



### A preliminary report on the implementation of eDNA-based techniques to biodiversity monitoring of fish from the Far East of Russia

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### Map of where we are





### Why do we need to use aquatic eDNA for it?

- 1. All we need is water.
- 2. There is no need to physically locate and/or capture individuals to determine whether it is present in the area.
- 3. The cost of surveys is relatively low.



Fish eDNA studies on the Far East of Russia are now concentrated on:

- Building the DNA barcode reference library based on the *COI* and *12S* rRNA mitochondrial markers. There are about 1200 fish species documented to date in Russia (including 35 endangered species).
  Reference database is still half-completed.
- **2. Express-monitoring** of **specially protected natural areas** (Far Eastern Marine Reserve) including detection of invasive species.
- 3. Non-invasive monitoring of endangered and threatened species:

- Sakhalin sturgeon (*Acipenser mikadoi* Hilgendorf, 1892)

1. Collecting eDNA.



### How do we use it



A modified sealant gun :)



### 2. eDNA isolation.



Modified backflushing technique (Kesberg, Schleheck, 2013)

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Modified backflushing technique (Kesberg, Schleheck, 2013)

Commercial kit whish is based on magnetic beads. Sintol Co., Russia.

### 2. eDNA isolation.





What have we done for today **1. Sakhalin sturgeon eDNA.** 



### Sampling site: Anyuiskiy fish hatchery







Water tank of 1000 liters with 10 sturgeon specimens from 2008 year generation.

In September of 2019 we had filtered 450 ml water from these tanks (0.45 µm syringe-filter) with 3 replicates. DNA is already isolated. <u>We are now developing the</u> <u>species-specific primers and probes</u>.

## 2. The development of express-monitoring techniques for fish species using eDNA.



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2. The development of express-monitoring techniques for fish species using eDNA.



Marine fishes (Sea of Japan/East Sea) TF13, **13 species.** 





Freshwater fishes (Lake Khanka) TF5, **16 species** 



Sturgeons (has no Sakhalin sturgeon) T1, **4 species** 

Touch pool (fishes and invertebrates) T3, **11 species** 

# 2. The development of express-monitoring techniques for fish species using eDNA.

- collecting and isolating eDNA
- implementing metabarcoding techniques with two sets of *twin-tagged* primers Leray COI and 12S rRNA MiFish
- using individual tag pair for each sample (replicate) for PCR
- normalizing and construct the common pool based on both markers
- inspecting the results, dereplicating, filtering, clustering and assigning OTUs to known taxa





Sending for sequencing to Novogen company

### 2. The development of express-monitoring techniques for fish species using eDNA.



Distribution of sequence lengths over all sequences

## 2. The development of express-monitoring techniques for fish species using eDNA.

Metabarcoding data processing was done based on **Begum** pipeline (Zepeda-Mendoza et al., 2016; Yang et al., 2020):

COI	VS	12S rRNA
Dereplication		Dereplication
Clustering (sumaclust)		Clustering (sumaclust)
blasting (blastn)		blasting (blastn)
Building OUT table based on MEGAN output		Building OUT table based on MEGAN output
lulu r package OTUs correction		lulu r package OTUs correction

Visualization

Visualization



Sturgeons T1, 4 species

COI

OTU0051

OTU0118

OTU0172

OTU0243



COI

12S rRNA



Marine fishes (Sea of Japan/East Sea) TF13, **13 species.** 

#### COI







Possible sources of contamination:

- Water intake (we didn't take a sample from it)
- DNA isolation (we didn't sequence a control from it)

In addition:

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- Salmonidae were everywhere

### Acknowledgements

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**Primorsky Aquarium** staff

Anyuiskiy fish hatchery staff

Hank yoy!