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New Distributional Record for Siganus vermiculatus (Valenciennes 1835) from the Veraval Fishing Landing Centre along Northwest Coast of India

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Abstract: A new distributional record of vermiculated spinefoot, *Siganus vermiculatus* (Valenciennes, 1835), belonging to the family Siganidae, for the first time from the northwest coast of India at Veraval fish landing centre (20°54'03" N 70° 22' 10" E) in Gir-Somnath district of the state of Gujarat on 23 March 2022. The morphometric and meristic characters of the specimen were measured using standard taxonomic keys. Further, DNA barcoding was carried out for the mitochondrial cytochrome oxidase subunit I gene from the tissues of the holotype specimen and phylogenetic studies using neighbor joining tree construction were done to ascertain the relationship and similarity with the specimens of the same species barcoded in the other places of southern India, and authentication of the specimens to *S. vermiculatus* was done. The species is reported from 900 km north of the previous nearest reported location.

Keywords: DNA sequencing, Gujarat, Siganus, Veraval, Vermiculatus, New distribution record, X-ray

The Siganidae family, also known as the rabbit fish family, is composed of a single accepted genus Siganus, with 29 species (Horton et al. 2022) possessing poisonous spines and having diurnal herbivore feeding behavior feeding mainly on benthic algae and microorganisms by scraping corals and rocks. Fifteen species have been reported from Indian waters of this family (Murugan and Namboothri 2012), out of which 2 species (S. canaliculatus and S. javus) were reported from Gujarat waters (Burman et al 2000). The common name rabbitfish is because of their rounded blunt snout, peaceful temperament and jaws having rabbit-like appearance. Siganid species can be identified by their color and morphological characteristics, such as snout shape, body depth, color patterns, shape of fins, etc., but some distinct key characters must be checked to prevent misidentification from closely related species (Woodland 1990). Siganids are marine-residing species that inhabit mainly reefs, sea grasses, mangroves, or shallow lagoons. They are important reef fishes that protect coral reefs from being smothered by algae. They are mostly marine, with a rare occurrence in estuaries, with the exception of S. vermiculatus, which is truly estuarine (Nelson 1994). S. vermiculatus can be cultured in ponds, tanks along with other fishes, crabs or as a mono cultured species. S. vermiculatus is one of the fastest growing species of genus Siganus. Efforts of captive breeding on a commercial basis are in progress (Anuraj et al. 2021). Siganids have venom glands in their dorsal, anal and pelvic fin spines that contain a painful toxin. The teeth are asymmetrical, bicuspid, and compressed into a single row. The dorsal fin comprise of 13 spines with 10 soft rays and the anal fin comprising 7 spines with 10 soft rays. They can attain a maximum length of 50 cm and have 23 vertebrates (Nelson 1994, Helfman et al 1997). The female siganids are larger than males in some but not all of the species (Kuiter 1993, Thresher 1984).

The present study has derived the meristic and morphological characteristics of the fish specimen collected from the western coast of India. Also, the gene sequence obtained was used to carry out BLAST with the NCBI GenBank database. Based on the maximum identity score, the first ten sequences were selected and aligned using multiple alignment software programs. The aim of the paper is, firstly, to report the presence of *S. vermiculatus* in Gujarat and the northward range extension of the species to about 900 km compared to its closest and previously recorded locations (i.e., Karwar coast).

MATERIAL AND METHODS

The study was carried out along the northwest coast of India, on the Veraval coast of the state of Gujarat (Fig. 1). The fish specimen was caught by FRP OBM using a bottom gill net from the inshore waters of Veraval (Fig. 2). The specieslevel identification was made by using standard taxonomic keys (Day 1888). The muscle and pectoral fin tissue samples were used for extracting DNA, and then its quality was evaluated on a 1.0% agarose gel. The fragment of the gene was amplified by PCR with primers FISH_F2–FISH_R2. A single discrete PCR amplicon band was observed when resolved on a 1% agarose gel. The PCR amplicon was purified by column purification to remove contaminants. The DNA sequencing reaction of the PCR amplicon was carried out with both primers using the BDT v3.1 cycle sequencing kit on an ABI 3730xl genetic analyzer. The gene sequence was used to carry out BLAST with the NCBI GenBank database. COI gene, approximately 617bp length located in the mitochondrial genome was compared with the NCBI data based on nucleotide homology and phylogenetic analysis to know the specimen at species level.

RESULTS AND DISCUSSION

Systematics

Kingdom: Animalia Phylum: Chordata Subphylum: Vertebrata Class: Actinopteri Subclass: Teleostei Order: Acanthuriformes Family: Siganidae Genus: *Siganus* Species: *vermiculatus*

Description: D. XIII 10, V. I 2-4 V, P. 14, A. VII 9, C. 16. Occurrence of 23 vertebrae (Fig. 3), bluish white body, head brownish or golden yellow with irregular blue lines making maze like pattern. Preopercular angle 91°-102°, strong overlapping scales cover cheeks, midline of thorax scaled, lacking pelvic ridges. Anterior nostril with low flange and slightly broadened posteriorly. Spines are stout, blunt or pungent and venomous. Head slightly concave above eye with head length 18.7% of standard length (SL) followed by head depth with 30.63% of SL. Snout length is 12.09% of SL. Eyes rounded with eye diameter 6.29% of SL, presence of forward directed spine in front of dorsal fin. First dorsal fin length is 6.34% of SL, second dorsal fin length with 10.56% of SL, third dorsal fin length with 12.5% of SL, fourth dorsal fin length with 12.79% of SL, fifth dorsal fin length with 13.05% of SL, sixth dorsal fin length with 12.17% of SL, seventh dorsal fin length with 12.5% of SL, eighth dorsal fin length with 12.5% of SL, ninth dorsal fin length with 12.84% of SL, tenth dorsal fin length with 11.20% of SL, eleventh dorsal fin length with 13.14% of SL, twelfth dorsal fin length with 11.85% of SL and thirteenth dorsal fin length with 11.21% of SL. Pelvic fin length is 16.05% of SL, pectoral fin length is 20.09% of SL, anal fin length is 15.94% of SL and caudal peduncle length is 4.9% of SL followed by caudal peduncle depth with 8.66% of SL. Caudal fin slightly emarginated; scales minute but distinct.

Table 1. Morphometric characters of <i>Siga</i> Character	Length (mm)
	0 ()
Total length	393.01
Standard length	308.27
Fork length	349.86
Head length	57.66
Snout length	37.28
Head depth	94.43
Snout to the end of preoperculum length	45.76
Orbit diameter	19.38
Upper-jaw length	17.95
Lower-jaw length	13.32
Caudal peduncle length	15.11
Caudal peduncle depth	26.70
Pectoral fin length	61.94
Pelvic fin length	49.47
Dorsal fin length	22.37
Anal fin length	49.15
Anal fin width	146.52
Dorsal fin base length	213.56
Anal fin base length	221.35
Pelvic fin base length	32.54
Opercular length	68.72
Predorsal length	75.56
Prepectoral length	70.12
Prepelvic length	88.24
Preanal length	161.92
nterorbital width	11.18
1 st anal fin spine length	26.56
2 nd anal fin spine length	38.54
3 rd anal fin spine length	41.52
4 th anal fin spine length	41.53
5 th anal fin spine length	39.54
$6^{ m th}$ anal fin spine length	41.55
7 th anal fin spine length	43.74
1 st dorsal fin spine length	19.53
2 nd dorsal fin spine length	32.54
3 rd dorsal fin spine length	38.55
4 th dorsal fin spine length	39.42
5 th dorsal fin spine length	40.24
ິ ^ຫ dorsal fin spine length	37.52
7 th dorsal fin spine length	38.53
B th dorsal fin spine length	38.52
^ʰ dorsal fin spine length	39.57
10 th dorsal fin spine length	34.52
11 th dorsal fin spine length	40.51
12 th dorsal fin spine length	36.52

 Table 1. Morphometric characters of Siganus vermiculatus

DNA Barcode: The mitochondrial cytochrome c oxidase (COI) gene, approximately 617bp length located in the mitochondrial genome (NCBI Sequence ID: OP476333) showed high similarity with *S. vermiculatus* based on nucleotide homology and phylogenetic analysis (Fig. 4) confirmed the fish sample at its species level.

Siganids belongs to the family Siganidae are found



Fig. 1. Possible fishing ground of OBM gill netter

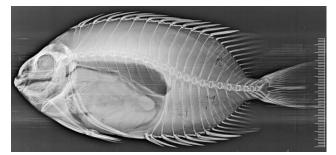


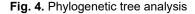
Fig. 3. X-ray of fish specimen

across the tropical and temperate Indo-West Pacific region and the Indian ocean. S. vermiculatus is commonly known for its light brownish body marked with irregular zigzag stripes. It was reported from the Veraval fishing landing centre from a gill netter, which is operated in nearshore water. The coral population in Gujarat is mostly found in the Gulf of Kachchh, but several reports support the existence of a patchy distribution of the coral in the intertidal and subtidal regions of Saurashtra (Raghunathan et al 2004). The fish is known to feed on algae growing on seagrasses, mangrove roots, and rocks. The coastal rocky shore of Gujarat, hence, can be a preferable feeding site for the species. This could be the result of the occurrence of species from Karwar to Veraval, as the southern Gujarat coast has a lacuna of rocky substratum. The fish is known to be one of the fastest-growing species, can feed on a variety of food items in captivity (EI-Dakar et al 2010), and is also tolerant to a wide range of salinity, temperature, and pH, making them an ideal candidate species for mariculture.



Fig. 2. Specimen of *Siganus vermiculatus* procured in this study

Siganus vermiculatus voucher VERM-SNF169 cytochrome c oxidase subunit 1 (CO1) gene, partial cds; mitochondrial
 Siganus vermiculatus voucher IRD BMF-198.2 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
 Siganus vermiculatus isolate F1707SM-38 from Bangladesh cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
 Siganus vermiculatus voucher BW-A7471 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
 Siganus vermiculatus voucher PGN136B cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
 Siganus vermiculatus voucher PGN136A cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
 Siganus vermiculatus voucher JAUFRSSSV cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial
 Siganus vermiculatus voucher PGN10B cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial



The taxonomic and DNA barcoding analyses have confirmed the collected specimen as Siganus vermiculatus. Globally, there are around 29 known species of Siganidae family (Froese and Pauly 2019), with 15 species described in India (Murugan and Namboothri 2012). On the west coast of India, three species of the Siganus genus are commonly available, among which S. vermiculatus has been reported to distribute upto Ratnagiri coast of Maharashtra (Metar et al., 2019). This study presents the first documentation of S. vermiculatus occurrence on the northwest coast of India, specifically at the Veraval fish landing centre. According to FAO identification sheets, S. vermiculatus can be distinguised from other Siganus species morphologically, by the presence of vermiculating lines on the sides, a characteristic observed in this study, which other signaus species do not possess. Additionally, S. vermiculatus is distinguished by having the longest last anal spine which aligns with the current study showing length of 43.74 mm in contrast, in S. luridus and S. spinus 3rd or 4th anal spine is the longest.

AUTHOR CONTRIBUTION

All the authors have significant contribution in the final manuscript. YM collected the fish sample and made the draft of the manuscript.

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