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BRIEF COMMUNICATIONS

Siganidae, a New Family of Fishes for the Russian Fauna

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Abstract—A representative of the family Siganidae, Mottled spinefoot (*Siganus fuscescens*), has been found for the first time in Russian waters. It is a Pacific, subtropical-equatorial, and Asian wide-ranging species: from the southern part of the Korean Peninsula and Japan to Papua New Guinea and Australia. In September 2013, it was collected in Far Eastern State Marine Reserve, Far East Branch, Russian Academy of Sciences, near Ostrovok Fal'shivyi Cape (42°26′ N, 130°47′ E).

Keywords: Mottled spinefoot *Siganus fuscescens*, Sea of Japan, new finding, tropical species

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Fishes of the family Siganidae (order Perciformes, subclass Actinopterigii) have been known since the middle of the Eocene (Berg, 1958). They are currently widespread in the coastal waters of the tropical Indo-Pacific region. The monotypic family comprises 28 species, which are distinguished mainly by their morphological features and body coloration (Nelson, 1984). Siganidae have never been recorded in Russian waters (Lindberg and Krasyukova, 1975; Sokolovskii et al., 2004; Parin et al., 2014).

The Pacific, subtropical-equatorial, and Asian Mottled spinefoot (*Siganus fuscescens*) is a wide-ranging species: distributed from the south part of the Korean Peninsula and Japan to Papua New Guinea and Australia (Woodland, 1990; Shimada, 2002; Riede, 2004). It lives in the shallow waters among algae and sea grasses (Randall et al., 1990; Lieske and Myers, 1994; Myers, 1999).

In September 2013, one representative of this species was collected in Far Eastern State Marine Reserve, Far Eastern Branch, Russian Academy of Sciences, near Ostrovok Fal'shivyi Cape (42°26′ N, 130°47′ E). Its description is provided in this report. The studied fish specimen is kept in the collection of the Institute of Marine Biology, Far East Branch, Russian Academy of Sciences (MIMB no. 28975).

Morphological features were measured according to the standard methods. A radiographic image was obtained with the help of a Faxitron Specimen Radiography System MX-20. DNA extraction for subsequent molecular-genetic analysis was performed using a PureLink Genomic DNA Kit (Invitrogen, United States). The cytochrome *b* gene was amplified by the method of polymerase chain reaction (PCR) with the forward (FishcytB-F 5'-ACCACCGTTGTTATTCAACTACAAGAAC-3') and reverse (TruccytB-R 5'-CCGACTTCCGGATTACAAGACCG-3') primers. The reaction mixture for PCR (10 μL) contained 6.4 μL deionized water, 0.5 μL dNTP (10 mM, deoxynucleotide triphosphate) mixture, 1 μL × PCR buffer (Evrogen, Russia), 0.4 μL $MgCl_2$ (50 mM), 0.3 μL forward and reverse primer solutions (10 mM), 0.1 μL Taq polymerase (Evrogen), and 1 μL genomic DNA solution. The temperature algorithm for PCR included preheating at 94°C for 2 min followed by 35 cycles as provided in the scheme: denaturation at 94°C for 30 s, annealing at 52°C for 40 s, and elongation at 72°C for 1 min; final elongation was carried out for 10 min. The results of DNA fragment amplification were verified using the electrophoresis of amplicons in a 1% agarose gel.

The sequencing reaction was carried out in 10 μL of the mixture containing 0.5 mM primer, 10–100 ng of the PCR product, and 1.0 μL of kit of BigDye Terminator Cycle Sequencing Kit v. 3.1 reagents. The reaction was performed according to the protocol to the BigDye Terminator Cycle Sequencing Kit. The reading of products of the sequencing reaction was performed on an ABI 3130xl genetic analyzer. The obtained sequence of nucleotides was used to identify the species in the BLAST (2014) application integrated in the international GenBank.

Fig. 1. Mottled spinefoot (*Siganus fuscescens*)—*TL* 325 mm (MIMB No. 28975), caught at the territory of Far Eastern State Marine Reserve, Far Eastern Branch, Russian Academy of Sciences near Ostrovok Fal'shivyi Cape, Sea of Japan.

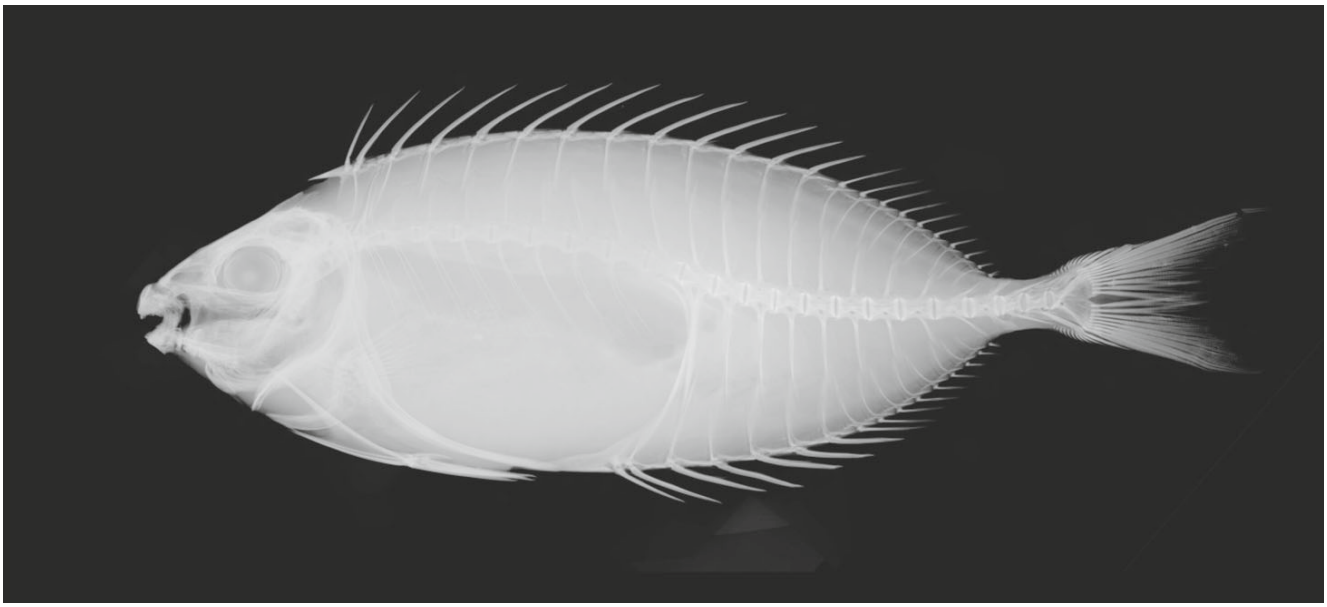

Fig. 2. Radiographic image of Mottled spinefoot (*Siganus fuscescens*) (MIMB no. 28975).

Siganus fuscescens (Houttuyn, 1782)—Mottled spinefoot **(Fig. 1)**

Material. MIMB no. 28975—one specimen, mature female *SL* 308 mm, *TL* 325 mm, September 4, 2013, 42°26′ N 130°47′ E, near Ostrovok Fal'shivyi Cape, Sea of Japan, collector A.V. Ratnikov.

Description. *D* XIII 10, *A*VII 9, *P* 16, *V* II 3, *vert.* 10 + 13 = 23, *sp.br.* 6 + 7 = 13.

Head 4.25 times in *SL*, largest body depth 2.7 times in *SL*, eye diameter 3.8 times in head length (*c*), snout length 2.8 times in *c*. Short snout, terminal nonprotractile mouth. Premaxillary bones without ascending appendages, jaws with dense rows of small incisor-like teeth having additional apexes; two pairs of nostrils, anterior nostrils with tubular-like flaps; a line drawn through anterior and posterior nostrils runs on eye upper margin. Well-developed false gills with 34 gill filaments. High body, compressed laterally, body depth-to-length ratio 2.7. Dorsal fin with 13 long spinous and ten soft branching rays. A forward-directed spine in front of dorsal fin. Anal fin with seven spines and nine branching rays. Anterior spines of dorsal fin 1.7 times longer last spine of dorsal fin. Last anal fin spine 2.5 times shorter than longest spine of this fin. Pectoral fins with 16 soft branching rays. Ventral fins

with two pairs of spines, ex- and internal, and membrane with two branching rays between them. Forked caudal fin with 38 rays, 24 of them branching; central rays at least half of longest rays in this fin. Anus shifted forward, directly behind ventral fins. Scales minute, smaller than in other species of family and easily detached.

Plastic features. Anteanal distance 107 mm, antedorsal distance 61 mm, anteventral distance 85 mm, head length 62 mm, postorbital distance 22 mm, horizontal eye diameter 16 mm, snout length 22 mm, interorbital distance 19 mm, largest body depth 98 mm, caudal peduncle depth 12 mm, body width before pectoral fin basement 36 mm, longest ray *D* 32 mm, longest ray *A* 29 mm.

Coloration. Silver belly, olive-colored back and body sides. This spinefoot species characterized by presence of small light spots on back and body sides, from 18 to 20 rows from highest point of lateral line to first spine of anal fin.

Genetic analysis. To identify the caught specimen, molecular-genetic analysis was used besides typological features. This type of analysis has proved its informativeness for spinefoot fish and is used for genetic barcoding (Lemer et al., 2007). Following the assembly and alignment, a region of the cytochrome *b* mtDNA gene with the length of 925 bp was obtained. BLAST program showed that our sequence was similar to that of *Siganus fuscescens* during the sequencing of mtDNA for this region. The mtDNA sequence used in this work was deposited in the international GenBank under the accession number of KM081654.

This finding of *S. fuscescens* indicates a possibility for this species to distribute well beyond the borders of its main habitat in the Indo-Malayan Region.

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