



# Species diversity of fish at the Wuzhizhou Island, South China Sea, based on environmental DNA

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Academic editor: Yahui Zhao

Received: 08 May 2024 | Accepted: 06 Jun 2024 | Published: 14 Jun 2024

Citation: Wang C, Ma Z, Cao K, Wang X, Xi R, Jiang T, Yang R, Xing Y (2024) Species diversity of fish at the Wuzhizhou Island, South China Sea, based on environmental DNA. Biodiversity Data Journal 12: e127120.

<https://doi.org/10.3897/BDJ.12.e127120>

## Abstract

## Background

Wuzhizhou Island (WZZ) is located in Haitang Bay in the northern region of Sanya, Hainan Island. The sea area surrounding WZZ represents a typical tropical marine ecosystem, characterised by diverse and complex habitats. Therefore, there is a rich variety of marine fish species at WZZ. The marine ecosystem of WZZ was seriously destroyed initially in the 1970s-1980s and recovered in the 1990s, then constructed as the first national tropical marine ranch demonstration area of China in 2019. As fish is an important high trophic vertebrate in the marine ecosystem, understanding the composition and distribution of fish species could help us to recognise the status of the ecosystem of WZZ and supply scientific data for construction of the national marine ranch demonstration area. This study used eDNA technology to investigate the composition of fish community surrounding WZZ and provided a scientific basis for realising and protecting the marine ecosystem of the South China Sea.

## New information

The WZZ is an offshore island in the South China Sea, harbouring abundant marine fish resources. Although previous research investigated fish species of WZZ, the data were, however, still incomplete due to limitation of sampling methods and survey seasons. In this study, we intended to take advantage of eDNA and supplement data of fish species at WZZ as much as possible. Based on eDNA, this study provided the data on 188 fish species (including nine undetermined species denoted by genus sp.) belonging to 17 orders, 63 families and 124 genera and they were the more comprehensive records of fish species surrounding WZZ. In addition, the information on Molecular Operational Taxonomic Units (MOTUs) for taxon identification was also provided, aiming to contribute to the establishment of a specific eDNA taxon database for fish of the South China Sea. This study included two datasets, which were occurrences of fish taxa at WZZ, as well as MOTUs sequences and geographical coordinate information of sampling sites. The "fish taxon occurrences" dataset presented records on taxonomic, distribution and habitat conditions of 188 fish species detected using eDNA, as well as the latitude and longitude information of the sampling sites, the "MOTUs information" dataset provided the MOTUs sequences, source of sequences, abundance of sequences for 188 fish species, also included the species matched in NCBI and the best NCBI BLAST sequence similarity.

## Keywords

marine ecosystem, occurrence of fish taxon, distribution, sequences of MOTUs, the South China Sea

## Introduction

The Hainan Island is located in the South China Sea, covers a land area of 35,400 km<sup>2</sup>, as well as having a vast sea area of nearly 2 million km<sup>2</sup> and 1,618 km of coastline (Lin et al. 2022). The coastal area of the Hainan Island is rich in habitats such as rocky, coral reefs, gravel as well as sandy and muddy substrates (Liu 2013), which breed complex biological communities and high biodiversity. The marine fish, as an important part of the marine ecosystem, plays a key role in material cycling and energy flow, as well as maintaining the ecological functions (Ault et al. 2022, Ziegler et al. 2023). Therefore, the study of fish diversity in specific marine areas is essential for monitoring and evaluating the status of the ecosystem and it is able to offer valuable insights for marine ecological restoration and protection (Zou et al. 2020).

The Wuzhizhou Island (WZZ) of Sanya City is an outlying island of Hainan Island, with an area of 1.48 km<sup>2</sup> and 5.7 km of coastline, charmingly resembling an irregular butterfly in shape (Luo et al. 2023). WZZ is located at Haitang Bay, affected by the tropical monsoon climate (Yin et al. 2023) and its northern coast is sandy and the southern coast is mainly rocky (Xu et al. 2020). Consequently, the water area at WZZ is distributed by abundant

marine fish resources. With the exploitation of WZZ over the past decades, its ecosystem was significantly damaged by human activities, such as overfishing, land reclamation, coral mining, dredging, aquaculture expansion and pollution (Zhang et al. 2006). However, these negative effects began to be eliminated in 1997 when the Wuzhizhou Company initiated tourism development on the Island (Huang et al. 2020). In 2010, WZZ embarked on a marine ranch construction project, leading to the recognition of it as the first national-level marine ranch demonstration area in Hainan Province by 2019 (Li et al. 2015, Wang et al. 2021, Luo et al. 2023). At present, the studies on fish diversity of WZZ are to be conducted, aimed to understand the status of fish species diversity and evaluate the effectiveness of the sea ranch.

The environmental DNA (eDNA) has been known as a useful tool to detect aquatic and semi-aquatic species by extracting DNA from environmental samples such as water and sediment (Rees et al. 2014, Pedersen et al. 2015). Indeed, this technique has been widely used to monitor marine fish species, especially tropical marine biodiversity (Gelis et al. 2021, Mathon et al. 2022, Xi et al. 2022, Zhang et al. 2023). Compared to major traditional marine monitoring methods, such as fishing nets and diving, eDNA could provide more species information and less harm to the wildlife (Jerde et al. 2011, Sales et al. 2021). This study applied eDNA technology to provide valuable data that enrich the database of tropical marine fish, which would be a benefit for protecting the ecosystem of the South China Sea.

## Sampling methods

**Description:** The sea area surrounding WZZ is located in Haitang Bay, coastal Sanya City, Hainan Province, China.

**Sampling description:** The sampling protocols referenced our previous research (Xing et al. 2022) and the main steps were as follows: the shallow seawater samples were collected using a 3 l hydrophore at six sampling sites in sea area surrounding WZZ in June 2022, as well as January and September 2023, the Hainan Province, China (Fig. 1). The distance between two sampling sites was more than 1 km. The three replicated 1 l water samples were collected at each sampling site (Fig. 2). The eDNA was collected by 0.45 µm MCE membrane filtration (Pall Whatman, UK) from water samples and each membrane enriched with DNA was stored individually in a 2 ml centrifuge tube at -10°C in the field. Meanwhile, 300 ml purified water was filtered to serve as a negative control in order to detect contamination.

**Step description:** The eDNA was extracted using E.Z.N.A. Water DNA Kit and protocols of the kit were followed. Before DNA extraction, the experimental bench and equipment were regularly cleaned using 5% bleach and then 75% ethanol, in order to prevent cross-contamination. The extracted DNA samples were stored at -20°C for subsequent experiments. PCR amplification was performed using "MiFish-U" primer sets for multiple fish species detection (Forward: GTCGGTAAAACCTCGTGCCAGC, Reverse: CATAGTG GGGTATCTAATCCCAGTTTG) (Miya et al. 2015). Both forward and reverse primers were

tagged with oligonucleotide designed by the Shanghai Biozeron Biotechnology Co. Ltd, China and each sample had a specific tag (Table 1). A PCR system was total 25  $\mu$ l volume, containing 4  $\mu$ l of 5 $\times$ FastPfu Buffer, 2  $\mu$ l of 2.5 mM dNTPs, 0.8  $\mu$ l Forward Primer (5  $\mu$ M), 0.8  $\mu$ l Reverse Primer (5  $\mu$ M), 0.4  $\mu$ l FastPfu Polymerase, 10 ng of Template DNA and 12  $\mu$ l ddH<sub>2</sub>O. The PCR reaction conditions were the following: pre-denaturation for 5 min at 95°C, followed by 32 cycles of denaturation (30 sec at 95°C), annealing (30 sec at 55°C) and elongation (45 sec at 72°C) and final elongation for 10 min at 72°C. And two negative controls (PCR blank) were set up in each PCR reaction, in order to monitor cross-contamination. The PCR products at each sampling site were verified at 2%. The libraries were built and then sequenced on an Illumina Novaseq platform (the Shanghai Biozeron Biotechnology Co. Ltd, China) using 150 bp paired-end sequencing.

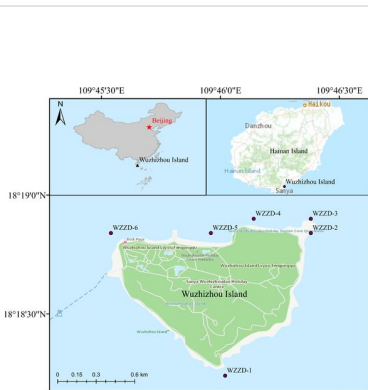


Figure 1. [doi](#)

Location of eDNA sampling sites.

The original sequences obtained from the Illumina Novaseq platform were initially processed using QIIME 2 software (Bolyen et al. 2019) and the end sequences demultiplexed, based on the tags and primers were removed from the end. The reads were then trimmed to 160-180 bp using CUTADAPT software (Martin 2011). Next, the data obtained by sequencing were spliced and filtered in order to obtain high-quality sequences, which were clustered into MOTUs using VSEARCH software with 97% similarity (Zhang et al. 2019). Finally, the sequences of MOTUs were aligned with NCBI-BLAST (<https://www.ncbi.nlm.nih.gov/BLAST>, version in March 2024) under the default parameter settings for taxonomic annotation (Djurhuus et al. 2017). We used the following criteria for taxonomic assignment: a) if the query sequence matched one locally occurring species in the NCBI database (<https://www.ncbi.nlm.nih.gov>) with  $\geq 97\%$  identity, the species was assigned, b) if the query sequence matched more than one locally occurring species in the NCBI with  $\geq 97\%$  identity, the lowest taxonomic level (i.e. genus or family) that contains all these species was assigned, c) if the query sequence matched a non-native species in the NCBI with  $\geq 97\%$  identity, meanwhile this non-native species belonged to the same genus

as the known native species, this genus was assigned. The sequences assigned to “NA” or assigned to humans, birds, mammals or amphibians were removed. The geographical distribution of each species was verified by the Species Catalogue of China. Volume 2, Animals, Vertebrates. V (Zhang et al. 2020) and the FishBase database (<http://www.fishbase.org/search.php>).

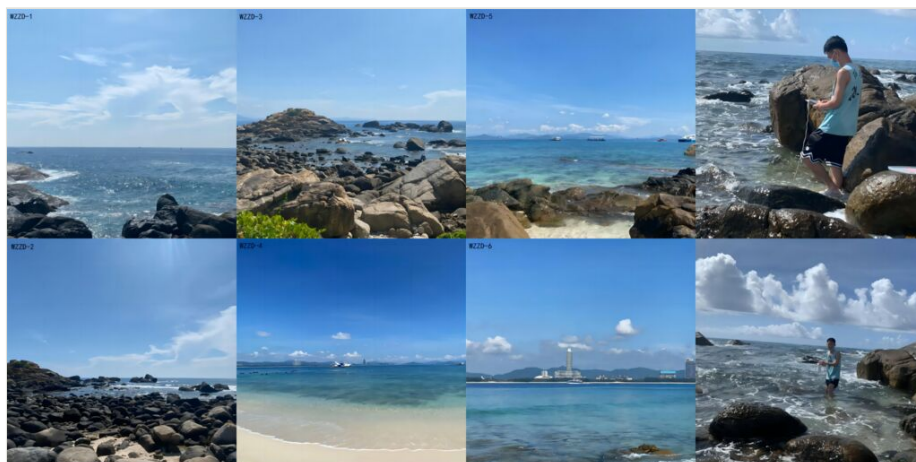


Figure 2. [doi](#)

Photographs of marine habitats and field sampling around WZZ.

Table 1.

The oligo tag sequences corresponding to the samples.

Sample ID	Forward Oligo Tags	Reverse Oligo Tags
2023-WZZD-1	TAACGA	CGCTT
2023-WZZD-2	TAACGA	GCCAGT
2023-WZZD-3	TAACGA	TCTCAGTC
2023-WZZD-4	TAACGA	CGCTGAT
2023-WZZD-5	AACCGAGA	TCACC
2023-WZZD-6	AACCGAGA	ATGCCT
2023-WZZD-NTC	AACCGAGA	CGCTT

## Geographic coverage

**Description:** We surveyed six localities in the sea area surrounding WZZ (Fig. 1). The investigation involved nearly 249325.426 m<sup>2</sup> measured using ArcGIS 10.8 software.

**Coordinates:** 18.304 and 18.316 Latitude; 109.759 and 109.773 Longitude.

## Taxonomic coverage

**Description:** In total, two classes, 17 orders, 63 families, 124 genera and 188 fish species (including nine undetermined species denoted by genus sp.), were detected using eDNA in the area surrounding WZZ.

### Taxa included:

Rank	Scientific Name
class	Chondrichthyes
class	Osteichthyes
order	Anguilliformes
order	Atheriniformes
order	Aulopiformes
order	Beloniformes
order	Beryciformes
order	Carcharhiniformes
order	Clupeiformes
order	Elopiformes
order	Gadiformes
order	Gasterosteiformes
order	Mugiliformes
order	Myliobatiformes
order	Perciformes
order	Pleuronectiformes
order	Scorpaeniformes
order	Siluriformes
order	Tetraodontiformes
family	Acanthuridae
family	Acropomatidae
family	Ambassidae
family	Ammodytidae
family	Apogonidae
family	Atherinidae

family	Balistidae
family	Belontiidae
family	Blenniidae
family	Bothidae
family	Bregmacerotidae
family	Caesionidae
family	Callionymidae
family	Carangidae
family	Carcharhinidae
family	Chaetodontidae
family	Chirocentridae
family	Cirrhitidae
family	Clupeidae
family	Cynoglossidae
family	Elopidae
family	Engraulidae
family	Ephippidae
family	Fistulariidae
family	Gerreidae
family	Gobiidae
family	Haemulidae
family	Hemiramphidae
family	Holocentridae
family	Kuhliidae
family	Kyphosidae
family	Labridae
family	Latidae
family	Leiognathidae
family	Lethrinidae
family	Lutjanidae
family	Malacanthidae

family	Monacanthidae
family	Mugilidae
family	Mullidae
family	Muraenidae
family	Myliobatidae
family	Nemipteridae
family	Ostraciidae
family	Pempheridae
family	Plesiopidae
family	Plotosidae
family	Pomacanthidae
family	Pomacentridae
family	Scaridae
family	Scatophagidae
family	Sciaenidae
family	Scombridae
family	Scorpaenidae
family	Serranidae
family	Siganidae
family	Sillaginidae
family	Sphyraenidae
family	Synphobranchidae
family	Synodontidae
family	Terapontidae
family	Tetraodontidae
family	Tripterygiidae
genus	<i>Abudefduf</i>
genus	<i>Acanthurus</i>
genus	<i>Acentrogobius</i>
genus	<i>Acropoma</i>
genus	<i>Aetobatus</i>



genus	<i>Alepes</i>
genus	<i>Aluterus</i>
genus	<i>Ambassis</i>
genus	<i>Ammodytes</i>
genus	<i>Anampses</i>
genus	<i>Andamia</i>
genus	<i>Arothron</i>
genus	<i>Atherinomorus</i>
genus	<i>Bathygobius</i>
genus	<i>Blenniella</i>
genus	<i>Branchiostegus</i>
genus	<i>Bregmaceros</i>
genus	<i>Caesio</i>
genus	<i>Callionymus</i>
genus	<i>Cantherhines</i>
genus	<i>Caranx</i>
genus	<i>Carcharhinus</i>
genus	<i>Centropyge</i>
genus	<i>Cephalopholis</i>
genus	<i>Chaetodon</i>
genus	<i>Cheilinus</i>
genus	<i>Chelon</i>
genus	<i>Chirocentrus</i>
genus	<i>Chrysiptera</i>
genus	<i>Cirrhitis</i>
genus	<i>Cirripectes</i>
genus	<i>Clupanodon</i>
genus	<i>Collichthys</i>
genus	<i>Coris</i>
genus	<i>Cromileptes</i>
genus	<i>Cynoglossus</i>

genus	<i>Decapterus</i>
genus	<i>Dendrophysa</i>
genus	<i>Diagramma</i>
genus	<i>Dysomma</i>
genus	<i>Echidna</i>
genus	<i>Ellochelon</i>
genus	<i>Elops</i>
genus	<i>Encrasicholina</i>
genus	<i>Engraulis</i>
genus	<i>Engyprosopon</i>
genus	<i>Enneapterygius</i>
genus	<i>Entomacrodus</i>
genus	<i>Epinephelus</i>
genus	<i>Exallias</i>
genus	<i>Favonigobius</i>
genus	<i>Fistularia</i>
genus	<i>Gazza</i>
genus	<i>Gerres</i>
genus	<i>Glossogobius</i>
genus	<i>Gymnomuraena</i>
genus	<i>Gymnothorax</i>
genus	<i>Halichoeres</i>
genus	<i>Helcogramma</i>
genus	<i>Hemigymnus</i>
genus	<i>Herklotsichthys</i>
genus	<i>Hypoatherina</i>
genus	<i>Hyporhamphus</i>
genus	<i>Istiblennius</i>
genus	<i>Istigobius</i>
genus	<i>Kuhlia</i>
genus	<i>Kyphosus</i>

genus	<i>Lagocephalus</i>
genus	<i>Lates</i>
genus	<i>Lethrinus</i>
genus	<i>Lutjanus</i>
genus	<i>Moolgarda</i>
genus	<i>Mugil</i>
genus	<i>Mugilogobius</i>
genus	<i>Myripristis</i>
genus	<i>Neopomacentrus</i>
genus	<i>Nuclequula</i>
genus	<i>Odontamblyopus</i>
genus	<i>Odonus</i>
genus	<i>Oedalechilus</i>
genus	<i>Osteomugil</i>
genus	<i>Ostorhinchus</i>
genus	<i>Ostracion</i>
genus	<i>Parablennius</i>
genus	<i>Parascorpaena</i>
genus	<i>Parupeneus</i>
genus	<i>Pelates</i>
genus	<i>Pempheris</i>
genus	<i>Platax</i>
genus	<i>Plectroglyphidodon</i>
genus	<i>Plesiops</i>
genus	<i>Plotosus</i>
genus	<i>Pomacentrus</i>
genus	<i>Pomadasys</i>
genus	<i>Pseudobalistes</i>
genus	<i>Pseudogobius</i>
genus	<i>Pterocaesio</i>
genus	<i>Rastrelliger</i>

genus	<i>Rhinecanthus</i>
genus	<i>Salarias</i>
genus	<i>Sardinella</i>
genus	<i>Sardinops</i>
genus	<i>Saurida</i>
genus	<i>Scarus</i>
genus	<i>Scatophagus</i>
genus	<i>Scolopsis</i>
genus	<i>Scomber</i>
genus	<i>Secutor</i>
genus	<i>Selar</i>
genus	<i>Siganus</i>
genus	<i>Sillago</i>
genus	<i>Sphyræna</i>
genus	<i>Spratelloides</i>
genus	<i>Stethojulis</i>
genus	<i>Stolephorus</i>
genus	<i>Terapon</i>
genus	<i>Thalassoma</i>
genus	<i>Thryssa</i>
genus	<i>Thunnus</i>
genus	<i>Trachinotus</i>
genus	<i>Trachurus</i>
genus	<i>Tylosurus</i>
genus	<i>Upeneus</i>
genus	<i>Zenarchopterus</i>
species	<i>Abudefduf notatus</i> (Day, 1870)
species	<i>Abudefduf septemfasciatus</i> (Cuvier, 1830)
species	<i>Abudefduf sexfasciatus</i> (Lacépède, 1801)
species	<i>Abudefduf sordidus</i> (Forsskål, 1775)
species	<i>Abudefduf vaigiensis</i> (Quoy & Gaimard, 1825)

species	<i>Acanthurus triostegus</i> (Linnaeus, 1758)
species	<i>Acentrogobius viganensis</i> (Steindachner, 1893)
species	<i>Acropoma japonicum</i> Günther, 1859
species	<i>Aetobatus narinari</i> (Euphrasen, 1790)
species	<i>Alepes djedaba</i> (Forsskål, 1775)
species	<i>Alepes kleinii</i> (Bloch, 1793)
species	<i>Alepes vari</i> (Cuvier, 1833)
species	<i>Aluterus scriptus</i> (Osbeck, 1765)
species	<i>Ambassis urotaenia</i> Bleeker, 1852
species	<i>Ammodytes personatus</i> Girard, 1856
species	<i>Anampses caeruleopunctatus</i> Rüppell, 1829
species	<i>Andamia tetradactylus</i> (Bleeker, 1858)
species	<i>Arothron stellatus</i> (Bloch & Schneider, 1801)
species	<i>Atherinomorus lacunosus</i> (Forster, 1801)
species	<i>Atherinomorus regina</i> (Seale, 1910)
species	<i>Bathygobius cotticeps</i> (Steindachner, 1879)
species	<i>Bathygobius hongkongensis</i> Lam, 1986
species	<i>Blenniella bilitonensis</i> (Bleeker, 1858)
species	<i>Branchiostegus argentatus</i> (Cuvier, 1830)
species	<i>Bregmaceros maclellandi</i> Thompson, 1840
species	<i>Caesio caerulea</i> Lacépède, 1801
species	<i>Callionymus meridionalis</i> Suwardji, 1965
species	<i>Cantherhines pardalis</i> (Rüppell, 1837)
species	<i>Caranx sexfasciatus</i> Quoy & Gaimard, 1825
species	<i>Caranx tille</i> Cuvier, 1833
species	<i>Carcharhinus melanopterus</i> (Quoy & Gaimard, 1824)
species	<i>Centropyge vrolikii</i> (Bleeker, 1853)
species	<i>Cephalopholis argus</i> Bloch & Schneider, 1801
species	<i>Cephalopholis boenak</i> (Bloch, 1790)
species	<i>Chaetodon auriga</i> Forsskål, 1775
species	<i>Chaetodon plebeius</i> Cuvier, 1831

species	<i>Chaetodon rafflesii</i> Anonymous [Bennett], 1830
species	<i>Chelon affinis</i> (Günther, 1861)
species	<i>Chelon haematocheilus</i> (Temminck & Schlegel, 1845)
species	<i>Chelon macrolepis</i> (Smith, 1846)
species	<i>Chirocentrus dorab</i> (Forsskål, 1775)
species	<i>Chrysiptera biocellata</i> (Quoy & Gaimard, 1825)
species	<i>Chrysiptera brownriggii</i> (Bennett, 1828)
species	<i>Chrysiptera glauca</i> (Cuvier, 1830)
species	<i>Chrysiptera unimaculata</i> (Cuvier, 1830)
species	<i>Cirrhitis pinnulatus</i> (Forster, 1801)
species	<i>Cirripectes imitator</i> Williams, 1985
species	<i>Clupanodon thrissa</i> (Linnaeus, 1758)
species	<i>Collichthys lucidus</i> (Richardson, 1844)
species	<i>Coris gaimard</i> (Quoy & Gaimard, 1824)
species	<i>Cromileptes altivelis</i> (Valenciennes, 1828)
species	<i>Cynoglossus robustus</i> Günther, 1873
species	<i>Decapterus macrosoma</i> Bleeker, 1851
species	<i>Decapterus maruadsi</i> (Temminck & Schlegel, 1843)
species	<i>Dendrophysa russelii</i> (Cuvier, 1829)
species	<i>Diagramma melanacrum</i> Johnson & Randall, 2001
species	<i>Dysomma anguillare</i> Barnard, 1923
species	<i>Echidna nebulosa</i> (Ahl, 1789)
species	<i>Echidna polyzona</i> (Richardson, 1845)
species	<i>Ellochelon vaigiensis</i> (Quoy & Gaimard, 1825)
species	<i>Elops machnata</i> (Forsskål, 1775)
species	<i>Encrasicholina heteroloba</i> (Rüppell, 1837)
species	<i>Encrasicholina punctifer</i> Fowler, 1938
species	<i>Engyprosopon multsquama</i> Amaoka, 1963
species	<i>Enneapterygius bahasa</i> Fricke, 1997
species	<i>Enneapterygius philippinus</i> (Peters, 1868)
species	<i>Entomacrodus caudofasciatus</i> (Regan, 1909)

species	<i>Entomacrodus decussatus</i> (Bleeker, 1858)
species	<i>Entomacrodus striatus</i> (Valenciennes, 1836)
species	<i>Entomacrodus thalassinus</i> (Jordan & Seale, 1906)
species	<i>Epinephelus fuscoguttatus</i> (Forsskål, 1775)
species	<i>Epinephelus multinotatus</i> (Peters, 1876)
species	<i>Epinephelus trimaculatus</i> (Valenciennes, 1828)
species	<i>Exallias brevis</i> (Kner, 1868)
species	<i>Favonigobius reichei</i> (Bleeker, 1854)
species	<i>Fistularia commersonii</i> Rüppell, 1838
species	<i>Gazza minuta</i> (Bloch, 1795)
species	<i>Gerres erythrourus</i> (Bloch, 1791)
species	<i>Gerres filamentosus</i> Cuvier, 1829
species	<i>Gerres oyena</i> (Forsskål, 1775)
species	<i>Glossogobius celebius</i> (Valenciennes, 1837)
species	<i>Gymnomuraena zebra</i> (Shaw, 1797)
species	<i>Gymnothorax chilospilus</i> Bleeker, 1864
species	<i>Gymnothorax fimbriatus</i> (Bennett, 1832)
species	<i>Gymnothorax flavimarginatus</i> (Rüppell, 1830)
species	<i>Gymnothorax kidako</i> (Temminck & Schlegel, 1846)
species	<i>Gymnothorax pictus</i> (Ahl, 1789)
species	<i>Gymnothorax undulatus</i> (Lacépède, 1803)
species	<i>Halichoeres argus</i> (Bloch & Schneider, 1801)
species	<i>Halichoeres marginatus</i> Rüppell, 1835
species	<i>Helcogramma fuscipectoris</i> (Fowler, 1946)
species	<i>Hemigymnus melapterus</i> (Bloch, 1791)
species	<i>Herklotsichthys quadrimaculatus</i> (Rüppell, 1837)
species	<i>Hypoatherina temminckii</i> (Bleeker, 1854)
species	<i>Hyporhamphus dussumieri</i> (Valenciennes, 1847)
species	<i>Istiblennius dussumieri</i> (Valenciennes, 1836)
species	<i>Istiblennius edentulus</i> (Forster & Schneider, 1801)
species	<i>Istigobius ornatus</i> (Rüppell, 1830)

species	<i>Kuhlia mugil</i> (Forster, 1801)
species	<i>Kyphosus bigibbus</i> Lacépède, 1801
species	<i>Kyphosus cinerascens</i> (Forsskål, 1775)
species	<i>Kyphosus vaigiensis</i> (Quoy & Gaimard, 1825)
species	<i>Lagocephalus spadiceus</i> (Richardson, 1845)
species	<i>Lates calcarifer</i> (Bloch, 1790)
species	<i>Lethrinus atkinsoni</i> Seale, 1910
species	<i>Lethrinus harak</i> (Forsskål, 1775)
species	<i>Lethrinus nebulosus</i> (Forsskål, 1775)
species	<i>Lethrinus ornatus</i> Valenciennes, 1830
species	<i>Lethrinus xanthochilus</i> Klunzinger, 1870
species	<i>Lutjanus argentimaculatus</i> (Forsskål, 1775)
species	<i>Lutjanus fulviflamma</i> (Forsskål, 1775)
species	<i>Lutjanus malabaricus</i> (Bloch & Schneider, 1801)
species	<i>Lutjanus monostigma</i> (Cuvier, 1828)
species	<i>Lutjanus stellatus</i> Akazaki, 1983
species	<i>Moolgarda seheli</i> (Forsskål, 1775)
species	<i>Mugil cephalus</i> Linnaeus, 1758
species	<i>Mugilogobius chulae</i> (Smith, 1932)
species	<i>Myripristis kuntee</i> Valenciennes, 1831
species	<i>Neopomacentrus cyanomos</i> (Bleeker, 1856)
species	<i>Nucequula nuchalis</i> (Temminck & Schlegel, 1845)
species	<i>Odontamblyopus lacepedii</i> (Temminck & Schlegel, 1845)
species	<i>Odonus niger</i> (Rüppell, 1836)
species	<i>Oedalechilus labiosus</i> (Valenciennes, 1836)
species	<i>Osteomugil speigleri</i> (Bleeker, 1858)
species	<i>Ostorhinchus cookii</i> (Macleay, 1881)
species	<i>Ostorhinchus fasciatus</i> (White, 1790)
species	<i>Ostracion cubicus</i> Linnaeus, 1758
species	<i>Parablennius yatabei</i> (Jordan & Snyder, 1900)
species	<i>Parascorpaena mossambica</i> (Peters, 1855)



species	<i>Parupeneus ciliatus</i> (Lacépède, 1802)
species	<i>Pelates quadrilineatus</i> (Bloch, 1790)
species	<i>Pempheris adusta</i> Bleeker, 1877
species	<i>Pempheris xanthoptera</i> Tominaga, 1963
species	<i>Platax teira</i> (Forsskål, 1775)
species	<i>Plectroglyphidodon dickii</i> (Liénard, 1839)
species	<i>Plectroglyphidodon leucozonus</i> (Bleeker, 1859)
species	<i>Plectroglyphidodon obreptus</i> (Whitley, 1948)
species	<i>Plesiops coeruleolineatus</i> Rüppell, 1835
species	<i>Plotosus lineatus</i> (Thunberg, 1787)
species	<i>Pomacentrus chrysurus</i> Cuvier, 1830
species	<i>Pomadasys maculatus</i> (Bloch, 1793)
species	<i>Pseudobalistes flavimarginatus</i> (Rüppell, 1829)
species	<i>Pseudogobius javanicus</i> (Bleeker, 1856)
species	<i>Pterocaesio digramma</i> (Bleeker, 1864)
species	<i>Rastrelliger kanagurta</i> (Cuvier, 1816)
species	<i>Rhinecanthus aculeatus</i> (Linnaeus, 1758)
species	<i>Salaria fasciatus</i> (Bloch, 1786)
species	<i>Sardinella gibbosa</i> (Bleeker, 1849)
species	<i>Sardinella lemuru</i> Bleeker, 1853
species	<i>Sardinops sagax</i> (Jenyns, 1842)
species	<i>Saurida undosquamis</i> (Richardson, 1848)
species	<i>Scarus psittacus</i> Forsskål, 1775
species	<i>Scarus rivulatus</i> Valenciennes, 1840
species	<i>Scatophagus argus</i> (Linnaeus, 1766)
species	<i>Scolopsis ciliata</i> (Lacépède, 1802)
species	<i>Scomber japonicus</i> Houttuyn, 1782
species	<i>Secutor ruconius</i> (Hamilton, 1822)
species	<i>Selar crumenophthalmus</i> (Bloch, 1793)
species	<i>Siganus canaliculatus</i> (Park, 1797)
species	<i>Siganus fuscescens</i> (Houttuyn, 1782)

species	<i>Siganus guttatus</i> (Bloch, 1787)
species	<i>Siganus spinus</i> (Linnaeus, 1758)
species	<i>Sillago sihama</i> (Forsskål, 1775)
species	<i>Sphyræna jello</i> Cuvier, 1829
species	<i>Spratelloides delicatulus</i> (Bennett, 1832)
species	<i>Spratelloides gracilis</i> (Temminck & Schlegel, 1846)
species	<i>Stethojulis bandanensis</i> (Bleeker, 1851)
species	<i>Stethojulis terina</i> Jordan & Snyder, 1902
species	<i>Stethojulis trilineata</i> (Bloch & Schneider, 1801)
species	<i>Stolephorus waitei</i> Jordan & Seale, 1926
species	<i>Terapon jarbua</i> (Forsskål, 1775)
species	<i>Thryssa kammalensis</i> (Bleeker, 1849)
species	<i>Thunnus tonggol</i> (Bleeker, 1851)
species	<i>Trachinotus baillonii</i> (Lacépède, 1801)
species	<i>Trachinotus ovatus</i> (Linnaeus, 1758)
species	<i>Trachurus japonicus</i> (Temminck & Schlegel, 1844)
species	<i>Tylosurus crocodilus</i> (Péron & Lesueur, 1821)
species	<i>Upeneus japonicus</i> (Houttuyn, 1782)
species	<i>Zenarchopterus dunckeri</i> Mohr, 1926
species	<i>Cheilinus</i> sp.
species	<i>Engraulis</i> sp.
species	<i>Enneapterygius</i> sp.
species	<i>Gymnomuraena</i> sp.
species	<i>Ostorhinchus</i> sp.
species	<i>Platax</i> sp.
species	<i>Sardinella</i> sp.
species	<i>Siganus</i> sp.
species	<i>Thalassoma</i> sp.

## Temporal coverage

**Data range:** 2022-6-26 - 2022-6-27; 2023-1-15 - 2023-1-17; 2023-9-06 - 2023-9-08.

## Usage licence

**Usage licence:** Creative Commons Public Domain Waiver (CC-Zero)

## Data resources

**Data package title:** Fish taxon-occurrences surrounding WZZ, Hainan Province, China based on eDNA

**Number of data sets:** 2

**Data set name:** Fish taxon-occurrences surrounding WZZ detected by eDNA

**Data format:** Darwin Core

**Description:** The dataset presents the results of 188 fish species detected by eDNA at six sampling localities surrounding WZZ and includes the latitude and longitude information of the sampling sites. Important information including the taxonomic, geographic location of the occurrence and habitat condition was provided (Suppl. material 1).

Column label	Column description
occurrenceID	Unique occurrence identifier.
scientificName	The full scientific name.
kingdom	The full scientific name of the kingdom in which the taxon is classified.
Phylum	The full scientific name of the phylum or division in which the taxon is classified.
Class	The full scientific name of the class in which the taxon is classified.
Order	The full scientific name of the order in which the taxon is classified.
Family	The full scientific name of the family in which the taxon is classified.
Genus	The full scientific name of the genus in which the taxon is classified.
taxonRank	The taxonomic rank of the most specific name in the scientificName as it appears in the original record.
locality	The specific description of the county from where specimens are collected.
county	The full, unabbreviated name of the next smaller administrative region than stateProvince (county, shire, department, etc.) in which the Location occurs.
stateProvince	The name of the next smallest administrative region than country (state, province, canton, department, region etc.) in which the Location occurs.
Country	The full, unabbreviated name of the country where the organism was collected.
waterBody	The name of the water body in which the Location occurs.

habitat	A category or description of the habitat in which the Event occurred.
locationID	A spatial region or named place. The locationID refers to serial number of each sampling site in this study.
decimalLatitude	The geographic latitude (in decimal degrees, using the spatial reference system given in geodeticDatum) of the geographic centre of a Location.
decimalLongitude	The geographic longitude (in decimal degrees, using the spatial reference system given in geodeticDatum) of the geographic centre of a Location.
geodeticDatum	The geographic information system (GIS) upon which the geographic coordinates given in decimalLatitude, decimalLongitude and meterElevation are based.
basisOfRecord	The specific nature of the data record.
eventDate	The date-time or interval during which a dwc:Event occurred. For occurrences, this is the date-time when the dwc:Event was recorded. Not suitable for a time in a geological context.
samplingProtocol	The names of, references to, or descriptions of the methods or protocols used during a dwc:Event.

**Data set name:** MOTUs information of fish species detected by eDNA

**Data format:** Darwin Core

**Description:** The dataset presents the nucleotides sequence, sequences source and abundance of sequences of each MOTU, as well as its matched species in NCBI (<https://www.ncbi.nlm.nih.gov/BLAST>) and the best NCBI BLAST sequence similarity, obtained through high-throughput sequencing, based eDNA samples collected from the sea area surrounding WZZ (Suppl. material 2).

Column label	Column description
scientificName	The full scientific name.
associatedSequences	A list (concatenated and separated) of identifiers (publication, global unique identifier, URI) of genetic sequence information associated with the Occurrence. The associatedSequences refers to MOTUs sequences of each scientificName.
organismQuantity	A number or enumeration value for the quantity of organisms.
organismQuantityType	The type of quantification system used for the quantity of organisms.
dateIdentified	The date on which the subject was determined as representing the Taxon.
identificationReferences	A list (concatenated and separated) of references (publication, global unique identifier, URI) used in the Identification.
identificationRemarks	Comments or notes about the Identification.

## Additional information

A total of 188 fish species (including nine undetermined species denoted by genus sp.) were detected using eDNA surrounding WZZ and fish fauna was analysed (Fig. 3). At the order level, Perciformes included the most species ( $n = 130$ ), accounting for 69.15% of the total number of fish species detected and occupied absolute advantage compared to other orders. The Clupeiformes ( $n = 14$ ) was the second largest order, accounting for 7.45%, followed by Anguilliformes ( $n = 11$ ) accounting for 5.85%. Additionally, the Mugiliformes and Tetraodontiformes both had eight species, accounting for 4.26%, respectively. The Atheriniformes and Belontiiformes both included three species, separately accounting for 1.60%, as well as the Pleuronectiformes containing two species and accounting for 1.06%. The rest of the orders, Aulopiformes, Beryciformes, Carcharhiniformes, Elopiformes, Gadiformes, Gasterosteiformes, Myliobatiformes, Scorpaeniformes and Siluriformes, all harboured only one species and 0.53% of the total number (Fig. 3). At the family level, the most dominant was Pomacentridae and it included 14 species, accounting for 7.45% of the total number. The second family is Blenniidae ( $n = 12$ , 6.38%), followed by Carangidae ( $n = 11$ , 5.85%). Most of the families had only one species (Fig. 3).

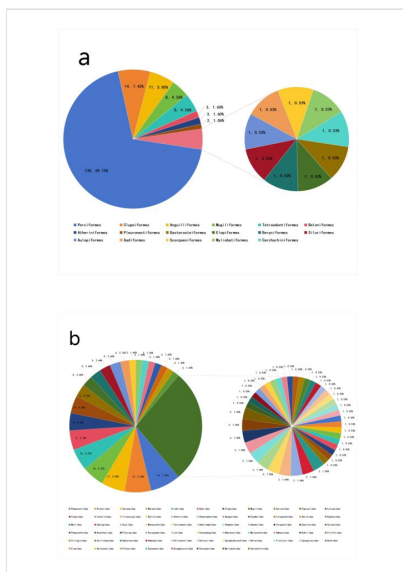


Figure 3. [doi](#)

The composition of fish fauna surrounding WZZ at the order level (a) and family level (b).

We compared the fish species richness detected by eDNA to that by fishing nets, in order to assess the effects of eDNA on species identification. A total of 115 fish species belonging to 11 orders and 49 families, as well as a total of 174 fish species belonging to two classes, 12 orders, 65 families and 123 genera were investigated at WZZ through trawl nets in 2019 and 2020-2021, respectively (Wang et al. 2021, Luo et al. 2023). According to our results, the eDNA could supply more information of fish species, compared to

traditional fishing nets. Meanwhile, the differences between the two monitoring methods in the number of family and order may be related to seasonal changes of the marine fish community. Although some species cannot be annotated using the NCBI database or only be identified at the genus level, based on MOTUs sequences, the eDNA datasets established in this study can help us to solve this problem to a certain extent.

## Acknowledgements

This study is funded by the Key Research and Development Programme of the Hainan Province (No.ZDYF2022SHFZ027), the Hainan Provincial Joint Project of Sanya-Yazhou Bay Science and Technology City Grant (No.320LH069) and Central Public-interest Scientific Institution Basal Research Fund, CAFS (NO.2023TD12). We appreciated help from the Hainan Wuzhizhou Tourism Development Co., Ltd during water sampling.

## Author contributions

Chongzhao Wang prepared datasets, analysed data and drafted the manuscript. Zhenhua Ma, Xin Wang, Kun Cao and Yingchun Xing performed the fieldwork. Rui Xi, Ting Jiang and Rui Yang performed eDNA laboratory work. All co-authors gave their comments on this manuscript.

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## Supplementary materials

### Suppl. material 1: Fish taxon-occurrences surrounding WZZ, Hainan Province, China based on eDNA [doi](#)

**Authors:** Chongzhao Wang, Zhenhua Ma, Kun Cao, Ting Jiang, Rui Yang, Rui Xi, Xin Wang, Yingchun Xing

**Data type:** dataset

**Brief description:** The dataset presents the results of 188 fish species detected by eDNA at six sampling localities surrounding WZZ, also above the latitude and longitude information of the sampling sites. The important information including taxonomic, geographic location of the occurrence and habitat condition was provided.

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### Suppl. material 2: MOTUs information of marine fish detected by eDNA [doi](#)

**Authors:** Chongzhao Wang, Zhenhua Ma, Kun Cao, Ting Jiang, Rui Yang, Rui Xi, Xin Wang, Yingchun Xing

**Data type:** dataset

**Brief description:** The dataset presents the nucleotides sequence, source of sequences and abundance of sequences of each MOTU, as well as its matched species in NCBI (<https://www.ncbi.nlm.nih.gov/BLAST>) and the best NCBI BLAST sequence similarity, obtained through high-throughput sequencing based eDNA samples collected from the area surrounding WZZ.

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