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Abstract

Background

The Wuzhizhou Island (WZZ) is located in the Haitang Bay at the northern region of the Sanya, Hainan Island. The sea area surrounding WZZ represents a typical tropical marine ecosystem, which is characterized by diverse and complex habitats. Therefore, there are a rich variety of marine fish species at WZZ area. The marine ecosystem of WZZ had experienced seriously destroyed in 1970s - 1980s, initially recovered in 1990s and constructed as the first national tropical marine ranch demonstration area of China in 2019. Obviously, the fish are important high trophic vertebrates in the marine ecosystem, understanding composition and distribution of fish species could help us to recognize status of ecosystem of WZZ and supply scientific data for construction of 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 realizing and protecting marine ecosystem of the South China Sea.

New information

The waters around WZZ are part of the South China Sea, and they have abundant marine fish resources. Although some researches have investigated fish species of WZZ, however, the data are still incomplete due to the limitation of sampling methods and survey seasons. In this study, we hope to take advantages of eDNA and try to supplement data of fish species at WZZ as many as possible. Based on eDNA, this study provides the data on 179 fish species and 9 fish genera belonging to 17 orders, 63 families and 124 genera, and they are more comprehensive records of fish species surrounding WZZ. In addition, the

information of Molecular Operational Taxonomic Units (MOTUs) for taxon identification are also provided, aiming to contribute to the establishment of a specific eDNA taxon database for fish of the South China Sea. This study includes two datasets, which are occurrence of fish taxa at WZZ area, as well as MOTUs sequences and geographical coordinate information of sampling sites. The "fish taxon occurrences" dataset presents records on taxonomic, distribution, habitat condition of 188 fish species detected using eDNA, as well as the latitude and longitude information of the sampling sites, the "MOTUs information" dataset provides the MOTUs sequences, source of sequences, abundance of sequences for 188 fish species, also includes the species matched in NCBI and the best NCBI Blast sequence similarity.

Keywords

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

Introduction

The Hainan Island is located in the South China Sea, covers a land area of 35,400 km², harbors a vast sea area of approximately 2 million km² and 1,618 km coastline (Lin et al. 2022). The coastal area of the Hainan Island is rich of habitats such as rocky, coral reefs, gravel as well as sandy and muddy substrates (Liu 2013), which breeds complex biological communities and high biodiversity. The marine fish, integral to the marine ecosystem surrounding the Hainan Island, play a key role in material cycling and energy flow, as well as maintaining ecological functions (Ault et al. 2022, Ziegler et al. 2023). Therefore, studying on diversity of fish species in a specific marine area is a vital measure for monitoring and evaluating status of its ecosystem, and offers valuable insights for the ecological restoration and protection (Zou et al. 2020).

The Wuzhizhou Island (WZZ) of the Sanya City is an outlying island of the Hainan Island, charmingly resembles an irregular butterfly in shape, with area of 1.48 km² and 5.7 km coastline (Luo et al. 2023). WZZ is located at the Haitang Bay, affected by tropical monsoon climate (Yin et al. 2023), and its northern coast is sandy and southern coast is mainly rocky (Xu et al. 2020). Consequently, the waters at WZZ are distributed by abundant marine fish resources. However, with the exploitation of WZZ over the past decades, alongside human-induced impacts such as overfishing, land reclamation, coral mining, dredging, aquaculture expansion and pollution, inflicted significant damages on its ecosystem (Zhang et al. 2006), and this negative trend began to be reverse 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 the 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 should be conducted, in order to understand status of fish species diversity and evaluate the effectiveness of the sea ranch.

Environmental DNA (eDNA) has been known as a useful tool to detect aquatic and semi-aquatic species through 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 net and diving, eDNA could provide more species information and less harm to the wild lifes (Jerde et al. 2011, Sales et al. 2021). This study applied eDNA technology to furnish valuable data so that enriches database of tropical marine fish, which is benefit to protect ecosystem of the South China Sea.

Sampling methods

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

Sampling description: The sampling protocols reference (Xing et al. 2022), and the main steps are as follows: the shallow seawater samples were collected using a 3L hydrophore at 6 sampling sites at waters surrounding WZZ in June, 2022, as well as January and September, 2023, the Hainan Province, P.R.mChina (Fig. 1). The distance between two sampling sites is not less than 1 km. The three replicate 1L water samples were collected at each sampling site (Fig. 2). The eDNA was collected by 0.45 μ m MCE membrane filtration (Pall Whatman, UK) from water samples, and the 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 follow the protocols of the kit. Before DNA extraction, the experimental bench sterile operating table and experimental equipment was regularly cleaned using 5% bleach first and then 75% ethanol, to prevent contamination. The extracted DNA samples were stored at -20°C for subsequent experiments. PCR amplification was performed using "MiFish-U" primer sets for fish multiple species detection (Forward :GTCGGTAAACTCGTGCCAGC, Reverse:

CATAGTGGGGTATCTAATCCCAGTTTG) (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 μ l volume, containing 4 μ l of 5 \times FastPfu Buffer, 2 μ l of 2.5 mM dNTPs, 0.8 μ l Forward Primer (5 μ M), 0.8 μ l Reverse Primer(5 μ M), 0.4 μ l FastPfu Polymerase, 10 ng of Template DNA and 12 μ l ddH₂O. The PCR reaction conditions were following: pre-denaturation for 5 min at 95 $^{\circ}\text{C}$, followed by 32 cycles of denaturation (30sec at 95 $^{\circ}\text{C}$), annealing (30sec at 55 $^{\circ}\text{C}$) and elongation (45sec at 72 $^{\circ}\text{C}$), and final elongation for 10 min at 72 $^{\circ}\text{C}$. And two negative controls (PCR blank) were set in each PCR reaction, so as to monitoring contamination. The PCR products at each sampling site were verified on 2%

agarose gels and then pooled in equal volumes. 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.

The original sequences obtained from the Illumina's Novaseq platform were initially processed using QIIME 2 software (Bolyen et al. 2019). The end sequence is demultiplexed based on the tags and primers are removed from the end. The reading is then trimmed to 160-180 bp using CUTADAPT software (Martin 2011). Next, the data obtained by sequencing were spliced and filtered to obtain high-quality sequences, which were clustered into MOTUs using VSEARCH software with 97% similarity (Zhang et al. 2019). Finally, the sequences of MOTU 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 match and $\geq 97\%$ identity, then specify the lowest taxonomic level (i.e. genus or family) that contains all these species, c) If the query sequence matches a non-native species in the NCBI with $\geq 97\%$ identity, and this non-native species belongs to the same genus as the known native species, so that genus is 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>).

Geographic coverage

Description: We surveyed six localities at the sea area surrounding WZZ (Fig. 1). The investigation involved nearly 249325.426 m² measured using ArcGIS 10.8 software.

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

Taxonomic coverage

Description: In total, 17 orders, 63 families, 124 genera and 188 fish species were detected used eDNA at the area surrounding WZZ.

Taxa included:

Rank	Scientific Name
kingdom	Animalia
phylum	Chordata
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	Belonidae
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>Cirrhitus</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>Sphyraena</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 mccllelandi</i> Thompson, 1840
species	<i>Caesio caeruleaurea</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>Cirrhites 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>Ellochelone 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>Engyprosonon multisquama</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 erythrouus</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 kuntzei</i> Valenciennes, 1831
species	<i>Neopomacentrus cyanomos</i> (Bleeker, 1856)
species	<i>Nuchequula 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>Salarias 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>Sphyaena 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>Thalassoma</i> sp.
species	<i>Siganus</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

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Data resources

Data package title: Fish taxon-occurrences surrounding WZZ, Hainan Province, P.R. 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 at the waters surrounding WZZ, also include the latitude and longitude information of the sampling sites. The important information including taxonomic, geographic location of the occurrence and habitat condition were 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 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

Total 179 fish species and 9 fish genera were detected using eDNA surrounding WZZ, and fish fauna was analyzed (Fig. 3). At the order level, Perciformes included the most species (n=130), accounting for 69.15% of 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 the Tetraodontiformes both had eight species, accounting for 4.26%, respectively. The Atheriniformes and Beloniformes both included three species, separately accounting for 1.60%, as well as the Pleuronectiformes

contained two species and accounted for 1.06%. The rest orders, Aulopiformes, Beryciformes, Carcharhiniformes, Elopiformes, Gadiformes, Gasterosteiformes, Myliobatiformes, Scorpaeniformes and Siluriformes, all harbored 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%). The most families had only one species (Fig. 3).

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. Total 115 fish species belonging to 11 orders and 49 families and a total of 174 fish species belonging to 2 classes, 12 orders, 65 families and 123 genera were investigated at WWZ through trawlnets in 2019 and 2020-2021, respectively (Wang et al. 2021, Luo et al. 2023). According to our results, the 188 fish species were detected, which could indicated that eDNA could supplied more fish species comparing to traditional fishing nets. Although there are some species cannot be annotated using NCBI database or only be identified at genus or family level based on MOTUs sequences, the eDNA datasets established in this study can help us to solve this problem to a certain extent.

Acknowledgements

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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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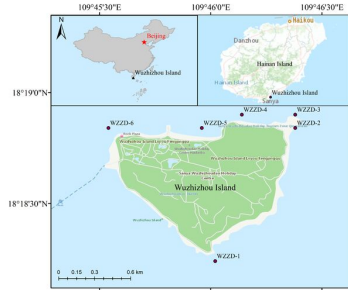


Figure 1.
Location of eDNA sampling sites.

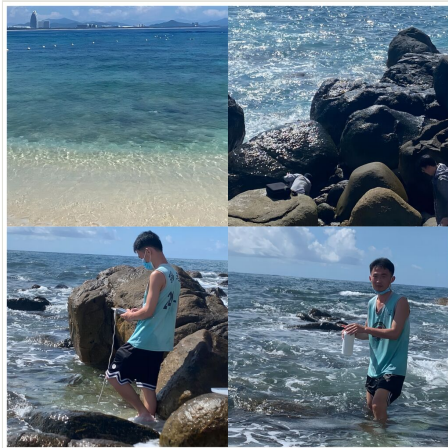


Figure 2.
Photographs of marine habitats and field sampling around WZZ.

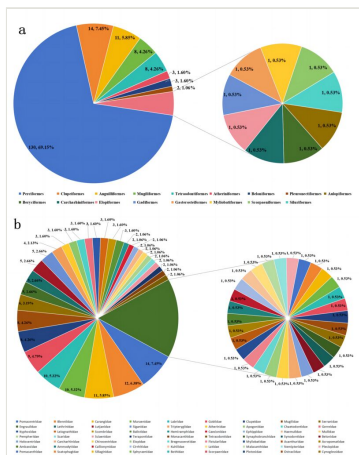


Figure 3.
 Figure 3. The composition of fish species of area surrounding the WZZ (a: at the order level, b: at the family level).

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

Supplementary materials

Suppl. material 1: Fish taxon-occurrences surrounding WZZ, Hainan Province, P.R.China based on eDNA

Authors: ChongzhaoWang, 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 at the waters 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 were provided.

[Download file](#) (239.22 kb)

Suppl. material 2: MOTUs information of marine fish detected by eDNA

Authors: ChongzhaoWang, 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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