



Towards conservation genomics in Arctic plant species

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Short background

Main causes of biodiversity loss

- ▶ Climate change
- ▶ Habitat fragmentation

- ▶ We do not have good knowledge on the distribution of vascular plant species in the Arctic!
 - ▶ Fragmentary, superficial, old, unsystematic
- ▶ Key information to evaluate conservation status is mostly highly insufficient
 - ▶ Population numbers, sizes, trends
 - ▶ Levels of genetic diversity and distinctiveness
 - ▶ Threats
 - ▶ Ecological requirements



Saxifraga nathorstii, endemic to a small area of East Greenland.
Photo: KB Westergaard

Future perspectives for arctic-alpine species

Range shifts polewards in latitude and upwards in altitude

- ▶ They may to a certain extent track their niches

Limited suitable habitats

- ▶ Establishment may be the limiting factor

Competition from colonizing species

- ▶ Species invading from adjacent vegetation
- ▶ Species adapted to warmer climates

Small, few and fragmented populations

- ▶ Little or no gene flow among populations
- ▶ Vulnerable for extinction
- ▶ Regionally Red Listed, perhaps also Panarctic Red Listed soon?
(CAFF Flora group project)

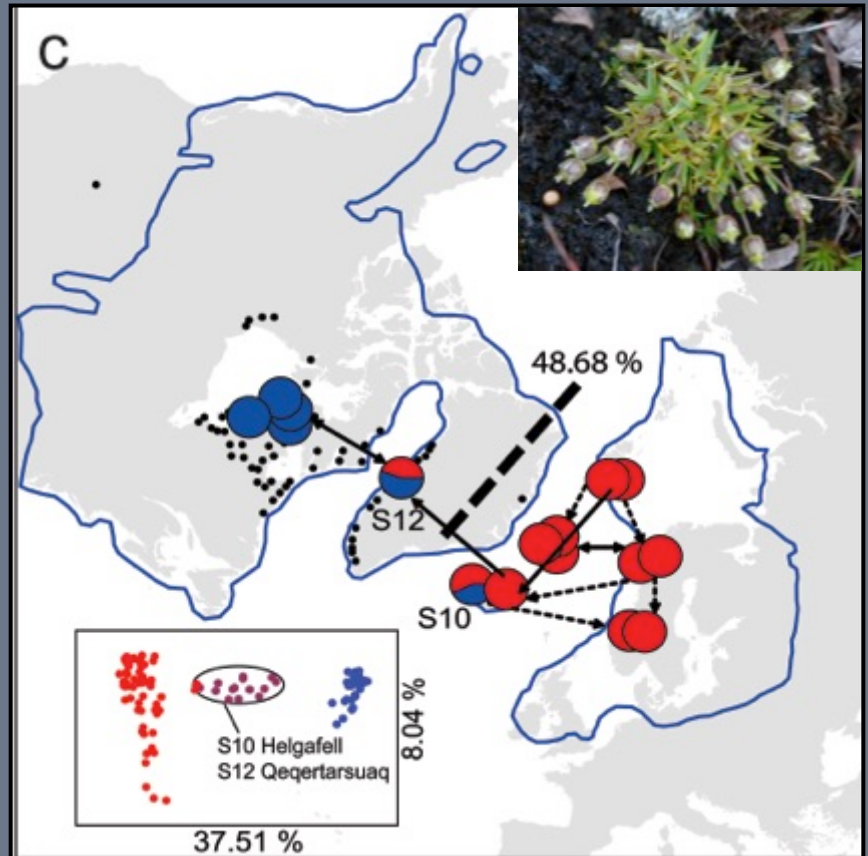
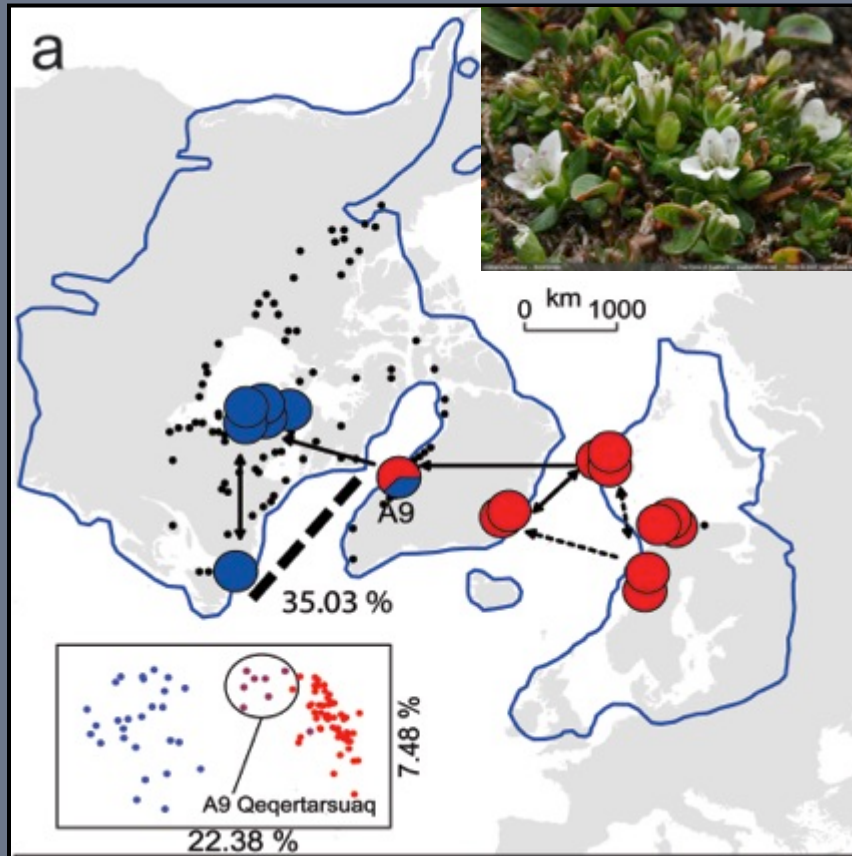
Also IG et al 2007. Frequent long-distance plant colonization in the changing Arctic. *Science*.

Conservation genetics

- ▶ Not many studies on Arctic plant species
- ▶ Studies have been based on neutral genetic markers due to methodological restrictions. This excludes the adaptive genetic variation important for species' survival.
- ▶ Unfortunately, the difference between neutral and adaptive genetic variation is mostly neglected in conservation management, potentially severely limiting better conservation plans.



Glacial history and conservation genetics of two rare arctic-alpine Caryophyllaceae



Arenaria humifusa

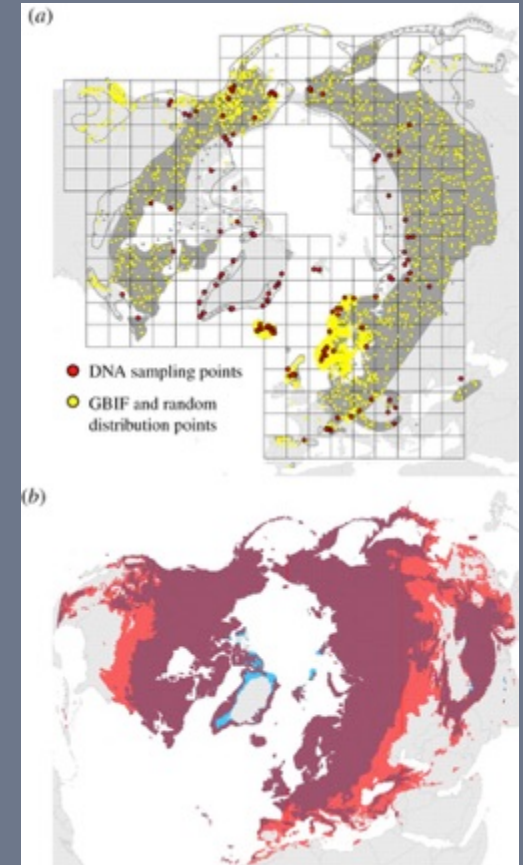
AFLP data

Sagina caespitosa

Westergaard KB *et al* 2011. Glacial survival may matter after all: nunatak signatures in the rare European populations of two west-arctic species. *Mol Ecol*.

Genetic consequences of habitat fragmentation and climate change

- ▶ Estimated loss of neutral genetic diversity and range reduction by year 2080
- ▶ The expected range reduction in the 27 northern species was larger than reported for temperate plants, and all were predicted to lose genetic diversity according to at least one scenario.
- ▶ The relationship between loss of genetic diversity and loss of range was nonlinear
- ▶ Loss of genetic diversity was explained by dispersal adaptation and genetic differentiation among populations.



Vaccinium uliginosum
(bog bilberry)

The genetic basis of local adaptation

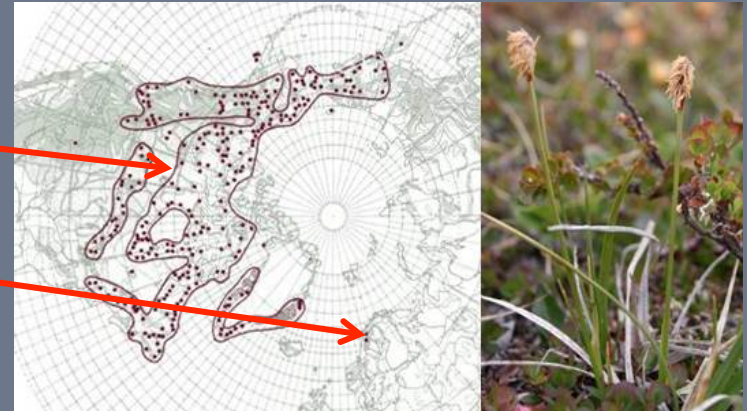
- ▶ It is increasingly important to improve our understanding of the genetic basis of local adaptation because of its relevance to climate change and conservation of genetic resources.
- ▶ Species response to climate change:
local adaptation, range shift, range reduction
- ▶ The genomic era is here!
- ▶ New genomic tools are now allowing genome-wide studies in non-model species
Shows great promise and is in high demand

Non-model species and moderate project budgets

- ▶ High-throughput sequencing technologies
- ▶ RAD (Restriction site Associated DNA) sequencing
 - ▶ Uses the flanking DNA-sequences of restriction sites of a restriction enzyme (RAD tags)
 - ▶ Once RAD tags are isolated, they can be used to identify and genotype mainly single nucleotide polymorphisms (SNPs)
 - ▶ a flexible method for sampling the genomes of multiple individuals in a population using high-throughput DNA sequencing
 - ▶ Rapid discovery and genotyping of SNP markers

Towards conservation genomics

- ▶ Double digest RAD sequencing (ddRAD-seq)
- ▶ Wide distribution and ecological amplitude in N-America
- ▶ Narrow ecological limits in Norway, *in situ* glacial survivor?
- ▶ Combine a large-scale phylogeographic pattern and an outlier analysis with local ecological data to find candidate loci for local adaptation



Carex scirpoidea ($2n=62$)

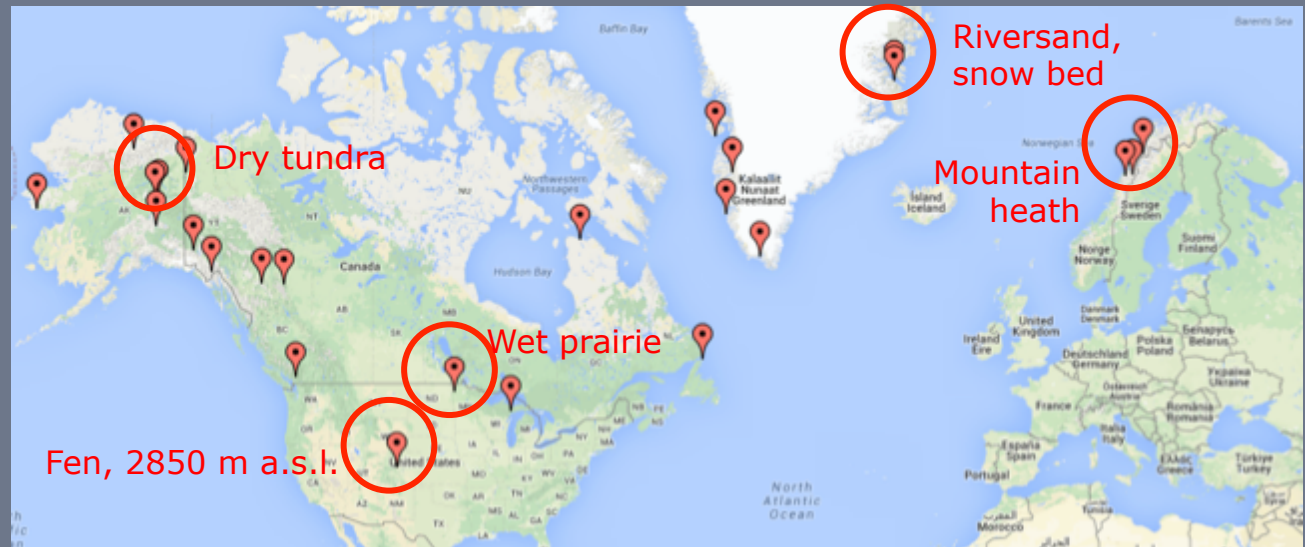
Prof. Hans Stenøien, NTNU, Norway

Prof. Alex Widmer, ETH, Switzerland

Prof. Rolf Holderegger, WSL, Switzerland

Ass. Prof. Leo Bruederle, Univ. Of Colorado Denver, USA

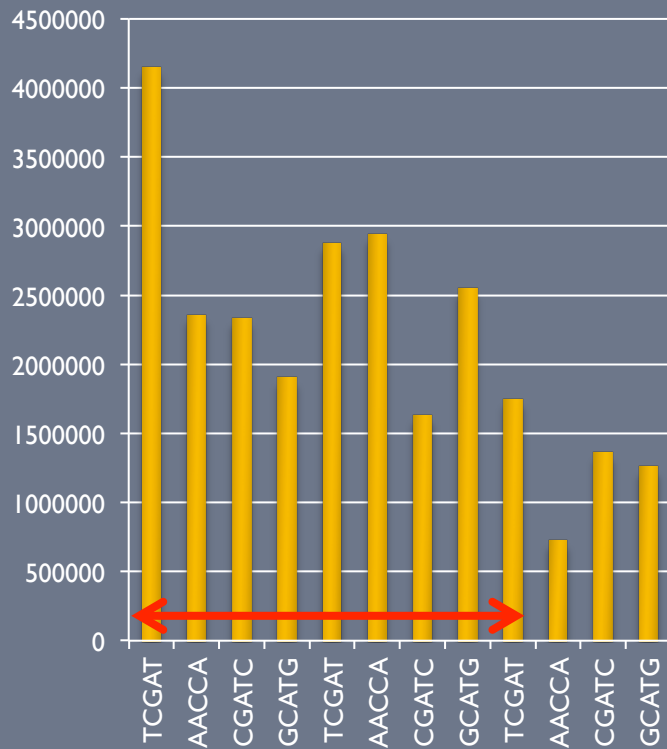
Material



- ▶ Phylogeography – 25 pops, ~320 inds
- ▶ 9 focal populations – search for candidate loci for local adaptation
 - ▶ 10 females & 10 males
 - ▶ Populations grow in very different habitats
 - ▶ Ecological data (available plant nutrients, soil temperature, associated species, climatic data)

All silica-dried material not collected by us in 2014 was collected during previous field work for other projects, and kept in the DNA-bank at the University of Oslo.

A glimpse of what we are waiting for...



- ▶ Estimation of genome size from 35 individuals (flow cytometry) – 400 Mb
- ▶ Aimed for 1 million reads per individual – will get more in the full run
- ▶ 2000-6000 shared SNPs among 80-90 % of the 9 individuals

Challenges and perspectives

- ▶ Evaluate how the inclusion of data on adaptive divergence adds information on the species' evolutionary potential, and how this affects the delimitation of conservation units
- ▶ Vast distributions and heavy logistics
- ▶ Genomics will enable highly demanded empirically based and sustainable conservation strategies for threatened and fragmented populations.



A person wearing a light-colored jacket and a hat is standing in a vast, open field with sparse vegetation. In the background, there are mountains under a blue sky with white clouds. A yellow thought bubble is positioned above the person, containing the text "Where are all the tiny, rare plants...?".

Where are all
the tiny, rare
plants...?

Thank you!



From the locality we named «*Carex scirpoidea*-heaven»
Mestersvig, Northeast Greenland National Park, 2014.