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

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

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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)

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*
Population structure using nuclear markers

Results using mtDNA and 16 microsatellites

- 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 (unpublished)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)
Study area

Three oceanic areas and the Southern area was independently analysed.
Relationship between temp. and cod catch

- **Sea of Japan**
  - Bottom temp.
  - $f(x)$

- **Hokkaido**
  - Bottom temp.
  - $f(x)$

- **Southern Area**
  - Bottom temp.
  - $f(x)$

- **Pacific Ocean**
  - Bottom temp.
  - $f(x)$
Different water responses at each ocean area,
Relationship between temp. and cod catch

Different water responses at each ocean area, Inhabiting in different temperature condition?
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*
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

<table>
<thead>
<tr>
<th>Site</th>
<th>Sample Number</th>
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</thead>
<tbody>
<tr>
<td>Sakaiminato</td>
<td>23</td>
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<tr>
<td>Noto</td>
<td>3</td>
</tr>
<tr>
<td>Sanpoku</td>
<td>15</td>
</tr>
<tr>
<td>Nikaho</td>
<td>19</td>
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<td>Monbetsu</td>
<td>7</td>
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<tr>
<td>Rausu</td>
<td>4</td>
</tr>
<tr>
<td>Doto (North)</td>
<td>19</td>
</tr>
<tr>
<td>Doto (South)</td>
<td>14</td>
</tr>
<tr>
<td>Tohoku — 10 sites</td>
<td>120</td>
</tr>
</tbody>
</table>

A total of 19 sites

234 samples
Genome-wide analysis showed,

- The southern individuals have different genetic structure ($K=2$)
- More detailed structure with respect to water bodies ($K=3$)
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* by Antão et al. (2008)
- *Bayenv2* by 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
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