Different responses to water temperature in two distinct groups of Pacific cod (Gadus macrocephalus) inhabiting around Japan

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Effects of climate change

http://faostat.fao.org

Shifting distribution

Changing migration patterns

Perry *et al.* (2005), Dulvy *et al.* (2008), Simpson *et al.* (2011)

Impacts in fisheries

- Increasing tropical fish catch Cheung *et al.* (2012)

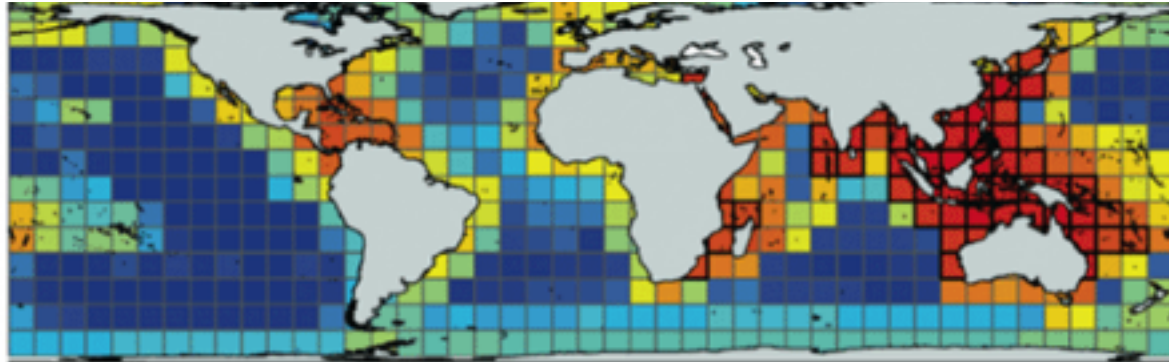- Changes in fishing area Pinsky & Fogarty (2012)
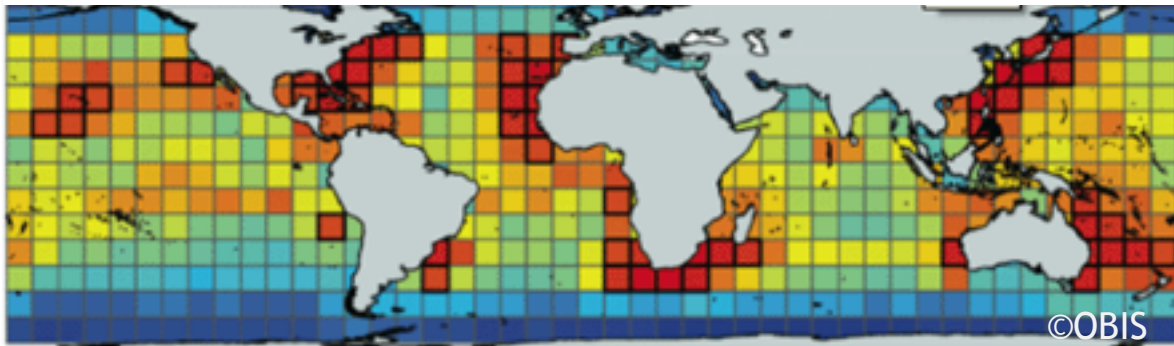
Animal distribution and environment

Many factors are involving to determine current animal distribution

Historical factors and natural selection cause creation of population structure

Coastal taxa

Oceanic taxa

©OBIS

Factors prevents creation of population structure

No obvious physical barriers in ocean

- Pelagic larvae Gaylord and Gaines (2000)

- Passive dispersal Thorson (1950)

- Long distance migration

  Roughgarden et al. (1988)

©FishChannel

Weak genetic structure due to high gene flow

Local adaptation is rare Conover at al. (2006)

Pacific cod *Gadus macrocephalus*

- Widely distributed in the North Pacific
- Mainly ranging along the continental shelf
- The most important species in bottom trawling along the Pacific coast of the northern Japan Narimatsu *et al.* (2010)
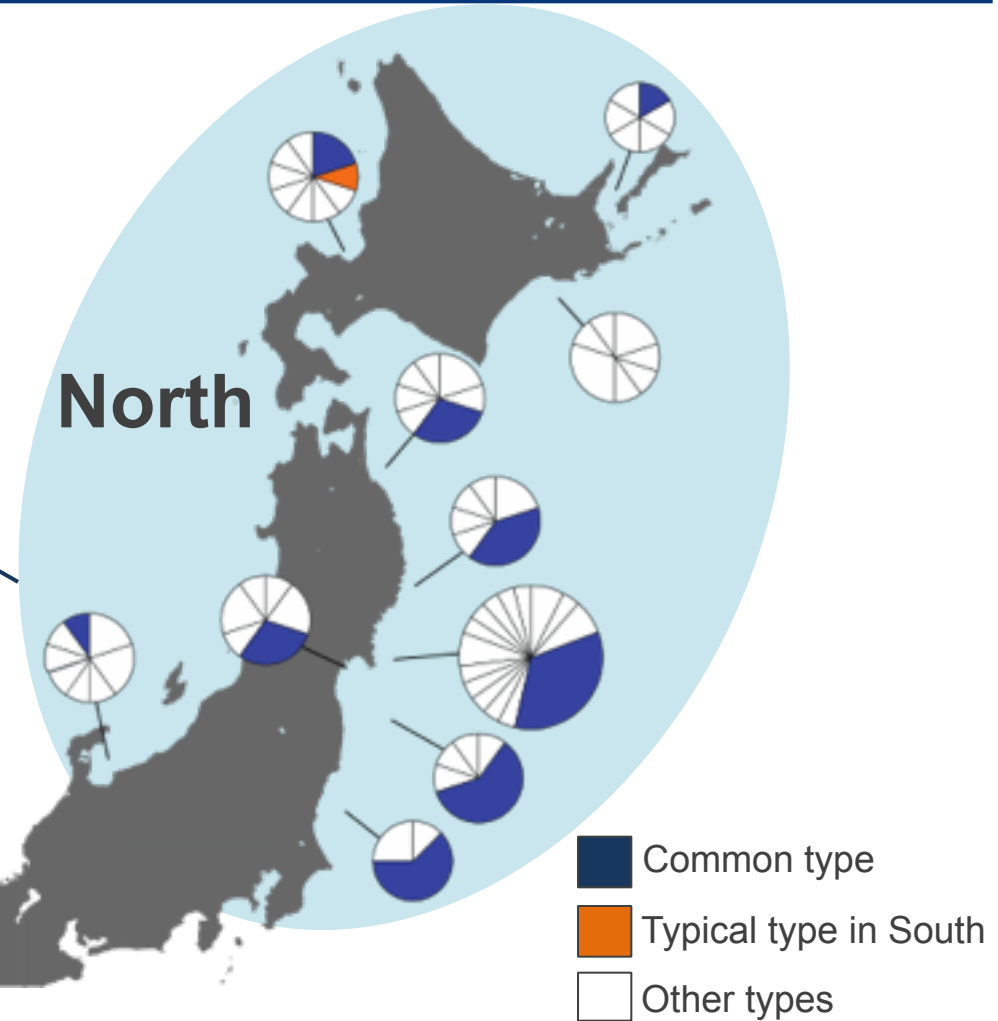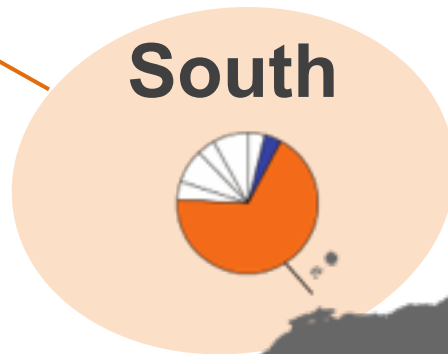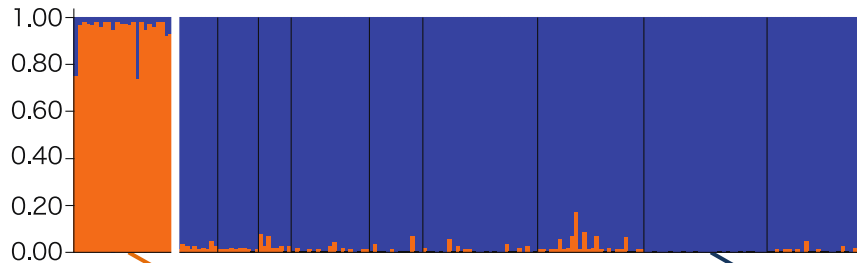
Pacific cod *Gadus macrocephalus*

Pacific cod *Gadus macrocephalus*

Bottom temperature

Japan Sea Proper Water

Oyashio

Tsushima

Kuroshio
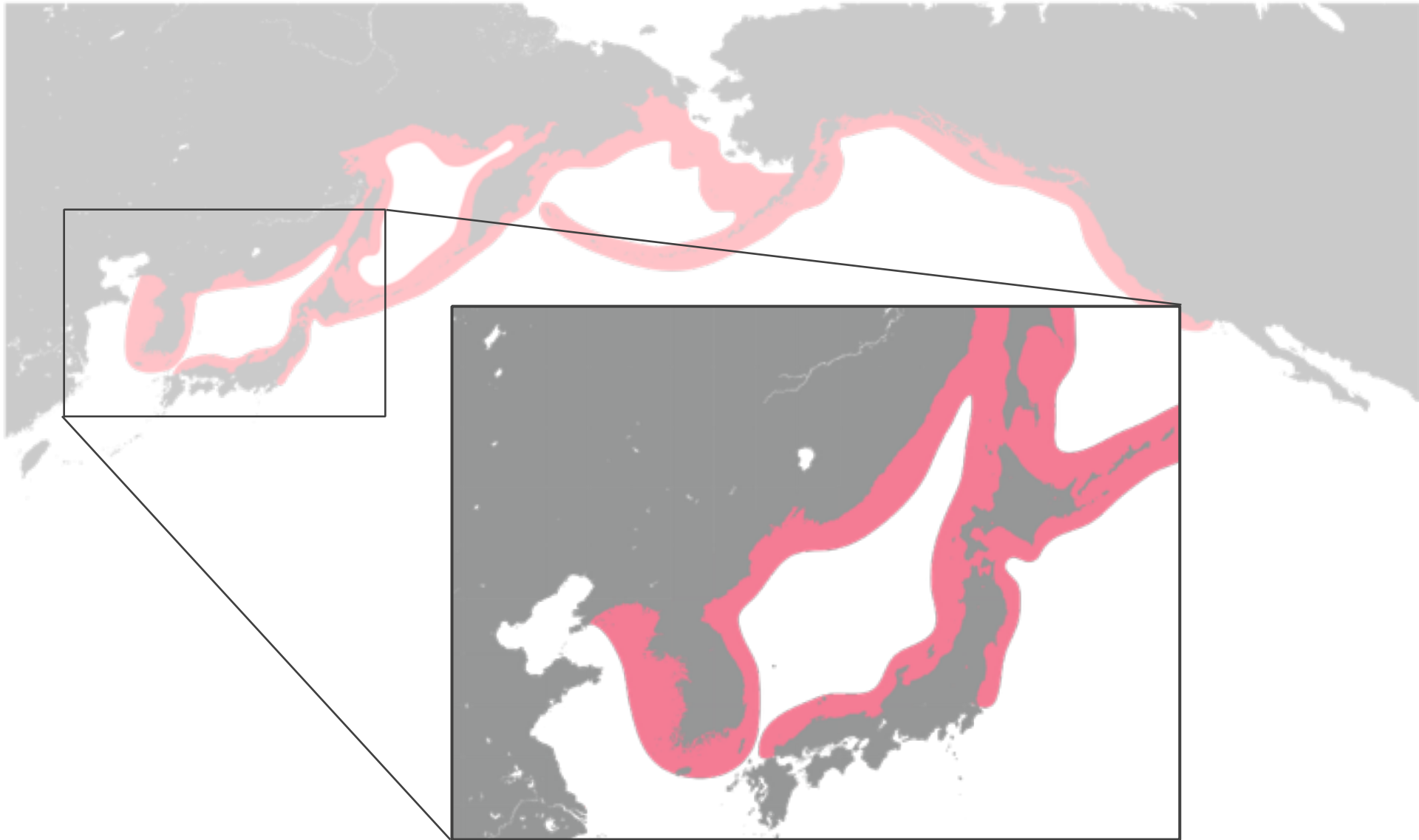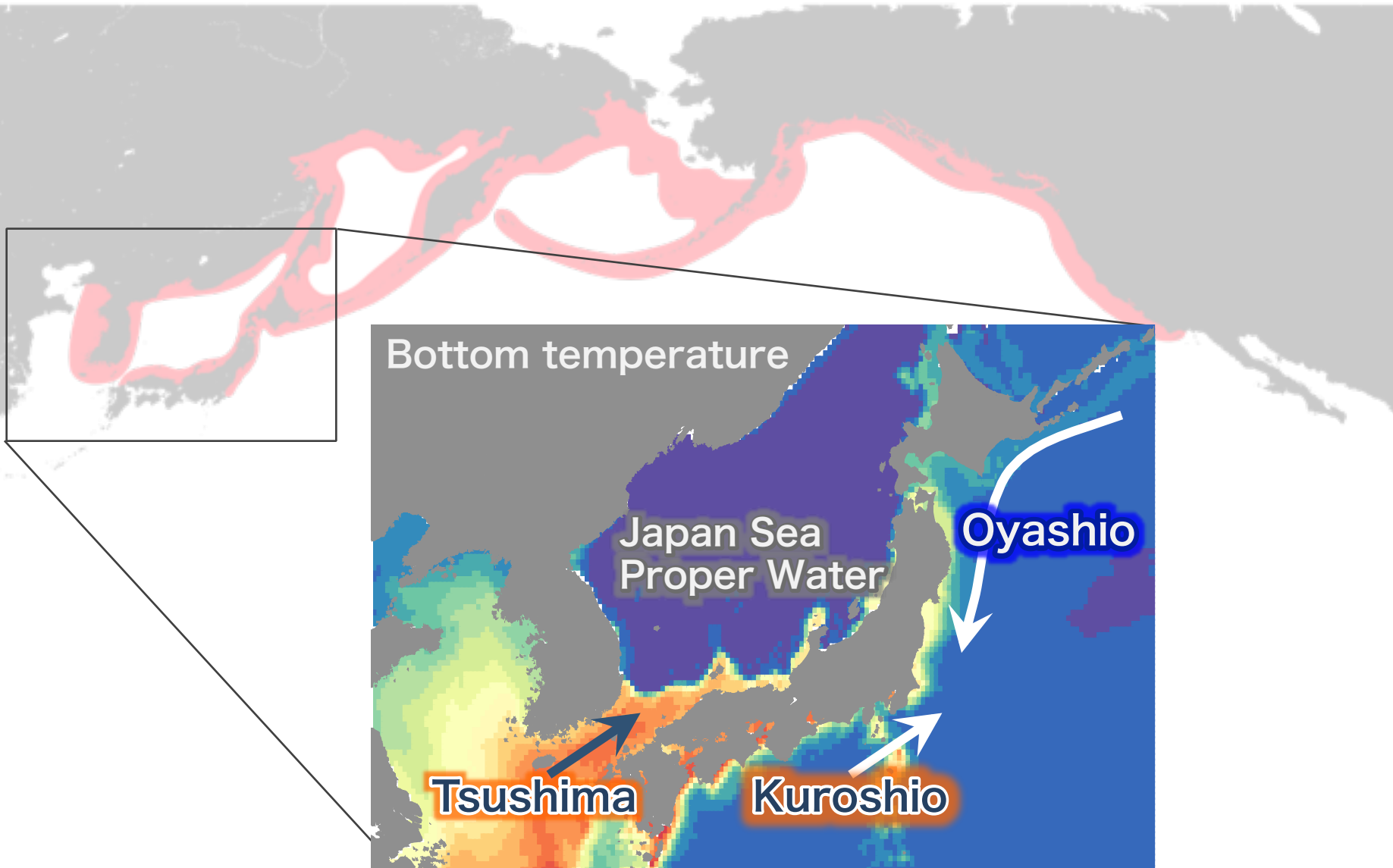
Population structure using nuclear markers

Results using mtDNA and
16 microsatellites

North

South

Common type

Typical type in South

Other types

- Southern population has a dominant haplotype
- Gene flow is limited between South and North

Suda *et al.* (unpublished)

Objectives

Ecological data

Estimation of optimum environment using statistical relationship between catch data and environmental data, water temperature.

Genetic data

Population genomics approach using RAD-seq
- Population structure
- Signature of natural selection, **Local Adaptation**

To reveal factors creating population differentiation and to evaluate adaptability to climate change

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Statistical analysis using GAM

General additive model (GAM)

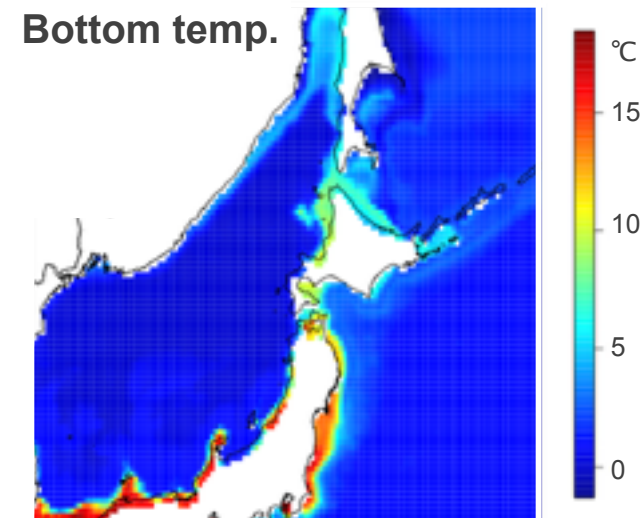Non-linear relationship between Env. factor and response factor

Distribution data

Cod catch from 1993–2012 (data in winter season)

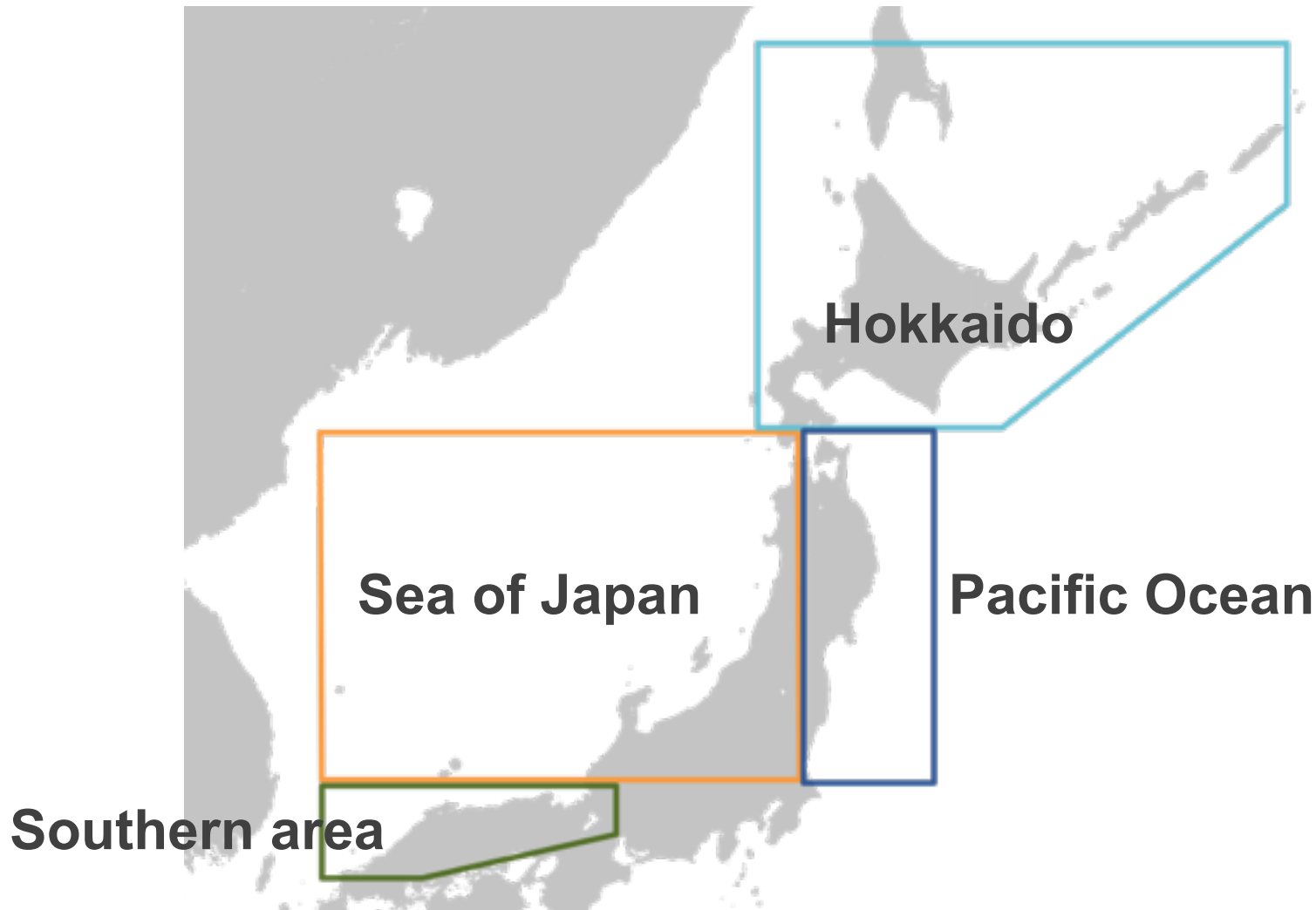*bottom trawling dataset published from the Fisheries Research Agency

Environmental data

Bottom temperature where cod were caught

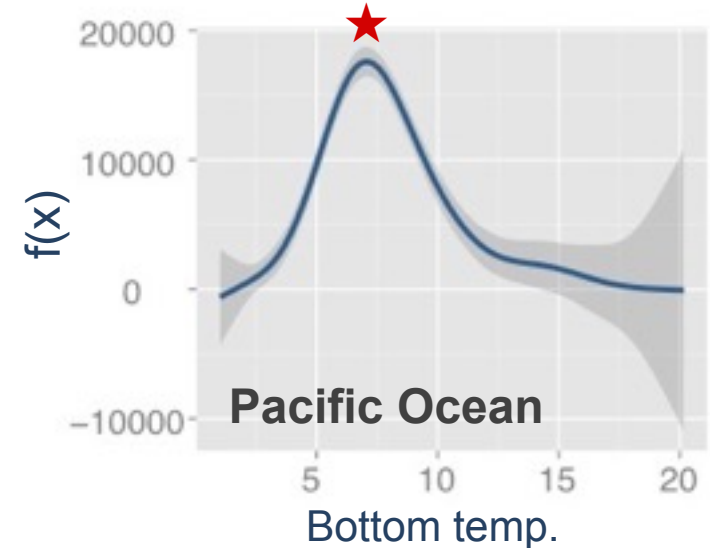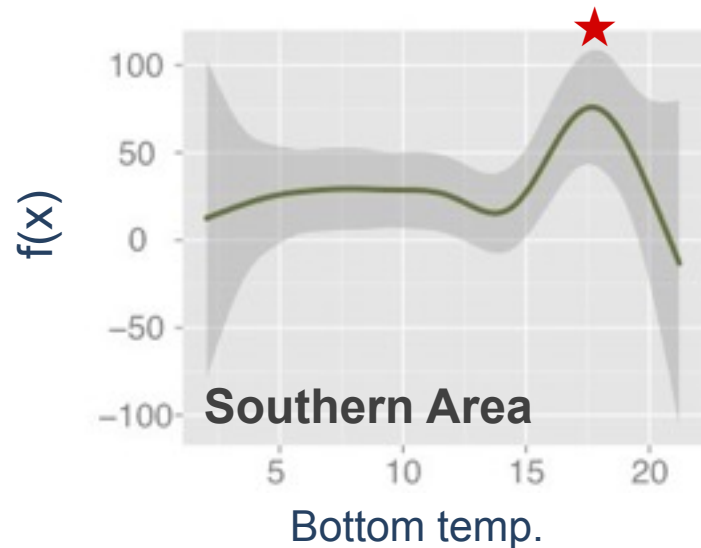*Japan Coastal Ocean Predictability Experiment (Miyazawa et al., 2009)

Bottom temp.

Study area

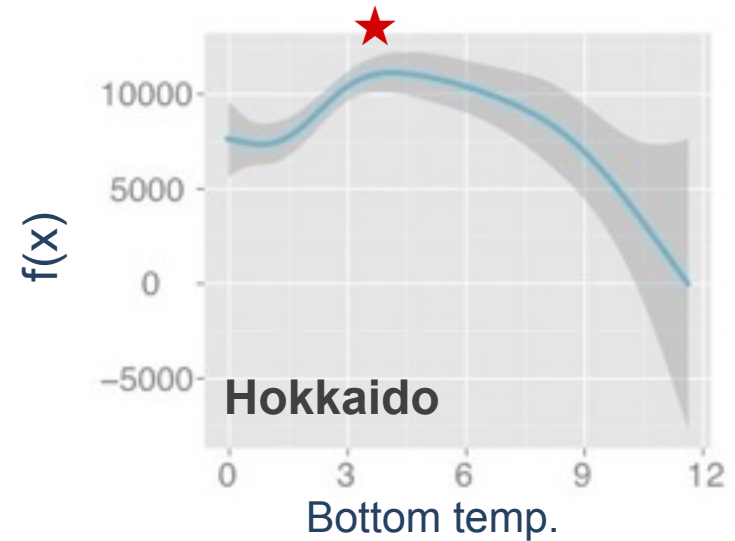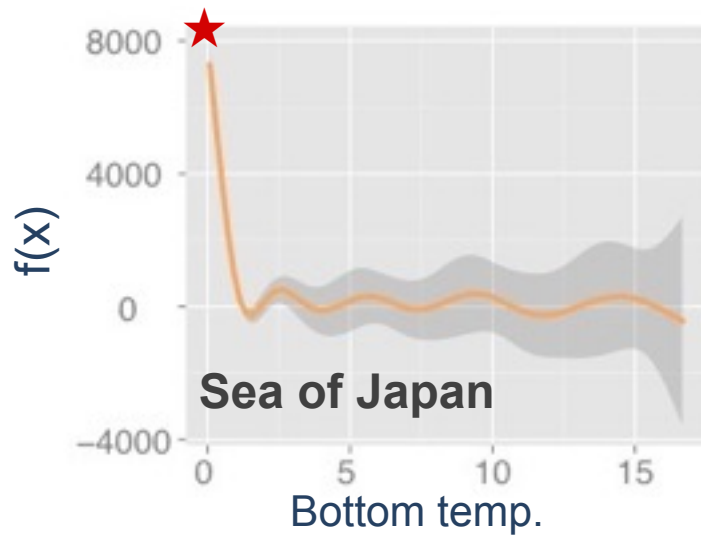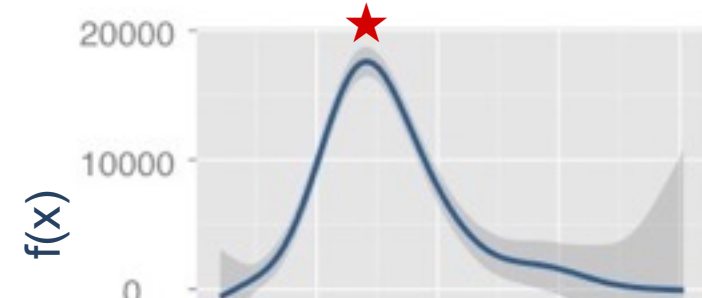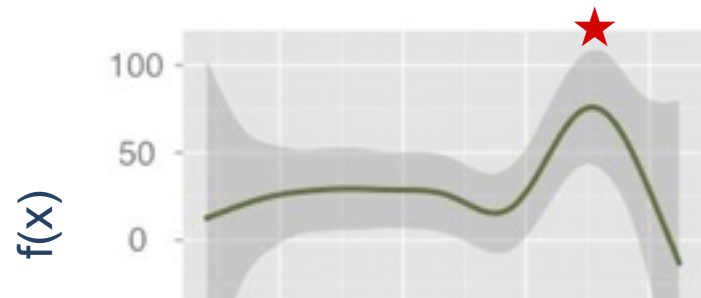Three oceanic areas and the Southern area was independently analysed.

Relationship between temp. and cod catch

Relationship between temp. and cod catch

Sea of Japan

Hokkaido

Bottom temp.

Bottom temp.
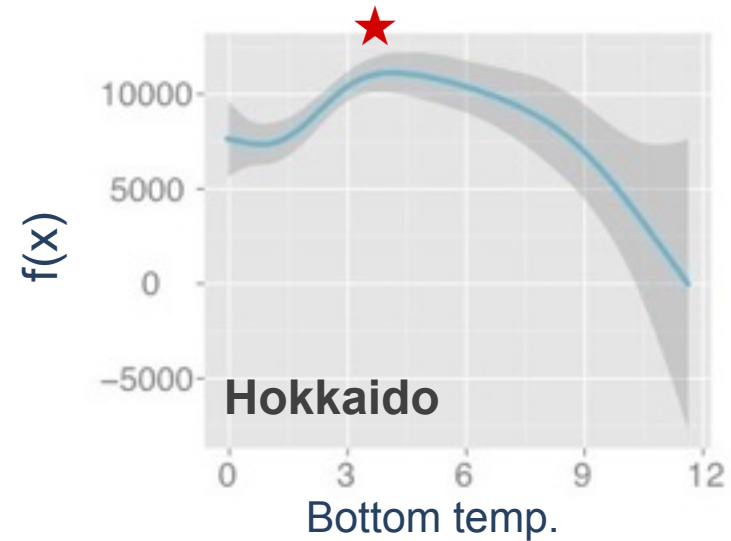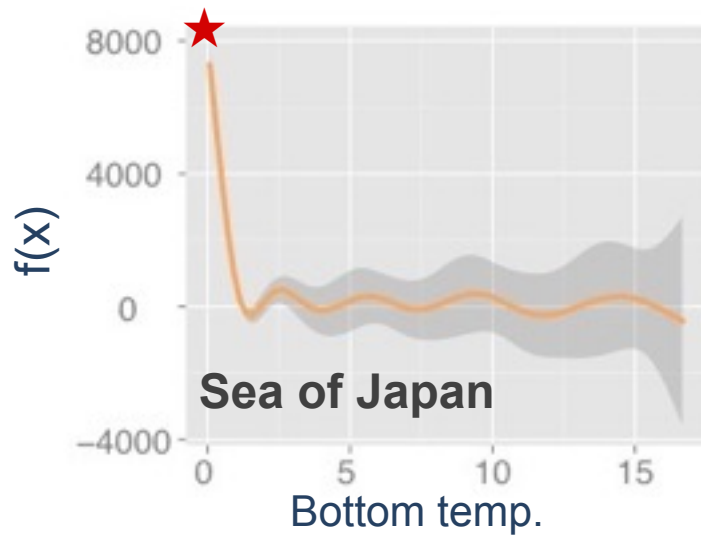
Different water responses at each ocean area,

Relationship between temp. and cod catch

Sea of Japan

Bottom temp.

Hokkaido

Bottom temp.
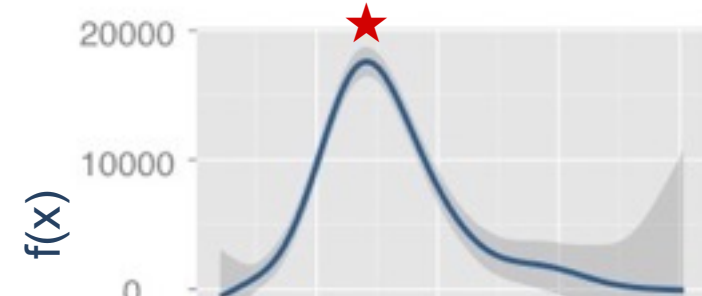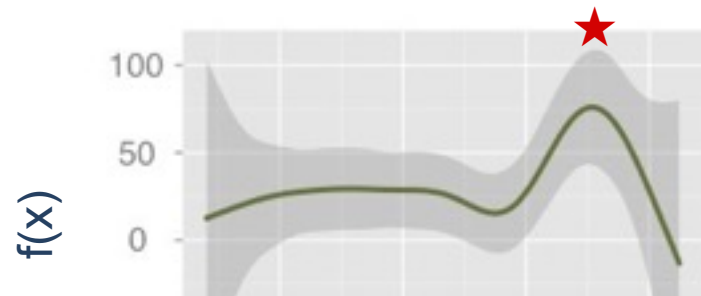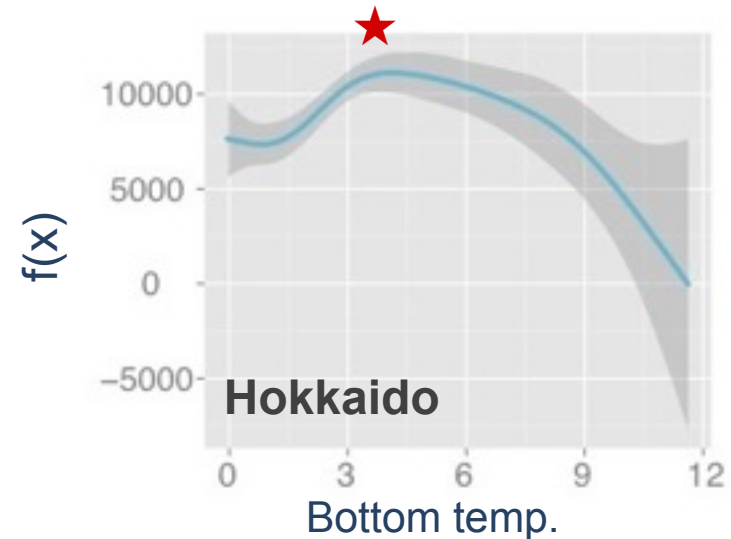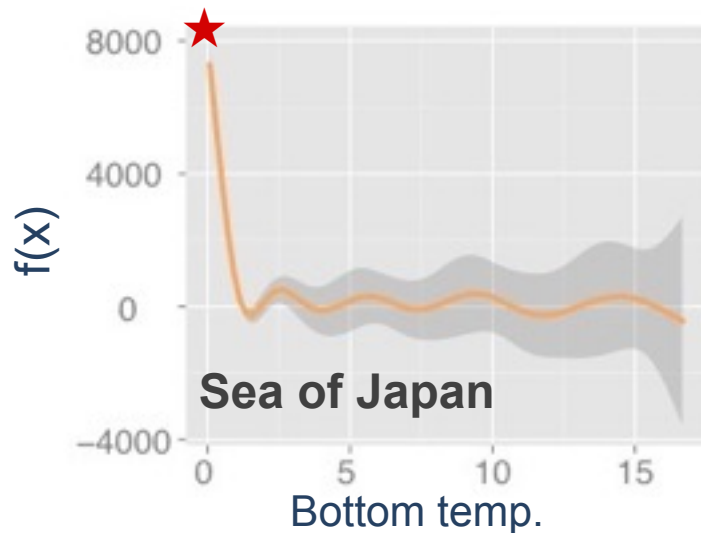
Different water responses at each ocean area, Inhabiting in different temperature condition?

Objectives

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Genetic data

Population genomics approach using RAD-seq
- Population structure
- Signature of natural selection, **Local Adaptation**

Restriction-site associated DNA (RAD) sequencing

- A technique using restriction enzyme to cut off DNA and sequence both side of restriction enzyme site using NGS

- Possible to obtain a high number of **Single Nucleotide Polymorphism (SNP)** in genome-wide, advantage in non-model organisms

- Possible to find candidate genes that are under selection, responding to env. change

Collection site and sample number

Site	Sample Number
Sakaiminato	23
Noto	3
Sanpoku	15
Nikaho	19
Otaru	10
Monbetsu	7
Rausu	4
Doto(North)	19
Doto(South)	14
Tohoku — 10 sites	120
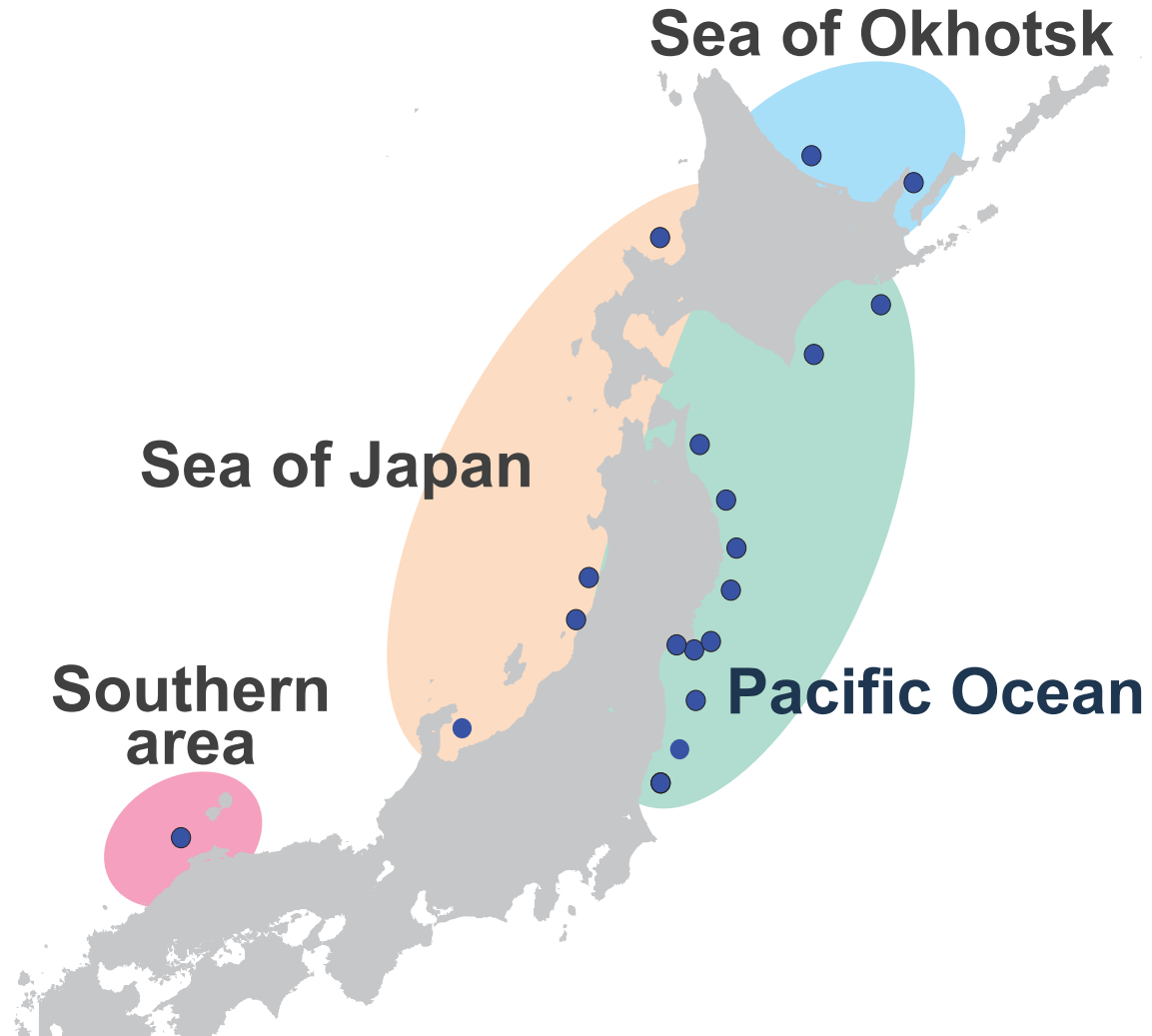
**A total of 19 sites
234 samples**

Sea of Okhotsk

Sea of Japan

Southern area

Pacific Ocean

Population structure and phylogenetic tree

Results from 1,925 SNPs
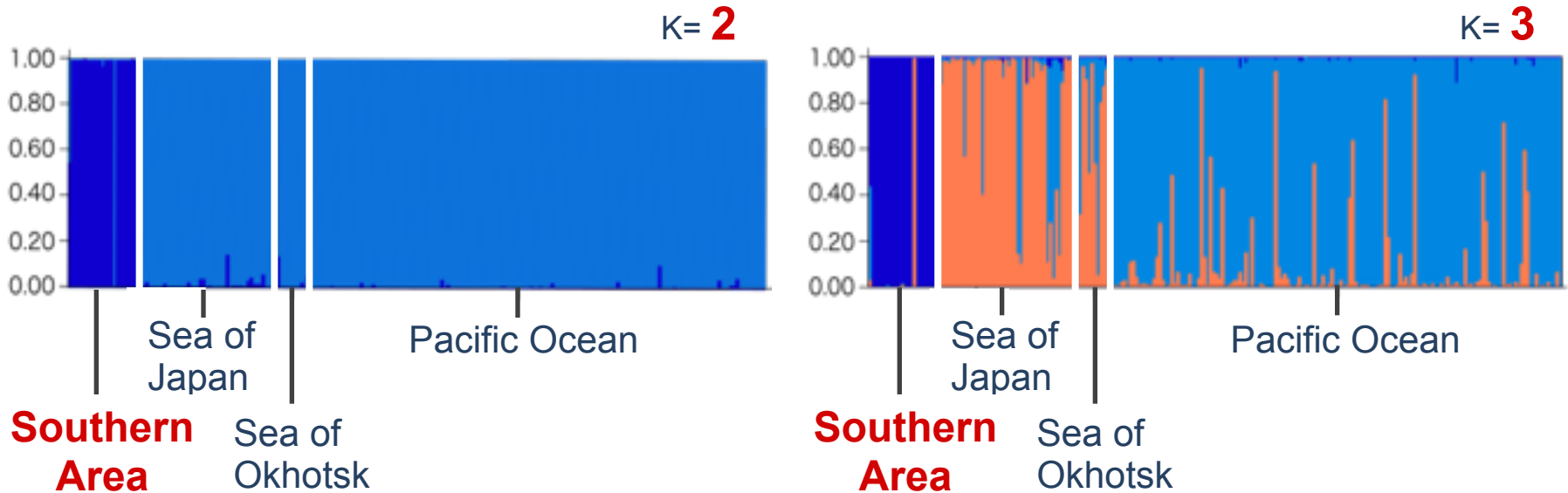
Genome-wide analysis showed,

- The southern individuals have different genetic structure (K=2)
- More detailed structure with respect to water bodies (K=3)

Population structure and phylogenetic tree

D$_A$ 0.005

Sea of Japan

Pacific Ocean

Sea of Okhotsk

Southern Area

non-rooted phylogenetic tree
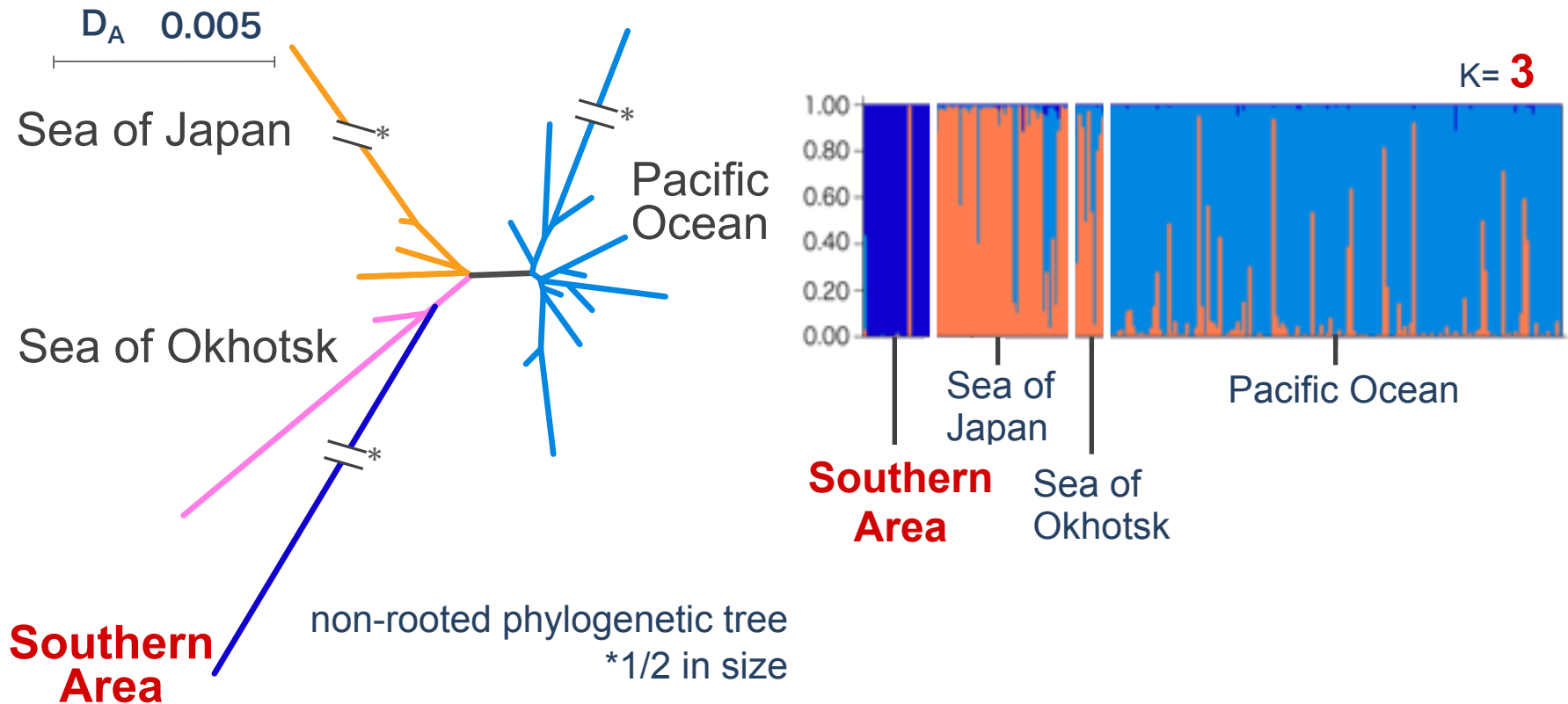*1/2 in size

K= **3**

Southern Area

Sea of Japan

Sea of Okhotsk

Pacific Ocean

- The southern population also phylogenetically different from others
- Gathered clades in each oceanic area

Detailed population structure can be observed with a high number of SNPs

Population structure and Natural selection

- **The southern individuals clearly differ from others**
- **High number of SNPs give more detailed population structures than ordinary nuclear markers**

Are there SNPs that are under selection?
responding to environmental changes?
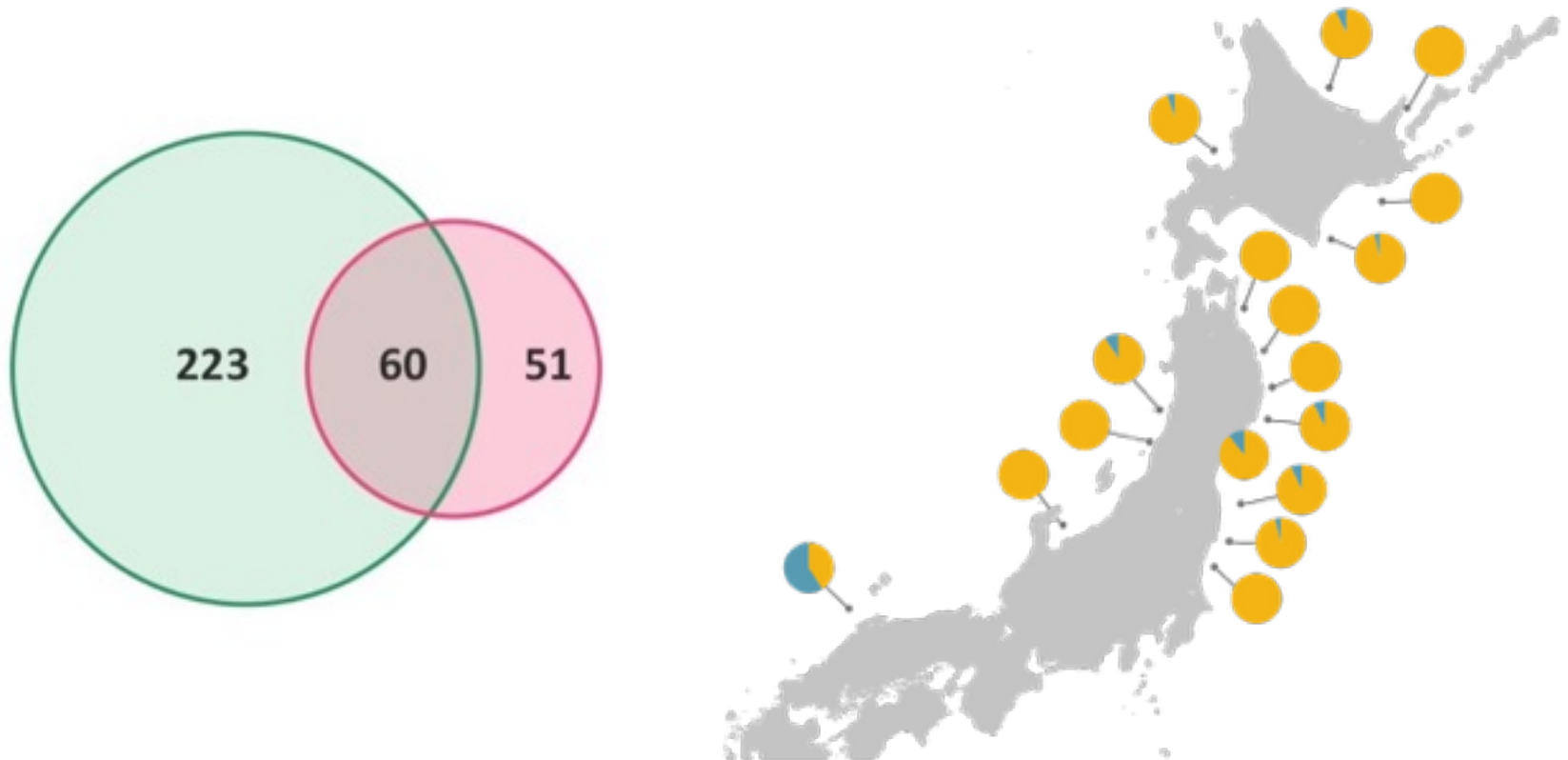
Lositan — Antão *et al.* (2008)

Bayenv2 — Günther & Coop (2013)

Multiple analyses are necessary to avoid false positive outliers

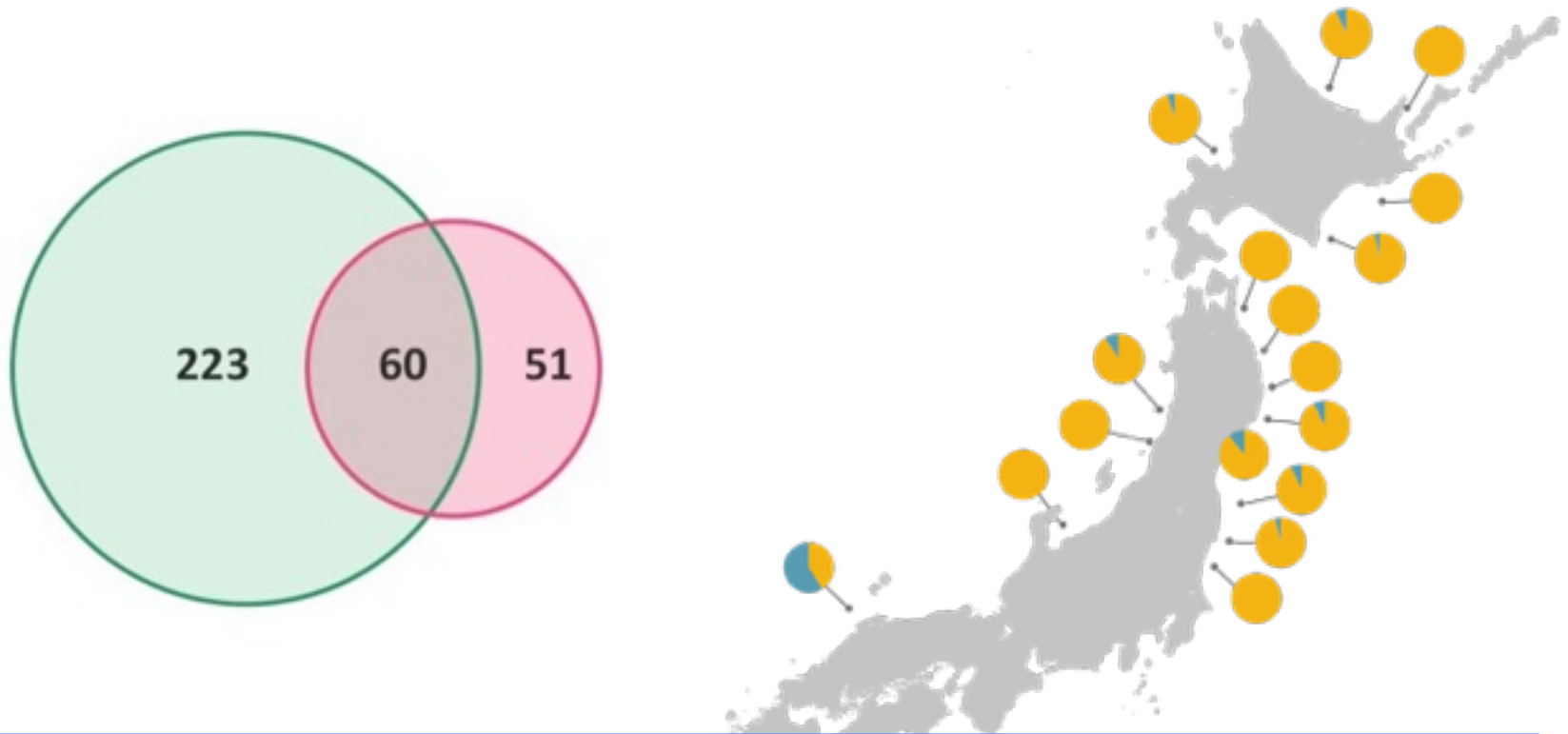# Outliers found in the southern population

60 outliers with the comparison of South and North population

- Signature of selection in southern population
- Necessary to identify loci correlate to environmental factors

Outliers found in the southern population

60 outliers with the comparison of South and North population

Identifying accurate outliers lead to reveal factors associating with local adaptation

Overall summary

Ecological data

Analysis of catch and env. data showed,
- The southern population may live in different temperature condition, possibly at higher temperature than other regions.
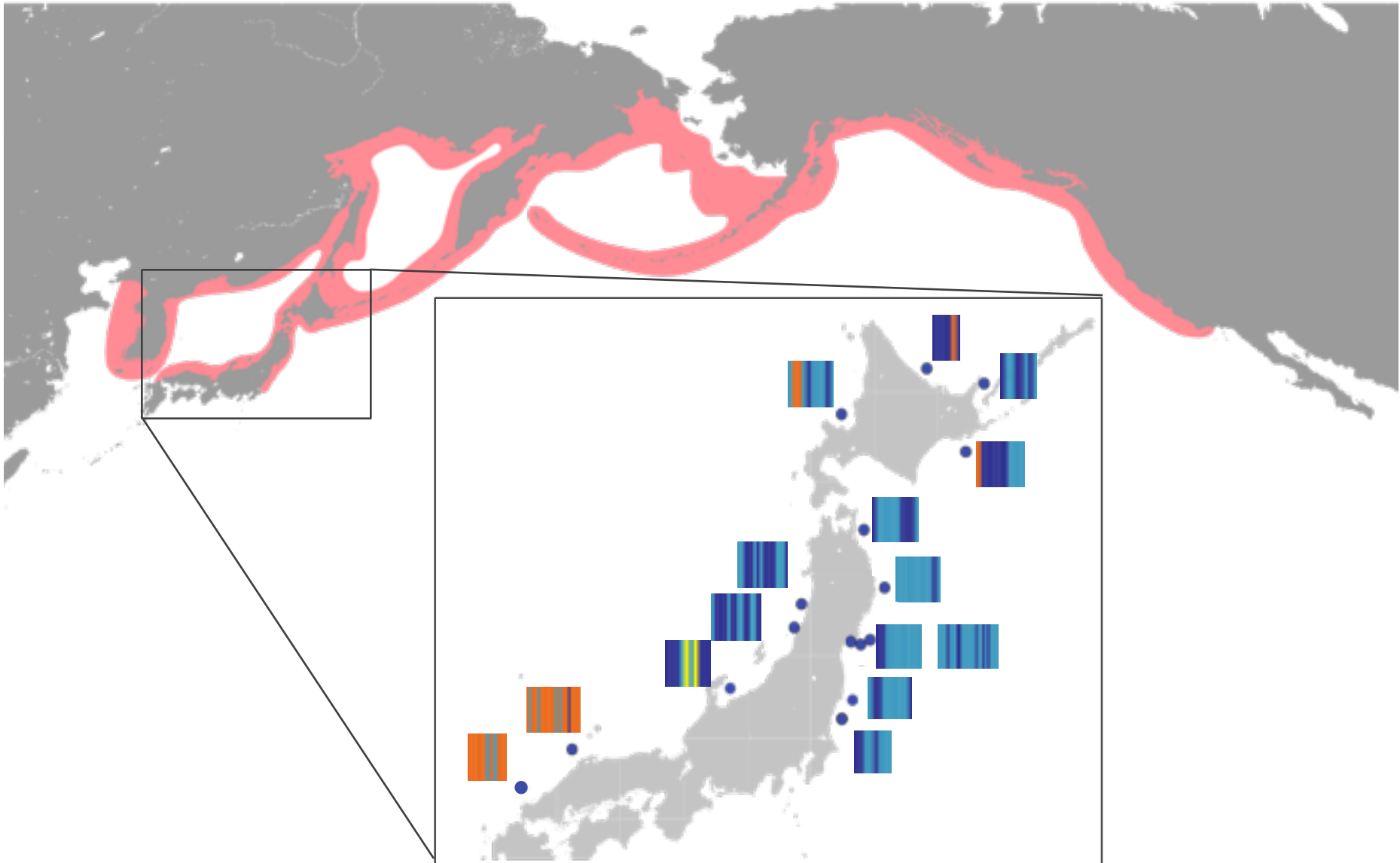
Genetic data

Genome-wide SNPs analysis,
- The southern population has clearly different genetic background.
- Detailed population structure was able to observe with many SNPs.
- Some SNPs showed signature of natural selection

More samples are required for further analysis

Acknowledgements

❖ Tohoku National Fisheries Research Institute

❖ FRA RV crews of "Wakataka Maru"

❖ JAMSTEC Hyper dolphin team

❖ JAMSTEC RV crews of "Natsushima"

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