

Molecular approaches to enhancing fish egg monitoring in the Pacific waters off Japan

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Egg and Larval Surveys

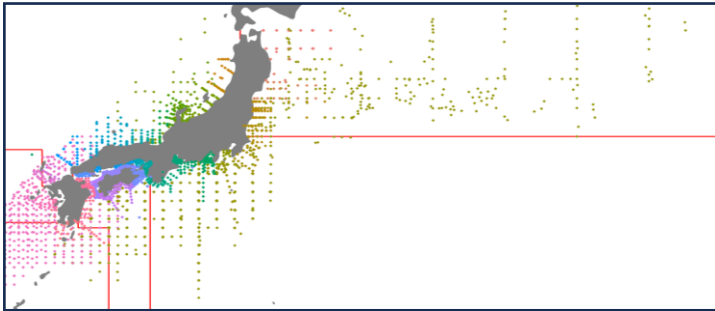
Purpose:

1. Monitoring the distribution of eggs and larvae.
2. Estimating the egg abundance and similar indicator values of egg and larvae distribution for use in resource assessment and basic research.

Analysis Targets: Eggs and larvae of multiple fish species, including sardine, anchovy, herring, and mackerel.

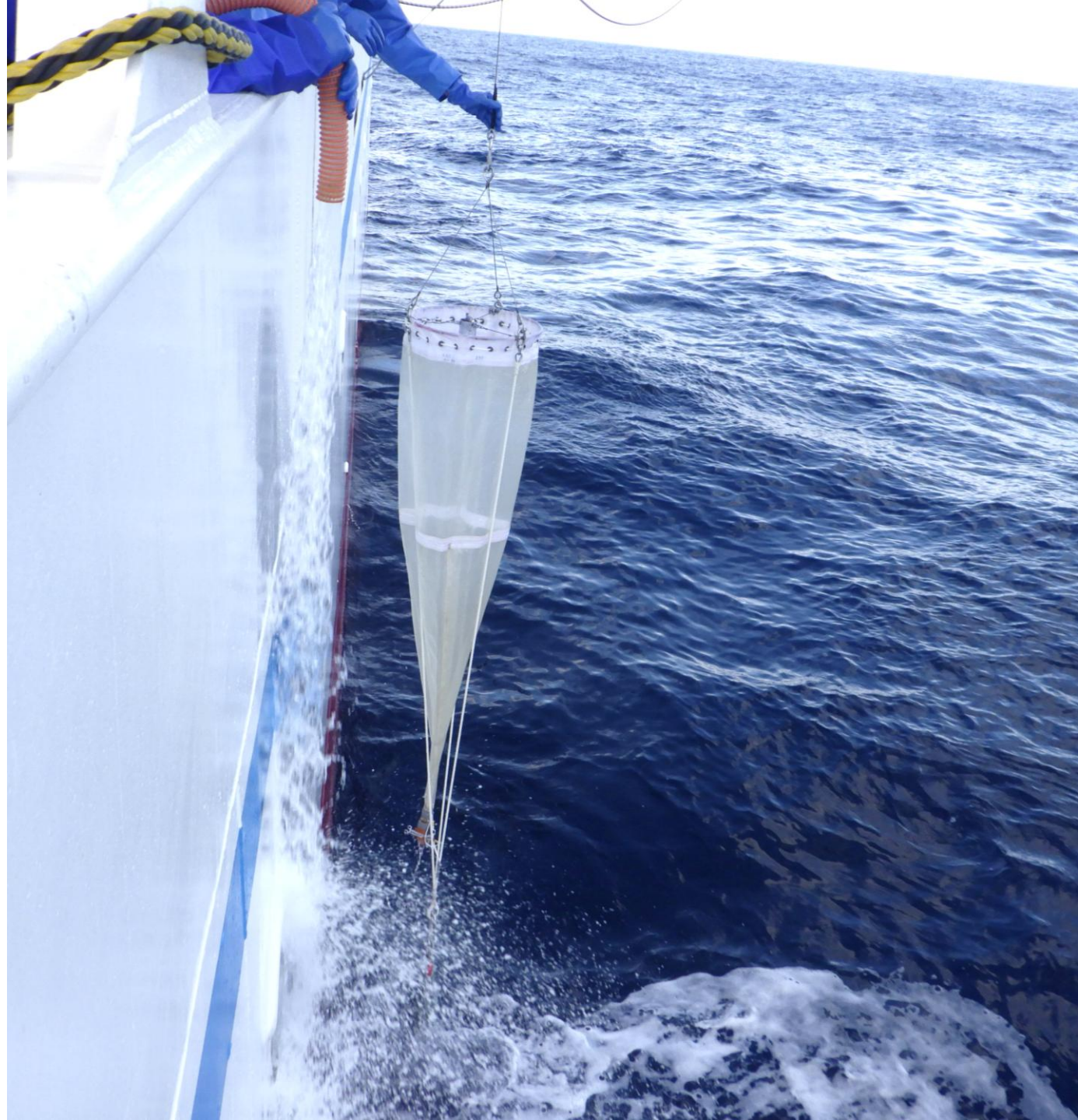
Survey Area:

(Example from Japan)



Fixation: 5% formalin

Identification: morphological characteristics



Traditional Identification Methods

- **Accurate identification** is crucial for:

- Estimating species distribution
- Understanding spawning patterns

- However, this method has **several limitations**:

- Time-consuming
- Heavily dependent on expert knowledge
- Lack of detailed information

➔ These issues lead to:

- **Difficulty in accurate identification**
- **Limited understanding of marine ecosystems**



Identifiability of species after fixation	number of species	example
Identification is possible	26	<i>Sardinops melanosticta</i> <i>Engraulis japonicus</i> <i>Etrumeus micropus</i> <i>Konosirus punctatusniphonius</i> <i>Trachurus japonicus</i>
Identifiable to a large taxonomic group is possible	46	<i>Beryx splendens</i>
Identifiable to species level in the late developmental stage	1	<i>Lateolabrax japonicus</i>
Identifiable to a large taxonomic group is possible at a late stage of development	15	<i>Trichiurus japonicus</i>
Identification is not possible	100	<i>Laemonema longipes</i> <i>Physiculus japonicus</i> <i>Seriola quinqueradiata</i>
Information insufficient to make a determination	46	
No information on eggs	other species*	

*Japanese fish species: 4210 species (Nakabou *et al.* 2013)



The types of eggs listed in the Japanese Fish Egg Guide (e.g. Ikeda *et al.* 2014), classified by morphological characteristics.

➡ Only a small number of species can be identified morphologically.

DNA Barcoding Introduction

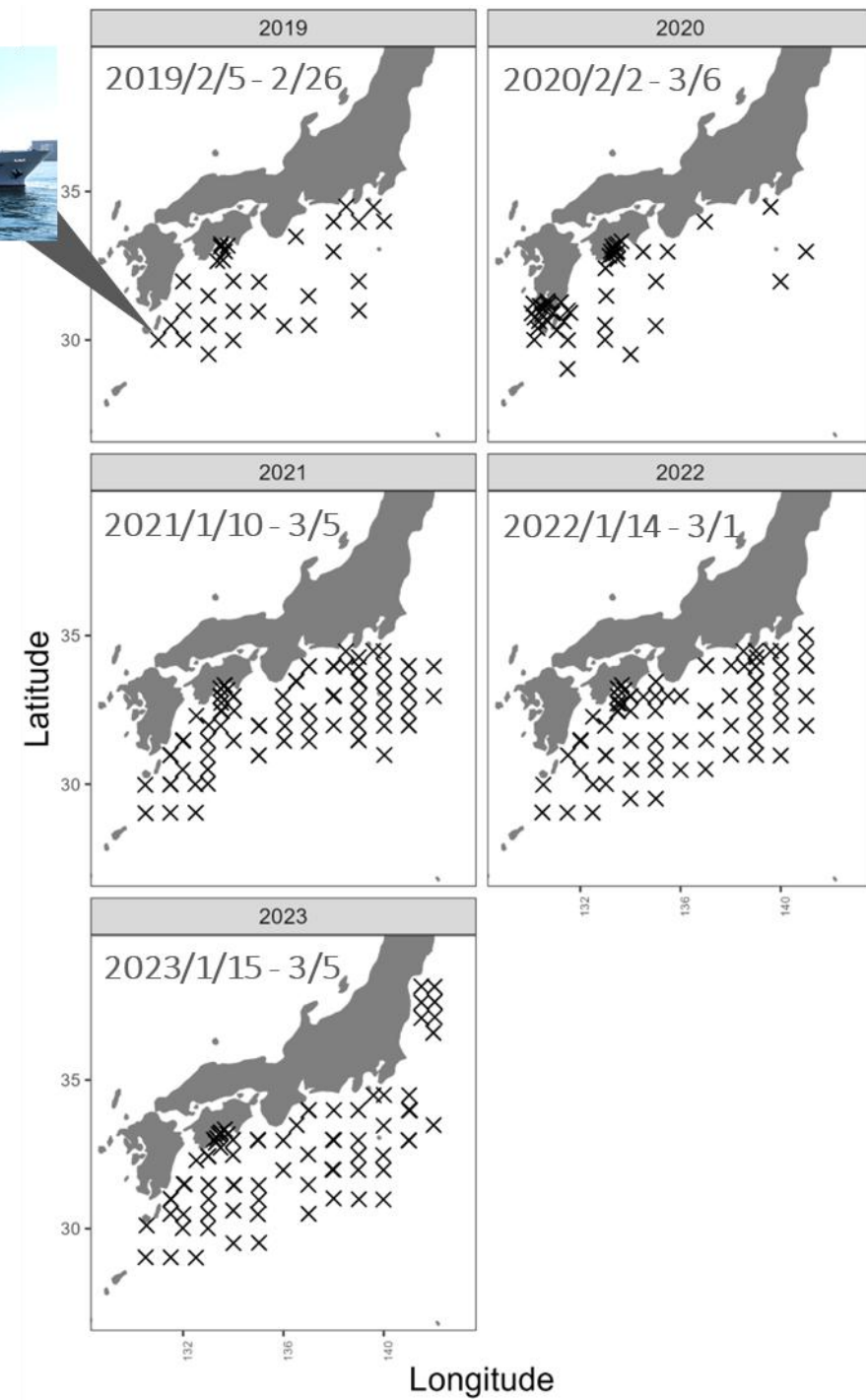
- **DNA barcoding** used to compare sequences with reference databases
 - Helps identify **spawning areas** and estimate **biomass** (Saitoh et al., 2009; Neira et al., 2015).
 - Traditional methods are **slow** and **contamination-prone**
- **Next-generation sequencing (Illumina MiSeq)** for **barcoding**
 - Fast and high-throughput
 - Effective for **mixed samples**
- **Universal primers** used to identify eggs to **genus or species level** (Miya et al., 2015)
 - Enables estimation of **relative abundance**

This method is faster, more reliable, and better suited for assessing fish egg diversity.

Materials and Methods

Egg Sampling and Preservation

- Covered inshore and offshore spawning grounds of small pelagic fish.
- January–March 2019–2023
- Specifications:
 - Diameter: 0.45 m
 - Mesh size: 0.335 mm
- Vertical towing

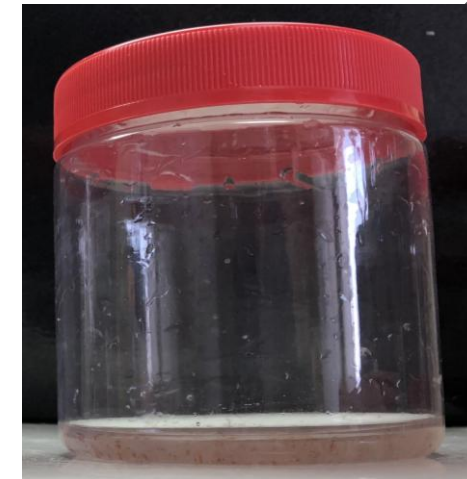
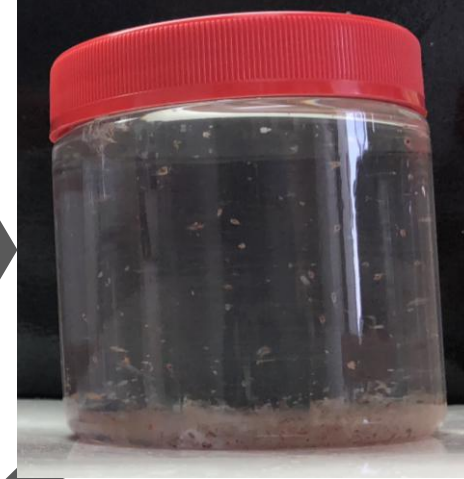


Materials and Methods

Specimen Processing Procedure for Plankton Samples

Method 1 (2019-2021)

- 1) **Sedimentation:** Allow the sample to settle for approximately 15 minutes.
- 2) **Removal of Excess Seawater:** Drain as much excess seawater as possible.
- 3) **Preservation:** Add 99% ethanol and a label to the sample. Store the sample in a freezer.



Materials and Methods

Specimen Processing Procedure for Plankton Samples

Method 2 (2022-2023)

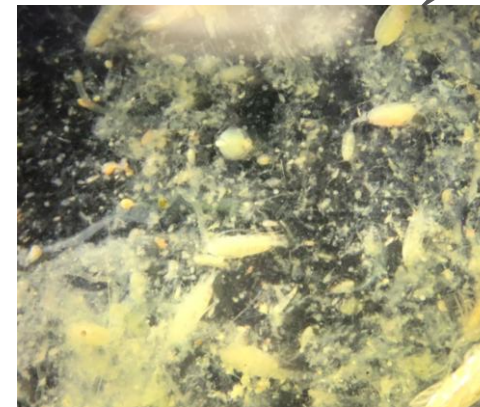
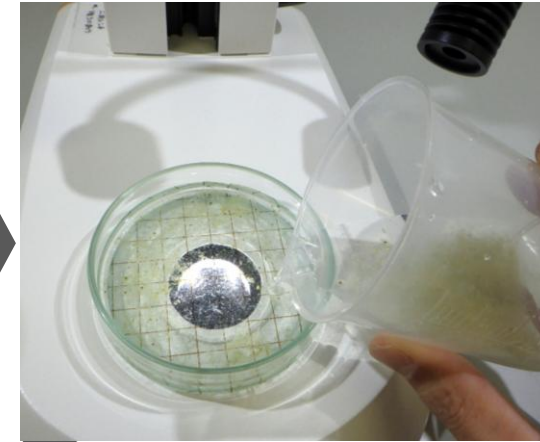
- 1) **Filtration:** Pour the plankton net sample into a tea strainer.
- 2) **Preservation:** Submerge the tea strainer with the sample in 99% ethanol. Store the sample in a freezer.



Materials and Methods

Morphological Identification of Fish Eggs

- Samples preserved in **5% formaldehyde** for morphological identification
- Eggs examined under **light microscopy** based on key traits:
 - Shape
 - Yolk and oil globules
 - Chorion texture
- Species identified:
Engraulis japonicus, *Etrumeus micropus*, *Laemonema longipes*, *Sardinops melanosticta*, *Scomber japonicus*, *Scomber australasicus*, *Trachurus japonicus*



Scomber japonicus



Engraulis japonicus

Materials and Methods

DNA Extraction and Analysis

DNA Extraction:

1. NaOH buffer or TE buffer
2. Crush egg, ultrasonicate at 55° C for 2 hours (2019 only).
3. Heat at 97° C for 20 minutes, neutralize with 1 M Tris–HCl (2019 only).

PCR and Sequencing:

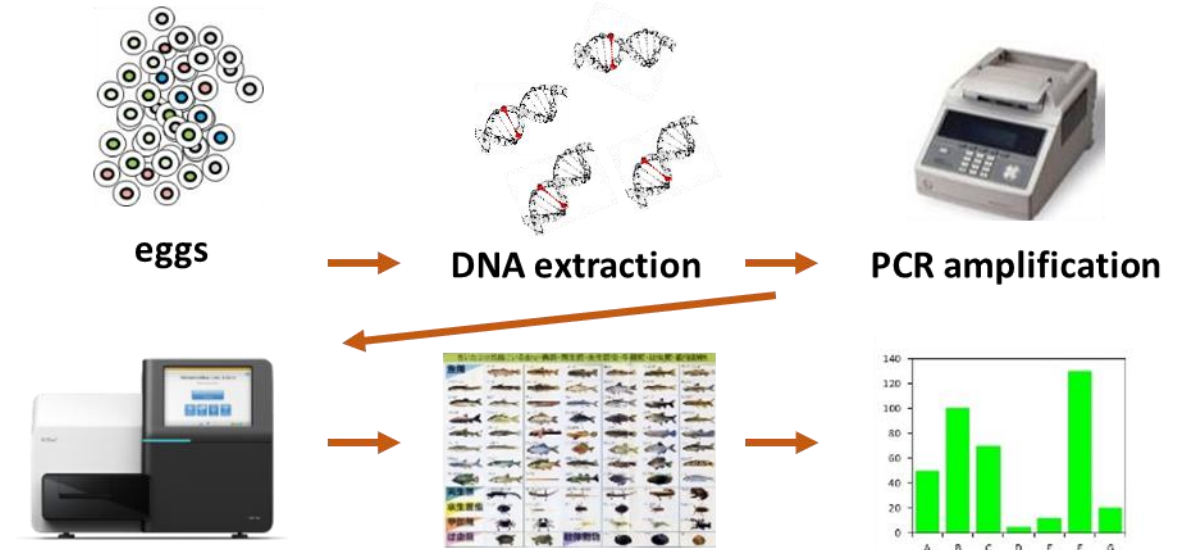
1. Amplify 12S rRNA genes with MiFish primers.
2. Two-step PCR:
 - First PCR: 1.0 µL DNA, 9 µL water, 12.5 µL GoTaq, 1.25 µL primers.
 - Conditions: 95° C for 3 min, 35 cycles of 95° C for 30 s, 60° C for 30 s, 72° C for 30 s.
 - Second PCR: Diluted first PCR products, dual-index primers. Conditions: 94° C for 3 min, 10-12 cycles of 94° C for 15 s, 59° C for 30 s, 68° C for 40 s.
1. Verify, purify, quantify, pool, and store at -30° C.

Bioinformatics:

1. Demultiplex, trim, filter, merge, align, and count operational taxonomic units (OTUs).
2. Deposit data in DDBJ.

Taxonomic Identification:

1. Download mtDNA, BLAST search.
2. Merge OTUs, detect and merge artificial OTUs.
3. Identify dominant OTUs (identity >0.980).

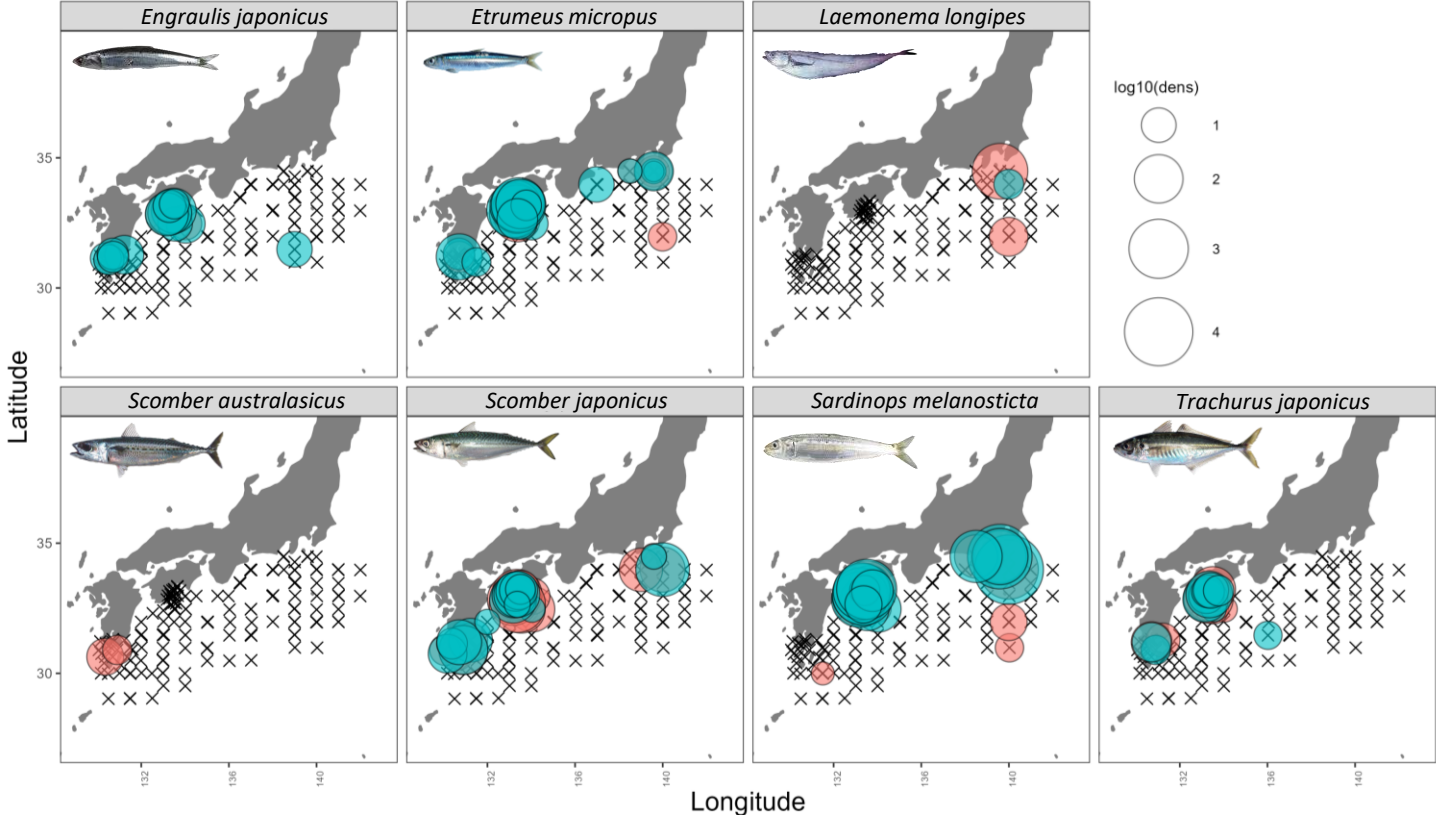


Results

Evaluating Ethanol Fixation Techniques: DNA vs. Morphological ID

Method 1
(2019-2021)

● Formalin-fixed
for morphological ID ● Supernatant discarded,
ethanol-fixed for DNA ID



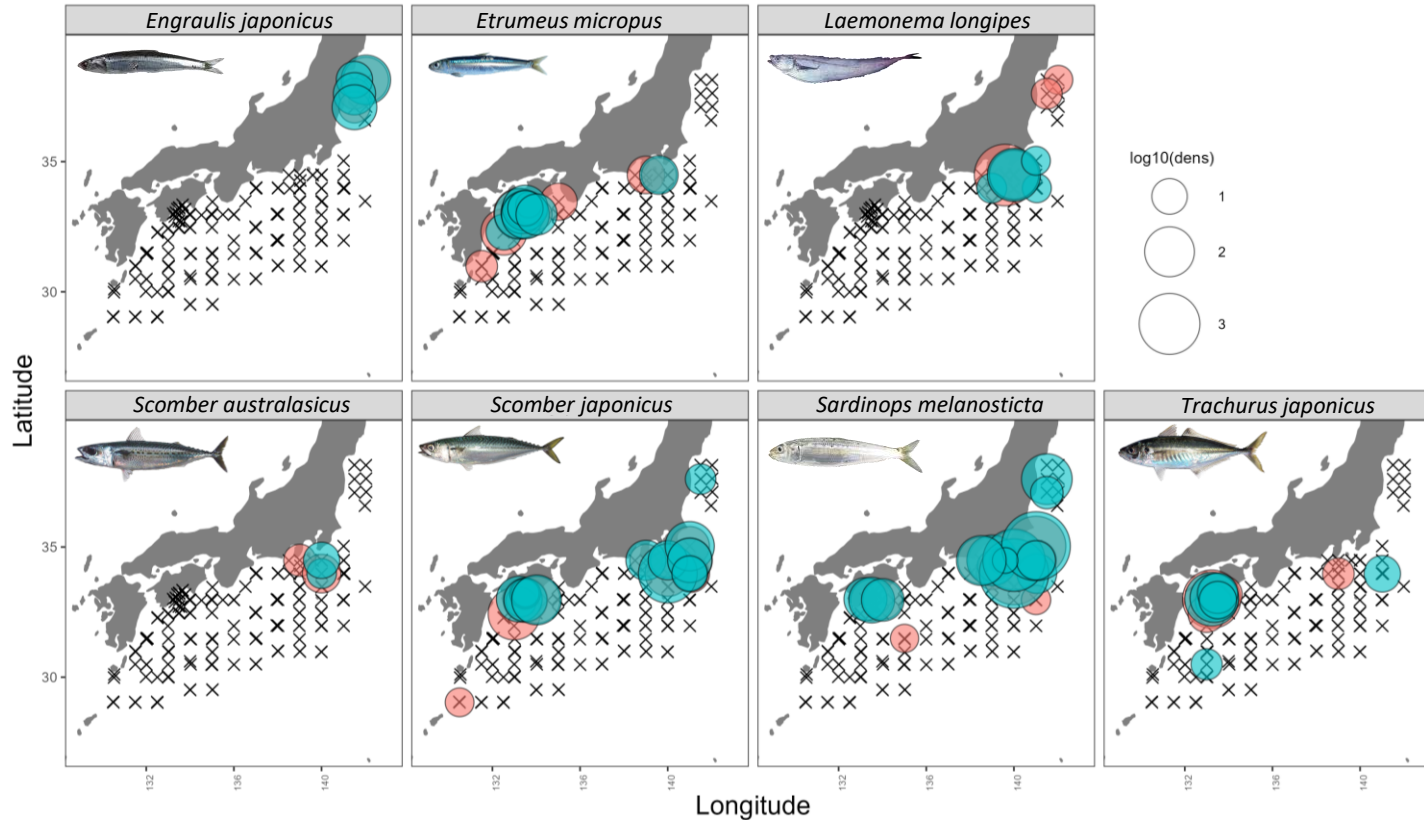
Results

Evaluating Ethanol Fixation Techniques: DNA vs. Morphological ID

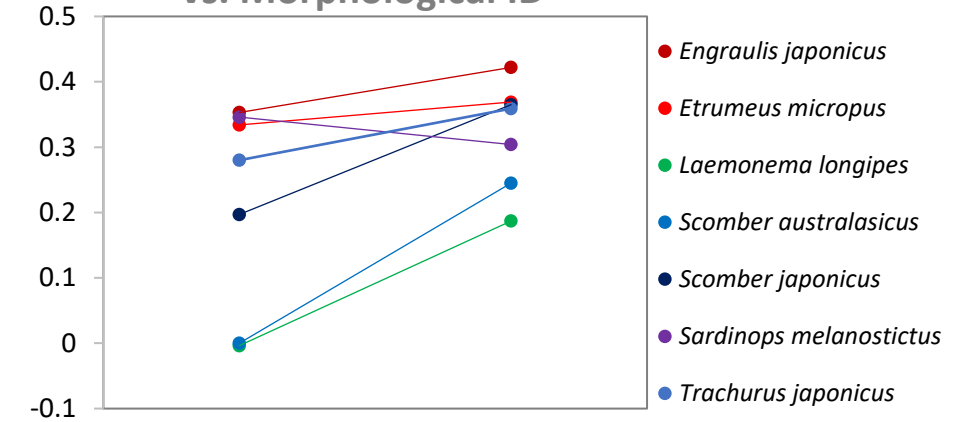
Method 2 (2022-2023)

● Formalin-fixed
for morphological ID

● Filtering with a Strainer,
ethanol-fixed for DNA ID



Cohen's Kappa vs. Morphological ID



Supernatant
discarded

Method 1 (2019-
2021)

Filtering with
a Strainer

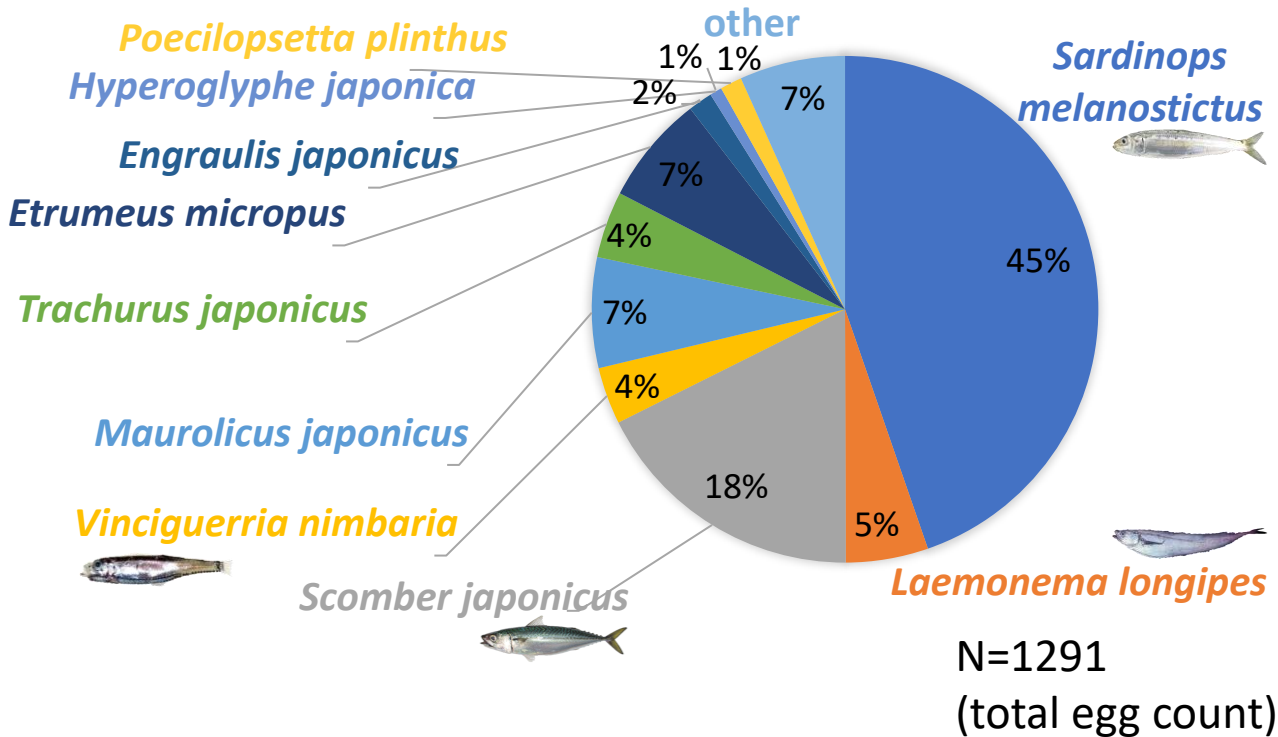
Method 2 (2022-
2023)

➡ The method using a strainer showed occurrences more closely aligned with morphological identification.

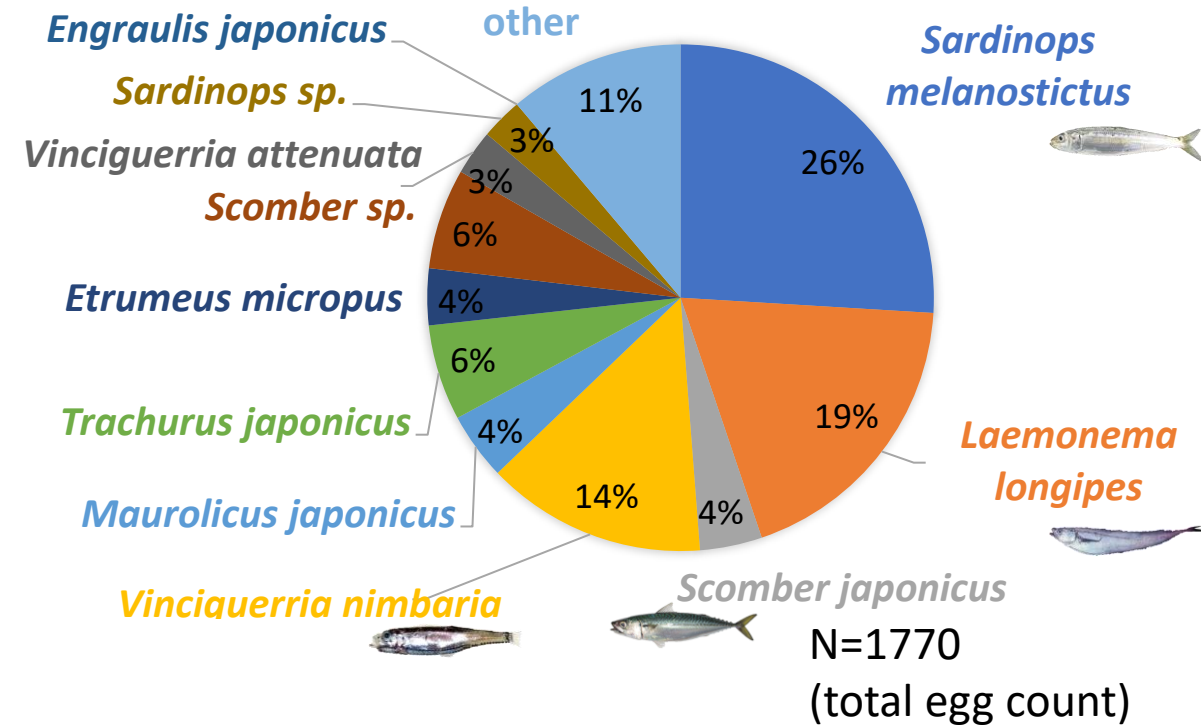
Results

Yearly Comparison (2019–2023)

2019-2021



2022-2023



➡ *Sardinops melanosticta*, *Laemonema longipes*, *Scomber japonicus*, and *Vinciguerrria nimbaria* account for 60% of occurrences. The proportion of species varies by year.

Results

Overview of Identified Fish eggs

family	species	family	species	family	species
Clupeidae	<i>Sardinops melanosticta</i>	Moridae	<i>Gadella jordani</i>	Bramidae	<i>Brama japonica</i>
	<i>Sardinops sp.</i>		<i>Laemonema longipes</i>		<i>Brama sp.</i>
Dussumieriidae	<i>Etrumeus micropus</i>		<i>Physiculus japonicus</i>	Caristiidae	<i>Caristius macropus</i>
Engraulidae	<i>Engraulis japonicus</i>	Macrouridae	<i>Coelorinchus hubbsi</i>	Sparidae	<i>Rhabdosargus sarba</i>
Argentinidae	<i>Glossanodon semifasciatus</i>		<i>Coelorinchus macrochir</i>		
Microstomatidae	<i>Lipolagus ochotensis</i>		<i>Nezumia convergens</i>		
Gonostomatidae	<i>Sigmops gracilis</i>	Melamphaidae	<i>Scopeloberyx sp.</i>		
Sternoptychidae	<i>Maurolicus japonicus</i>	Berycidae	<i>Beryx sp.</i>		
	<i>Polyipnus matsubarai</i>	Trachichthyidae	<i>Aulotrachichthys sp.</i>		
	<i>Sternoptyx diaphana</i>	Aulostomidae	<i>Aulostomus chinensis</i>		
Phosichthyidae	<i>Vinciguerrria attenuata</i>	Macroramphosidae	<i>Macroramphosus sp.</i>		
	<i>Vinciguerrria nimbaria</i>	Mugilidae	<i>Mugil cephalus</i>		
Chauliodontidae	<i>Chauliodus macouni</i>	Atherinidae	<i>Atherion elymus</i>		
	<i>Chauliodus sloani</i>	Triglidae	<i>Chelidonichthys sp.</i>		
	<i>Chauliodus sp.</i>		<i>Lepidotrigla guentheri</i>		
Melanostomiidae	<i>Opostomias mitsuii</i>		<i>Lepidotrigla sp.</i>		
Stomiidae	<i>Stomias atriventer</i>	Hoplichthyidae	<i>Hoplichthys fasciatus</i>		
	<i>Stomias sp.</i>		<i>Hoplichthys sp.</i>		
Synodontidae	<i>Synodus cf. oculus</i>	Howellidae	<i>Howella sp.</i>		
	<i>Synodus sp.</i>	Serranidae	<i>Caprodon schlegelii</i>		
Myctophidae	<i>Benthosema pterotum</i>		<i>Selenanthias analis</i>		
	<i>Dasyscopelus asper</i>	Callanthiidae	<i>Callanthias japonicus</i>		
	<i>Nannobrachium sp.</i>	Branchiostegidae	<i>Branchiostegus sp.</i>		
	<i>Notoscopelus japonicus</i>	Scombroidae	<i>Scombrops boops</i>		
	<i>Symbolophorus californiensis</i>	Carangidae	<i>Kaiwarinus equula</i>		
Lophotidae	<i>Lophotus capellei</i>		<i>Trachurus japonicus</i>		

Proportions of Identified Eggs by Taxonomic Level

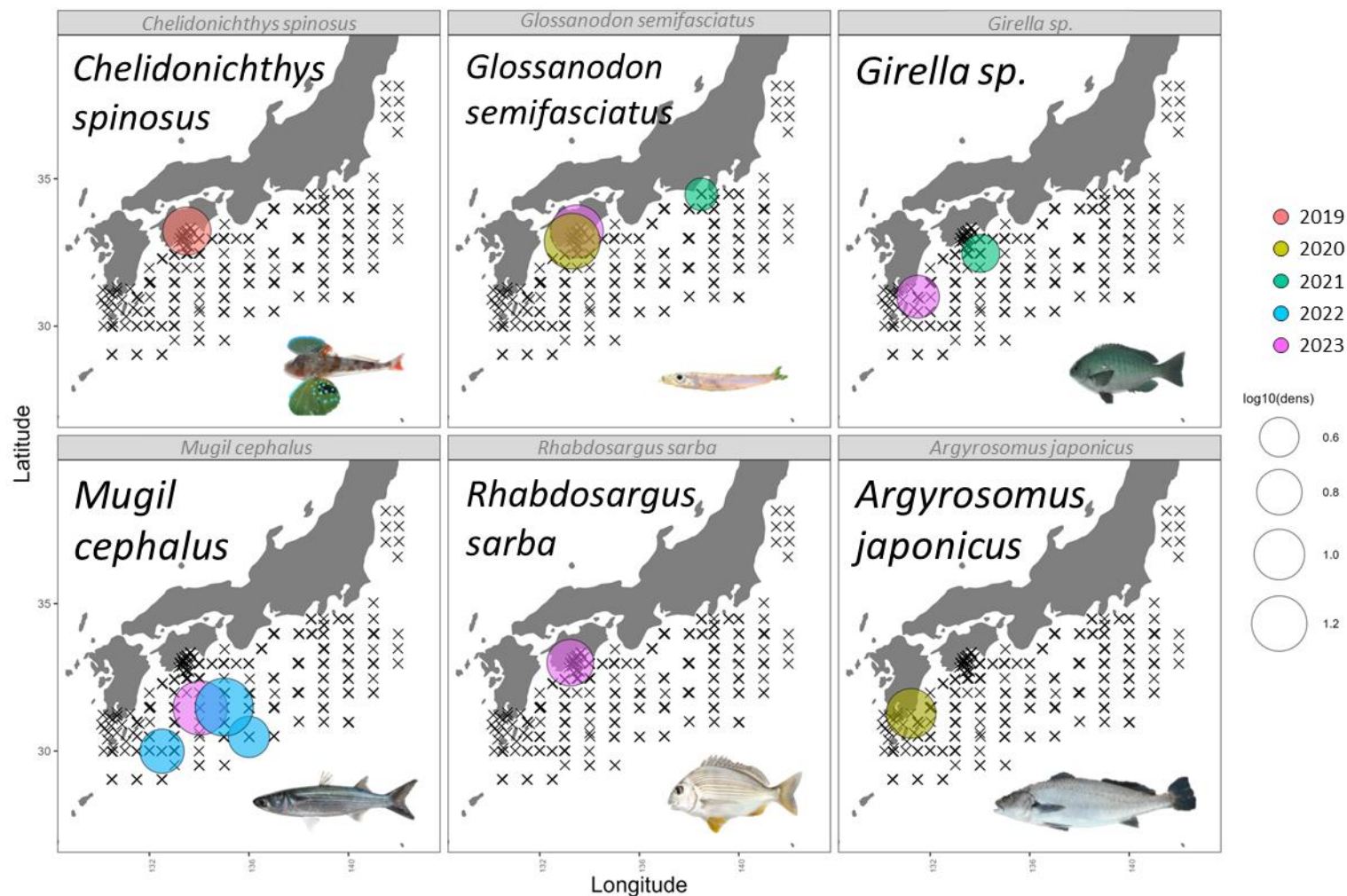
Taxonomic Level	Proportion
species level	69%
genus level	26%
family level	5%

N=80
(number of OTUs)

	<i>Scomber japonicus</i>
	<i>Scomber sp.</i>
	<i>Glyptocephalus zachirus</i>
	<i>Poecilopsetta plinthus</i>
	<i>Cynoglossidae sp.</i>

Results

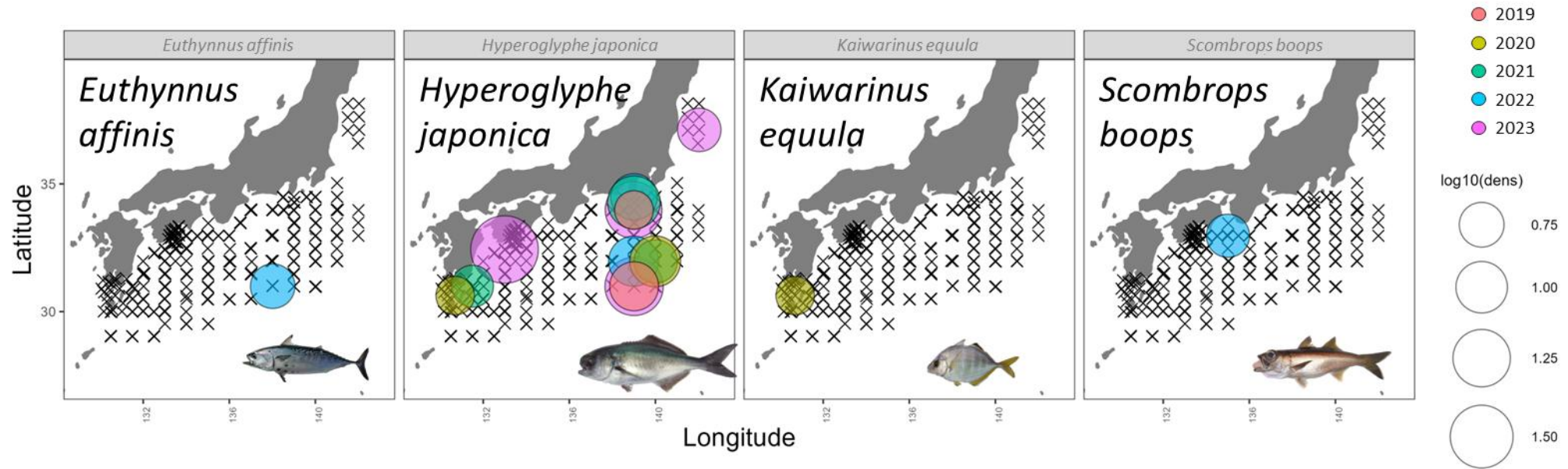
Newly Recorded Key Fish eggs



➡ They are an important commercial fish, but their eggs had never been recorded in the region before.

Results

Species with No Prior Morphological Descriptions



➡ These species are also important commercial fish, but there is no information on the morphology of their eggs. This is the first insight into their distribution.

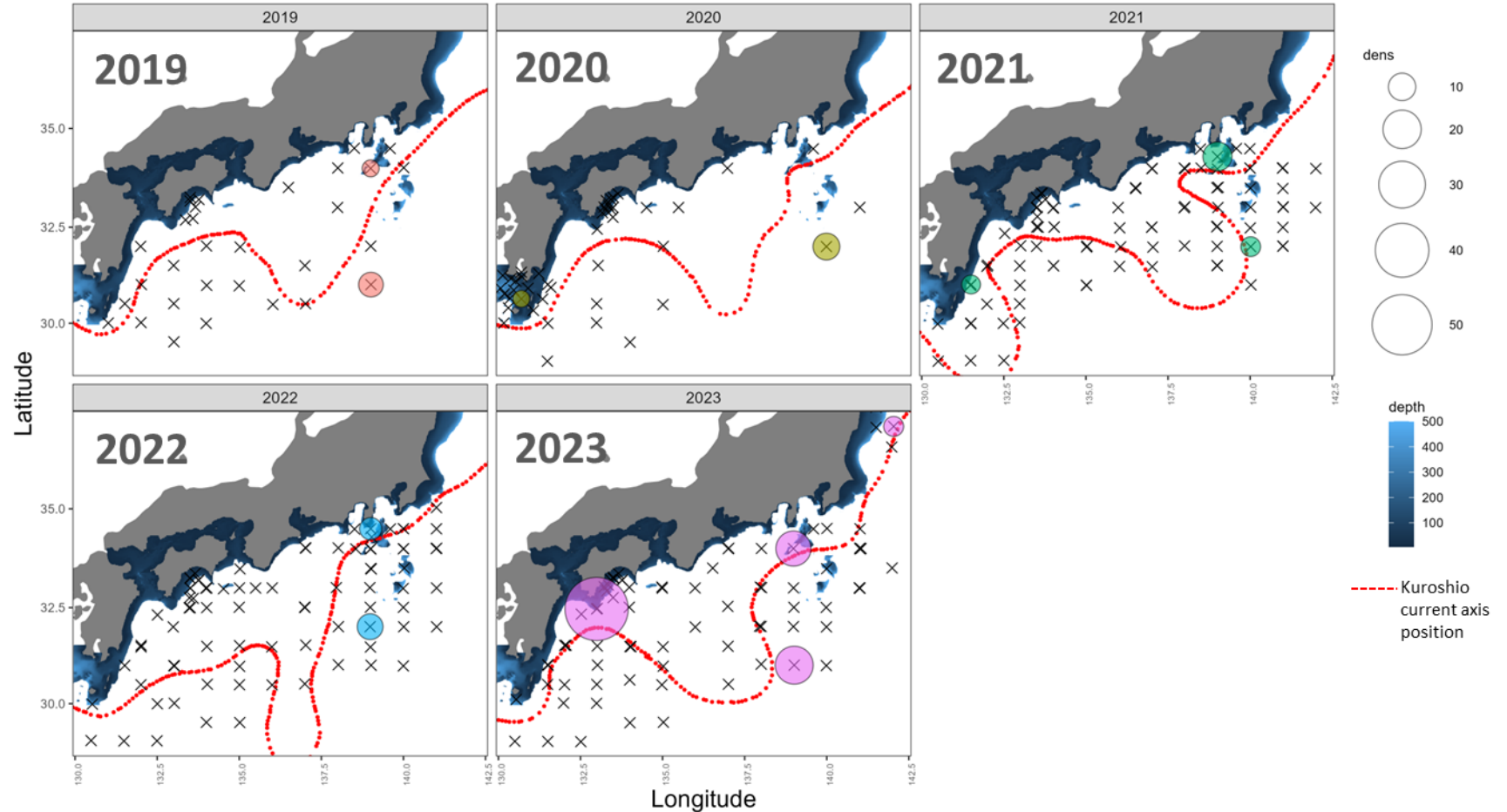
Results

Species with No Prior Morphological Descriptions

Hyperoglyphe japonica

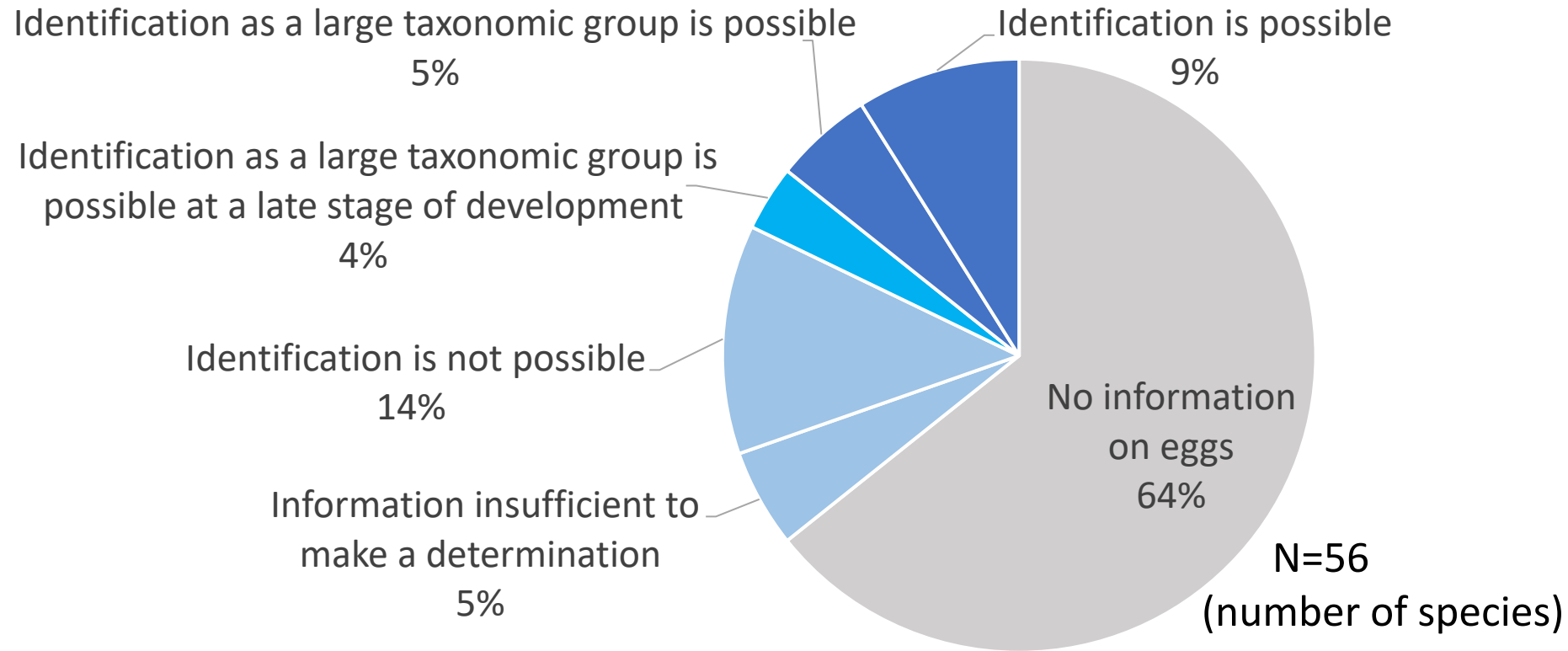


- Mid-water zones near Japan
- Deep-sea handline fishing — around the Izu Islands and off the Kii Peninsula



➡ The eggs of *Hyperoglyphe japonica* have been identified around the Satsunan and Izu islands, providing valuable information for estimating spawning grounds.

Morphological Identification Possibilities



The types of eggs listed in the Japanese Fish Egg Guide (e.g. Ikeda *et al.* 2014), classified by morphological characteristics.

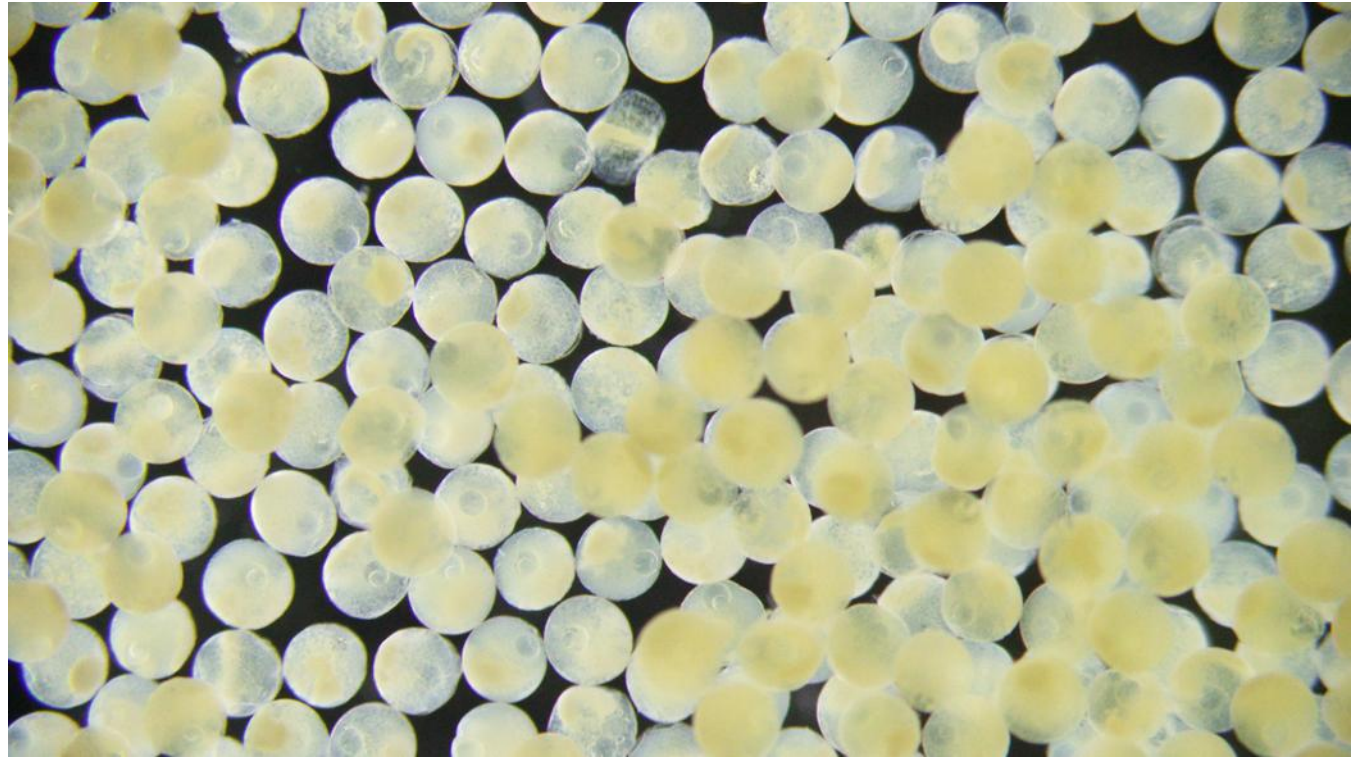
➡ 64% of which lack morphological trait information. Only 9% of the remaining species can be identified at the species level.

Significance of the Study

- A wide range of species was detected, including those lacking prior morphological descriptions
- Eggs of commercially important species were found, offering new occurrence records
- The method is applicable to many species, allowing comprehensive assessment of egg diversity



Thank you for your attention



Diaphus theta