



The phylogeographic structure of Arctic char (*Salvelinus alpinus*); a candidate model species to predict the effects of climate change in the Arctic

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Introduction

Freshwater fish communities of the Arctic and subarctic regions of Europe are sparse and include few fish species, compared to the tens, hundreds and thousands found in more southerly regions. However, while true at the species level, increasing numbers of studies provide compelling evidence that within these few species biologically important allopatric and sympatric population diversity is widespread, particularly for the dominant salmonid species, Atlantic salmon (*Salmo Salar*), brown trout (*Salmo trutta*) and Arctic char (*Salvelinus alpinus*).

Climatic models have forecasted pronounced changes in climatic conditions and these changes may have adverse effects in the Arctic and subarctic. The changes may be large regarding the ecology of many valuable species that are utilized in fisheries and in aquaculture. It is very important to understand how the changes will affect the biota to react to the threats and to encourage the opportunities involved. We chose a model species that is especially important for the Nordic societies. The Arctic char is well suited to be used as a model species to understand the effects of climate change. Arctic char is an arctic fish species with circumpolar distribution. Already, it can be seen that Arctic char is retreating from its southernmost locations, for example in Iceland.

Materials and methods

A total of 1600 individuals of the genus *Salvelinus* were included in this study with the vast majority of them belonging to the species *Salvelinus alpinus*. Five regions of the *Salvelinus* mitochondrial genome covering the D-loop region and parts of four coding genes (ND1, ND2, ND5 and ND6) were selected for the sequencing using the 454 sequencing platform from Roche.



Results

The sequence coverage (number of sequence reads) supporting the SNPs per individual, was 39.4 (± 12.6). The alignment analysis yielded a total of 546 polymorphic loci, with the greatest number of SNPs identified in the second D-loop region (128) and the region with the lowest number of SNPs being in the ND1 gene (71).



Figure 1. A map displaying the 93 sampling sites used for this study.

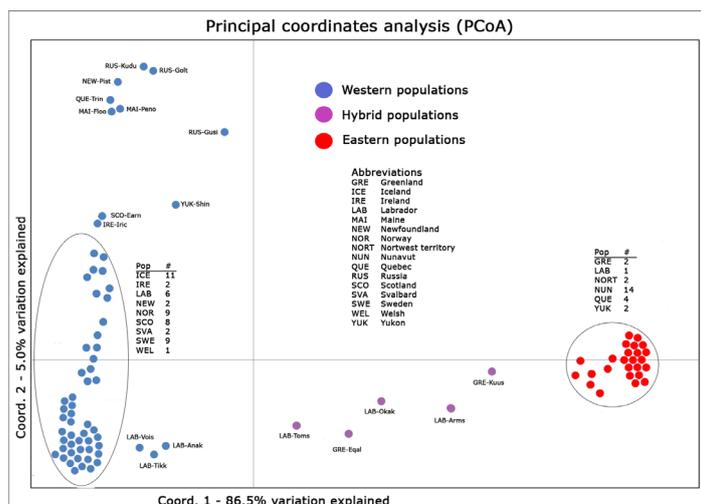


Figure 2. Principal coordinates analysis (PCoA) for the genetic distance (Tamura K. and Nei M. (1993)) between 93 groups of *Salvelinus alpinus*.

Discussion

Intraspecific genetic diversity in Arctic char was studied as well as the subdivision of phylogeographic groups of Arctic char into western and eastern groups and the hybrid zone in between. Within this research the evolution and the divergence of the Arctic char was mapped. This section of the NORDCHAR project uses new genetic methodologies to analyse the phylogeography and the genetic divergence, within and among Arctic char populations. The Arctic char is possibly well suited as a model species for monitoring changes in the Nordic areas and these results can be used to understand and investigate further both historical and contemporary parts of the phylogeographic structure of the species. All this information can be used to forecast the development of the species associated with climate warming.

This project was funded by NordForsk



NordForsk

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