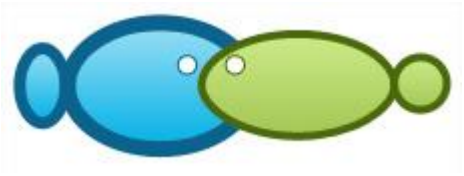

First record of *Corica soborna* in the downstream Mahakam River, East Kalimantan, Indonesia, based on morphological and molecular evidence

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Abstract. The Ganges river sprat (*Corica soborna*) is a freshwater fish of economic value, belonging to the Clupeidae family and Clupeiformes order. This species is primarily distributed across India and Southeast Asia, inhabiting downstream river areas, estuaries, and coastal waters. In Indonesia, *C. soborna* has only been reported in the lower Musi River (South Sumatra), the Kapuas River, Padang Tikar, and Pemangkat (West Kalimantan). However, prior to this study, the presence of *C. soborna* in the downstream Mahakam River, East Kalimantan, had not been documented. This study aimed to identify and verify fish specimens suspected to be *C. soborna* from the downstream Mahakam River, East Kalimantan, Indonesia based on morphological and molecular characteristics. Fish specimens resembling *C. soborna* were collected from a local fisherman in the downstream Mahakam River at Muara Sanga Sanga Village, Samarinda City, East Kalimantan, Indonesia. Laboratory identification was conducted through morphometric and meristic analysis, as well as COI gene sequencing followed by nucleotide BLAST comparison with GenBank. Three specimens were collected, with total lengths ranging from 49.55 to 51.11 mm. Morphometric comparisons between Mahakam River specimens and a reference specimen (*C. soborna* NHM.OUF-993) from India showed minor differences in body depth, pre-dorsal length and head width among the 21 characters measured. Meanwhile, the 13 meristic characters showed no significant variation. Molecular identification based on a 642 bp fragment of the COI gene revealed 97% identity and maximum score of 1.066 with *C. soborna* from Bangladesh (GenBank accession no. MK572140). The integration of morphometric, meristic, and molecular data confirms that the fish specimens from the Downstream Mahakam River are indeed *C. soborna*, establishing a new distributional record for this species in East Kalimantan.
Key Words: Clupeidae, COI gene, identification, morphometric, meristic.

Introduction. The Mahakam River in East Kalimantan is considered as one of the most important freshwater systems in Indonesia, sustaining high ichthyofaunal diversity that includes both endemic and migratory fish species (Christensen 1992; Kottelat et al 1995; Jusmaldi et al 2019; Jusmaldi et al 2025). Ichthyological studies in the downstream areas of the Mahakam, however, have been sparse, focusing mostly on economically important or larger species (Suyatna et al 2010; Suyatna et al 2017). This has resulted in a lack of coverage in region-specific checklists for some important species, like clupeids, despite their significant role as forage fish in trophic webs (Hunnam 2021).

The Ganges river sprat, *Corica soborna* (Hamilton, 1822) is among the less documented species, primarily known from the Ganges-Brahmaputra River systems as well as the brackish-freshwater transitional zones of Bangladesh, northeastern India, and Myanmar, with additional records from the Bharathapuzha River in Kerala, as well as from Malaysia, Singapore and Indonesia, in Southeast Asia (Whitehead 1985; Kottelat 2013; Prasad et al 2020).

This small clupeid fish has been studied in terms of its local fishery importance and ecological role in South Asian countries (Khatun et al 2022; Kabir & Rabbane 2021). In Indonesian waters, *C. soborna* has been reported in the downstream Musi River in South Sumatra, Padang Tikar, Pemangkat, and the Kapuas River in West Kalimantan (Whitehead 1967). Meanwhile, information regarding the presence of *C. soborna* in the

Mahakam River, East Kalimantan, has never been reported (Kottelat 1995; Suyatna et al 2017; Jusmaldi et al 2019; Jusmaldi et al 2025).

One type of fish caught by fishermen in the downstream area of the Mahakam River, East Kalimantan, is locally known as lurai fish or river anchovy (a clupeid species). It is consumed for its savory flesh, but does not contribute significantly to commercial fisheries due to its small size and lack of market attention. Therefore, research reports on the valid identity and biological aspects of the lurai fish from downstream the Mahakam River are still unknown (Jusmaldi et al 2023).

The difficulty in identifying clupeid species morphologically stems from overlapping meristic counts, ontogenetic variation, and morphological convergence (Stern et al 2016). As a result, modern taxonomic research shifts more often to integrative methods that combine traditional morphometrics and molecular analyses (Ergüden & Turan 2005). Traditional morphometric and meristic analyses continue to play a crucial role in fish taxonomy, particularly in regions with rich but understudied biodiversity. These methods, which include precise measurements of body structures and counts of anatomical features such as fin rays and scales, are widely used to distinguish between morphologically similar species or to detect intraspecific variation (Muchlisin 2013). Furthermore, complex or ambiguously morphologically characterized groups have become easier to identify with DNA barcoding of mitochondrial cytochrome oxidase I (COI) sequences (Hebert et al 2003; Ward et al 2005).

This research was initiated following the collection of several clupeid specimens, locally known as lurai fish, from fishermen in the downstream Mahakam River, which exhibited morphological resemblance to *C. soborna*. Initial morphological traits, including body shape, fin ray counts, scale counts, scute counts, and finlets suggested alignment with the genus *Corica*, but species-level identification needed molecular validation. Previous ichthyological surveys in this region are known to avoid using molecular techniques, which poses a significant obstacle in terms of our taxonomic knowledge (Suyatna et al 2017).

This study aimed to confirm the presence of *C. soborna* in the Mahakam River, East Kalimantan, through an integrative approach combining morphological diagnostics and DNA barcoding. By comparing COI sequences from Mahakam specimens with reference data from GenBank, the study evaluates genetic divergence to verify species identity and potentially establish a new distributional record for East Kalimantan. This research addresses a critical biogeographical gap in Southeast Asian freshwater ichthyofauna and provides essential baseline data for biodiversity conservation and sustainable resource management in the region.

Material and Method

Study area and sample collection. During ichthyological surveys in September 2024, three fish specimens resembling *C. soborna* were collected from a local fisherman in the downstream Mahakam River at Muara Sanga Sanga Village (S 00°36’34.76”, E 117°17’49.44”), Samarinda City, East Kalimantan, Indonesia (Figure 1). Fish samples were photographed using a digital camera to document their fresh coloration before fixation. After photographing, one specimen was preserved in 96% ethanol for molecular analysis, while the remaining two were fixed in 5% formalin for morphological examination. In the laboratory, a muscle tissue sample was aseptically excised from the ethanol-preserved specimen, transferred into a labeled cryovial, and stored at - 20°C for subsequent DNA extraction. All specimens, including those preserved in ethanol and formalin, were cataloged and deposited as voucher material at the Ecology and Animal Systematics Laboratory, Faculty of Mathematics and Natural Sciences, Mulawarman University, Samarinda City, Indonesia (Voucher Codes: EAS-MSC_UNMUL_ CS01–03).

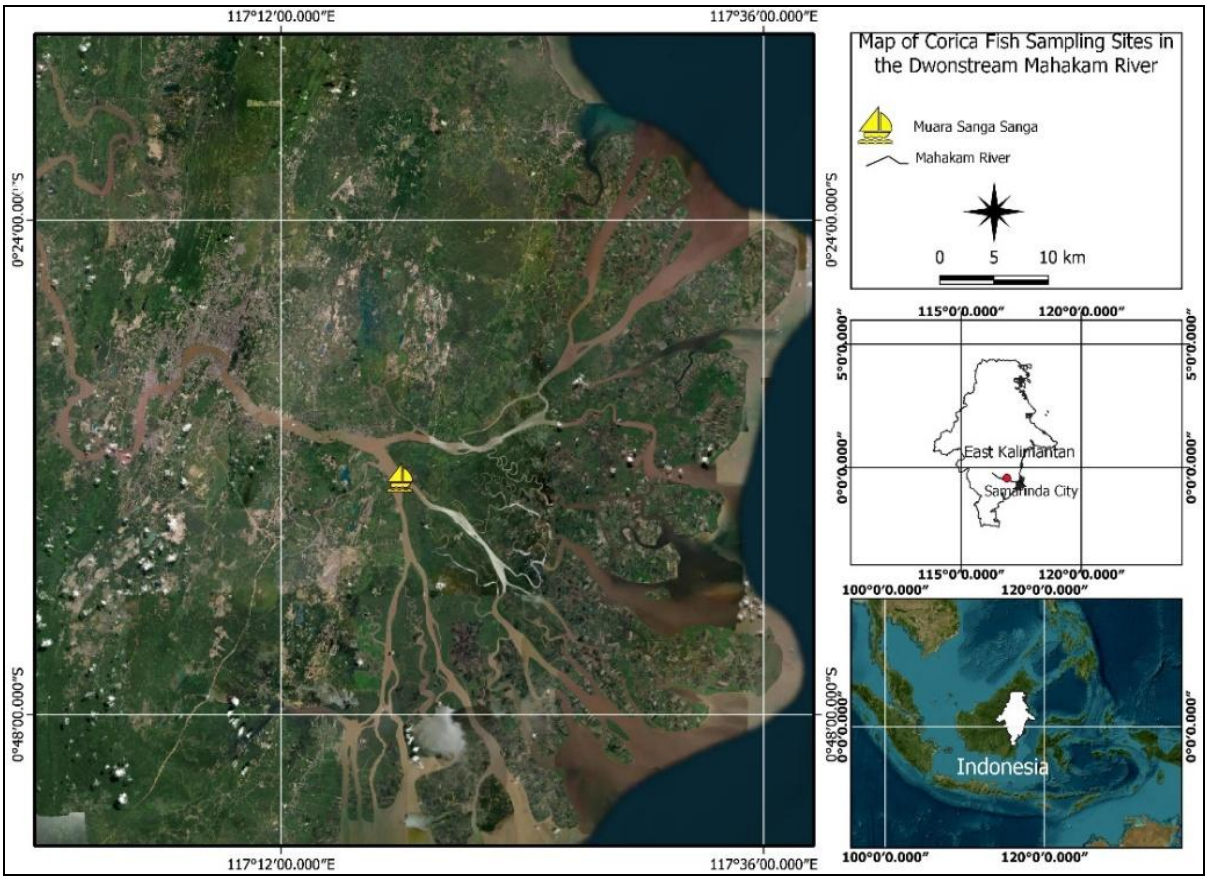

Figure 1. Sampling locations of resembling *Corica soborna* in the downstream Mahakam River, East Kalimantan, Indonesia.

Morphological measurements and identification. Morphological identification was conducted using standard taxonomic keys for clupeid fishes (Whitehead 1985) and (Munroe et al 1999). Each specimen (CS01-CS03) was subjected to a series of morphometric and meristic measurements based on Prasad et al (2020) methods. Morphometric measurements were taken using a digital caliper with a precision of 0.01 mm, including 21 morphometric characters (Figure 2). Thirteen meristic characters were assessed by counting key anatomical features, such as fin rays, scales, scutes, and finlets (Figure 3). All measurements followed standard ichthyological procedures under consistent positioning and preservation conditions.

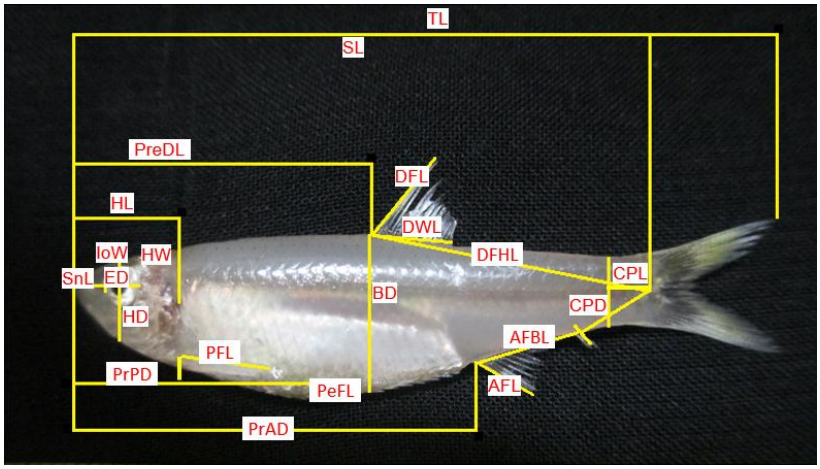

Figure 2. Morphometric measurements of resembling *Corica soborna* from the downstream Mahakam River, East Kalimantan, Indonesia.

The description of the abbreviations from Figure 2 are as follows: TL (Total Length) represents the distance from the tip of the snout to the end of the caudal fin); SL (Standard Length) is the distance from the tip of the snout to the base of the caudal fin (caudal peduncle); PreDL (Predorsal Length) is the distance from the tip of the snout to the origin of the dorsal fin; HL (Head Length) is the distance from the tip of the snout to the posterior edge of the operculum; SnL (Snout Length) is the distance from the tip of the snout to the anterior margin of the eye; ED (Eye Diameter)is the horizontal distance across the eye; IoW (Interorbital Width) is the distance between the upper margins of the orbits (eyes); HW (Head Width) is the maximum width of the head; HD (Head Depth) is the maximum vertical depth of the head; PFL (Pectoral Fin Length) is the length of the longest ray of the pectoral fin; PeFL (Pelvic Fin Length) is the length of the longest ray of the pelvic fin; PrPD (Prepelvic Distance) is the distance from the tip of the snout to the origin of the pelvic fin; PrAD (Preanal Distance) is the distance from the tip of the snout to the origin of the anal fin; DFL (Dorsal Fin Length) is the length of the base of the dorsal fin; DWL (Dorsal Fin Width) is the length of the longest ray of the dorsal fin; DFHL (Dorsal Fin Height Length) is the maximum height of the dorsal fin; BD (Body Depth) represents the greatest vertical depth of the body; AFBL (Anal Fin Base Length) is the length of the base of the anal fin; AFL (Anal Fin Length) is the length of the longest ray of the anal fin; CPD (Caudal Peduncle Depth) is the vertical depth of the caudal peduncle; and CPL (Caudal Peduncle Length) is the horizontal distance from the posterior end of the anal fin base to the base of the caudal fin.

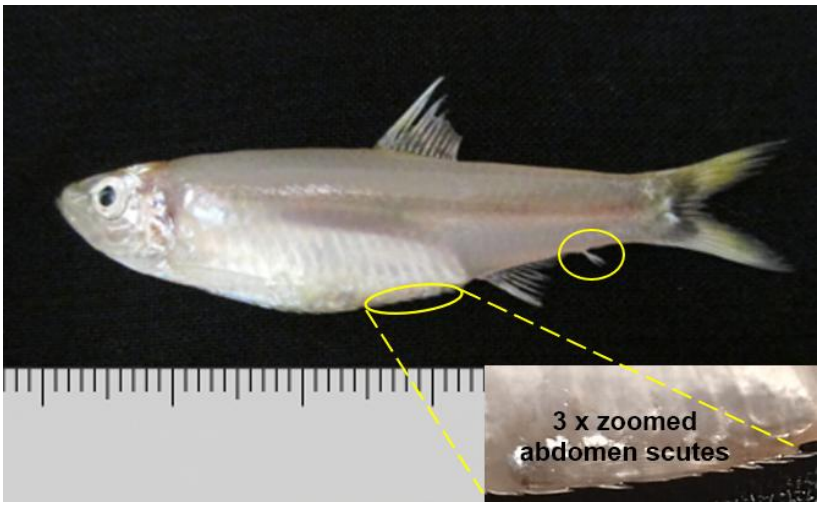

Figure 3. Meristic counts of resembling *Corica soborna* from the downstream Mahakam River, East Kalimantan, Indonesia.

To confirm the species identity, the morphometric and meristic data obtained in this study were compared with reference values from published descriptions of *C. soborna*. Morphometric characters were standardized by expressing them as percentages of standard length (SL) and head length (HL), thereby minimizing the impact of size variation among individuals.

Molecular identification. Genomic DNA was extracted from muscle tissue (specimen CS01) using the QIAGEN DNeasy Blood & Tissue Kit, adhering to the manufacturer's guidelines, under sterile conditions. DNA quality and concentration were evaluated using a NanoDrop™ spectrophotometer. Subsequently, a 658 bp fragment of the cytochrome c oxidase subunit I (COI) gene, located at the 5' region, was amplified through PCR with the primer set FishF1 (5'-TCAACCAACCACAAAGACATTGGCAC-3') and FishR1 (5'-TAGACTTCTGGGTGGCCAAAGAATCA-3') (Ward et al 2005).

PCR reactions were prepared in a total volume of 25 µL, consisting of 23 µL of PCR Master Mix and 2 µL of DNA template, and homogenized by brief centrifugation for 30 seconds. Amplification was conducted in an ASTEC GeneAtlas Thermal Cycler (Astec Co. Ltd.) using a mixture containing 12.5 µL of Taq polymerase, 8.5 µL of ultrapure water,

and 1 µL of each of the forward and reverse primers. The thermal cycling profile comprised an initial denaturation at 95°C for 1 minute, followed by 35 cycles of denaturation at 95°C for 15 seconds, annealing at 55°C for 15 seconds, and extension at 72°C for 30 seconds. A final extension step was performed at 72°C for 3 minutes, after which the reaction was held at 6°C for 6 minutes. PCR amplicons were checked on 1% agarose gels, purified with the PureLink™ PCR purification kit, and sequenced at First BASE Laboratories (Malaysia) using the ABI PRISM 3730xl Genetic Analyzer with BigDye® Terminator v3.1 chemistry

The results of the nucleotide sequences were then manually edited using BioEdit software based on a chromatogram (Alzohairy 2011). The edited nucleotide sequences were then aligned using Clustal W in the MEGA X software (Molecular Evolutionary Genetics Analysis) (Kumar et al 2018). The resulting sequences were analyzed using BLASTn with a ≥97% identity and query coverage threshold, and the verified sequence was submitted to GenBank (NCBI accession code OR607963) via the Barcode Submission Tool with complete metadata and annotations.

To validate molecular identification, a DNA barcoding approach was applied by constructing a Neighbor-Joining (NJ) tree using MEGA X software (Kumar et al 2018). The COI sequences from Mahakam specimens were aligned with reference sequences of *C. soborna* and closely related clupeids retrieved from GenBank. Genetic distances were calculated using the Kimura 2-parameter (K2P) model, and node support was tested with 1,000 bootstrap replicates. The NJ tree was used to assess clustering patterns and confirm species-level placement of the Mahakam specimens.

Results. Materials examined: specimen voucher EAS-MSC_UNMUL_CS01-03, from the downstream Mahakam River at Muara Sanga-Sanga Village (S 00°36’34.76”; E 117°17’49.44”), East Kalimantan, Indonesia. Key identifying features: *C. soborna* is a small clupeid species, with recorded total lengths up to 53 mm (Hossain 2017) and standard lengths around 41.6 mm (Prasad et al 2020). This species exhibits a moderately elongate, laterally compressed body, characterized by a pronounced ventral keel. The abdominal keel is equipped with 17–18 ventral scutes, usually arranged as 10–11 pre-pelvic scutes followed by 6–8 post-pelvic scutes (Hamilton 1822; Whitehead 1985; Kottelat et al 1993). This species has a terminal mouth, and the second supramaxilla is equal to or marginally longer than the maxillary blade. Teeth in the jaws are minute or entirely absent. The lower limb of the first gill arch bears 19–21 gill rakers, a feature that distinguishes *C. soborna* from the sympatric *Corica laciniata*, which possesses a greater number (23–27) and fewer predorsal bones (9 vs. 12 in *C. soborna*) (Whitehead 1985). Species of *Clupeichthys* may also have a separate anal finlet, but differ in having prominent teeth along the sides of the jaws. The dorsal fin is inserted above the pelvic fin origin and contains two simple rays followed by 12–14 branched rays. The pectoral fin has 12–13 rays, and the pelvic fin, positioned slightly anterior to the dorsal fin origin, has one simple and seven branched rays. The anal fin bears two simple and 12–13 branched rays, with the last two rays forming a distinct finlet. A deeply forked caudal fin with 18 principal rays and subtly darkened edges characterizes the species (Prasad et al 2020). Scales are small, cycloid, and the lateral line is absent. The number of scales in the lateral series ranges from 40 to 42 (Jayaram 2010). Predorsal bone counts are usually 12 (Whitehead 1985), though Kottelat (1993) recorded 9 in some material. These meristic and skeletal counts, together with the absence or minuteness of teeth, the proportionally long second supra-maxilla, and the anal finlet, form the key diagnostic combination distinguishing *C. soborna* from its congeners and closely related taxa.

The present specimen matches the general description provided by Hamilton (1822), Whitehead (1985), and Kottelat et al (1993). Minor morphological differences were observed when specimens from the downstream Mahakam River, East Kalimantan, were compared with *C. soborna* (NHM.OU.F-993) from Bangladesh, as reported by Prasad et al (2020). The observed minor variations in the morphometric characters of *C. soborna* from the downstream Mahakam River are presented in Table 1.

Table 1

Morphometric characters of *Corica soborna* from the downstream Mahakam River, East Kalimantan, Indonesia

No	*Morphometric characters*	*Specimens voucher in this study*			*Corica saborna (Prasad et al 2020)*
		CS01	*CS02*	*CS03*	
1	Total length (mm)	51.11	51.38	49.55	50.5
2	Standard length (mm)	42.11	41.90	40.59	41.6
3	Head length (mm)	9.63	9.74	9.97	9.0
	% of standard length				
4	Body depth	24.48	25.18	25.70	20.4
5	Head length	22.87	23.25	24.46	21.6
6	Head depth	16.24	16.40	16.09	16.9
7	Head width	7.70	7.68	7.64	9.2
8	Eye diameter	7.43	7.59	7.64	7.9
9	Snout length	7.12	7.09	6.80	6.4
10	Inter orbital width	5.72	5.70	6.16	4.8
11	Dorsal fin base length or dorsal fin width	14.77	15.20	15.03	14.6
12	Pre-dorsal distance	53.29	54.32	54.07	50.8
13	Dorsal fin length	19.52	19.24	19.71	19.1
14	Dorsal fin origin to hypural distance	45.52	45.70	46.93	46.2
15	Pectoral fin length	16.17	16.16	16.70	17.3
16	Pelvic fin length	13.80	13.77	13.75	13.7
17	Caudal peduncle length	12.37	12.82	12.76	11.0
18	Caudal peduncle depth	10.57	10.31	10.59	9.2
19	Pre-pelvic distance	50.84	51.50	50.04	49.0
20	Pre-anal distance	71.88	71.86	71.64	70.7
21	Anal fin base length	17.05	17.09	17.02	17.7
22	Anal fin length	12.30	12.34	12.24	12.1
	% of head length				
23	Head depth	78.03	78.53	78.09	78.3
24	Head width	41.91	41.25	40.12	42.5
25	Eye diameter	36.50	36.65	36.59	36.6
26	Snout length	30.11	30.49	29.69	29.8
27	Inter orbital width	23.71	23.54	22.57	22.2

In particular, the Mahakam River specimens exhibited a greater body depth (24.48–25.70% SL) and a longer pre-dorsal distance (53.29–54.32% SL) than the Indian specimens from the Godavari River, Bangladesh (20.4% SL and 50.8% SL, respectively), while displaying a slightly narrower head width (40.12–41.91% HL vs. 42.5% HL). Conversely, the meristic characters showed no appreciable variation (Table 2), with most counts in the Mahakam specimens falling within the range reported by *C. soborna* from Prasad et al (2020). Minor differences were observed in certain counts, such as transverse scale rows (8 vs. 9), pre-pelvic scutes (9–10 vs. 10), post-pelvic scutes (7–8 vs. 8), and dorsal or pectoral fin rays (III+12–13 vs. III+13), but these variations are within the intraspecific range typically reported for clupeid fishes.

Analysis of the partial COI gene confirmed the identity of the Mahakam specimens as *C. soborna*, with the highest BLAST matches showing 96.12–97.00% similarity to sequences from Bangladesh and other reference vouchers available in GenBank (https://www.ncbi.nlm.nih.gov/) (Table 3).

Table 2

Meristic characters of *Corica soborna* from the downstream Mahakam River, East Kalimantan, Indonesia

No	*Meristic characters*	*Specimens voucher in this study*			*Corica saborna (Prasad et al 2020)*
		CS01	*CS02*	*CS03*	
1	Scales in lateral line	41	40	40	41
2	Transverse scale rows	8	8	8	9
3	Pre pelvic scutes	10	10	9	10
4	Post pelvic scutes	8	8	7	8
5	Pre-dorsal scales	17	16	15	17
6	Pre-pelvic scales	15	13	13	14
7	Pre-anal scales	24	23	23	23
8	Dorsal fin rays	III+13	III+13	III+12	III+13
9	Pectoral fin rays	I+13	I+13	I+12	I+13
10	Pelvic fin rays	I+7	I+7	1+7	I+7
11	Anal fin rays + (finlet)	III+12+(2)	III+11+(2)	III+11+(2)	III+11+ (2)
12	Principal caudal fin rays	17	18	18	18
13	Procurrent caudal fin rays	12	12	12	12

Table 3

Identification of *Corica soborna* from the downstream Mahakam River (NCBI accession code OR607963) using COI partial gene

No	*GenBank accession number*	*Closest match according to the COI gene sequence*	*No. of bases*	*Max. score*	*% match*
1	MK572140	*C. soborna* from Bangladesh	655	1.066	97.00
2	KY124368	*C. soborna* voucher DUZM012	661	1.055	96.55
3	KX455892	*C. soborna* voucher ZMUD:012	696	1.053	96.26
4	MK572137	*C. soborna* from Bangladesh	655	1.050	96.53
5	MK572139	*C. soborna* from Bangladesh	652	1.050	96.53
6	MK572138	*C. soborna* from Bangladesh	655	1.050	96.53
7	LC823283	*C. soborna* MHBSFMSTU	655	1.044	96.37
8	KX164004	*C. soborna*	647	1.014	96.12
9	MK359875	*C. soborna* isolate bf21	615	959	96.24
10	MK777249	*Corica laciniata* voucher DOS05827	400	686	97.74

The highest sequence similarity (97.00%) was obtained with *C. soborna* from the Godavari River, Bangladesh (GenBank accession MK572140), showing high alignment coverage (655 bp) and a maximum score of 1.066. Slightly lower similarities (96.12–96.55%) were observed with other *C. soborna* sequences, whereas one close match (97.74%) corresponded to *Corica laciniata* (MK777249) but with lower alignment coverage (400 bp) and a maximum score of 686. The neighbor-joining tree based on COI sequences (Figure 4) clustered the Mahakam specimens with reference *C. soborna* sequences from Bangladesh and India, supported by high bootstrap values (>95%). The Mahakam clade was distinct yet closely allied with South Asian sequences, suggesting either recent divergence or historical gene flow within the species' biogeographic range.

Field observations indicated that *C. soborna* in the downstream Mahakam River primarily occupied vegetated river margins with muddy substrates. Physico-chemical measurements at capture sites recorded dissolved oxygen (DO) levels of 3.70–4.17 mg L^{-1}, pH of 6.68–6.96, water temperature of 27.50–28.40°C, total dissolved solids (TDS) of 50–80 mg L^{-1}, water transparency of 19–29 cm, depths of 2.80–3.60 m, and current velocities of 0.65–1.07 m s^{-1}. Riparian vegetation along the left bank comprised a mosaic of shrubs and scattered trees dominated by *Ficus racemosa*, *Barringtonia acutangula*, and *Syzygium* spp., interspersed with tall grasses (*Saccharum spontaneum*) and aquatic

creepers (*Ipomoea aquatica*). This vegetation assemblage typifies a freshwater riparian community adapted to periodic inundation and fluctuating water levels in lower river reaches. The associated fish fauna included *Arius maculatus*, *Leiognathus equulus*, *Ambassis* sp., *Stolephorus* sp., *Toxotes jaculatrix*, and *Paraplotosus* sp., reflecting a mixture of freshwater and euryhaline species characteristic of transitional riverine–estuarine habitats.

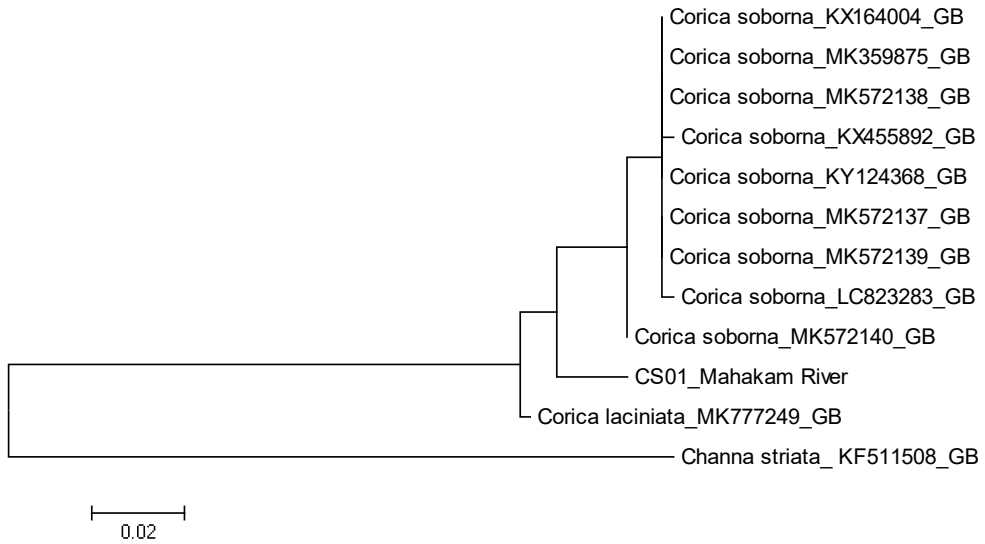

Figure 4. Neighbor-joining phylogenetic tree based on COI gene sequences showing the placement of CS01_Mahakam River relative to reference taxa.

Discussion. Deviations in body depth, pre-dorsal length, and head width indicate morphological plasticity in response to local environmental pressures (Table 1), whereas a range of slight differences in meristic counts, particularly in the transverse scale rows (Table 2), fall within the common variation observed in clupeid fishes, which are widely documented to show intraspecific meristic variability and environmentally induced, such as scale row counts across populations in response to environmental gradients like temperature, chlorophyll-a, pH, and dissolved oxygen (Sartimbul et al 2018; Stroganov et al 2021). These morphometric shifts may reflect ecomorphological adaptation to the ecohydraulic conditions of the Mahakam River, which is characterized by complex flow regimes, seasonal flooding, and high sediment loads (Jusmaldi et al 2023). Increased body depth can improve maneuverability and stability in lentic or turbid habitats (Langerhans 2008; Franssen et al 2013), whereas an elongated pre-dorsal region may contribute to enhanced propulsion efficiency under variable flow velocities (Norton 1995). The invariance of meristic traits supports the idea that environmental pressures more readily influence morphometric plasticity than genetically constrained meristic features (Swain et al 2005).

Molecular identification based on partial COI sequences (Table 3) corroborates the morphological assignment. The highest BLAST match (97.00%) was to *C. soborna* from Bangladesh (GenBank: MK572140), with high alignment coverage (655 bp) and maximum score (1.066). Slightly lower matches (96.12–96.55%) were obtained with other *C. soborna* accessions, while a close match (97.74%) to *Corica laciniata* (MK777249) exhibited lower alignment coverage (400 bp), suggesting conserved COI sequence motifs within the genus. Phylogenetic reconstruction using the Neighbor-Joining method (Figure 4) placed the Mahakam River specimen (CS01) within the *C. soborna* clade, distinctly separated from *Corica laciniata*, reinforcing species-level identification.

The congruence between morphological variation and molecular identity supports the hypothesis that the Mahakam River population represents *C. soborna* exhibiting localized morphological adaptation without significant genetic divergence at the COI locus. This pattern aligns with observations in other small clupeid fishes, where habitat-driven morphometric plasticity occurs despite high mitochondrial sequence conservation

(Ward et al 2005; Hubert et al 2008). The findings emphasize the utility of integrating morphometric and DNA barcoding methods for detecting fine-scale population differences and assessing adaptive responses in isolated freshwater fish populations.

Morphometric, meristic, and COI barcode analyses confirmed the downstream Mahakam River population as *C. soborna*, with body shape variation reflecting ecohydraulic adaptation rather than genetic divergence. Increased body depth and pre-dorsal length likely enhance swimming performance in turbid, variable-flow habitats, while stable meristic traits indicate genetic constraint. The high COI sequence similarity with Bangladesh populations suggests rapid phenotypic plasticity in response to environmental pressures, highlighting the importance of integrating morphological and molecular approaches to evaluate habitat-driven variation and inform freshwater fish conservation. The occurrence of *C. soborna* in the Mahakam River constitutes a new species record for the river system in East Kalimantan, providing novel ichthyofaunal data for the region.

Conclusions. This study provides the first confirmed record of *C. soborna* from the Mahakam River, East Kalimantan, Indonesia. An integrative approach combining morphometric, meristic, and mitochondrial COI barcode analyses verified species identity. Morphological variation in body depth, pre-dorsal length, and head width suggests ecohydraulic adaptation to local flow regimes and habitat conditions, whereas the stability of meristic traits indicates underlying genetic constraints. The high COI sequence similarity (97%) to Bangladesh populations supports the occurrence of phenotypic plasticity under differing environmental pressures. These findings extend the known biogeographic distribution of *C. soborna* and underscore the ecological role of large tropical rivers as dispersal corridors for clupeid fishes.

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Conflict of interest. The authors declare that there is no conflict of interest.

References

Alzohairy A. M., 2011 BioEdit: An important software for molecular biology. GERF Bulletin of Biosciences 2(1):60-61.

Christensen M. S., 1992 Investigations on the ecology and fish fauna of the Mahakam River in East Kalimantan (Borneo) Indonesia. International Review of Hydrobiology 77(4):593-608.

Ergüden D., Turan C., 2005 Examination of genetic and morphologic structure of sea-bass (*Dicentrarchus labrax* L., 1758) populations in Turkish coastal waters. Turkish Journal of Veterinary and Animal Sciences 29(3):727-733.

Franssen N. R., Stewart L. K., Schaefer J. F., 2013 Morphological divergence and flow-induced phenotypic plasticity in a native fish from anthropogenically altered stream habitats. Ecology and Evolution 3(14):4648-4657.

Hamilton F., 1822 An account of the fishes found in the River Ganges and its branches. Archibald Constable and Company, Edinburg, 405 p.

Hebert P. D. N., Cywinska A., Ball S. L., deWaard J. R., 2003 Biological identifications through DNA barcodes. Proceedings of the Royal Society B: Biological Sciences 270(1512):313-321.

Hossain M. Y., Hossen M. A., Nawer F., Khatun D., Pramanik M. N. U., Parvin M. F., Yahya K., 2017 New maximum size records and length–weight relationships for two species, *Corica soborna* (Hamilton, 1822) and *Mystus bleekeri* (Day, 1877), from the Ganges River (NW Bangladesh). Journal of Applied Ichthyology 33(6):1-2.

Hubert N., Hanner R., Holm E., Mandrak N. E., Taylor E., Burridge M., Watkinson D., Dumont P., Curry A., Bentzen P., Zhang J., April J., Bernatchez L., 2008 Identifying Canadian freshwater fishes through DNA barcodes. *PLoS ONE* 3(6):e2490.
Hunnam K., 2021 The biology and ecology of tropical marine sardine. Reviews in Fish Biology and Fisheries 31(3):405-435.
Jayaram K. C., 2010 The freshwater fishes of the Indian region. 2nd Edition, Narendra Publishing House, Delhi, 616 p.
Jusmaldi, Hariani N., Doq N., 2019 [Diversity, potentiality, and conservation status of fish fauna in the upper Mahakam's tributaries, East Kalimantan]. Jurnal Iktiologi Indonesia 19(3):391-410. [in Indonesian]
Jusmaldi, Nuramelia N., Arif M. F., Hendra M., Rukmi D. S., Rosadi I., 2023 [Biological aspects and habitat of lurai fish (*Corica soborna* Hamilton, 1822) from the Lower Mahakam River, East Kalimantan]. Berita Biologi 22(3):343-356. [in Indonesian]
Jusmaldi, Savira H., Hariani N., 2025 [Diversity and conservation status of ichthyofauna in the Mahakam River, Long Iram District, East Kalimantan]. Berita Biologi 24(1):171-186. [in Indonesian]
Kabir M. A., Rabbane M. G., 2021 Genetic diversity of Ganges River sprat, *Corica soborna*, from Kaptai Lake and Kirtankhola River in Bangladesh. Fisheries & Aquatic Life 29(4):239-245.
Khatun D., Hossain M. Y., Hossain M. F., Mawa Z., Rahman M. A., Hasan M. R., Islam M. A., Rahman M. A., Hassan H. U., Sikha S. N., 2022 Population parameters of a freshwater clupeid, *Corica soborna* (Hamilton, 1822) from the Ganges River, Northwestern Bangladesh. Pakistan Journal of Zoology 54(3):1279-1290.
Kottelat M., Whitten A. J., Kartikasari S. N., Wirjoatmodjo S., 1993 Freshwater fishes of Western Indonesia and Sulawesi. Periplus Editions, Hong Kong, 293 p.
Kottelat M., 1995 The fishes of the Mahakam River, East Borneo: an example of the limitations of zoogeographic analyses and the need for extensive fish survey in Indonesia. Tropical Biodiversity 2(3):401-426.
Kottelat M., 2013 The fishes of the inland waters of Southeast Asia: a catalogue and core bibliography of the fishes known to occur in freshwaters, mangroves and estuaries. The Raffles Bulletin of Zoology 27:1-663.
Kumar S., Stecher G., Li M., Knyaz C., Tamura K., 2018 MEGA X: Molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution 35(6):1547-1549.
Langerhans R. B., 2008 Predictability of phenotypic differentiation across flow regimes in fishes. Integrative and Comparative Biology 48(6):750-768.
Muchlisin Z. A., 2013 Morphometric variations of Rasbora group (Pisces:Cyprinidae) in Lake Laut Tawar, Aceh Province, Indonesia, based on truss character analysis. HAYATI Journal of Biosciences 20(3):138-143.
Munroe T. A., Wongratana T., Nizinski M. S., 1999 Clupeidae. Herrings (also, sardines, shads, sprats, pilchards and menhadens). In: FAO species identification guide for fishery purposes. The living marine resources of the WCP. Vol. 3. Batoid fishes, chimaeras and bony fishes Part 1 (Elopidae to Linophrynidae). Carpenter K. E., Niem V. H. (eds), FAO, Rome, 2067 p.
Norton S. F., 1995 A functional approach to ecomorphological patterns of feeding in cottid fishes. Environmental Biology of Fishes (44):61-78.
Prasad K. K., Younus M., and Srinivasulu C., 2020 Occurrence of *Corica soborna* Hamilton, 1822 (Clupeiformes: Clupeidae) in the Godavari basin, India. Journal of Threatened Taxa 12(17):17361-17365.
Sartimbul A., Rohadi E., Ikhsani S. N., Listiyaningsih D., 2018. Morphometric and meristic variations among five populations of *Sardinella lemuru* Bleeker, 1853 from waters of Bali Strait, northern and southern-east Java and their relation to the environment. AACL Bioflux 11(3):744-752.
Stern N., Rinkevich B., Goren M., 2016 Integrative approach revises the frequently misidentified species of *Sardinella* (Clupeidae) of the Indo-West Pacific Ocean. Journal of Fish Biology 89(4):2282-2305.

Stroganov A. N., Semenova A. V., Rybakov M. O., Smirnov A. A., 2021 Variability of morphobiological characteristics of the Pacific herring *Clupea pallasii* from Arctic and Pacific populations. Journal of Ichthyology 61(3):407-417.
Suyatna I., Bratawinata A. A., Sidik A. S., Ruchaemi A., 2010 Demersal fishes and their distribution in estuarine waters of Mahakam Delta, East Kalimantan. Biodiversitas 11(4):204-210.
Suyatna I., Mislan, Rahman A., Winata A., Wijaya Y. I., 2017 A biophysical observation of Mahakam River around Tanjung Una of Kutai Kartanegara, Indonesia. Biodiversitas 18(2):623-632.
Swain D. P., Hutchings J. A., Foote C. J., 2005 Environmental and genetic influences on stock identification characters. In: Stock identification methods. Cadrin S. X., Friedland K. D., Waldman J. R. (eds), Academic Press, San Diego, USA, 719 p.
Ward R. D., Zemlak T. S., Innes B. H., Last P. R., Hebert P. D. N., 2005 DNA barcoding Australia's fish species. Philosophical Transactions of the Royal Society B: Biological Sciences 360(1462):1847-1857.
Whitehead P. J. P., 1967 The clupeoid fishes described by Lacepède, Cuvier & Valenciennes. Bulletin of the British Museum (Natural History), Zoology Supplement 2, 180 p.
Whitehead P. J. P., 1985 FAO species catalogue. Clupeoid fishes of the world (suborder Clupeoidei). An annotated and illustrated catalogue of the herrings, sardines, pilchards, sprats, shads, anchovies and wolf-herrings. 1st edition. FAO Fisheries Synopsis No. 125, Vol. 7, Part 1. Food and Agriculture Organization of the United Nations, Rome, 303 p.

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