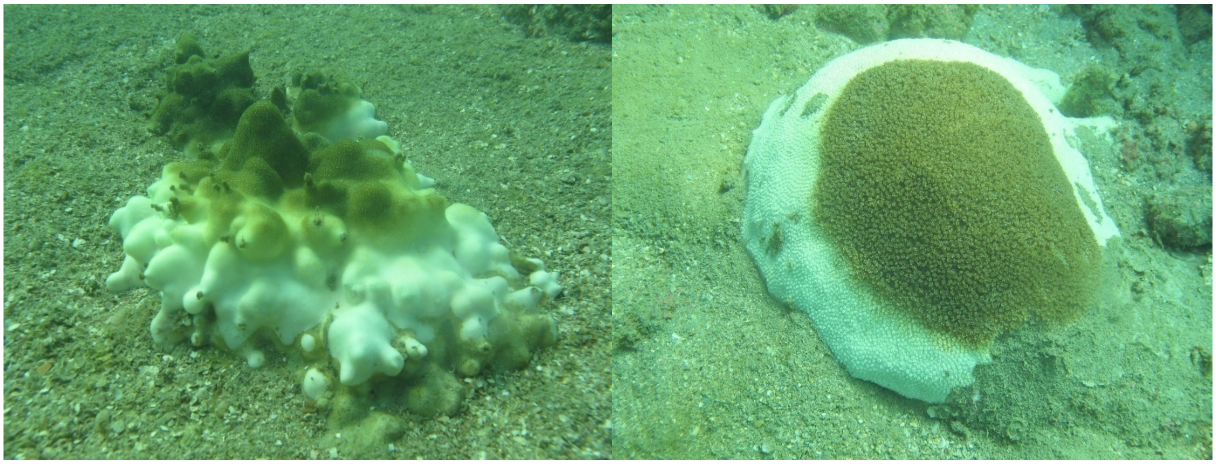


Figure 29. Picture shows coral reef are suffering from coral bleaching at St. Martin’s Island

12 Research highlight/findings:

- A total of 125 coral fish species had been found in St Martin`s Island which were identified morphologically. Among these 14 species were observed only by scuba diving.
- One hundred and eleven (111) species of fish have have assessed by DNA barcoding which are found in St Martin`s Island. The DNA barcodes were submitted to the NCBI GenBank and BOLD syatem and already accepted by these databases.
- A total of 32 fish species had been newly documented during this study as their new distributional record in Bangladesh
- Three (03) species had been found as new distributional records not only in Bangladesh marine water but also in the Bay of Bengal.
- In the population genetic study, the globally endangered scalloped hammerhead Shark, *S. lewini* (by IUCN) showed a unique population genetic structure (i.e. a single genetic stock) in the Bay of Bengal region. This result indicates the existance of a nursery ground for this species in the Bay of Bengal which suggests the necessity of a separate monitoring and conservation strategy for this species.
- The study shows that *S. lewini* population of the Bay of Bengal has undergone a recent population expansion after experiencing bottleneck. The expansion started approximately 558,000 years ago.
- A total of 332 operational taxonomic units, OTUs (i.e. probable species number) of zooplankton were found by DNA metabarcoding technique from 6 samples of two different sampling zones where 137 numbers of OTUs ensured 98% match with NCBI reference database and 67 number of OTUs were identified up to species level under 9 numbers of phylum.
- The fish and zooplankton diversity suggest that the SMI still has moderately good marine biodiversity and the unique population structure of *S. lewini* indicates the uniqueness of this habitat for its coral associated organisms. However, the island is facing high level of ecosystem degradation due to anthropogenic causes. So, it is urgently needed to declare marine protected area (MPA) to save this only coral Island of Bangladesh.

B. Implementation Position

1. Procurement:

Description of equipment and capital items	**PP Target**		**Achievement**		**Remarks**
	Phy (#)	**Fin (Tk)**	**Phy (#)**	**Fin (Tk)**	
(a) Office equipment (Computer-01)	59500		59500	59500	100% Achivement
(b) Lab &field equipment					
(c) Other capital items					

2. Establishment/renovation facilities: n/a

Description of facilities	Newly established		Upgraded/refurbished		Remarks
	PP Target	Achievement	PP Target	Achievement	

3. Training/study tour/ seminar/workshop/conference organized: n/a

Description	Number of participant			Duration (Days/weeks/ months)	Remarks
	Male	Female	Total		
(a) Training					
(b) Workshop					

C. Financial and physical progressig in Tk

Items of expenditure/activities	Total approved budget	Fund received	Actual expenditure	Balance/ unspent	Physical progress (%)	Reasons for deviation
A. Contractual staff salary	754716	754716	754716	0	100	-
B. Field research/lab expenses and supplies	2206758	2206758	2206758	0	100	-
C. Operating expenses	528803	528803	528803	0	100	-
D. Vehicle hire and fuel, oil & maintenance	335182	335182	335182	0	100	-
E. Training/workshop/seminar etc.	0	0	0	0		-
F. Publications and printing	15000	15000	15000	0	100	-
G. Miscellaneous	58080	58080	58080	0	100	-
H. Capital expenses	59500	59500	59500	0	100	-
Total	**3958039**	**3958039**	**3958039**	0	100	-

D. Achievement of Sub-project by objectives: (Tangible form)

Specific objectives of the sub-project	Major technical activities performed in respect of the set objectives	Output(i.e. product obtained, visible, measurable)	Outcome(short term effect of the research)
To build a precise inventory of coral associated fish based on DNA barcoding along with morphometrics	1. Sample collection and taking photographs 2. Morpho-meristic study 3. Molecular study: Genomic DNA extraction, Polymerase chain reaction, PCR	1. 125 coral associated fish species have been found 2. Thirty-two (32) fish species have been newly recorded in Bangladesh 3. Over 250 DNA	1. Finding several new species within short time survey signifies the needs of more long term study. 2. The study indicates uniqueness of SMI ecosystem with it's own stocks of

	purification, Sanger sequencing, Sequence data analysis	barcode sequences have been determined for coral fish of Bangladesh and submitted to GenBank and BOLD database.	organisms. 2. Data supports the justification of urgency of declaration MPA to SMI.
To assess population genetic structure of an ecologically/commercially important fish or shell fish species found in the island area.	1. Sample collection of globally endangered scalloped hamer headed Shark inhabits near sea area of SMI 2. Morpho-meristic study 3. Molecular study: Genomic DNA extraction, Polymerase chain reaction, PCR purification, DNA sequencing, Sequence data analysis by bioinformatics program	1. Genetic diversity was determined. 2. Uniq and non-panmictic population was found for BoB. 3. Expanded population was found.	1. The study discovered the BoB as a potential nursery ground for globally endangered hamer headed Shark. 2. Findings suggest immediate conservation steps for this species through coordination of all BoB countries.
To assess the diversity of zooplankton by DNA metabarcoding through next generation sequencing (NGS).	1. Sample collection by zooplankton net through horizontal and vertical pulling. 3. Molecular study: Genomic DNA extraction, Polymerase chain reaction, PCR purification, Next generation sequencing (NGS), Sequence data analysis by	1. A total of 332 operational taxonomic units, OTUs (i.e. probable species number) of zooplankton found 2. Sixty seven (67) OTUs were identified up to species level underlelongs to 9 phyla.	1. The results signifie the effectiveness of DNA metabarcoding for marine biodiversity analysis in the microscopic level in Bangladesh. 2. The study suggests usefulness of DNA metabarcoding

	bioinformatics program		technology for breeding and nursery ground detection for sustainable marine fisheries condservation.

E. Materials Development/Publication made under the Sub-project:

Publication	**Number of publication**		**Remarks (e.g. paper title, name of journal, conference name, etc.)**
	Under preparation	**Completed and published**	
Technology bulletin/ booklet/leaflet/flyer etc.			
Journal publication	03		
Information development			
Other publications, if any		Several	Several abstracts have been published in conference book of different conferences in 2018 and 2019. Different poster presentations on research progress won awards. Please see **Annexure**.

F. Technology/Knowledge generation/Policy Support (as applied):

i. Generation of technology (Commodity & Non-commodity)

- Thirty-two (32) new species rcords together from a single ecosystem
- Three (03) new records of fish species in the Bay of Bengal

i

- Nursery ground of scalloped hamer headed shark in BoB
- DNA barcode library for coral associated fishes of Bangladesh
- Usufulness of NGS for biodiversity assessment in microscopic level

iii. Technology transferred that help increased agricultural productivity and farmers' income

- Data and information ventilated to the Environment department of Bangladesh through a round table discussion in the support of justification of MPA declaration and management.

iv. Policy Support

- Would support respective department/s of Bangladesh governement for declaration of MPA to Saint Martin's Island.

G. Information regarding Desk and Field Monitoring

i. Desk Monitoring [description & output of consultation meeting, monitoring workshops/seminars etc.):

- CRG Sub- Project Implementation Progress Workshop/Seminar held in BARC, Farmgate, Dhaka on 21 December 2017. Found satisfactory
- CRG Sub-Project Final output Workshop held in BARC, Farmgate Dhaka on 19-20 September 2018. Found satisfactory

ii. Field Monitoring (time& No. of visit, Team visit and output):

- Field monitoring had been carried out by NATP team at Sher-e-Bangla Agricultural University on September 2018 and the team expressed satisfaction with the research progress.
- Desk monitoring had also been done by Research System (SAURES), Sher-e-Bangla Agricultural University.

H. Lesson Learned

i) Thirty-two (32) records of coral associated fish for the first time and three (03) new records of fish species in the Bay of Bengal were discovered from SMI only from 02 years' study which indicates high species diversity of SMI. Therefore, the island should be immediately declared as MPA to conserve its biodiversity. More intensive study is needed for assessment of accurate biodiversity in SMI.

ii) Population genetic study suggests there is a nursery ground of globally endangered scalloped hamer headed Shark in the Bay of Bengal.

iii) Year round monitoring of zooplankton by DNA metabarcoding can be an effective tool for microbiodiversity study of an ecosystem and for identifying nursery and spawning ground of a particular fish species and other marine organisms.

I. Challenges (if any)

a. Due to heavy roughness and rolling of the sea it was diffuclt to collect zooplankton samples in the summer season, even sometimes in winter also for adverse weather condition.

b. Since the samplings are conducted in regular basis it was highly necessary to permanently rent one or two room for the project tenure in the St. Martin's Island for using as field station. This station would be used as the store house of the biological samples and field instruments which are regularly used in samplings. This rented room could be also used for initial processing of the samples.

c. It was needed at least 3-5 years project for successful monitoring and survey of the fishes of a coral island for the presence of high fish diversity.

…………………………………………………………	**…………………………………………………………**
Signature of the Principal Investigator	Counter signature of the Head of the organization/authorized representative
Date ………………………….	Date …………………………..
Seal	Seal

References

BOBLME (2015) Report on Saint Martin’s Island ecosystem boundary, Bangladesh.

Carter E, Soemodinoto A. and White A. (2010). Guide for Improving Marine Protected Area Management Effectiveness in Indonesia. Bali, Indonesia: The Nature Conservancy Indonesia Marine Program, xi + 51p.

Castillo-Olgu_ın, E. M. Uribe-Alcocer, and P. D_ıaz-Jaimes (2012) Assessment of the population genetic structure of Sphyrna lewini to identify conservation units in the Mexican Pacific. Cienc. Mar. 38:635–652.

Castro JI (1993) The Shark nursery of Bulls Bay, South Carolina, with a review of the Shark nurseries of the southeastern coast of the United States. *Environmental Biology of Fishes*, 38, 37–48.

Chapman DD, Pinhal D, Shivji MS (2009) Tracking the fin trade: Genetic stock identification in western Atlantic scalloped hammerhead Sharks Sphyrna lewini. Endang Species Res 9: 221–228.

Clement M, Posada D and Crandall KA (2000) TCS: a computer program to estimate gene genealogies. Mol. Ecol. 9, 1657–1659.

Colin R. T., M. Begon and Harper J L (2014) Glossary. In: Essential of Ecology (Fourth Edition). Willey Online Library.

Compagno LJV (1984) FAO Species Catalogue. Vol. 4. Parts 1 & 2, Sharks of the world. *FAO Fisheries Synopsis*, p. 125.

Duncan KM, Martin AP, Bowen BW and and Couet H G DE (2006) Global phylogeography of the scalloped hammerhead Shark (*Sphyrna lewini*). Molecular Ecology 15: 2239–2251.

Excoffier L (2004) Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. Mol. Ecol. 13: 853–864.

Excoffier L, Smouse PE, Quattro JM (1992) Analysis of molecular varuance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data. Genetics 131: 479-491.

Frantine-Silva W, Sofia SH, Orsi ML, Almeida FS (2015) DNA barcoding of freshwater ichthyoplankton in the Neotropics as a tool for ecological monitoring. Molecular Ecology Resources 15(5): 1226–1237.

Garces Len. R, Pido MD, Tupper MH, Silvestre GT (2013) Evaluating the management effectiveness of three marine protected areas in the Calamianes Islands, Palawan Province, Philippines: Process, selected results and their implications for planning and management. Ocean & Coastal Management. 81: 49-57

Gibbard P and Head MJ (2009) Definition of the quaternary system/era and the Pleistocene series/epoch. Quaternaire **20**(2):125-133

Gray J S. (1997) Marine biodiversity: patterns, threats and conservation needs. Biodiversity and Conservation 6: 153–175.

Hajibabaei M, Singer GAC, Hebert PDN. And Hickey DA (2007) DNA barcoding: how it complements taxonomy, molecular phylogenetics and population genetics. TRENDS in Genetics 23(4): 167–172.

Harpending RC (1994) Signature of ancient population growth in a low-resolution mitochondrial DNA mismatch distribution. Hum. Biol. 66: 591–600

Hasan M M (2009) Tourism and Conservation of Biodiversity: A Case Study of St. Martins Island, Bangladesh. Law, Social Justice & Global Development Journal (LGD) (1): 1-12.

Hebert PDN, Cywinska A, Ball SL. and deWaard JR (2003) Biological identifications through DNA barcodes. Proceedings of the Royal Society London Bioogical Scences 270:313–321.

Heileman S, Bianchi G, and Funge-Smith S (2009) In: The UNEP large marine ecosystems: A perspective on changing conditions in LMEs of the world's regional seas. pp. 237-251, Edited by K. Sherman and G. Hempel, United Nations Environement Programme, Nairobi, Kenya. Vol. 82.

Hewitt GM (2000) The genetic legacy of the Quaternary ice ages. Nature 405: 907-913.

Hoegh-Guldberg O. (1999) Climate change, coral bleaching and the future of the world’s coral reefs. Marine and Freshwater Research 50, 839–866.

Hossain MM, Sulatana D, Ormond R and PJ, Siisddiqui (2009) Diversity of coral associated fishes in the St. Martin’s Island, Bangladesh. J. Taxononomy and Biodiversity Research, 3:1-8

Hughes TP, Bellwood DR and Connolly SR (2002) Biodiversity hotspots, centres of endemicity, and the conservation of coral reefs. Ecological Letters 5: 775–784.

Imbrie J, Boyle EA, Clemens SC, DuVy A, Howard WR, Kukla G, Kutzbach J, Martinson DG, McIntyre A, Mix AC, Molfino B, Morley JJ, Peterson LC, Pisias NG, Prell WL, Raymo ME, Shackleton NJ, Toggweiler JR (1992) On the structure and origin of major glaciation cycles, 1. Linear responses to Milankovitch forcing. Paleoceanography **7**:701-738

IUCN Bangladesh (2015). National framework for establishing and managing marine protected areas (MPAs) in Bangladesh. IUCN, International Union for Conservation and Nature, Bangladesh country office, Dhaka, Bangladesh, Pp xi+106.

Kajiura SM and Holland KN (2002) Electroreception in juvenile scalloped hammerhead and sandbar Sharks. *Journal of Experimental Biology*, **205**, 3609–3621.

Klimley AP, Butler SB (1988) Immigration and emigration of a pelagic fish assemblage to seamounts in the Gulf of California related to water mass movements using satellite imagery. *Marine Ecology Progress Series*, 49, 11–20.

Knowlton N (1993) Sibling species in the sea. Annual Review of Ecology and Systematics 24, 189-216.

Knowlton N (2000) Molecular genetic analyses of species boundaries in the sea. Hydrobiologia 420:73–90.

Kohler NE, Turner PA (2001) Shark tagging: a review of conventional methods and studies. Environmental Biology of Fishes, 60, 191–223.

Lambeck K, Esat TM, Potter EK (2002) Links between climate and sea levels for the past three million years. Nature **419**:199-206

Leray M and Knowlton N (2015) DNA barcoding and metabarcoding of standardized samples reveal patterns of marine benthic diversity. PNAS 22(7): 2076–2081.

Li, X.Y., Papavassiliou, S. and Ruehrup, S. eds., 2012. Ad-hoc, Mobile, and Wireless Networks: 11th International Conference, ADHOC-NOW 2012, Belgrade, Serbia, July 9-11, 2012. Proceedings (Vol. 7363). Springer.Lieske E and Myers RF (2001) Coral Reef Fishes; Indo-pacific and Caribbean. Harper Collins Pub. London, 400pp

Lindeque PK, Parry HE, Harmer RA, Somerfield PJ and Atkinson A (2013) Next Generation Sequencing Reveals the Hidden Diversity of Zooplankton Assemblages. PLoS ONE 8(11): e81327. doi:10.1371/ journal.pone.0081327.

Liu JX, Gao TX, Yokogawa K, Zhang YP (2006a) Differential population structuring and demographic history of two closely related fish species, Japanese sea bass (*Lateolabrax japonicus*) and spotted sea bass (*Lateolabrax maculatus*) in Northwestern Pacific. Mol Phylogenet Evol **39**:799-811

Lund R (1990) Chondrichthyan life history styles as revealed by the 320 million years old Mississippian of Montana. *Environmental Biology of Fishes*, **27**, 1–19.

Meyer CL, Holland KN, Papastamatiou YP (2005) Sharks can detect changes in the geomagnetic field. *Journal of the Royal Society Interface*, **2**, 129–130.

Mollah AR (1997) Status of corals and associated resources in Bangladesh. In: Proceedings of the Regional Workshop on the Conservation and Sustainable Management of Coral Reefs. (Proceedings No.22) CRSARD, Madras. pp 37-51

Nance HA, Klimley P, Galván-Magaña F, Martínez-Ortíz, Marko PB (2011) Demographic processes underlying subtle patterns of population structure in the scalloped hammerhead Shark, *Sphyrna lewini*. PLoS ONE 6(7): e21459.

Ovenden JR, Kashiwagi T, Broderick D, Giles J, Salini J (2009) The extent of population genetic subdivision diVers among four codistributed Shark species in the Indo-Australian archipelago. BMC Evol Biol 9:40

Ovenden JR, Morgan JAT, Street R, Tobin A, Simpfendorfer C, Macbeth W, Welch D (2011) Negligible evidence for regional genetic population structure for two Shark species R*hizoprionodon acutus* (Rüppell, 1837) and *Sphyrna lewini* (GriYth & Smith, 1834) with contrasting biology. Mar Biol 158:1497–1509.

Ovenden, J R, Morgan JAT, Street R, Tobin A, Simpfendorfer C, Macbeth W, et al. (2011) Negligible evidence for regional genetic population structure for two Shark species *Rhizoprionodon acutus* (Ruppell, 1837) and *Sphyrna lewini* (Griffith, Smith, 1834) with contrasting biology. Mar. Biol. 158:1497–1509.

Ovenden, JR, Kashiwagi T, Broderick D, and Salini J (2009) The extent of population genetic subdivision differs among four co-distributed Shark species in the Indo-Australian archipelago. BMC Evol. Biol. 9:40.

Pearman J K, El-Sherbiny MM, Lanzén A, Al-Aidaroos AM and Irigoien X (2014) Zoplankton diversity across three Red Sea reefs using pyrosequencing. Frontiers in Marine Science. 01 (27): 1-11.

Pinhal, D, Shivji MS, Vallinoto M, Chapman DD, Gadig OBF, and Martins C (2012) Cryptic hammerhead Shark lineage occurrence in the western South Atlantic revealed by DNA analysis. Mar. Biol. 159:829–836.

Plaisance L, Knowlton N, Paulay G, Meyer C (2009) Reef-associated crustacean fauna: biodiversity estimates using semi-quantitative sampling and DNA barcoding. Coral Reefs 28:977–986.

Rajasuriya, A, Zahir H, Venkataraman K Islam Z and Tamelender J (2004) Status of coral reefs in South Asia: Bangladesh, India, Maldives, Sri Lanka. Pp 213-233. In D. Souter and O. Linden (eds.) Coral reef degredation in the Indian Ocean Status Report, Sweded: CORDIO.

Raymond M and Rousset F (1995) An exact test for population differentiation. Evolution 49: 1280-1283.

Rogers AR (1995) Genetic evidence of Pleistocene population explosion. Evolution 49:608-615

Rogers AR and Harpending H (1992) Population growth makes waves in the distribution of pairwise genetic difference. Mol. Biol. Evol. 9: 552–569.

Savolainen V, Cowan RS, Vogler AP, Roderick GK and Lane R (2005) Towards writing the encyclopedia of life: an introduction to DNA barcoding. Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences 360:1805–1811.

Schmitt T and Hewitt GM (2004) Molecular biogeography of the arctic-alpine disjunct burnet moth species Zygaena exulans (Zygaenidae, Lepidoptera) in the Pyrenees and Alps. Journal of Biogeography 31: 885-893.

Schneider S, Roessli D and Excoffier L (2000) Arlequin: a software for population genetics data analysis. Ver 2.000. Genetics and Biometry Laboratory, Department of Anthropology, University of Geneva, Geneva.

Simpfendorfer CA, Milward NE (1993) Utilization of a tropical bay as a nursery area by Sharks of the families Carcharhinidae and Sphyrnidae. *Environmental Biology of Fishes*, **37**, 337–345.

Spaet J LY, Rima Jabado W, Henderson AC, Moore ABM and Berumen M L (2015) Population genetics of four heavily exploited Shark species around the Arabian Peninsula. Ecology and Evolution 2015; 5(12): 2317–2332.

Spaet JLY, Rima WJ, Aaron CH, Alec BMM, Michael L (2015) Population genetics of four heavily exploited Shark species around the Arabian Peninsula. Ecology and Evolution 5(12): 2317–2332.

Spalding MD, Ravilious C, and Green EP (2001) United Nations Environment Programme, World Conservation Monitoring Centre. World Atlas of Coral Reefs. University of California Press: Berkeley. 416 pp.

Springer S (1967) Social organization of Shark populations. In: *Sharks, Skates and Rays* (eds Gilbert PW, Matheswon RF, Rall DP), pp. 149–174. Johns Hopkins University Press, Baltimore.

Sultana D (2008) Diversity and distribution of coral associated fishes in the St. Martin‘s Island. Bangladesh. Thesis paper, Inst. of Marine Sci. and Fisheries, Univ. Chittagong, Bangladesh.114pp.

Tajima F (1989) Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. Genetics 123: 585-595

Templeton AR, Crandall KA, Sing CF (1992) A cladistic analysis of phenotype associations with haplotypes inferred from restriction endonuclease mapping and DNA sequence data. III. Cladogram estimation. *Genetics*, 132, 619–633.

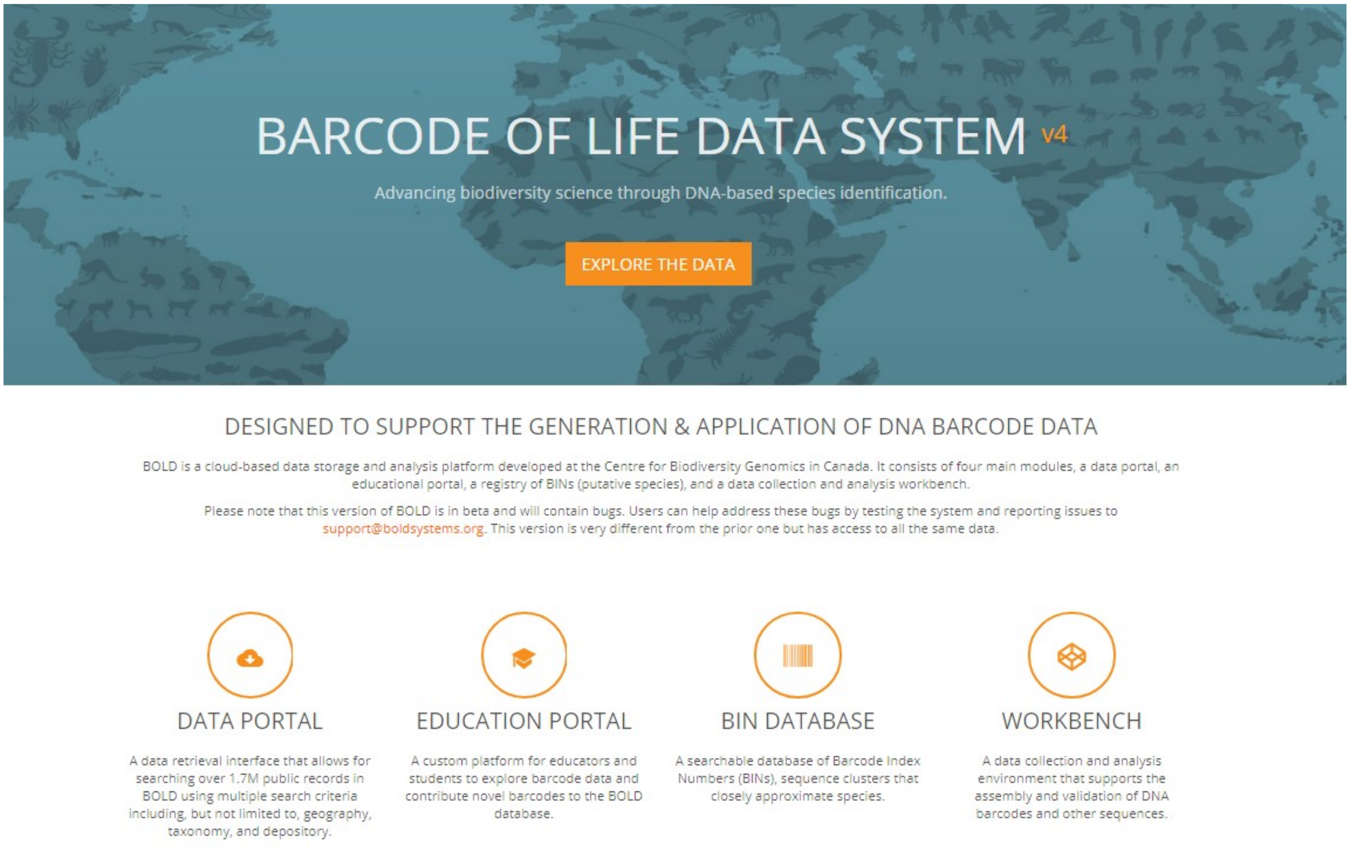
Thomas JRC, Willette DA, Carpenter KE, Santos MD (2014) Hidden Diversity in Sardines: Genetic and Morphological Evidence for Cryptic Species in the Goldstripe Sardinella, Sardinella gibbosa (Bleeker, 1849) 9(1): 1-10.

Tomascik T, (1997) Management Plan for Resources of Narikel Jinjira (St. Martin's Island). National Conservation Strategy Implementation Project 1, Ministry of Environment and Forest, Government of Bangladesh. Pp 125.

Ward RD, Zemlark TS, Innes BH, Last PR and Hebert PDN (2005) DNA barcoding Australia’s fish species. Philosophical Transactions Royal Society of London. Series B., 1716 p.

Wilkinson C (2002). Status of Coral Reefs of the World, Australian Institute of Marine Science.

<u>Annex 01</u>. Submitted species in BOLD Database i.e. *Cryptocentrus maudae* [Anyone can search and get information on the identified species from BOLD database for further research and knowledge]



BARCODE OF LIFE DATA SYSTEM v4

Advancing biodiversity science through DNA-based species identification.

DESIGNED TO SUPPORT THE GENERATION & APPLICATION OF DNA BARCODE DATA

BOLD is a cloud-based data storage and analysis platform developed at the Centre for Biodiversity Genomics in Canada. It consists of four main modules, a data portal, an educational portal, a registry of BINs (putative species), and a data collection and analysis workbench.

Please note that this version of BOLD is in beta and will contain bugs. Users can help address these bugs by testing the system and reporting issues to support@boldsystems.org. This version is very different from the prior one but has access to all the same data.

DATA PORTAL

A data retrieval interface that allows for searching over 1.7M public records in BOLD using multiple search criteria including, but not limited to, geography, taxonomy, and depository.

EDUCATION PORTAL

A custom platform for educators and students to explore barcode data and contribute novel barcodes to the BOLD database.

BIN DATABASE

A searchable database of Barcode Index Numbers (BINs), sequence clusters that closely approximate species.

WORKBENCH

A data collection and analysis environment that supports the assembly and validation of DNA barcodes and other sequences.

F1707SM- 02 - DNA Barcoding of Coral Associated Fish of Saint Martin’s Island , Bangladesh [SAU]

Copyright (2018)
ShereBangla Agricultural University

Process ID: SAU002-18
Identification: Cryptocentrus maudae
Identified by Kazi Ahsan Habib
Collected in Bangladesh, Chittagong
by Habib,K.A., Neogi, A.K., Nahar, N.
Institution Storing: Sher-e-Bangla Agricultural University, Department of Fisheries Biology and Genetics, Aquatic Bioresource Research Lab
Field ID: F1707SM- 02
Museum ID: F1707SM- 02

Tags

Comments

Recent Activities

Timestamp	Who	Action
Jul-21, 2018 06:38	Kazi Ahsan Habib	Modify-Specimen
Jul-21, 2018 06:38	Kazi Ahsan Habib	New-Image(s)
Jul-20, 2018 14:13	BOLD Data Manager	New-Record

Comments

Specimen Details

Sample ID: F1707SM- 02
Process ID: SAU002-18
Project: SAU
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Field ID: F1707SM- 02
Museum ID: F1707SM- 02
Collection Code: F1707SM- 02
Reference Link:
Note:

Voucher Status:
Tissue Descriptor:
Sex:
Reproduction:
Life Stage:
Extra Info:
Associated Taxa:
Associated Specimens:

Taxonomy

Phylum: Chordata
Class: Actinopterygii
Order: Gobiiformes
Family: Gobiidae
Subfamily: Gobiinae
Genus: Cryptocentrus
Species: Cryptocentrus maudae

Identification: Cryptocentrus maudae
Rank: Species
Identifier: Kazi Ahsan Habib
Identification Method:
Identifier Institution: Sher-e-Bangla Agricultural University
Identifier Email: ahsan.sau@gmail.com
Taxonomy Note:

Barcode Index Numbers

BIN: BOLD:ADN9569

Collection Data

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Type: Member
Max Divergence in BIN: N/A
Distance to NN: 7.38% (p-dist)

Phylum:
Class:
Order:
Family:
Subfamily:
Genus:
Species:

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Region/County: Cox` Bazar
Sector: Teknaf
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Lat/Lon: 20.611, 92.326
Elevation: 4 m
Elevation Accuracy:
Depth:
Depth Accuracy:
Collection Event ID:
Collection Notes:

Collector: Habib,K.A., Neogi, A.K., Nahar, N.
Date Collected: 15-Jul-2017
Date Accuracy:
Time Collected:
Site Code:
Habitat: Coral
Sampling Protocol:
Coord. Source:
Coord. Accuracy

Map

Sequence View for Process ID: SAU003-18

Specimen Details Current

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Process ID:	SAU003-18
Project:	SAU
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Taxon:	Valenciennea muralis
Rank Name:	species
Sampling Protocol:	N/A
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Kingdom:	Animals

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Marker Code	Sequence Length	GC	Ambiguous	Trace Count
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COI-5P

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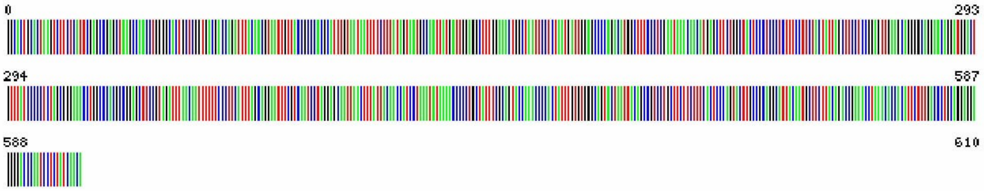

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Amino Acid Sequence

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Sequence Metadata

Genbank Accession:	N/A
Translation Matrix:	Vertebrate Mitochondrial
Last Updated:	2019-01-12 01:06:07.212459
Sequence Runsite:	Sher-e-Bangla Agricultural University, Department of Fisheries Biology and Genetics, Aquatic Bioresource Research Lab

COI-5P Tags & Comments

Sequencing Date	2018-03-12 17:18:30
Trace Direction	F
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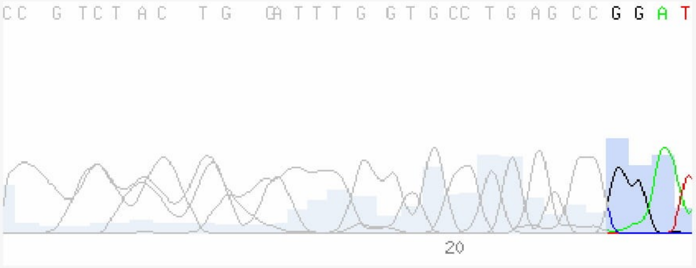
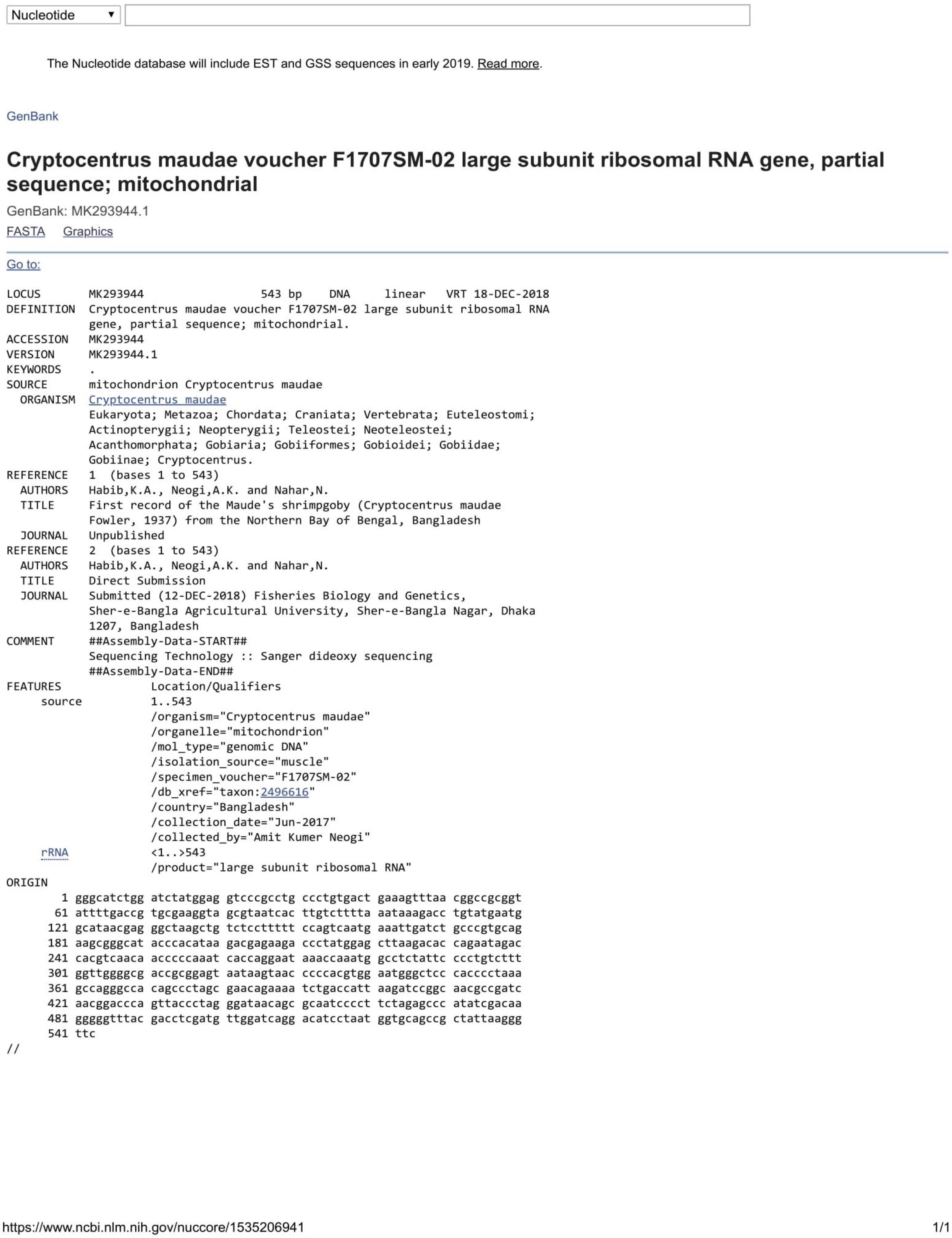
Trace Runsite	Sher-e-Bangla Agricultural University, Department of Fisheries Biology and Genetics, Aquatic Bioresource Research Lab



Annex 2. Submitted species in NCBI Database i.e. *Cryptocentrus maudae*
[Anyone can see and download DNA sequence of the identified species from NCBI database]



The Nucleotide database will include EST and GSS sequences in early 2019. Read more.

GenBank

Cryptocentrus maudae voucher F1707SM-02 large subunit ribosomal RNA gene, partial sequence; mitochondrial

GenBank: MK293944.1

FASTA Graphics

Go to:

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REFERENCE   1  (bases 1 to 543)
  AUTHORS   Habib,K.A., Neogi,A.K. and Nahar,N.
  TITLE     First record of the Maude's shrimpgoby (Cryptocentrus maudae
            Fowler, 1937) from the Northern Bay of Bengal, Bangladesh
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 543)
  AUTHORS   Habib,K.A., Neogi,A.K. and Nahar,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-DEC-2018) Fisheries Biology and Genetics,
            Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka
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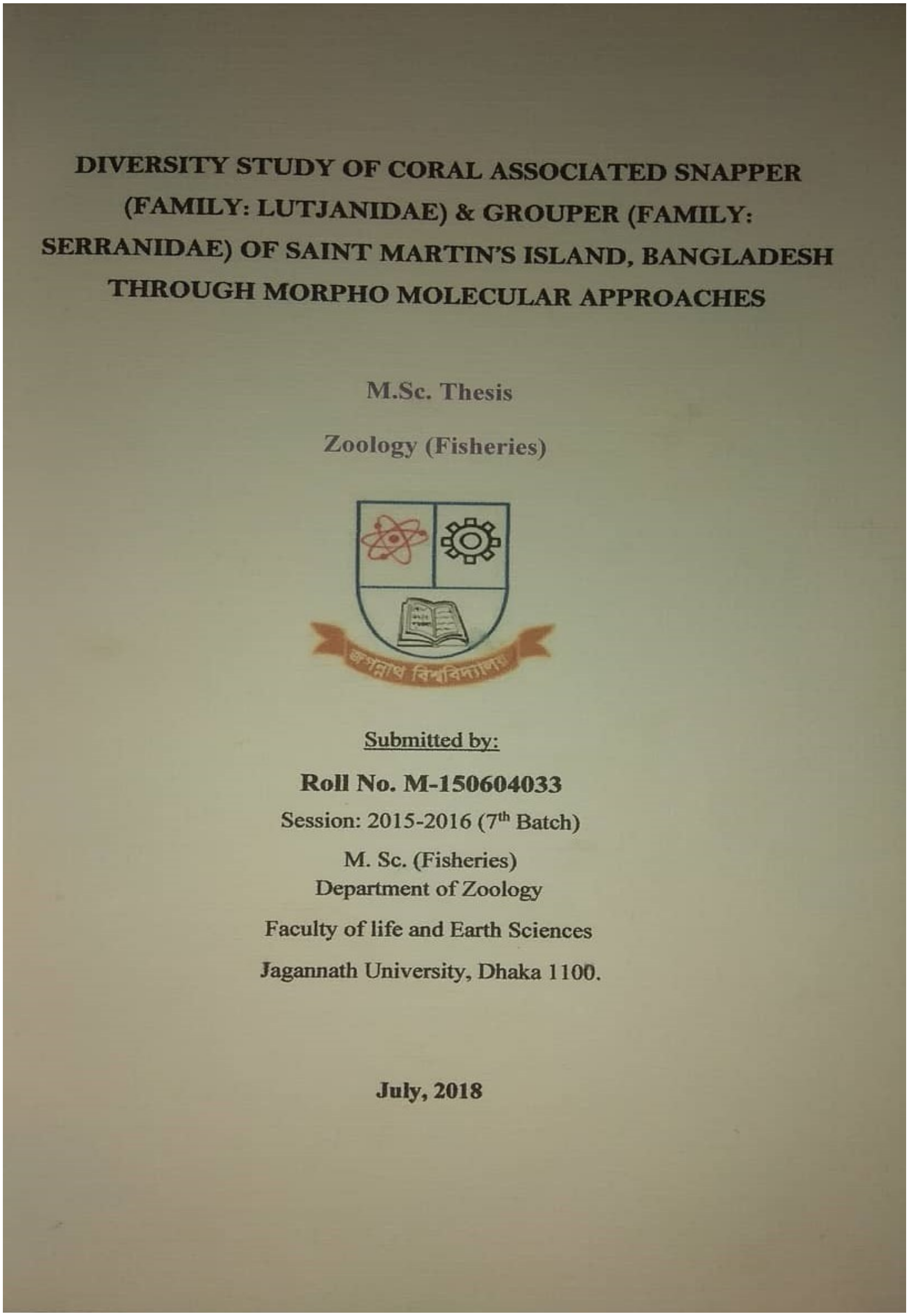
Annex 3: MS thesis published on the research work of this project



DIVERSITY STUDY OF CORAL ASSOCIATED SNAPPER (FAMILY: LUTJANIDAE) & GROUPER (FAMILY: SERRANIDAE) OF SAINT MARTIN'S ISLAND, BANGLADESH THROUGH MORPHO MOLECULAR APPROACHES

M.Sc. Thesis

Zoology (Fisheries)

জগন্নাথ বিশ্ববিদ্যালয়

Submitted by:

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Session: 2015-2016 (7th Batch)
M. Sc. (Fisheries)
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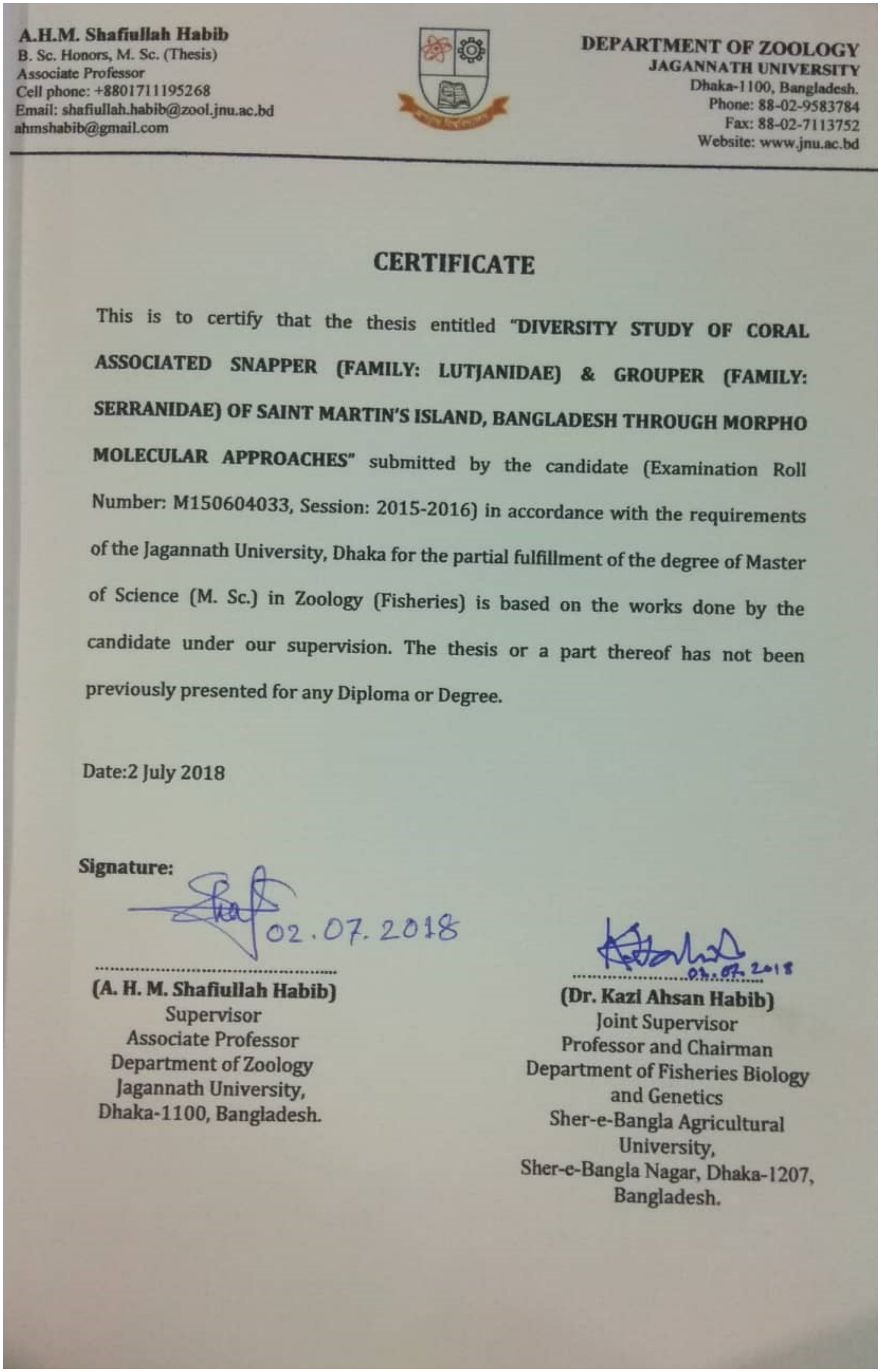
July, 2018



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CERTIFICATE

This is to certify that the thesis entitled **"DIVERSITY STUDY OF CORAL ASSOCIATED SNAPPER (FAMILY: LUTJANIDAE) & GROUPER (FAMILY: SERRANIDAE) OF SAINT MARTIN'S ISLAND, BANGLADESH THROUGH MORPHO MOLECULAR APPROACHES"** submitted by the candidate (Examination Roll Number: M150604033, Session: 2015-2016) in accordance with the requirements of the Jagannath University, Dhaka for the partial fulfillment of the degree of Master of Science (M. Sc.) in Zoology (Fisheries) is based on the works done by the candidate under our supervision. The thesis or a part thereof has not been previously presented for any Diploma or Degree.

Date:2 July 2018

Signature:

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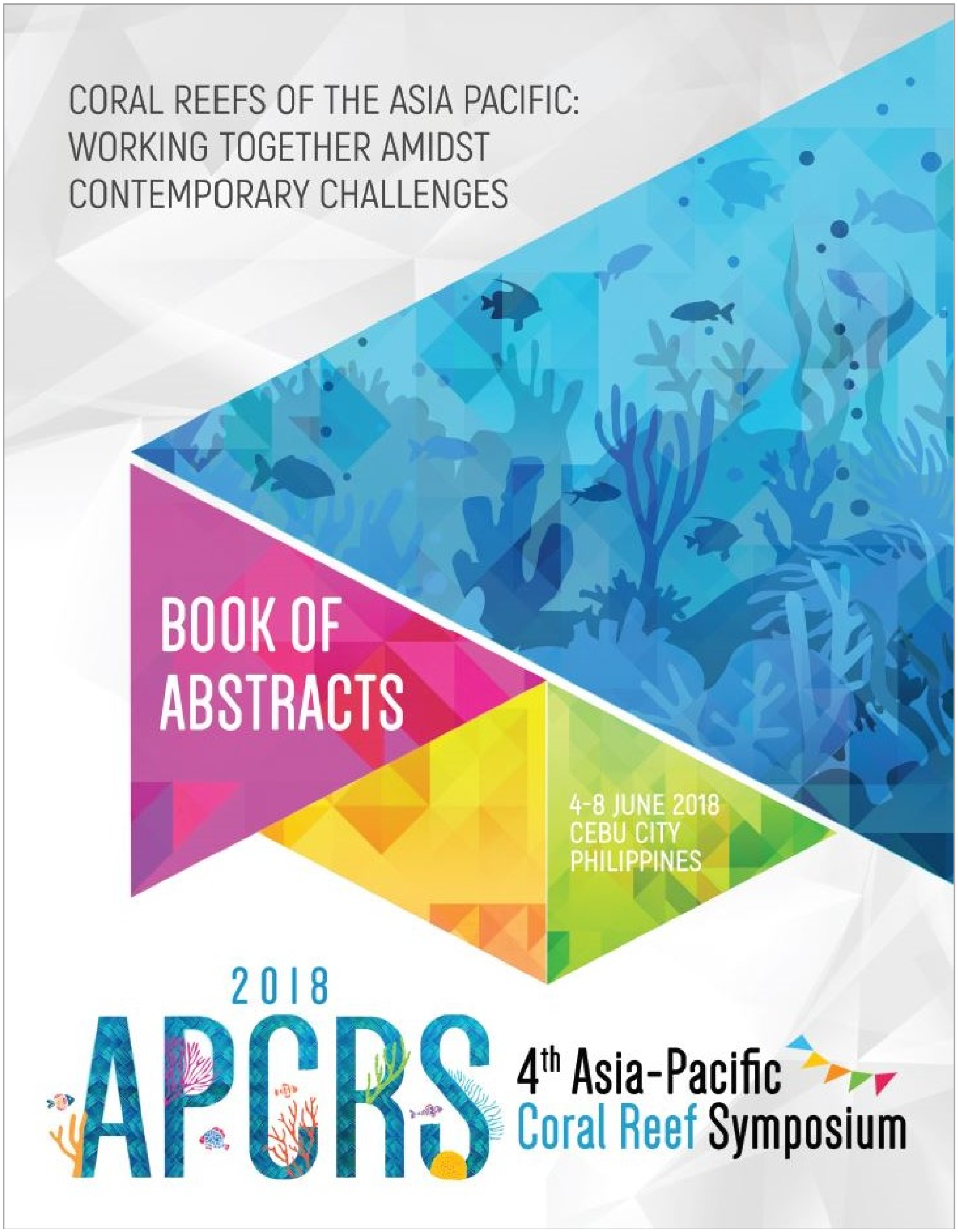
Annex 4: Published abstracts in different conferences



CORAL REEFS OF THE ASIA PACIFIC:
WORKING TOGETHER AMIDST
CONTEMPORARY CHALLENGES

BOOK OF
ABSTRACTS

4-8 JUNE 2018
CEBU CITY
PHILIPPINES

2018
APCRS
4th Asia-Pacific
Coral Reef Symposium

BEC-253

DNA barcoding of coral associated fishes of Saint Martin's Island of Bangladesh

Kazi Ahsan Habib, Amit Kumer Neogi, Najmun Nahar, Provakor Sarkar, Kabir Ikramul Haque

The current rate of species description using traditional keys is extremely slow and typically require specialized expertise which have severely limited the understanding of coral reef biodiversity. DNA barcoding is an advance tool to identify unique, cryptic and new species from marine ecosystems and reveals undisclosed biodiversity than previously estimated. Saint Martin's Island is the only coral island in Bangladesh. The island was declared an Ecologically Critical Area (ECA). There is lack of information on different biodiversity data such as a complete species inventory, recruitment process etc. for conservation and designing effective Marine Protected Area (MPA). Present study aims to assess the diversity and make an updated inventory of coral associated fishes of the island using DNA barcoding, and to build a reference library of DNA barcodes. From November to till date, 75 species of fish were collected from the reef environment of the Island. Collected samples were first identified by examining morphometric characteristics and then assessed by DNA barcoding. Until now, 50 fish species have been successfully barcoded. The study provided several new records of fish species in Bangladesh viz., *Valenciennea muralis* (Valenciennes, 1837), *Blenniella periophthalmus* (Valenciennes, 1836), *Leiognathus longispinis* (Valenciennes, 1835), *Johnius amblycephalus* (Bleeker, 1855), *Pomadasys guoraca* (Cuvier, 1829).

Aquaculture and Fisheries for Achieving SDGs

BOOK OF ABSTRACTS

8th Biennial Fisheries Conference & Research Fair 2019

30-31 March

BFRF Bangladesh Fisheries Research Forum

Bangladesh Fisheries Research Forum (BFRF)

ADDITION OF THIRTY-TWO NEW RECORDS TO THE FISH INVENTORY OF BANGLADESH FOUND OFF SAINT MARTIN'S ISLAND THROUGH MORPHOLOGICAL ANALYSIS AND DNA BARCODING

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DNA barcoding appears to be an advance approach for taxonomic identification, characterization, and discovery of newer species, facilitating biodiversity studies. A study has been conducted to assess the diversity of reef associated fishes found off Saint Martin's Island of Bangladesh and to prepare DNA barcode library of them. The fishes were collected from May 2017 to July 2018. Species level identification was carried out using morphological characters according to original descriptions.DNA barcode information on the mitochondrial COI gene and/or 16S rRNA gene sequences was obtained for molecular identification of the collected samples. Sequences were matched with the DNA sequence data of NCBI and BOLD database using BLAST search engine and phylogenetic analysis was made using computer program MEGA. A total of 128 marine fish species were successfully DNA barcoded from SMI belonging to 49 families of 9 orders. Most importantly, a total of 32 marine fish species have been confirmed as a new distributional records in Bangladesh, of which 26 species are reef associated. These newly recorded reef fishes are *Ostorhinchus cookie, Lepidamia kalosoma, Istiblennius dussumieri, Blenniella periophthalmus, Caranx heberi, Valenciennea muralis, Amblyeleotris downingi, Cryptocentrus cyanotaenia, Istigobius ornatus, Plectorhinchus macrospilus, Bodianus neilli, Pomadasys andamanensis, Pomadasys guoraca, Lethrinus crocineus, Lutjanus fulvus, Parupeneus indicus, Parapercis clathrate, Filimanus similis, Chromis cinerascens, Chlorurus rhakoura, Plectropomus pessuliferus, Sphyraena putnamae, Synodus variegatus, Apogonichthyoides pseudotaeniatus, Cryptocentrus maudae*and *Stegastes apicalis.* The other non-reef fish species are *Leiognathus daura, Leiognathus longispinis, Equulites leuciscus, Opistognathus variabilis, Chrysochir aureus* and *Saurida micropectoralis.* Among the newly recorded fish species, the order Perciformes solely contributes 30 number of species (93%). The present study endows the remarkable addition of species record to the country's fish inventory.

Aquaculture and Fisheries for Achieving SDGs

BOOK OF ABSTRACTS

8th
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Fisheries
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Research
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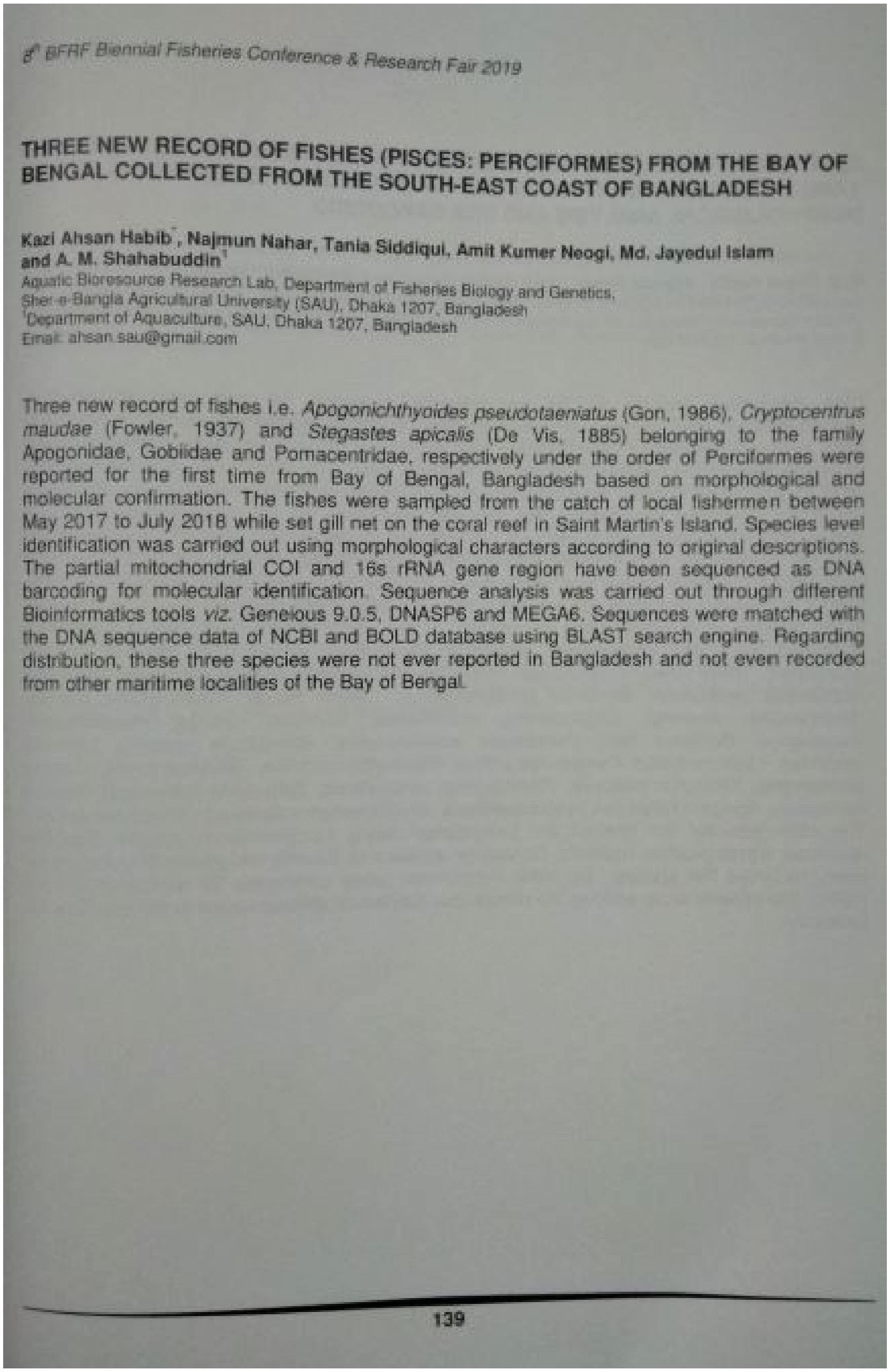
Bangladesh Fisheries Research Forum (BFRF)



THREE NEW RECORD OF FISHES (PISCES: PERCIFORMES) FROM THE BAY OF BENGAL COLLECTED FROM THE SOUTH-EAST COAST OF BANGLADESH

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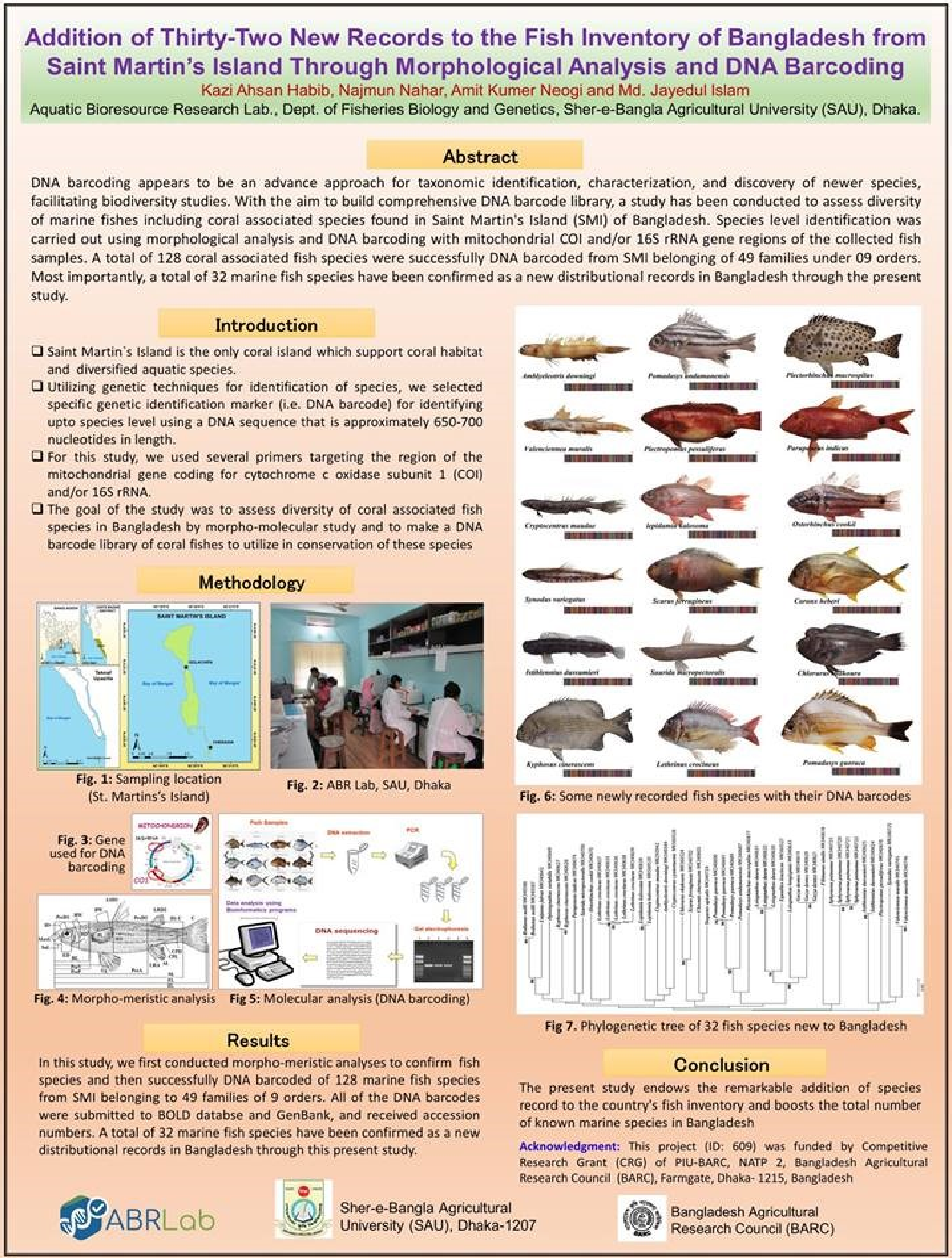
Three new record of fishes i.e. *Apogonichthyoides pseudotaeniatus* (Gon, 1986), *Cryptocentrus maudae* (Fowler, 1937) and *Stegastes apicalis* (De Vis, 1885) belonging to the family Apogonidae, Gobiidae and Pomacentridae, respectively under the order of Perciformes were reported for the first time from Bay of Bengal, Bangladesh based on morphological and molecular confirmation. The fishes were sampled from the catch of local fishermen between May 2017 to July 2018 while set gill net on the coral reef in Saint Martin's Island. Species level identification was carried out using morphological characters according to original descriptions. The partial mitochondrial COI and 16s rRNA gene region have been sequenced as DNA barcoding for molecular identification. Sequence analysis was carried out through different Bioinformatics tools *viz.* Geneious 9.0.5, DNASP6 and MEGA6. Sequences were matched with the DNA sequence data of NCBI and BOLD database using BLAST search engine. Regarding distribution, these three species were not ever reported in Bangladesh and not even recorded from other maritime localities of the Bay of Bengal.

Annex 5: Award received from different Conference for Poste/Oral Presentation

Poster-1:



Addition of Thirty-Two New Records to the Fish Inventory of Bangladesh from Saint Martin's Island Through Morphological Analysis and DNA Barcoding

Kazi Ahsan Habib, Najmun Nahar, Amit Kumer Neogi and Md. Jayedul Islam

Aquatic Bioresource Research Lab., Dept. of Fisheries Biology and Genetics, Sher-e-Bangla Agricultural University (SAU), Dhaka.

Abstract

DNA barcoding appears to be an advance approach for taxonomic identification, characterization, and discovery of newer species, facilitating biodiversity studies. With the aim to build comprehensive DNA barcode library, a study has been conducted to assess diversity of marine fishes including coral associated species found in Saint Martin's Island (SMI) of Bangladesh. Species level identification was carried out using morphological analysis and DNA barcoding with mitochondrial COI and/or 16S rRNA gene regions of the collected fish samples. A total of 128 coral associated fish species were successfully DNA barcoded from SMI belonging of 49 families under 09 orders. Most importantly, a total of 32 marine fish species have been confirmed as a new distributional records in Bangladesh through the present study.

Introduction

- ☐ Saint Martin's Island is the only coral island which support coral habitat and diversified aquatic species.
- ☐ Utilizing genetic techniques for identification of species, we selected specific genetic identification marker (i.e. DNA barcode) for identifying upto species level using a DNA sequence that is approximately 650-700 nucleotides in length.
- ☐ For this study, we used several primers targeting the region of the mitochondrial gene coding for cytochrome c oxidase subunit 1 (COI) and/or 16S rRNA.
- ☐ The goal of the study was to assess diversity of coral associated fish species in Bangladesh by morpho-molecular study and to make a DNA barcode library of coral fishes to utilize in conservation of these species

Methodology

Fig. 1: Sampling location (St. Martins's Island)

Fig. 2: ABR Lab, SAU, Dhaka

Fig. 3: Gene used for DNA barcoding

Fig. 4: Morpho-meristic analysis

Fig 5: Molecular analysis (DNA barcoding)

Fig. 6: Some newly recorded fish species with their DNA barcodes

Fig 7. Phylogenetic tree of 32 fish species new to Bangladesh

Results

In this study, we first conducted morpho-meristic analyses to confirm fish species and then successfully DNA barcoded of 128 marine fish species from SMI belonging to 49 families of 9 orders. All of the DNA barcodes were submitted to BOLD databse and GenBank, and received accession numbers. A total of 32 marine fish species have been confirmed as a new distributional records in Bangladesh through this present study.

Conclusion

The present study endows the remarkable addition of species record to the country's fish inventory and boosts the total number of known marine species in Bangladesh

Acknowledgment: This project (ID: 609) was funded by Competitive Research Grant (CRG) of PIU-BARC, NATP 2, Bangladesh Agricultural Research Council (BARC), Farmgate, Dhaka- 1215, Bangladesh

ABRLab

Sher-e-Bangla Agricultural University (SAU), Dhaka-1207

Bangladesh Agricultural Research Council (BARC)

Best poster presentation award at 8th Biennial Fisheries Conference and Research Fair 2019

Poster-2:

DIVERSITY ASSESSMENT OF SCLERACTINIAN CORAL WITH FIFTEEN NEW RECORDS FROM SAINT MARTIN'S, ISLAND, BANGLADESH

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[1]Aquatic Bioresource Research Lab., Department of Fisheries Biology and Genetics, Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh, [2]Research Center for Oceanography, Indonesia.

Abstract

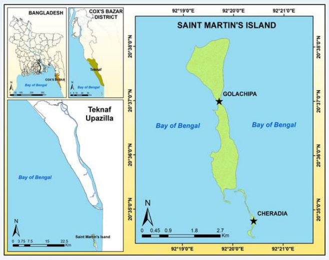
Coral reefs are one of the most biologically diverse ecosystems and home of thousands of marine species. Saint Martin's Island is the only place in Bangladesh where coral colonies are found and still supporting coral reef ecosystem. To investigate the present status and diversity, several expeditions has been made offshore of St. Martin's Island. Result shows 15 Scleractinian species belongs to 7 families and 9 genera were newly recorded in Bangladesh water. However, the present investigation increases the total number of hard coral species to 81 belonging 12 families found in this island.

Background Information

Coral reefs are a vital natural resource found in tropical waters throughout the world (Spalding et al. 2001). Although they occupy less than 1% of the ocean floor, but are inhabited by at least 25% of all marine species (Gray 1997, Hoegh-Guldberg 1999). In Bangladesh, St. Martin's have only coral aggregations in shallow waters along with seagrass beds, soft coral habitats and rocky habitats. Coral communities extend to about 200m offshore of St. Martin' s Island with maximum coral cover of 7.6% and colony density of 1.3m^2 and comprise 66 hard coral species belonging to 22 genera and 10 families (Tomasick, 1997; Mollah, 1997). The present study deals with the status and diversity of hard coral at St. martin`s Island, Bangladesh.

Methodology

Sampling on under water coral diversity was conducted during the dry season (November to February) from 2017 to 2018 at St. martins island Bangladesh. Species Identification was done according to Veron et al., 2018 and Suharsono 2008. The photograph of the specimens was taken on up to 1-5 meters employing scuba diving with the help of professional scuba diver.



Results and Discussion

A total of 45 Scleractinian species under 09 family and 16 genera were recorded during the coral sampling (Fig A). Among them, 15 species were recorded as new distribution record from Bangladesh. Among them *Pavona clavus* and *Favites halicora* are found most abundant species. However, human intervention on coral reef destruction has been documented significantly.

Figure A. 1. *Acropora hyacinthus*, 2. *Pavona clavus*, 3. *Coscinaraea exesa*, 4. *Tubastrea faulkneri*, 5. *D. lizardensis*, 6. *D. maritima*, 7. *D. veroni*, 8. *Goniastrea stelligera*, 9. *Favites acuticollis*, 10. *F. melicerum*, 11. *Favites complanata*, 12. *Favites pentagona*, 13. *Plesiastrea versipora*,13. *Goniopora albiconus*, and 15. *Goniopora norfolkensis*

Indiscriminate anchoring of boats, ship grounding, fishing on coral reef habitat, throwing garbage to the water, etc. In these most damages has been caused by anchoring of hundreds of life boats that use very sharp metal anchors. Also observed soft and hard substrate on coral reef in surrounding of ship grounding and propeller actions of mechanical boats.

Conclusion

The coral population of St. martin`s island has been decreasing remarkably over the years, and currently, it has reached an alarming level. This study indicates there are some few coral diversity is exist here. So, Government intervention is immediately needed to save the coral biodiversity of this island.

Acknowledgment: **Authors are thankful to Mr. S.M. Atiqur Rahman and Sharif Sarwar for supporting by underwater photography and Prof. Suharsono, RCO, IIS to confirm the species identification.**

Best poster presentation award at 8th Biennial Fisheries Conference and Research Fair 2019

Poster-3:

UNDERWATER VISUAL CENSUS REVEALS SEVEN NEW RECORDS OF REEF-ASSOCIATED FISH FROM SAINT MARTIN'S ISLAND, BANGLADESH

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Abstract

Coral reefs are one of the most biologically diverse ecosystems in the world and play important roles for reef fish assemblages. To investigate the present status and diversity of reef-associated fish of St. Martin's Island, a study has been made through UVC methods from November 2017 to April 2018. In this study, we found 42 reef-associated fish species under 13 families. Among them 7 species of 4 families were identified as the first distributional records from Bangladesh.

Background Information

Underwater Visual Census (UVC) methods are used worldwide to assess shallow marine habitats and are particularly known for supporting conservation decisions in coral reefs. Coral reefs are a vital natural resource found in tropical waters throughout the world (Spalding et al. 2001). Although they occupy less than 1% of the ocean floor, but are inhabited by at least 25% of all marine species (Gray 1997, Hoegh-Guldberg 1999). In Bangladesh, St. Martin's have only coral aggregations in shallow waters along with seagrass beds, soft coral habitats and rocky habitats where reef fish found and its located in the northeastern part of the Bay of Bengal, Bangladesh. The present paper deals with the present status and diversity of reef-associated fish of St. Martin's Island through UVC methods.

Methodology

To investigate the present status and diversity of reef-associated fish of St. Martin's Island, a study has been made through UVC methods from November 2017 to April 2018. The survey was carried out up to five (05) meters water depth and off-field identification of fish was done from the captured photo at Aquatic Bioresource Research Lab, SAU, Dhaka.

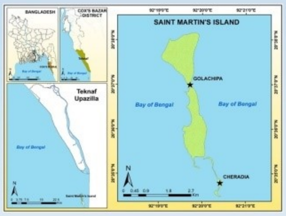

Figure: **a.** *Pomacentrus simsiang*, **b**. *Pomacentrus aquilus*, **c**. *Labroides dimidiatus*, **d**. *Halichoeres hortulanus*, **e.** *Scolopsis igcarensis*, **f.** *Pomacanthus sextriatus* ,**g**. *Blenniella periophthalmus.*

Results and Discussion

We found 42 reef-associated fish species under 13 families. Among them 7 species of 5 families were identified as the first distributional records from Bangladesh which are *Pomacentrus simsiang*, *Pomacentrus aquilus*, *Labroides dimidiatus*, *Halichoeres hortulanus*, *Pomacanthus sextriatus*, *Blenniella periophthalmus* and *Scolopsis igcarensis*. Among these *P. simsiang* and *P. aquilus* were reported for the first time in the Bay of Bengal. However, human intervention on coral reef destruction has been documented significantly which leads habitat losses of reef fishes.

Conclusion

Although the reef fish population of St. martin`s Island has been decreasing remarkably over the years and currently, it has reached an alarming level, but there are some few reef fish diversity is still exist here. So, Government intervention is immediately needed to save the coral biodiversity of this island.

Acknowledgment: This project (ID: 609) was funded by Competitive Research Grant (CRG) of PIU-BARC, NATP 2, Bangladesh Agricultural Research Council (BARC), Farmgate, Dhaka- 1215, Bangladesh . Authors are thankful to Mr. S.M. Atiqur Rahman and Sharif Sarwar for supporting by underwater photography.

Best poster presentation award in 1st International Conference on Sustainable Fisheries2019

Annex 6. List of recorded fishes from St. Martin's during the study periods

Sl. No	LAB CODE	Class	ORDER	FAMILY	*SPECIES*	DNA Barcode
1	F1803SM-18	Actinopterygii	Scorpaeniformes	Dactylopteridae	*Dactyloptena orientalis*	MK340606, MK340607
2	F1803SM-51	Elasmobranchii	Myliobatiformes	Dasyatidae	*Neotrygon indica*	MK340668
3		Actinopterygii	Anguilliformes	Muraenidae	*Gymnothorax favagineus*	-
4	F1712SM-07	Actinopterygii	Aulopiformes	Synodontidae	*Trachinocephalus myops/Synodus myops*	MK340735, MK340736
5	F1712SM-22	Actinopterygii	Aulopiformes	Synodontidae	*Saurida micropectoralis*	MK335881, MK335882, MK340700, MK340701
6	F1803SM-47	Actinopterygii	Aulopiformes	Synodontidae	*Synodus variegatus*	MK335889, MK340725
7	F1712SM-01	Actinopterygii	Beloniformes	Exocoetidae	*Cheilopogon furcatus*	MK335846, MK335847, MK340601, MK340602
8	F1801SM-11	Actinopterygii	Beloniformes	Belonidae	*Ablennes hians*	MK340570, MK340571
9	F1710SM-09	Actinopterygii	Beryciformes	Holocentridae	*Sargocentron rubrum*	MK340697, MK340698, MK340699
10	F1803SM-45	Actinopterygii	Beryciformes	Holocentridae	*Myripristis hexagona*	MK340664, MK335869
11	F1707SM-48	Actinopterygii	Perciformes	Acanthuridae	*Acanthurus xanthopterus*	MK340579
12	F1802SM-13	Actinopterygii	Perciformes	Acanthuridae	*Ostorhinchus cookii*	MK340670, MK335872
13	F1803SM-33	Actinopterygii	Perciformes	Apogonidae	*Lepidamia kalosoma*	MK340634
14	F1711SM-27	Actinopterygii	Perciformes	Blenniidae	*Istiblennius dussumieri*	MK340623, MK340624, MK335853, MK335854
15		Actinopterygii	Perciformes	Blenniidae	*Blenniella periophthalmus*	-

16	F1707SM-12	Actinopterygii	Perciformes	Carangidae	*Caranx sexfasciatus*	MK340592, MK340593, MK340594, MK340595
17	F1707SM-40	Actinopterygii	Perciformes	Carangidae	*Alectis indica*	MK340580, MK340581
18	F1708SM-03	Actinopterygii	Perciformes	Carangidae	*Megalaspis cordyla*	MK340662
19	F1708SM-14	Actinopterygii	Perciformes	Carangidae	*Alepes kleinii*	MK340582, MK340583
20	F1709SM-01	Actinopterygii	Perciformes	Carangidae	*Scomberoides tol*	MK340711
21	F1709SM-02	Actinopterygii	Perciformes	Carangidae	*Scomberoides commersonnianus*	MK340708, MK340709
22	F1711SM-22	Actinopterygii	Perciformes	Carangidae	*Scomberoides lysan*	MK340710
23	F1801SM-03	Actinopterygii	Perciformes	Carangidae	*Ulua mentalis*	MK340738
24	F1801SM-04	Actinopterygii	Perciformes	Carangidae	*Caranx heberi*	MK340591, MK335844
25	F1803SM-01	Actinopterygii	Perciformes	Carangidae	*Gnathanodon speciosus*	MK340622
26	F1803SM-17	Actinopterygii	Perciformes	Carangidae	*Seriolina nigrofasciata*	MK340712
27	F1802SM-06	Actinopterygii	Perciformes	Chaetodontidae	*Chaetodon decussatus*	MK340600
28		Actinopterygii	Perciformes	Chaetodontidae	*Heniochus acuminatus*	-
29	F1708SM-16	Actinopterygii	Perciformes	Drepaneidae	*Drepane longimana*	MK340610, MK340611
30	F1803SM-22	Actinopterygii	Perciformes	Echeneidae	*Echeneis naucrates*	MK340612
31	F1801SM-02	Actinopterygii	Perciformes	Ephippidae	Platax teira	MK340675, MK340676
32	F1707SM-02	Actinopterygii	Perciformes	Gobiidae	*Cryptocentrus maudae*	MK293942, MK293944
33	F1707SM-03	Actinopterygii	Perciformes	Gobiidae	*Valenciennea muralis*	MK340745, MK340746, MK335891
34	F1708SM-10	Actinopterygii	Perciformes	Haemulidae	*Pomadasys maculatus*	MK340692, MK340693
35	F1709SM-	Actinopterygii	Perciformes	Haemulidae	*Pomadasys*	MK340689,

	08				*guoraca*	MK340690, MK340691
36	F1712SM-14	Actinopterygii	Perciformes	Haemulidae	*Pomadasys argyreus*	MK340688
37	F1803SM-19	Actinopterygii	Perciformes	Haemulidae	*Pomadasys andamanensis*	MK340687
38	F1804SM-21	Actinopterygii	Perciformes	Haemulidae	*Diagramma pictum*	MK340608, MK340609
39	F1707SM-39	Actinopterygii	Perciformes	Kyphosidae	*Kyphosus cinerascens*	MK340627
40	F1710SM-07	Actinopterygii	Perciformes	Labridae	*Thalassoma lunare*	MK340733, MK340734, MK340735
41	F1710SM-12	Actinopterygii	Perciformes	Labridae	*Cheilinus chlorourus*	MK335845
42		Actinopterygii	Perciformes	Labridae	*Bodianus neilli*	-
43	F1712SM-15	Actinopterygii	Perciformes	Lactariidae	*Lactarius lactarius*	MK340629
44	F1707SM-09	Actinopterygii	Perciformes	Leiognathidae	*Gazza dentex*	MK340619, MK340620, MK340621
45	F1707SM-29	Actinopterygii	Perciformes	Leiognathidae	*Leiognathus daura*	MK340630, MK340631, MK340632, MK335857, MK335858, MK335859
46	F1708SM-13	Actinopterygii	Perciformes	Leiognathidae	*Leiognathus longispinis*	MK340633, MK335860
47	F1803SM-37	Actinopterygii	Perciformes	Lethrinidae	*Lethrinus crocineus*	MK340636, MK340637, MK340638, MK340639
48	F1709SM-14	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus fulvus*	MK340642, MK335865
49	F1708SM-05	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus johnii*	MK340643, MK340644
50	F1709SM-07	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus madras*	MK340655, MK340656, MK340657
51	F1709SM-11	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus lemniscatus*	MK340645, MK340646, MK340647,

						MK340648
52	F1709SM-13	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus lunulatus*	MK340649, MK340650, MK340651
53	F1710SM-32	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus lutjanus*	MK340652, MK340653, MK340654
54	F1711SM-01	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus rivulatus*	MK340658, MK340659, MK340660
55	F1803SM-02	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus erythropterus*	MK340640
56	F1803SM-41	Actinopterygii	Perciformes	Lutjanidae	*Lutjanus russellii*	MK340661
57	F1803SM-48	Actinopterygii	Perciformes	Menidae	*Mene maculata*	MK340663
58	F1712SM-06	Actinopterygii	Perciformes	Mullidae	*Upeneus guttatus*	MK340739
59	F1712SM-09	Actinopterygii	Perciformes	Mullidae	*Upeneus sulphureus*	MK340740, MK340741, MK340742, MK340743
60	F1801SM-07	Actinopterygii	Perciformes	Mullidae	*Upeneus tragula*	MK340744
61	F1803SM-38	Actinopterygii	Perciformes	Mullidae	*Parupeneus indicus*	MK340674, MK335873
62	F1710SM-10	Actinopterygii	Perciformes	Nemipteridae	*Scolopsis vosmeri*	MK340705, MK340706, MK340707
63	F1712SM-16	Actinopterygii	Perciformes	Nemipteridae	*Nemipterus peronii*	MK340666, MK340667
64	F1802SM-01	Actinopterygii	Perciformes	Nemipteridae	*Nemipterus japonicus*	MK340665
65		Actinopterygii	Perciformes	Pinguipedidae	*Parapercis clathrata*	-
66	F1712SM-24	Actinopterygii	Perciformes	Polynemidae	*Filimanus similis*	MK340618, MK335852
67	F1707SM-45	Actinopterygii	Perciformes	Pomacanthidae	*Pomacanthus annularis*	MK340679
68	F1707SM-04	Actinopterygii	Perciformes	Pomacentridae	*Abudefduf septemfasciatus*	MK340573
69	F1707SM-16	Actinopterygii	Perciformes	Pomacentridae	*Pomacentrus tripunctatus*	MK335876

70	F1710SM-14	Actinopterygii	Perciformes	Pomacentridae	*Chromis cinerascens*	MK340603, MK335848
71	F1802SM-05	Actinopterygii	Perciformes	Pomacentridae	*Abudefduf sordidus*	MK340576
72	F1802SM-08	Actinopterygii	Perciformes	Pomacentridae	*Abudefduf septemfasciatus*	MK340573
73	F1803SM-12	Actinopterygii	Perciformes	Pomacentridae	*Stegastes apicalis*	MK340724, MK335888
74	F1802SM-18	Actinopterygii	Perciformes	Scaridae	*Scarus ferrugineus*	
75	F1708SM-07	Actinopterygii	Perciformes	Sciaenidae	*Johnius amblycephalus*	MK340625
76	F1708SM-08	Actinopterygii	Perciformes	Sciaenidae	*Protonibea diacanthus*	MK340694, MK340695
77	F1708SM-12	Actinopterygii	Perciformes	Sciaenidae	*Otolithes ruber*	MK340671
78	F1708SM-19	Actinopterygii	Perciformes	Sciaenidae	*Chrysochir aureus*	MK340604, MK335850
79	F1709SM-06	Actinopterygii	Perciformes	Sciaenidae	*Otolithoides pama*	MK340672
80	F1709SM-12	Actinopterygii	Perciformes	Sciaenidae	*Pterotolithus maculatus*	MK340696
81	F1708SM-20	Actinopterygii	Perciformes	Scombridae	*Rastrelliger kanagurta*	-
82	F1707SM-08	Actinopterygii	Perciformes	Serranidae	*Epinephelus erythrurus*	MK340613, MK340614, MK340615, MK340616
83	F1710SM-06	Actinopterygii	Perciformes	Serranidae	*Cephalopholis boenak*	MK340596
84	F1710SM-34	Actinopterygii	Perciformes	Serranidae	*Cephalopholis formosa*	MK340597, MK340598, MK340599
85	F1803SM-43	Actinopterygii	Perciformes	Serranidae	*Plectropomus pessuliferus*	MK340678, MK335875
86	F1803SM-68	Actinopterygii	Perciformes	Serranidae	*Epinephelus fuscoguttatus*	MK340617, MK335851
87		Actinopterygii	Perciformes	Serranidae	*Cromileptes altivelis*	-
88	F1707SM-01	Actinopterygii	Perciformes	Siganidae	*Siganus javus*	MK340716

89	F1707SM-32	Actinopterygii	Perciformes	Siganidae	*Siganus canaliculatus*	MK340713, MK340714, MK340715
90	F1707SM-38	Actinopterygii	Perciformes	Siganidae	*Siganus vermiculatus*	MK340717
91	F1707SM-28	Actinopterygii	Perciformes	Sillaginidae	*Sillago sihama*	MK340718, K340719
92	F1707SM-19	Actinopterygii	Perciformes	Sparidae	*Acanthopagrus berda*	MK340577, MK340578
93	F1708SM-01	Actinopterygii	Perciformes	Sphyraenidae	*Sphyraena putnamae*	MK340720, MK340721, MK340722, MK340723, MK335884, MK335885, MK335886, MK335887
94	F1708SM-04	Actinopterygii	Perciformes	Stromateidae	*Pampus argenteus*	MK340673
95	F1707SM-25	Actinopterygii	Perciformes	Terapontidae	*Terapon jarbua*	MK340726, MK340727, MK340728
96	F1708SM-02	Actinopterygii	Perciformes	Terapontidae	*Terapon theraps*	MK340729, MK340730
97	F1712SM-26	Actinopterygii	Perciformes	Trichiuridae	*Trichiurus gangeticus*	MK340605
98	F1709SM-16	Actinopterygii	Anguilliformes	Ophichthidae	*Ophisurus serpens*	MK340605
99		Actinopterygii	Scorpaeniformes	Platycephalidae	*Platycephalus indicus*	MK986641
100		Actinopterygii	Scorpaeniformes	Scorpaenidae	*Pterois russelii*	MK560529
101		Actinopterygii	Perciformes	Chaetodontidae	*Chaetodon octofasciatus*	-
102		Actinopterygii	Tetraodontiformes	Diodontidae	*Diodon hystrix*	-
103		Actinopterygii	Siluriformes	Plotosidae	*Plotosus lineatus*	-
104	F1710SM-31	Actinopterygii	Perciformes	Caesionidae	*Caesio cuning*	MK340588, MK340589, MK340590
105		Actinopterygii	Scorpaeniformes	Scorpaenidae	*Pterois volitans*	-
10	F1803SM-	Actinopterygii	Perciformes	Opistognathid	*Opistognathus*	MK340669

6	24			ae	*variabilis*	
107	F1803SM-67	Actinopterygii	Perciformes	Haemulidae	*Plectorhinchus macrospilus*	MK561628, MK335874
108	F1803SM-54	Actinopterygii	Perciformes	Gobiidae	*Amblyeleotris downingi*	MK340584
109	F1707SM-35	Actinopterygii	Perciformes	Labridae	*Halichoeres nigrescens*	MK840723
110	F1804SM-20	Actinopterygii	Ostraciidae	Tetraodontiformes	*Tetrosomus gibbosus*	MK340731
111	F1803SM-21	Actinopterygii	Scorpaeniformes	Synanceiidae	*Minous monodactylus*	MK340610
112	F1804SM-15	Actinopterygii	Tetraodontiformes	Balistidae	*Balistoides viridescens*	MK560530
113	F1804SM-02	Actinopterygii	Perciformes	Leiognathidae	*Equulites leuciscus*	MK560527
114	F1802SM-11,12	Actinopterygii	Perciformes	Gobiidae	*Istigobius ornatus*	MK335855, MK335856
115	F1711SM-15	Actinopterygii	Beloniformes	Hemiramphidae	*Hemiramphus far*	MK561619
116	F1803SM-67	Actinopterygii	Perciformes	Haemulidae	*Plectorhinchus macrospilus*	MK561628, MK335874
117	F1803SM-16	Actinopterygii	Perciformes	Apogonidae	*Apogonichthyoides pseudotaeniatus*	-
118	F1803SM-55	Actinopterygii	Perciformes	Gobiidae	*Cryptocentrus cyanotaenia*	MK560526, MK561627
119	F1803SM-69	Actinopterygii	Perciformes	Scaridae	*Chlorurus rhakoura*	MK560524, MK561629
120	F1804SM-23	Actinopterygii	Tetraodontiformes	Tetraodontidae	*Chelonodontops patoca*	MK560528
121	F1804SM-19	Actinopterygii	Pleuronectiformes	Soleidae	*Heteromycteris oculus*	MK560525
122	F1804SM-01	Actinopterygii	Perciformes	Leiognathidae	*Aurigequula longispina*	MK560522
123	F1803SM-13	Actinopterygii	Perciformes	Lobotidae	*Lobotes surinamensis*	MK560523
124	F1804SM-16	Actinopterygii	Perciformes	Acanthuridae	*Acanthurus mata*	-
125	F1803SM-39	Actinopterygii	Tetraodontiformes	Balistidae	*Sufflamen fraenatum*	-