

A report on anomalies in pelvic fin and pectoral filament of two species of genus *Setipinna* (Swainson, 1839) from east coast of India

Shardul S. Gangan, A. K. Jaiswar*, A. Pavan-Kumar, S. Jahageerdar, W. S. Lakra & Gopal Krishna

ICAR- Central Institute of Fisheries Education, Panch Marg, off Yari Road,
Versova, Andheri (West), Mumbai – 400 061, Maharashtra, India
[E mail – akjaiswar@cife.edu.in]

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Present study consists the instances of anomalies in two species of genus *Setipinna* i.e. accessory pectoral filament in *S. phasa*, (Hamilton, 1822) and absence of pelvic fin in the *S. taty* (Valenciennes, 1848), collected from east coasts of India. Comparison of twenty seven morphometric measurements and twelve meristic characters of the abnormal with normal specimens confirmed abnormality. Furthermore, genetic divergence value of mitochondrial COI and 16S rRNA confirmed that both normal and abnormal specimens belong to the respective species. These abnormalities might have occurred in early stages of development. Abnormalities have affected only morphological aspects and not growth of the fish.

[Key words: *Setipinna phasa*, *S. taty*, anomalies, environmental factors, morphometric and meristic characters]

Introduction

Any change in the normal body structure of the fish, either external or internal, is termed as abnormality. External abnormalities include growth, lesions, wounds, unusual scale patterns, changes in body colour and physical deformities such as curved spine or blindness etc¹. Internal abnormalities are observed in form of changes in the liver, the intestines, the reproductive organs, or the presence of parasites². The abnormalities also include lack of certain body part³, regeneration of fins⁴, accessory fin⁵ and absence of pelvic fin^{6, 7}. Smith *et al.*⁸ described a guide for the assessment of external and internal anomalies in Fish. Dawson⁹⁻¹¹ and Dawson and Heal¹² published the bibliography of anomalies of fishes. Several other types of anomalies have been reported by various authors like anophthalmia in *Mystus tengra*¹³, morphological irregularities in the Indian oil sardine *Sardinella longiceps*¹⁴, abnormalities in larval fishes exposed to dissolve saxitoxin¹⁵, absence of part of snout in two rays³, abnormal rays^{16, 17}, an unusual ovary in the Indian oil sardine, *Sardinella longiceps*¹⁸, abnormalities of the operculum in gillhead bream *Sparus aurata*¹⁹, an accessory fin in *Esox lucius*⁵, regenerated caudal fin in *Sardinella longiceps*²⁰, abnormal mackerel, *Rastrelliger kanagurta* from India²¹. Patten²² recorded abnormal freshwater fishes from Washington Streams. Swan²³ found double-

mouth deformity in a trout, *Salmo trutta*. Hubbs²⁴ reported elongated fins in adult individuals of *Notropis metallicus* while the frequency of occurrence of abnormalities in fishes of Georgia Estuary was reported by Dahlberg²⁵.

Setipinna phasa and *S. taty* belong to the family Engraulidae (Clupeiforme). *S. phasa* is distributed in the Ganges system, from diamond harbour on the Hooghly to Allahabad on the Ganges, perhaps further also in the rivers and estuaries of Odisha while *S. taty* is distributed along the entire Bay of Bengal, India²⁶. The species of *Setipinna* are known as hairfin anchovy because of their hair like first ray of pectoral fin²⁷. Both the species show wide tolerating to salinity²⁸. During a taxonomic study on engraulids of India, abnormal specimens of *S. phasa* and *S. taty* were recorded from east coast. The taxonomic details of both the specimens are reported in this communication.

Materials and Methods

Specimens of two abnormal *Setipinna* species were collected along the coast of West Bengal.(Fig. 1).

The abnormal specimen of *S. phasa* (222.50 mm in standard length) were collected from Diamond harbor (22° 11' N; 88° 14'E) on 20th November 2014, having accessory pectoral filament and *S. taty* (120.05 mm in standard length) from Digha (21.68°N 87.55°E) on

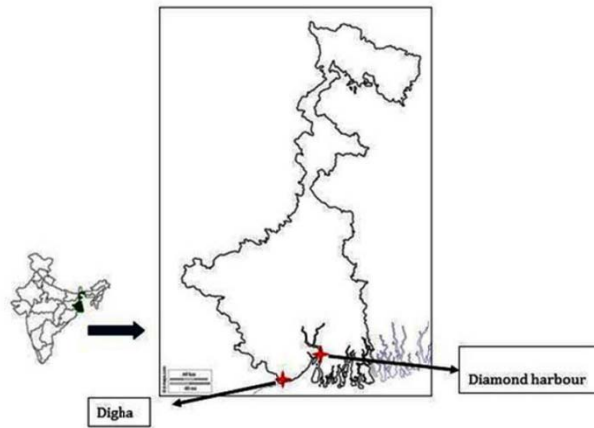


Fig 1 Study area map Diamond harbor and Digha landing centres of West Bengal.

Fig. 1 — Study area map Diamond harbor and Digha landing centres of West Bengal

17th November 2014 that lacked pelvic fins. The specimens were preserved in the museum of ICAR-Central Institute of Fisheries Education, Mumbai, India. During the present study thirty normal specimens each of *S. phasa* and *S. taty* were also studied for comparison. The specimens were identified and differentiated based on the description given by different authors²⁸⁻³⁴. The morphometric measurements and meristic characters were measured and counted, respectively³⁵ following standard procedures. A total of twenty seven morphometric measurements and eight meristic characters were compared between the normal and deformed specimens. Similarly, six characters proportional to head length and twenty one characters proportional to the standard length were compared to know the difference between normal and abnormal specimens, if any (Table 1).

Total genomic DNA was isolated from the caudal fin of normal and abnormal specimens using phenol-chloroform method³⁵. Mitochondrial cytochrome *c* oxidase subunit (COI) and 16S rRNA partial genes were amplified using reported primers^{36, 37, 38}. PCR was performed in the 25 μ l reaction volume containing 100 ng template DNA, 10 pmol of each specific primer, 200 μ M of each dNTPs, 1.0 units of Taq DNA polymerase and 1xTaq buffer containing 1.5 mM MgCl₂. The thermocycler was programmed for initial denaturation at 94 °C for 4 min, followed by 35 cycles of 94 °C for 30 sec, annealing temperature specific to the primer pair 54 °C for 30 sec, 72 °C for 30 sec for denaturation, annealing and extension, with final extension at 72 °C for 10 min. The amplicons

were purified and sequenced commercially using PCR primers (Xcelaris lab, Ahemadabad, India). Genetic distance values and Neighbor-Joining tree were constructed using MEGA7 software³⁹.

Results

Analysis of morphometric and meristic characters of all specimens of both the species confirmed that specimens belong to *S. phasa* and *S. taty*. In the abnormal specimen of *S. phasa*, there were two filaments; inner one was shorter than outer, instead of one at the right side (Fig. 2, 3), while the abnormal specimen of *S. taty* lacked pelvic fin (Fig. 4, 5).

The morphometric ratios of standard length to pectoral fin base length were considerably high on the right side of the abnormal specimen of *S. phasa* than normal (Table 1). The abnormal specimens of *S. taty* did not show any sign of external thickening, sign or scar of any injury in the pelvic area; the region was covered with normal scales (Fig. 5). There was no scar of any injury too. The meristic characters of abnormal specimens of both the species revealed counts within the range of the normal specimens (Table 2). For Further confirmation, Mitochondrial COI (550 bp) and 16S rRNA (500bp) sequences were analyzed for pairwise genetic distance values. Both the genes showed very low divergence (0.000-0.005) between normal and abnormal specimens (Table. 3). The Neighbor Joining (NJ) tree showed conspecific clustering of abnormal specimens with normal specimens with significant bootstrap for both the genes (Fig. 6) indicating similar genetic makeup of normal and abnormal specimens.

Discussion

Many reasons have been sighted for developing abnormalities in aquatic organisms including fishes⁴⁰. The abnormalities observed in the specimen of *S. phasa* might have arisen from an unusual development of the muscle buds during the early embryonic period. A similar abnormality was observed as accessory pectoral fin in *Esox lucius*⁵. The combined pelvic and anal fins was recorded in *Notropis metallicus* that has resulted in slower swimming and jerky movements²⁴.

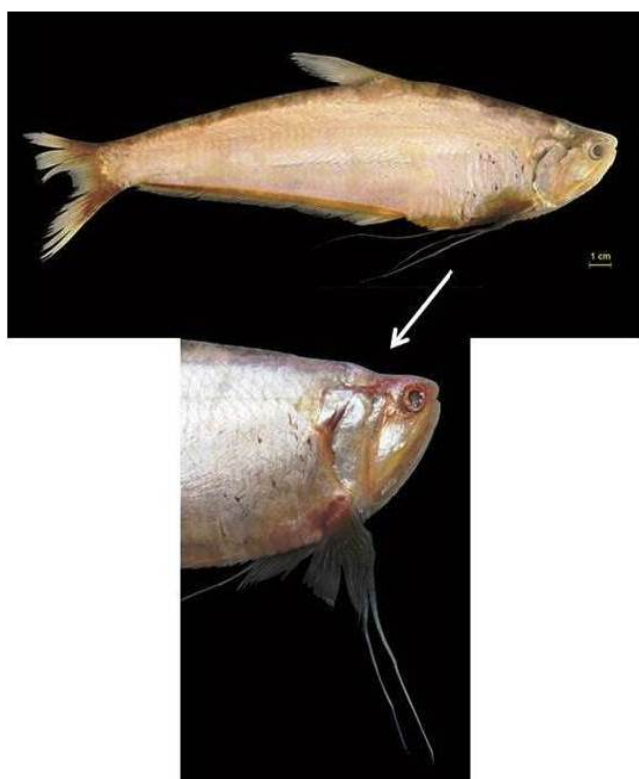
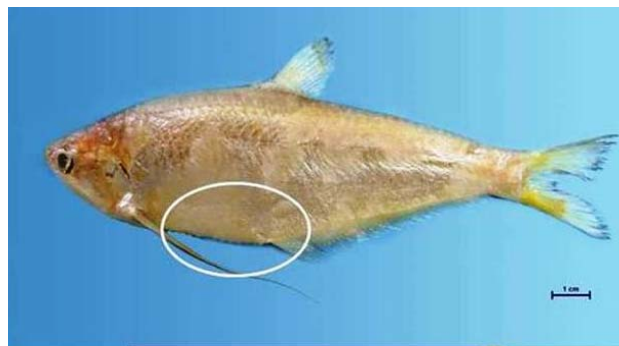
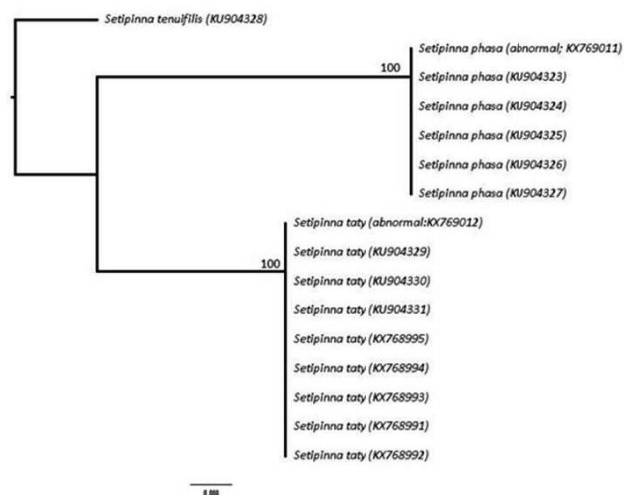
Absence of paired fins have been reported in clupeid *Brevoortia patronus* from Gulf of Menhaden⁴¹; absence of pelvic fin in *Thrissina baelama*⁴², *Brevoortia smithi*⁴³, Atlantic menhaden *Brevoortia tyrannus*⁴⁴, rainbow sardine *Dussumieria*

Table 1 — Biometric data of *S. taty* and *S. phasa* specimens collected from Diamond harbour and Digba fish landing centre, West Bengal, India.

	Abnormal specimen of <i>S. taty</i> mm	Normal specimen <i>S. taty</i> (n = 30) Range (mm)	Mean±SD	Abnormal specimen of <i>S. phasa</i> mm	Normal specimen <i>S. phasa</i> (n = 30) Range (mm)	Mean SD
In % of HL						
Snout length	16.35	16.49-19.65	17.66±0.86	14.89	13.55-17.40	15.68±0.98
Post orbital head length	59.45	56.56-60.73	58.44±1.18	68.91	62.39-66.76	65.16±1.24
Inter orbital width	34.12	29.28-35.15	32.57±1.66	28.73	28.35-30.92	29.59±0.78
Eye diameter	26.75	25.40-28.10	26.60±0.57	18.25	18.09-22.32	19.96±1.04
Upper jaw length	88.09	86.47-93.18	90.22±1.87	84.98	81.08-89.43	85.11±2.22
Lower jaw length	78.95	78.08-84.51	81.02±1.98	76.19	72.13-81.18	76.36±2.51
In % of SL						
Head length	19.31	18.40-19.47	18.93±0.30	16.72	15.63-17.20	15.68±0.98
Dorsal fin base length	9.54	8.92-9.77	9.45±0.22	7.63	7.23-8.19	7.71±0.30
Anal fin base length	46.51	43.91-48.46	46.02±0.94	55.03	53.07-57.09	54.64±1.06
Pelvic fin base length	Absent	1.66-1.93	1.76±0.08	1.41	1.23-1.58	1.40±0.09
Pelvic fin length	Absent	7.25-7.82	7.47±0.13	6.80	6.24-6.98	6.59±0.19
Pectoral fin base length (Left)	4.26	3.97-4.36	4.23±0.11	4.68	4.25-4.90	4.57±0.15
Pectoral filament length (Left)	66.81	63.22-72.60	67.80±1.91	40.06	42.00-51.03	46.20±2.25
Length of second ray of pectoral fin (Left)	17.15	18.05-20.30	18.99±0.60	17.63	17.61-20.76	19.37±0.81
Pectoral fin base length (Right)	NA	NA	NA	4.85	3.86-6.4	4.64±0.52
Pectoral filament length (Right)	NA	NA	NA	46.97	42.54-78.23	48.46±8.33
Second pectoral filament length (Right)	Absent	Absent	Absent	34.19	Absent	Absent
Length of third ray of pectoral fin (Right)	NA	NA	NA	19.68	17.19-30.32	20.19±2.87
Distance between tip of snout to dorsal fin	47.56	44.88-49.41	46.79±1.13	45.20	42.52-46.02	44.39±0.83
Distance between tip of snout to anal fin	49.99	48.89-53.08	51.53±0.91	41.82	39.56-44.15	41.51±1.17
Distance between tip of snout to pelvic fin	Absent	32.78-37.04	35.15±0.86	33.39	29.69-33.81	31.39±1.06
Distance between tip of snout to pectoral fin	19.83	18.84-21.02	20.18±0.55	17.60	16.54-18.78	17.57±0.55
Distance between origin anal fin to origin of dorsal fin	34.11	32.34-33.98	33.26±0.44	28.59	25.76-30.02	27.60±1.07
Maximum body depth	33.88	31.55-33.60	32.75±0.49	27.81	25.25-29.26	26.94±0.97
Distance between origin of pectoral fin to origin of pelvic fin	absent	14.19-16.28	15.24±0.56	16.41	13.79-16.54	15.01±0.66
Distance between origin of pectoral fin to origin of anal fin	50.29	27.91-33.23	31.18±1.19	26.47	24.34-28.79	26.29±1.00
Distance between origin of pelvic fin to the origin of anal fin	absent	15.45-17.79	16.65±0.52	10.75	9.31-13.31	11.71±

*acuta*⁴⁵ and significantly less number of scutes than the normal specimen was observed in *Thryssa malabarica*⁴⁶. Patten²² reported fused pelvic, absence of one pelvic

fin, degenerate pelvic, abnormalities in vertebrae, caudal fin, anal fin, head and body in freshwater fishes of Washington streams. He opined that the

Fig. 2 — Normal *S. phasa* (with single pectoral filament on side).Fig.3 — Abnormal *S. phasa* (with two pectoral filament on right side)Fig.4 — Normal *S. taty* (with pelvic fin).Fig. 5 — Abnormal *S. taty* (without pelvic fin)Fig. 6 — NJ tree of *Setipinna* species using 16S rDNA gene.

abnormalities were the result of electro fishing or some disturbances in early development stages. A wide range of physical, chemical and biological factors may cause body anomalies of different types in the fish species, in natural and reared conditions⁴⁷. The cause of these abnormalities also due to be exposure of the fishes to various kinds of pollutants (chemical/thermal) during the early developmental stages. Hence in recent times, the instances and reports on abnormalities are appearing very frequently, probably a result of increasing anthropogenic activities in the aquatic ecosystems.

Table 2 — Meristic counts for normal and abnormal fishes collected from Diamond harbor and Digba landing centres of West Bengal, India.

Meristic characters	Abnormal Specimen of <i>S. taty</i>	Normal specimen <i>S. taty</i> (n = 30)	Abnormal Specimen of <i>S. phasa</i>	Normal specimen of <i>S. phasa</i> (n = 30)
Pre pelvic keeled scutes	NA	21-24	16	14-15
Post pelvic keeled scutes	NA	10-13	6	6-7
Total keeled scutes	34	31-37	22	20-22
Pectoral filaments (Left)	1	1	1	1
Pectoral filaments (Right)	1	1	2	1
Unbranched + anal fin rays	iii 51	iii 48-56	iii 75	iii 69-76
Pectoral filament (Left) reaches to the anal fin rays	41	37-53	25	18-38
Lower gill rakers	19	17-19	18	18-19

Table 3 — Genetic distance values (Kimura 2 Parameter model) for COI and 16S rRNA genes of *Setipinna* species

Specimen code		SPA	SP1	SP2	SP3	SP4	STA	ST1	ST2	ST3	ST4	ST5	STF
SPA	<i>S. phasa</i> (abnormal)		0.000	0.000	0.000	0.000	0.097	0.097	0.097	0.097	0.097	0.097	0.092
SP1	<i>S. phasa</i> 1	0.005		0.000	0.000	0.000	0.097	0.097	0.097	0.097	0.097	0.097	0.092
SP2	<i>S. phasa</i> 2	0.000	0.005		0.000	0.000	0.097	0.097	0.097	0.097	0.097	0.097	0.092
SP3	<i>S. phasa</i> 3	0.000	0.005	0.000		0.000	0.097	0.097	0.097	0.097	0.097	0.097	0.092
SP4	<i>S. phasa</i> 4	0.000	0.005	0.000	0.000		0.097	0.097	0.097	0.097	0.097	0.097	0.092
STA	<i>S. taty</i> (abnormal)	0.207	0.205	0.207	0.207	0.207		0.000	0.000	0.000	0.000	0.000	0.068
ST1	<i>S. taty</i> 1	0.200	0.198	0.200	0.200	0.200	0.005		0.000	0.000	0.000	0.000	0.068
ST2	<i>S. taty</i> 2	0.200	0.198	0.200	0.200	0.200	0.005	0.000		0.000	0.000	0.000	0.068
ST3	<i>S. taty</i> 3	0.200	0.198	0.200	0.200	0.200	0.005	0.000	0.000		0.000	0.000	0.068
ST4	<i>S. taty</i> 4	0.200	0.198	0.200	0.200	0.200	0.005	0.000	0.000	0.000		0.000	0.068
ST5	<i>S. taty</i> 5	0.200	0.198	0.200	0.200	0.200	0.005	0.000	0.000	0.000	0.000		0.068
STF	<i>S. tenuifilis</i>	0.201	0.201	0.201	0.201	0.201	0.184	0.180	0.180	0.180	0.180	0.180	

Conclusion

The accessory pectoral filament in *S. phasa* is probably due to the unusual development of the muscle buds during the early embryonic stages. Absence of paired pelvic fin in *S. taty* may be the anthropogenic disturbance, possibly the pollutants, in early stages of development. Since *S. taty* is not a migratory and probable schooling fish and the absence of pelvic fin may not affect its survival as the juveniles sustained subsequently. However, the abnormality in both the species did not affect the overall growth and development. Morphological and molecular investigations confirmed that the characters found to be different in two specimens, from the normal specimens, do not indicate new species.

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