Challenges for fish in warmer waters:

The Case of the Arctic Char

Sigurdur Gudjonsson

*Genetic Resources for Food and Agriculture in a Changing Climate*

*Lillehammer, Norway 27-29. January 2014*
Nordchar
Climate change/Global warming

Nordic Partners

[Logos of the Nordic partners]

Other partners

[Logos of the other partners]

A Nordic Council of Ministers funded project
Nordforsk
Nordchar

- Nordic partners
- Iceland - Institute of Freshwater Fisheries IFF and Matis/Procaria
- Sweden – Swedish University of Agricultural Sciences SLU
- Norway – Norwegian Institute for Nature Science NINA
- Other partners
  - Scotland – Inverness College, University of Highlands and Islands
  - Canada – Fisheries and Oceans, Memorial University of Newfoundland and University of Waterloo.
Nordchar

• The fish species arctic char is used as a model species to evaluate what happens as climate gets warmer

• The project uses both ecology and genetics
Nordchar

- **Work packages**
  - 1. Sampling and recording of biological parameters and life history (age, size at maturity, anadromy etc)
  - 2. Genotyping, data storage and handling and analyzes
    Development of synchronized genetic tool **Link 1 and 2**
  - 3. Project management and network organization. Meetings and interactions with stakeholders (managers, government, fisheries and aquaculture)
Nordchar

Climate change/Global warming
Climate change/Global warming

Global Warming Projections

- CCSR/NIES
- CCCma
- CSIRO
- Hadley Centre
- GFDL
- MPI
- NCAR PCM
- NCAR CSM

Temperature Anomaly (°C)

1900 1950 2000 2050 2100
Climate change/Global warming

Global Warming Predictions

2070-2100 Prediction vs. 1960-1990 Average

Based on HadCM3

Temperature Increase (°C)
Freshwater fish vs marine

• Marine fish are more migrant and can in many instances move as condition changes
• This can be seen in different distribution range of many species as ocean temperature and ocean currents change
• Freshwater fish are sometimes landlocked and can not move.
• Some freshwater fish species like many salmonids migrate to sea and can possibly go to new river systems
Increased distribution and population size of mackerel

Mackerel caught by Icelandic fishing vessels
Salmonids

- Salmonids are the most important fish species in fresh waters in the Nordic countries. Many population also go to sea for feeding
- Atlantic salmon both in rivers (recreational fisheries) and in aquaculture
- Brown trout in rivers and lakes (fisheries)
- Arctic char in rivers and lakes (fisheries) and increasingly in aquaculture
Importance

• It is important part of our heritage in the Nordic countries to fish in our lakes and rivers
• Salmonids are very important and highly valuated
• The image of the wild salmon, „the king of fishes“ swimming up steep, clean rivers is very important also for salmon aquaculture
• The same applies for char aquaculture. The image of wild fish from the cold, clean arctic waters is very important
Why Arctic char?

- *Salvelinus alpinus* – a model organism for assessing biodiversity responses to climate change in northern regions

- Fish that spawns in freshwater

- Wide distributional range with genetic character of most populations little influenced anthropomorphic influences

- Generalist and very plastic, with both phenotypic and genotypic responses to environmental change

- Life history responsive to temperature e.g. anadromy vs residency
Arctic char distribution
Arctic char (*Salvelinus alpinus*)

- Fish that spawn in freshwater
- Some populations are anadromous i.e. Fish go to sea for some months in the summer, overwinter in freshwaters
- Genetically different populations
- Generalist and very plastic
- Many different phenotypes
- Very variable life history
- Size at first maturity from 6 cm to 60 cm
- In some populations fish spawn once in other populations often etc
Four phenotypic morphs from a single lake
Nordchar

• Use Arctic char (*Salvelinus alpinus*) as a model species to evaluate effects of climate change

  • **Direct effects** of temperature (or climatic factors, i.e. precipitation, hydrology, ocean currents, sea temperature)

  • Temperature can exceed the species tolerance at some levels and life stages (~20°C)

  • **Indirect effects** through competition, food abundance, tolerance to diseases and parasites etc.
Changes can already be seen

• **Distribution** - population in south Iceland have collapsed in stock size.

• Many possible causes

• – competition with other species, brown trout (*Salmo trutta*) and a new invasive species flounder (*Platichthys flesus*).

• - susceptibility to some parasites increases with higher temperature for example PKD caused by *Tetracapsuloides bryosalmonae* (*Myxozoa*).

• **Life history changes** – Faster growth and younger mature char
Proportion of char and brown trout
Decrease of char population size

![Graph showing the decrease of char population size over years with different categories of catch: Hvítá rod catch, Hvítá-net catch, and Catch at seai.]
Decrease in population size

- Surveys in lakes in South and West Iceland
- Catch of char in fixed fishing effort
- In the 1980’s 400-800 char caught
- In the 2010’s 0-10 char caught
Nordchar

**Expected changes.**

- Distribution changes, char in warmer (south) locations will decrease or disappear. Distribution area will shrink. Brown trout and salmon will take over southerly areas (Brook trout and salmon in America)
- Anadromous char will decrease in southern part of the new distribution areas and increase in the northern part as areas become ice-free.
- Life history changes. Faster growth - shorter life span, more fluctuation (fewer age-classes).
- More difficult fisheries management
Study of genetic adaptation

- Mapping analyzes
- Genome scans
- Transcription profiling
- Candidate genes for climate change adaptation
- Many knowledge gaps and a lot to be learned
- Local adaptation – better understanding of environment and adaptation over large scale
Nordchar

• Map and evaluate this valuable resource
• Produce map of genetic diversity and pattern for Arctic char
• Map the life history variability and pattern of Arctic char
• Phylogeographical tree for the species
Why mtDNA?

- *Mitochondrial Genome* – a window on climate related biodiversity responses in the nuclear genome.
  
  - Interacts with nuclear genome to produce enzyme system underpinning energy production (OXPHOS – oxidative phosphorylation)
  
  - Genetic character can be expected to be sensitive to environmental temperature conditions in poikilotherms such as Arctic char
  
  - Natural selection will act to optimize genetic diversity that provides for the most efficient delivery of energy needs
  
  - Genetic responses will be tied to nuclear responses and help target important genes and gene functions in the nuclear genome
  
  - Genetic responses can be used to monitor climate response
Char populations life history data from literature and project partners
Work Programme in genetics

• Phase I

• **Objective** — to obtain a robust overview of the nature and extent of genetic variation across the mtDNA genome across the species’ range

• **Purpose** — to identify genome regions with the highest levels of variation and allow more populations to be screened for same resource i.e. optimize the overall information gained

• Phase II

• **Objective** — to undertake a detailed analysis of phylogenetic and selective differentiation among populations within and among locations across the species range

• **Purpose** — to understand the extent to which interpopulation variation is related to phylogenetic and adaptive divergence
Primer Design

• Salvelinus alpinus mitochondrion, complete genome is 16,659 bp (NC_000861).

• Primers for 28 amplicons were designed by Matis using NC_000861 sequence; amplicon size varied from 531-745 (mean 604 bp).
Work Programme – Phase I (completed)

Samples

- 520 samples assembled from 11 different countries: Finland, Canada, England, France, Greenland, Iceland, Ireland, Norway, Russia, Scotland, Sweden

- 128 geographically and phylogenetically representative samples chosen for biodiversity overview

- The DNA were extracted using Qiagen DNeasy Blood & Tissue Kit, concentration measured and equilibrated, and quality tested by pre-PCR.

- Samples that did not work well enough were replaced with new samples, generally from the same location and QC tested.
Sample sites in Phase 1
Work Programme – **Phase I** (completed)

**Genetic sequencing**

Two runs required due to technical problems
Work Programme – Phase I (completed)

Results: observed individual variants

- 4449 variants were identified with GS amplicon analyzer in the combined analysis (2270 in first run only)
- Applying criteria 1, 2 and 3 yields a total of 468 SNPs
- 93 out of the 468 SNPs are only found in one individual
Phylogenetic tree from phase 1
Work Programme – Phase I (completed)

Preliminary Results: population differentiation

e.g. geographic patterns

• Very highly diverged lineages show a regional distribution e.g. in eastern North America

• Moderately diverged lineages can be widely geographically dispersed

• Moderately diverged lineages can be sympatric within lakes and river systems
Focus:
Disentangle phylogenetic and adaptive components of genetic relatedness/ID temperature selection responses

Work Programme – Phase I (completed)
Design of Phase II Analysis

Genomic Sampling
Three-way trade-off
Work Programme – Phase I (completed)

Results: amplicon selection for Phase II

<table>
<thead>
<tr>
<th>Region</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Length</th>
<th>NGS Reads Only</th>
<th>NGS Covered</th>
<th>Depth</th>
<th>Homozygous</th>
<th>SNP Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>D-loop</td>
<td>1</td>
<td>998</td>
<td>995</td>
<td>10</td>
<td>55</td>
<td>35</td>
<td>10.1405</td>
<td>0.0551</td>
</tr>
<tr>
<td>12S rRNA</td>
<td>1067</td>
<td>2013</td>
<td>947</td>
<td>2</td>
<td>15</td>
<td>13</td>
<td>63.3333</td>
<td>0.0194</td>
</tr>
<tr>
<td>16S rRNA</td>
<td>2006</td>
<td>3705</td>
<td>1620</td>
<td>10</td>
<td>16</td>
<td>16</td>
<td>64.0154</td>
<td>0.0154</td>
</tr>
<tr>
<td>tRNA-Leu</td>
<td>7766</td>
<td>3548</td>
<td>75</td>
<td>4</td>
<td>4</td>
<td>0</td>
<td>12.795</td>
<td>0.0333</td>
</tr>
<tr>
<td>ND1 gene</td>
<td>3541</td>
<td>4815</td>
<td>975</td>
<td>26</td>
<td>40</td>
<td>14</td>
<td>21375</td>
<td>0.04155</td>
</tr>
<tr>
<td>tRNA-Met</td>
<td>4961</td>
<td>5029</td>
<td>69</td>
<td>2</td>
<td>3</td>
<td>1</td>
<td>40468</td>
<td>0.0448</td>
</tr>
<tr>
<td>ND2 gene</td>
<td>9160</td>
<td>6739</td>
<td>1050</td>
<td>9</td>
<td>20</td>
<td>10</td>
<td>26.9511</td>
<td>0.0254</td>
</tr>
<tr>
<td>rep-ori</td>
<td>6296</td>
<td>6331</td>
<td>36</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>2641</td>
<td>0.0278</td>
</tr>
<tr>
<td>rRNA-Cys</td>
<td>6332</td>
<td>6398</td>
<td>67</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>22332</td>
<td>0.0478</td>
</tr>
<tr>
<td>rRNA-Trp</td>
<td>6498</td>
<td>6491</td>
<td>72</td>
<td>2</td>
<td>3</td>
<td>1</td>
<td>24428</td>
<td>0.0427</td>
</tr>
<tr>
<td>COX1 gene</td>
<td>6471</td>
<td>8051</td>
<td>1552</td>
<td>30</td>
<td>37</td>
<td>7</td>
<td>41.9128</td>
<td>0.0286</td>
</tr>
<tr>
<td>tRNA-Asp</td>
<td>6097</td>
<td>8170</td>
<td>74</td>
<td>3</td>
<td>3</td>
<td>0</td>
<td>24665</td>
<td>0.04054</td>
</tr>
<tr>
<td>COX2 gene</td>
<td>8185</td>
<td>8876</td>
<td>691</td>
<td>7</td>
<td>12</td>
<td>5</td>
<td>57.8832</td>
<td>0.01787</td>
</tr>
<tr>
<td>tRNA-Lys</td>
<td>8376</td>
<td>8949</td>
<td>74</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>74</td>
<td>0.0165</td>
</tr>
<tr>
<td>ATP6 gene</td>
<td>8951</td>
<td>9118</td>
<td>161</td>
<td>3</td>
<td>3</td>
<td>0</td>
<td>96</td>
<td>0.02086</td>
</tr>
<tr>
<td>ATP8 gene</td>
<td>9109</td>
<td>9782</td>
<td>684</td>
<td>18</td>
<td>19</td>
<td>1</td>
<td>86</td>
<td>0.02778</td>
</tr>
<tr>
<td>COX1 gene</td>
<td>9792</td>
<td>10577</td>
<td>785</td>
<td>7</td>
<td>27</td>
<td>10</td>
<td>29.1111</td>
<td>0.04851</td>
</tr>
<tr>
<td>tRNA-Gly</td>
<td>10977</td>
<td>10946</td>
<td>70</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>70</td>
<td>0.0429</td>
</tr>
<tr>
<td>ND1 gene</td>
<td>10647</td>
<td>10997</td>
<td>391</td>
<td>10</td>
<td>11</td>
<td>1</td>
<td>319.9994</td>
<td>0.0184</td>
</tr>
<tr>
<td>ND1 gene</td>
<td>10997</td>
<td>12000</td>
<td>69</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>22</td>
<td>0.0498</td>
</tr>
<tr>
<td>ND1 gene</td>
<td>12000</td>
<td>1136</td>
<td>297</td>
<td>3</td>
<td>4</td>
<td>1</td>
<td>74.25</td>
<td>0.02347</td>
</tr>
<tr>
<td>ND1 gene</td>
<td>11356</td>
<td>12471</td>
<td>1306</td>
<td>42</td>
<td>46</td>
<td>4</td>
<td>30.3039</td>
<td>0.03392</td>
</tr>
<tr>
<td>tRNA-Asc</td>
<td>12732</td>
<td>13205</td>
<td>69</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>34.9834</td>
<td>0.02899</td>
</tr>
<tr>
<td>tRNA-Ser</td>
<td>12606</td>
<td>12874</td>
<td>69</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>34.9834</td>
<td>0.02899</td>
</tr>
<tr>
<td>ND1 gene</td>
<td>13749</td>
<td>14787</td>
<td>1053</td>
<td>41</td>
<td>61</td>
<td>10</td>
<td>30.1475</td>
<td>0.03317</td>
</tr>
<tr>
<td>ND2 gene</td>
<td>14784</td>
<td>15535</td>
<td>722</td>
<td>28</td>
<td>29</td>
<td>1</td>
<td>18</td>
<td>0.05286</td>
</tr>
<tr>
<td>C1071 gene</td>
<td>15178</td>
<td>16128</td>
<td>1141</td>
<td>11</td>
<td>11</td>
<td>7</td>
<td>6.8189</td>
<td>0.03758</td>
</tr>
</tbody>
</table>

No SNP discovered
Two types used:

- **Phylogenetic samples N=60**
  - various named *Salvelinus* species
  - generally 1-2 individuals per species

- **Population samples N=1540**
  - Wide range of regions and countries e.g. eastern Russia, western Russia, Baltic Russia, Alaska, Western Canadian Arctic, eastern Canadian Arctic, Eastern North America including Maine, West Greenland, Iceland, Norway, Finland, Sweden, Britain, Ireland
  - Includes sympatric morphs
  - 10-25 individuals/population
Sample sites in phase 2
Focus of Analyses and Publications

- Intra genomic description and distribution of polymorphism in the char mtDNA genome
- Phylogenetic relationships among populations at the inter- and intraspecific level
- Evidence for selection acting on variation and relationship of population divergence at polymorphisms with environmental temperature, life history
- Patterns of divergence among sympatric morphs
Nordchar

• These information can be used to forecast the development of the species associated with climate warming.
• These will give information on how other important species will react.
• Nordchar is a 3 year program
• Nordchar will hopefully be a stepping stone to larger international studies on both the effect of climate change and the arctic char with strong Nordic interests
• Extend analysis to encompass 16sRNA, COX1, COX3, ND4, ATP6 and CYTOB genes using same samples: efficient given that samples assembled, DNA extracted and primers already exist

• Screen more population for informative phylogenetic and candidate selected genes to provide a more robust analysis

• Explore linkage of potentially selected polymorphisms to variation in linked nuclear OXPHOS genes
Further research

• Map the genetic variation of our most important fish species
• Learn more on local adaption
• Forecast future distribution of the most important fish species
• Forecast changes in life history and important populations parameters (age and size at maturity)
• Prepare for more difficult fishery management (Fewer year-classes – more fluctuation in stock size)
Forecast of char distribution in Sweden

Hein et al. 2012
Thank you for the attention