

Mapping of Arctic circumpolar marine biodiversity – new challenges and new genetic methods

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INSTITUTE OF MARINE RESEARCH
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Genetic investigations on herring (*Clupeas harengus*) in northeast Atlantic

Institute of Marine Research, Bergen

Gunnar Nævdal et al. (- 1978)

Knut E. Jørstad et al. (1978 -)



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Jørstad, K.E., D.P.F. King & G. Nævdal. 1991. Population structure of Atlantic herring, *Clupea harengus* L. J. Fish Biol. 39 (Suppl. A): 43–52.

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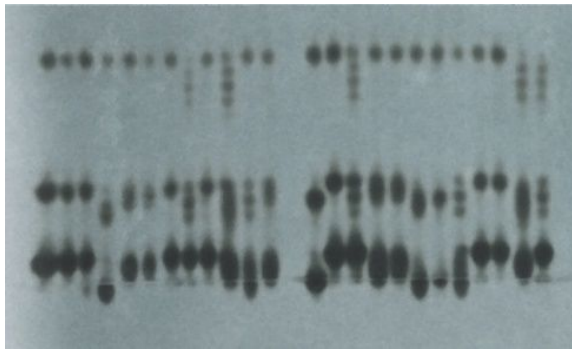
R/V "Johan Ruud", 0-group herring survey, Desember 1980

Starch gel electrophoreses conducted on the research vessel

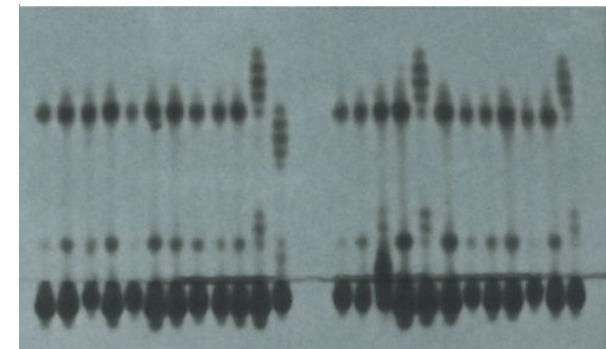
Technician: Ole Ingar Paulsen

Lactate dehydrogenase staining (*LDH-1**; *LDH-2**)

Balsfjord herring banding pattern

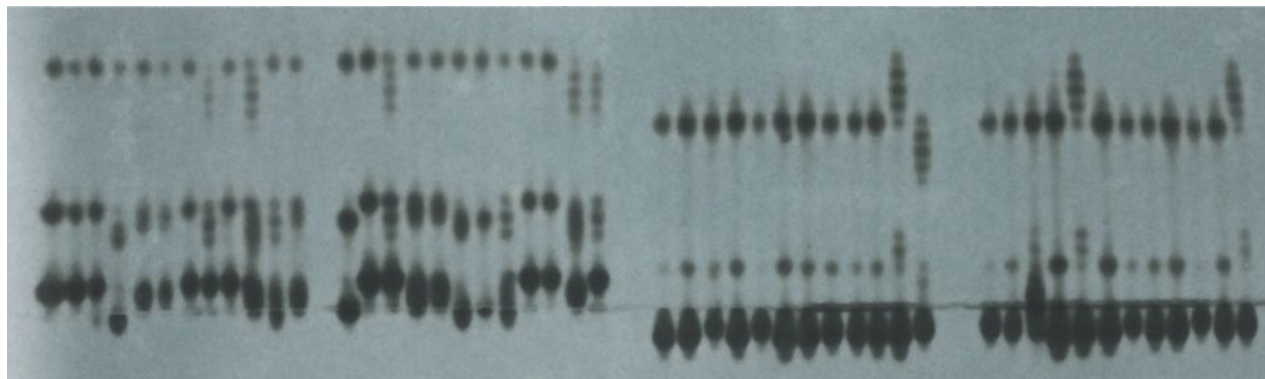


"Normal banding pattern"



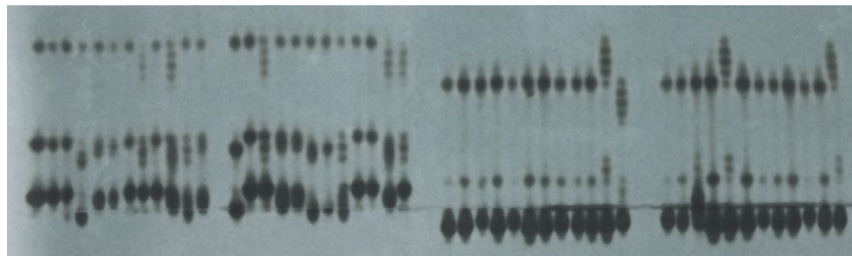
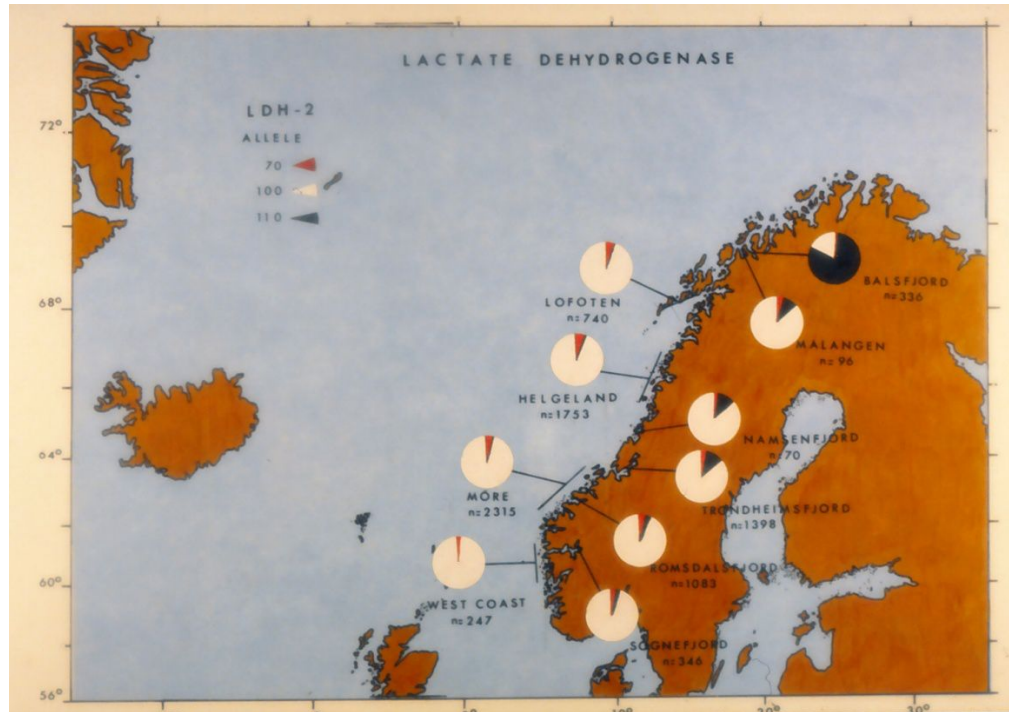
Technical
problems?

Control analyses (same gel)



Jørstad, K.E. & G. Nævdal. 1981. ICES C.M.

Jørstad, K.E. & G. Nævdal, 1983. Genetically distinct populations of herring.



Population structure of Atlantic herring, *Clupea harengus* L.

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ATLANTIC HERRING GENETICS

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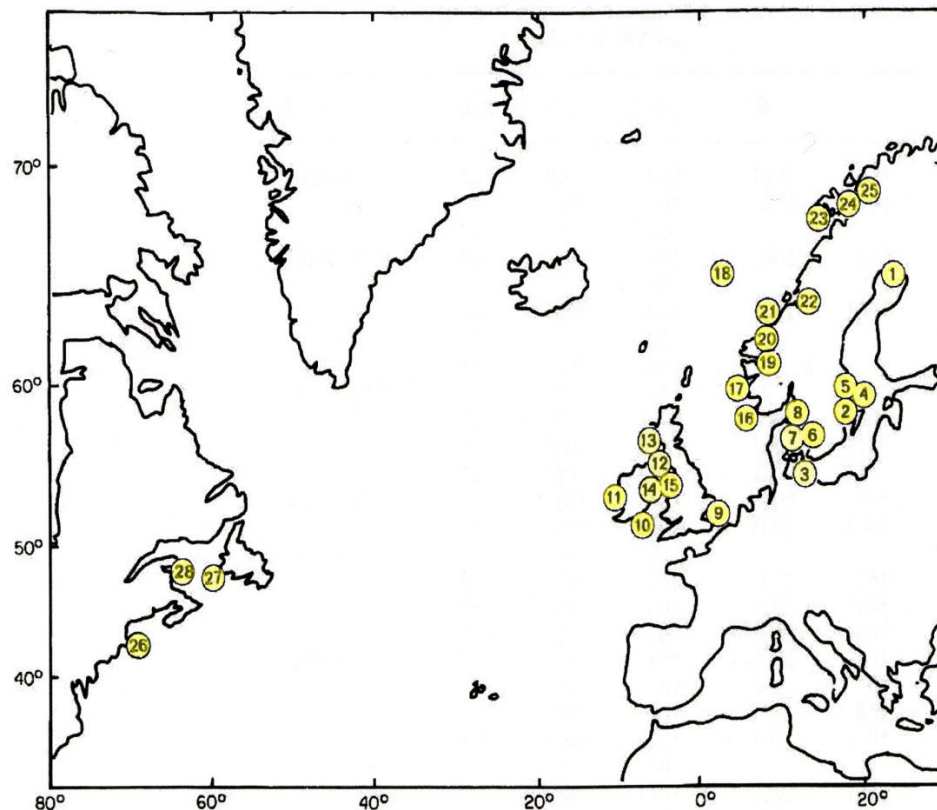


FIG. 1. Sampling localities of herring in the north Atlantic Ocean. The numbers and references (A–E) are given in Table I.



50

K. E. JØRSTAD ET AL.

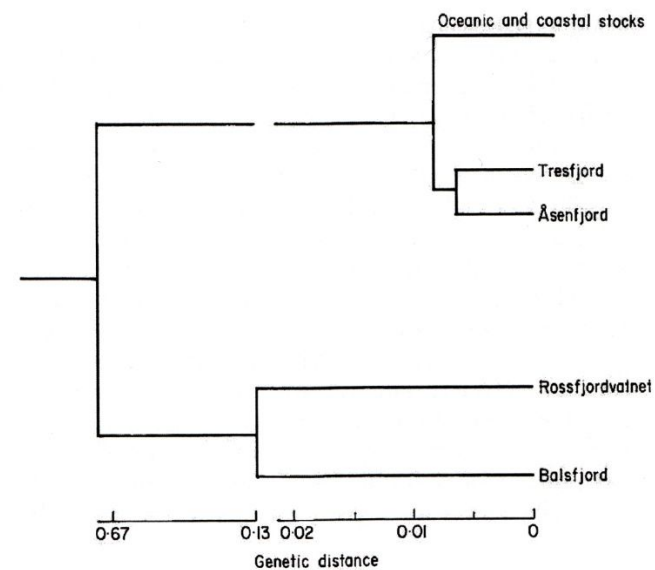


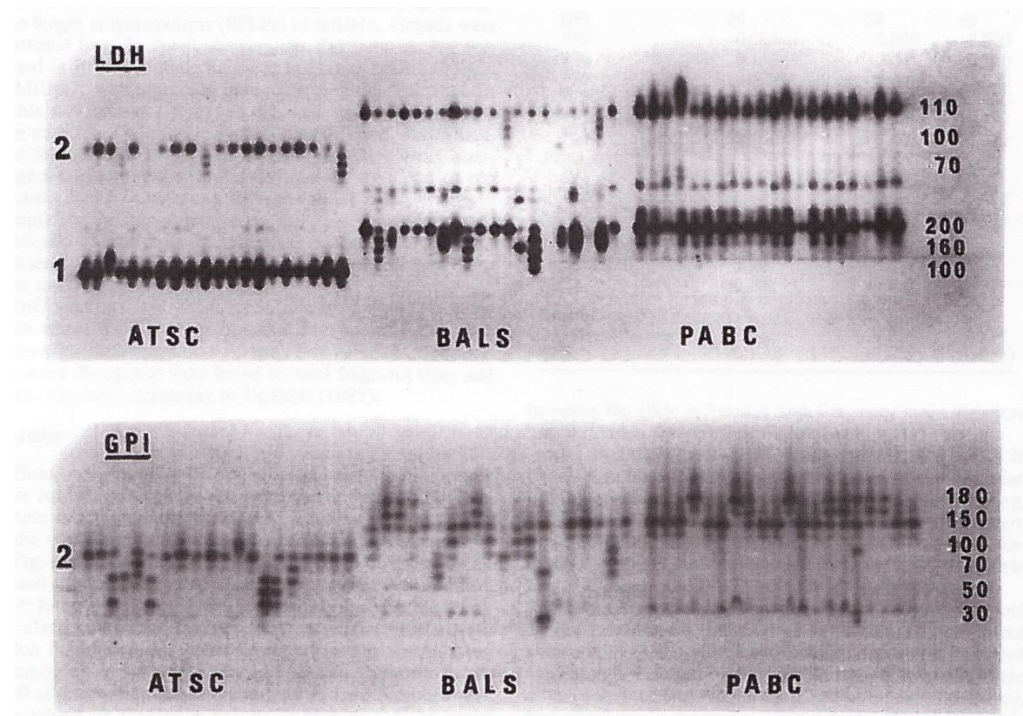
FIG. 2. Dendrogram generated by UPGMA cluster analysis showing the major genetic groupings among North Atlantic herring populations.

Genetic Comparison Between Pacific Herring (*Clupea pallasii*) and a Norwegian Fjord Stock of Atlantic Herring (*Clupea harengus*)

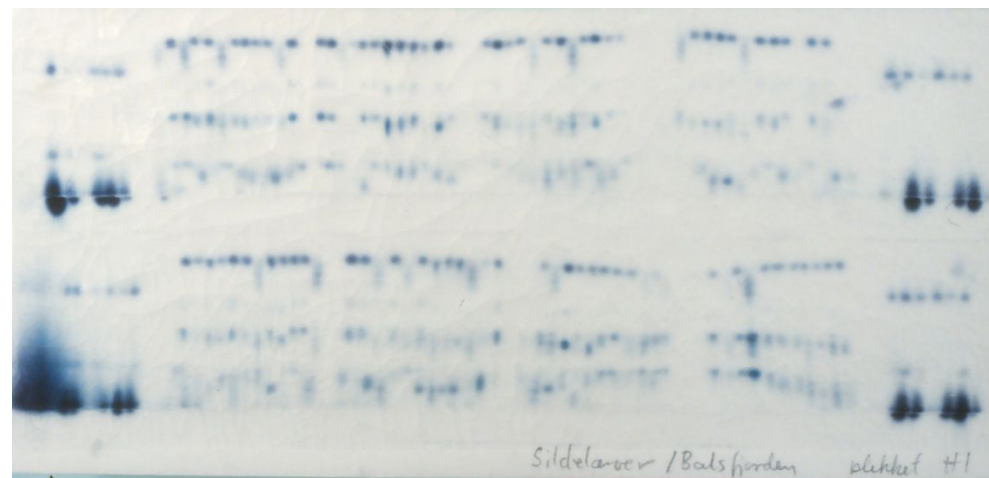
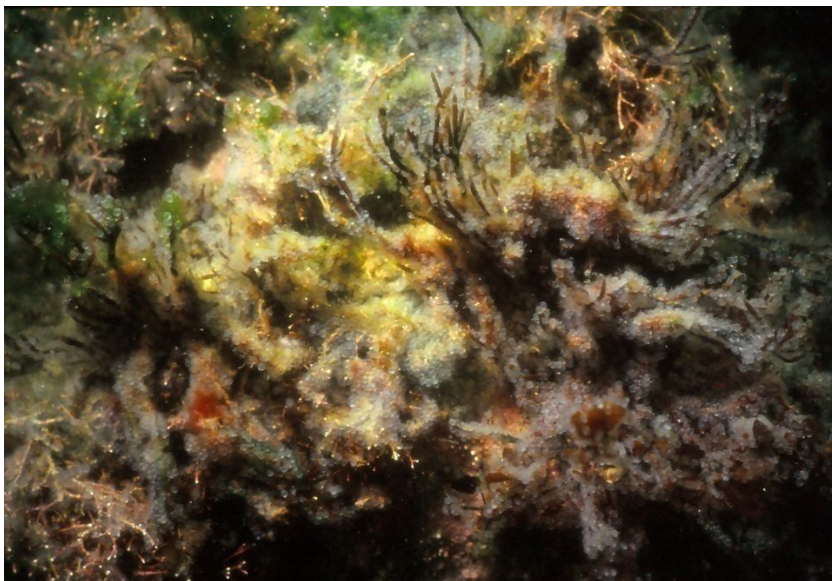
K.E. Jørstad, G. Dahle, and O.I. Paulsen

Institute of Marine Research, Div. of Aquaculture, P.O. Box. 1870 Nordnes, N-5024 Bergen, Norway

Jørstad, K.E., G. Dahle, and O.I. Paulsen. 1994. Genetic comparison between Pacific herring (*Clupea pallasii*) and a Norwegian fjord stock of Atlantic herring (*Clupea harengus*). Can. J. Fish. Aquat. Sci. 51(Suppl. 1): 233-239.



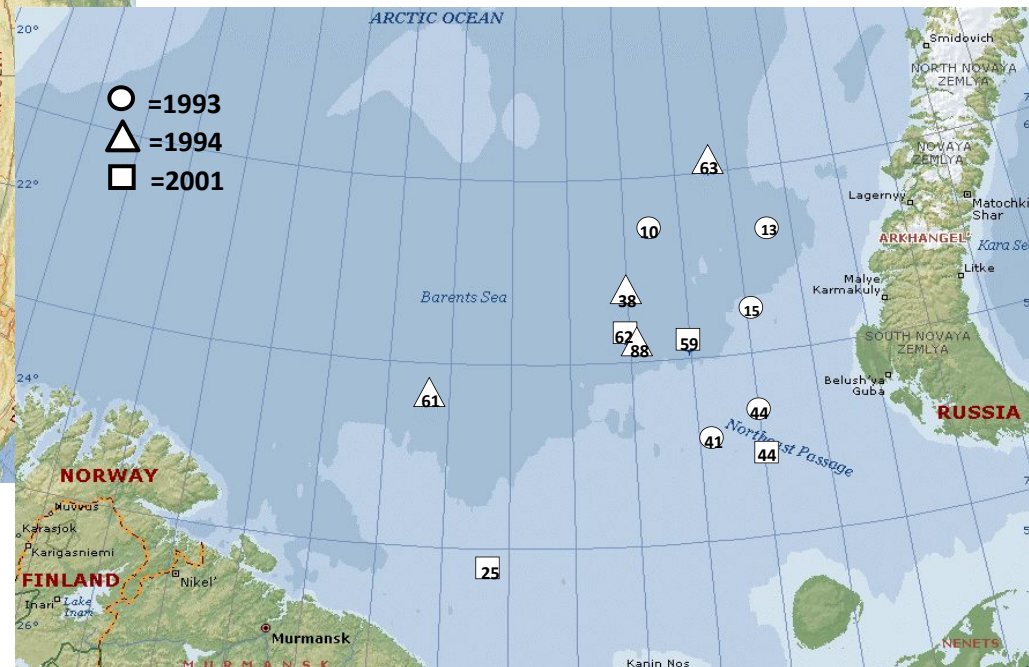
Balsfjord herring – intertidal spawning site (spring)



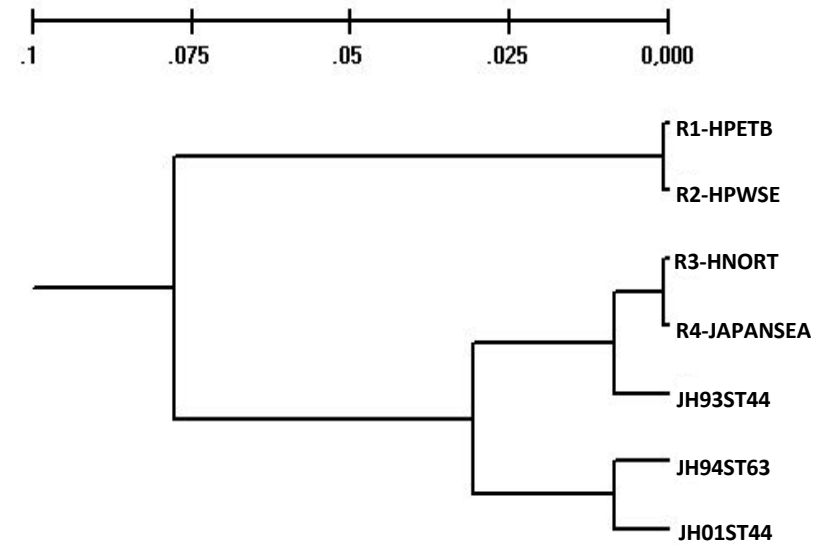
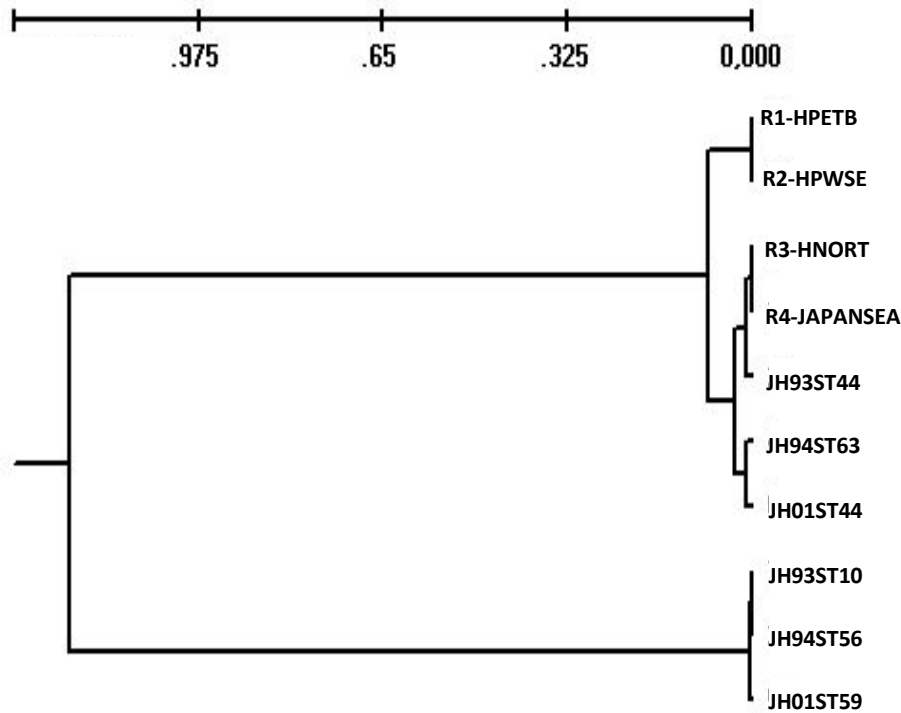
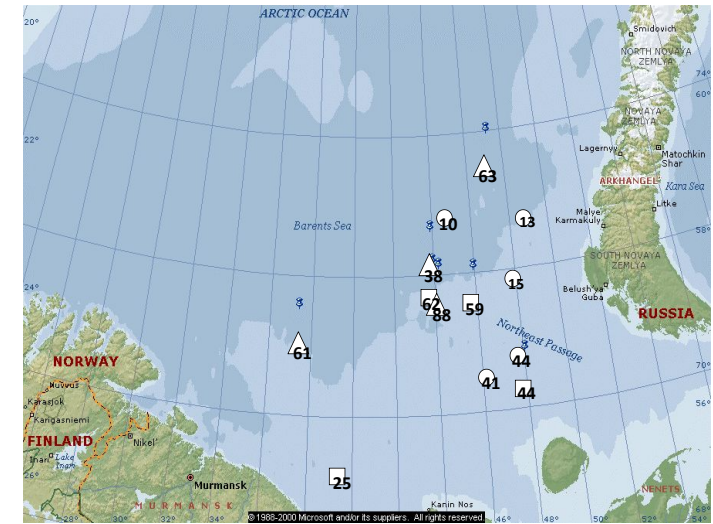
Evidence for two highly differentiated herring groups at Goose Bank in the Barents Sea and the genetic relationship to Pacific herring, *Clupea pallasii*

Knut E. Jørstad

Institute of Marine Research, Department of Aquaculture, Postbox 1970, Nordnes, 5817 Bergen, Norway (e-mail: knut.joerstad@imr.no)



Jørstad, 2004



RESEARCH ARTICLE

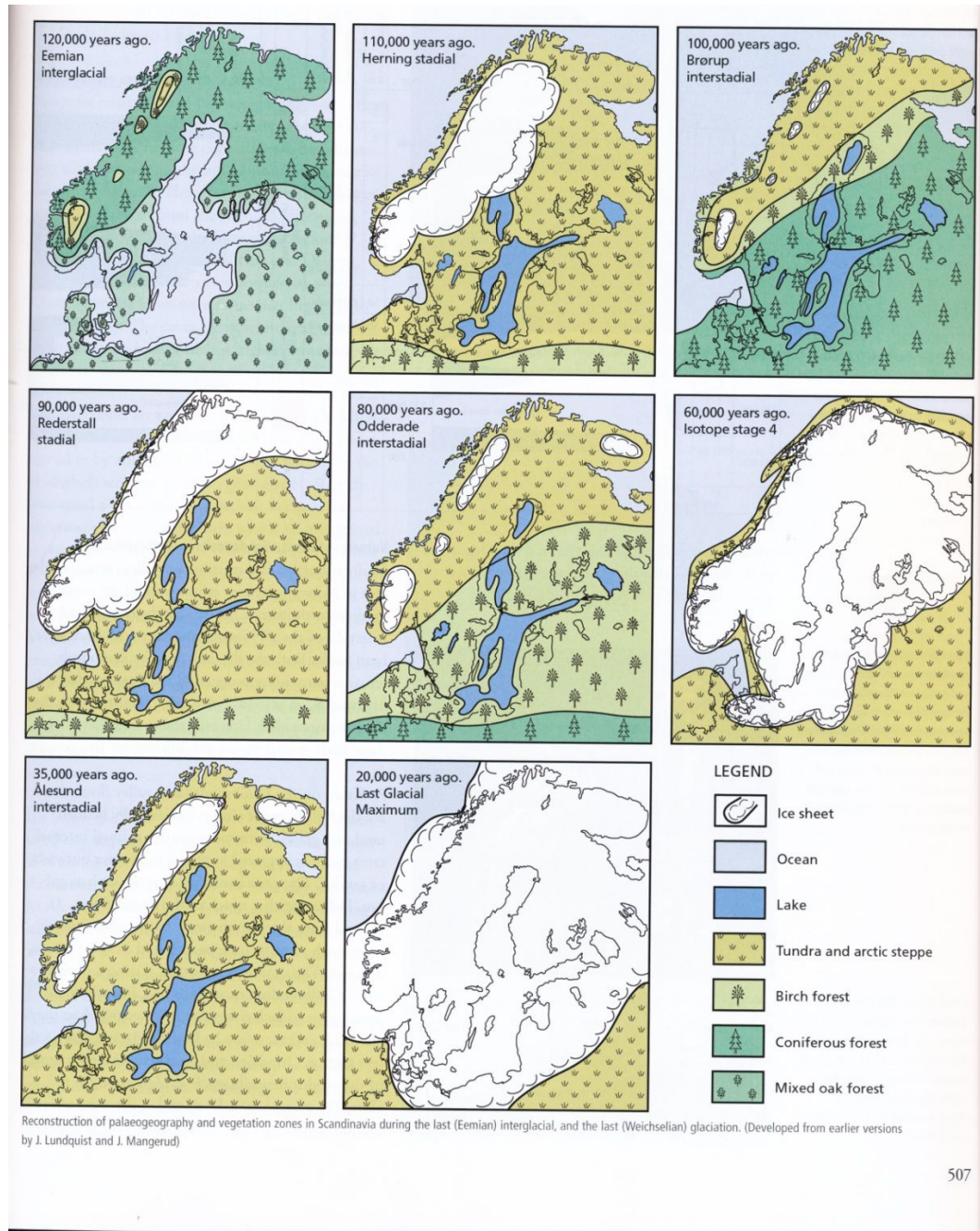
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Phylogeography of amphi-boreal fish: tracing the history of the Pacific herring *Clupea pallasii* in North-East European seas

Hanna M Laakkonen^{1*}, Dmitry L Lajus², Petr Strelkov² and Risto Väinölä¹

Vorren, T.O. and Mangerud, J. 2008.
Glaciations come and go.

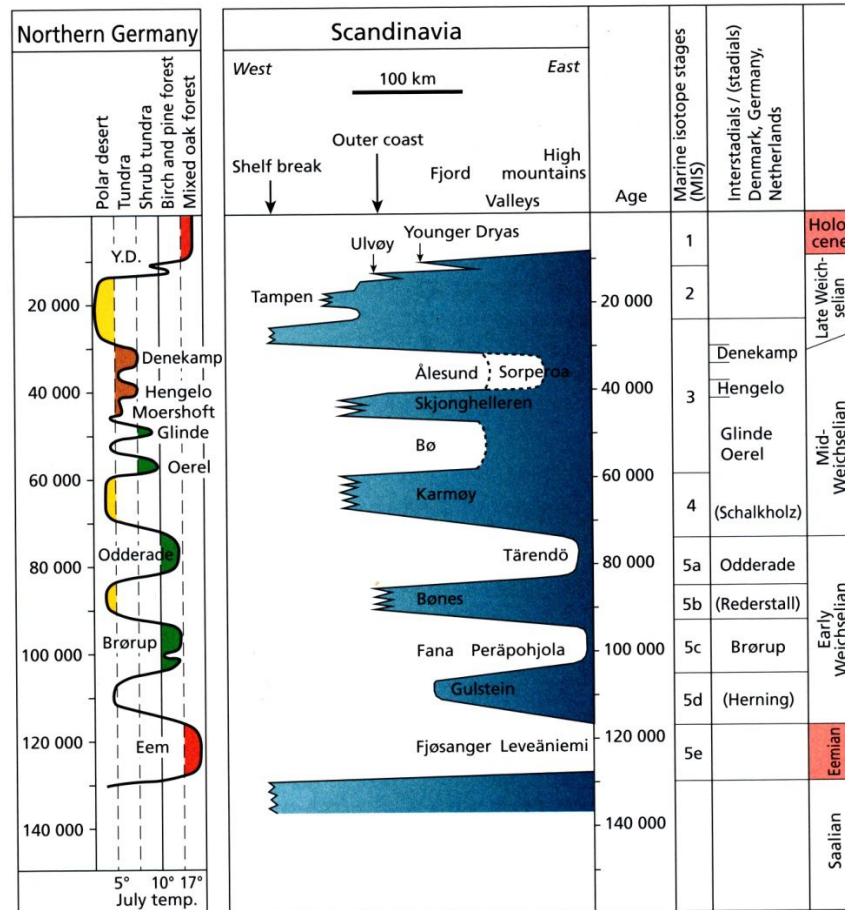
In: Ramberg, I.B., Bryhni, I., Nøttvedt, A. and Rognes, K. (eds.). The making of a land – geology of Norway. Trondheim. Norsk Geologisk Forening.

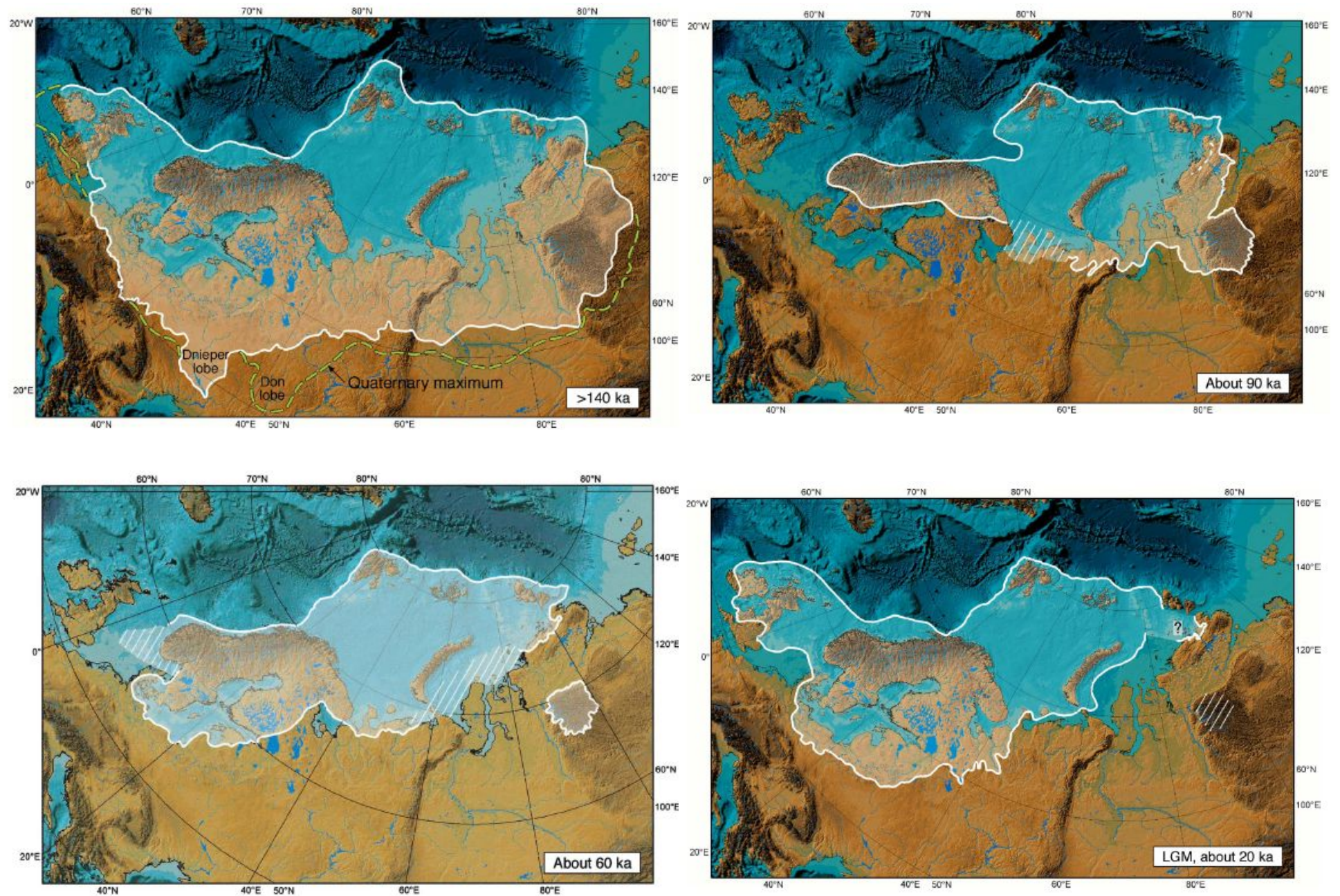


Vorren, T.O. and Mangerud, J. 2008. Glaciations come and go.

In: Ramberg, I.B., Bryhni, I., Nøttvedt, A. and Rognes, K. (eds.).
The making of a land – geology of Norway. Trondheim. Norsk Geologisk Forening.

Curves, termed *time-distance diagrams* by geologists, illustrating how the distribution of the Scandinavian and Barents Sea-Svalbard Ice Sheets varied during the last glaciation. The curves are designed to show the relative position of the ice margin. For example, there was no Scandinavian ice sheet during the Eemian interglacial. Thereafter, glaciers began to develop in the mountains, valley glaciers formed, and at some locations extended into the fjords during the Guldstein/Herning stadial some 110,000 years ago. This interval was succeeded by the milder Brørup Interstadial, during which the ice margin receded. An equivalent curve for Svalbard is also shown, but in this case the centre of the ice sheet is thought to have been located on Kong Karls Land or further east. The column on the extreme left shows vegetation types and July temperatures in northern Germany. (Figure modified from J. Mangerud et al.)





Svendsen et al. (2004). Quaternary Science Review 23: 1229-1271.



Berlevågfishen – en nordnorsk torskefisk med aner i Stillehavet

Den første berlevågfishen ble oppdaget i en fiskelast i Berlevåg i 1932. Siden da er det vitenskapelig bare registrert 57 eksemplarer av denne sjeldne torskefisk – alle utenfor kysten av Nord-Norge. Berlevågfishen, *Theragra finnmarchica*, ble lenge betraktet som en egen art som var beslektet med alaskalyren, *Theragra chalcogramma*, i Stillehavet. Nye genetiske og morfologiske undersøkelser viser imidlertid at berlevågfish og alaskalyr er én og samme art til tross for den store geografiske avstanden mellom de to bestandene. For å understreke det nære slektskapet til atlantisk torsk, *Gadus morhua*, har vi foreslått det nye vitenskapelige artsnavnet *Gadus chalcogrammus* for både bestanden i Nord-Norge og i Stillehavet.

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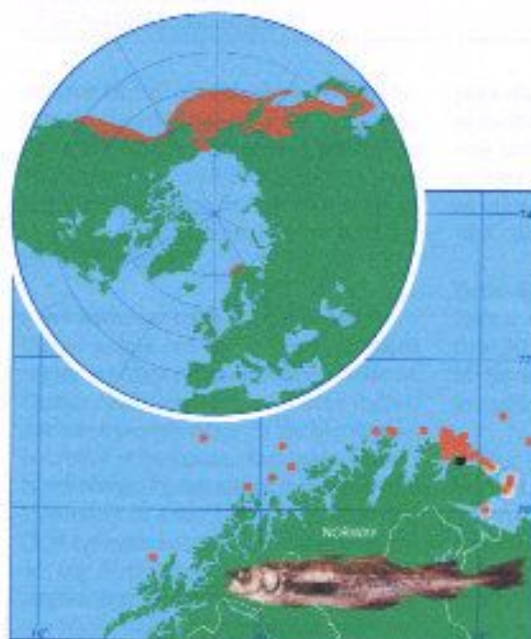
svein-erik.fjeldsen@uit.no

Ingvar Byrkjedal, UiB

ingvar.byrkjedal@umb.uib.no

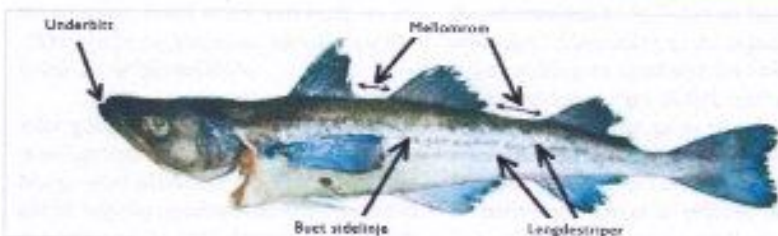
Koefoeds pionerarbeid

På mange måter er 1932 et merkeår for forståelsen av torskefiskenes evolusjonære opprinnelse og geografiske utbredelse på den nordlige halvkule. Gunnar Rollefson (1899–1976), den senere så kjente fiskeforskeren ved Havforskningsinstituttet, var da statens fiskeriinspektør i Øst-Finnmark. Midt i mai dette året oppdaget han tre eksemplarer av en hittil ukjent torskefisk i en fiskelast i Berlevåg. To av eksemplarene ble sendt til Havforskningsinstituttet for nærmere undersøkelser. Det skulle



Figur 1.11.1

Utbredelsen av torskefisk *Gadus chalcogrammus*. Bemerk den geografiske avstanden mellom bestanden i Nord-Norge (berlevågfish) og i Stillehavet (alaskalyr). Enkeltobservasjoner av berlevågfish er vist for perioden 1932–2008. Berlevåg er markert med en sort firkant. The geographical distribution of the gadoid species *Gadus chalcogrammus*. The municipality of Berlevåg is denoted by a filled square.



Figur 1.11.2

Noen markante kjennetegn for berlevågfishen, *Gadus chalcogrammus*. Berlevågfish tas mest på line i fiskeriene etter hyse og torsk. Some morphological characters of the Berlevågfish, *Gadus chalcogrammus*.

The taxonomic status of *Theragra finnmarchica* Koefoed, 1956 (Teleostei: Gadidae): perspectives from morphological and molecular data

1. I. Byrkjedal*,
2. D. J. Rees,
3. J. S. Christiansen,
4. S.-E. Fevolden

Journal of Fish Biology

Volume 73, Issue 5, pages 1183–1200, October 2008

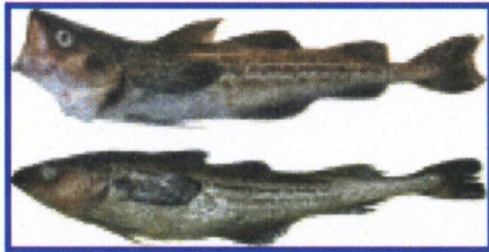


Figure 4. Examples of *Theragra finnmarchica* from northern Norway (upper; ZMUB V-255/06) and *Theragra chalcogramma* from Alaska (lower; ZMUB 15590).

Research article

Open Access

A mitogenomic approach to the taxonomy of pollocks: *Theragra chalcogramma* and *T. finnmarkica* represent one single species

Anita Ursvik¹, Ragna Breines¹, Jørgen Schou Christiansen², Svein-Erik Fevolden², Dag H Coucheron¹ and Steinar D Johansen^{*1,3}

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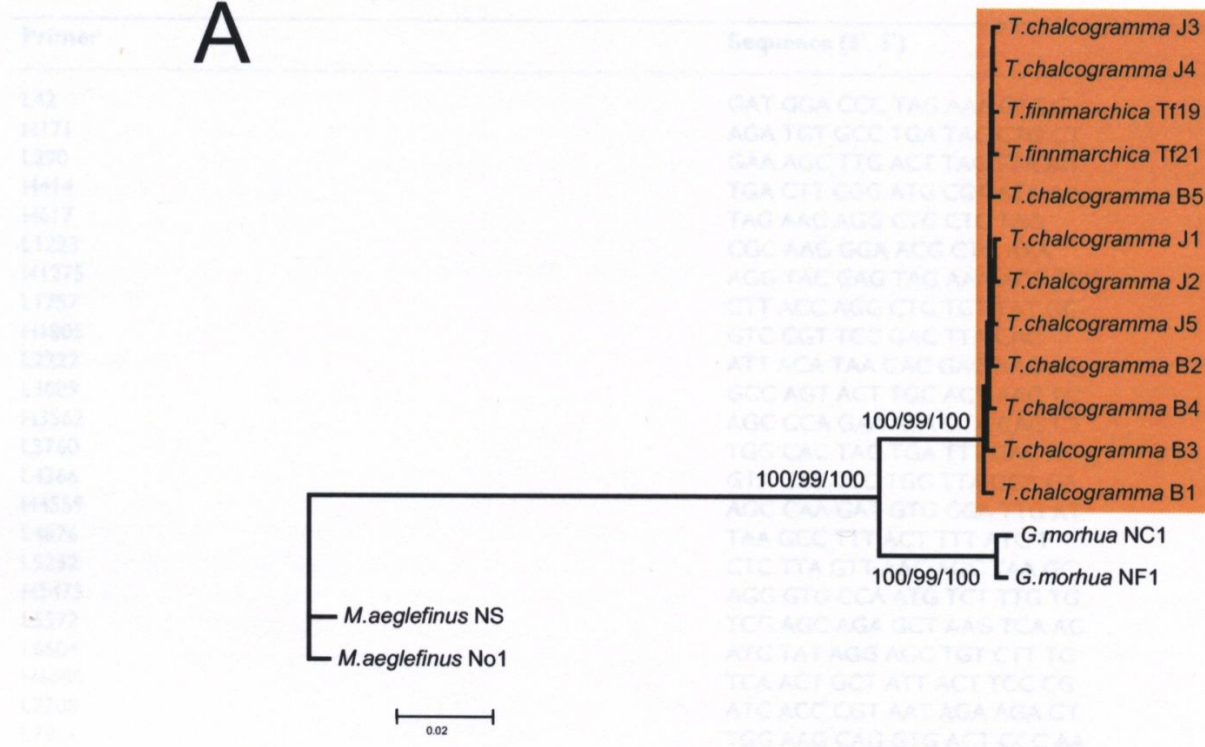
BMC Evolutionary Biology 2007, 7:86 doi:10.1186/1471-2148-7-86

Accepted: 7 June 2007

BMC Evolutionary Biology 2007, 7:86

<http://www.biomedcentral.com/1471-2148/7/86>

Table 3: PCR and DNA sequencing primers



Atlantic observation of *Calanus marshallae* (Copepoda; Calanoida)

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ABSTRACT: An observation of *Calanus marshallae* Frost, 1974, on the Atlantic side of the Polar Ocean is reported. Copepods were identified by comparing nucleotide sequences of mitochondrial 16S ribosomal RNA with a previously reported sequence from the Pacific region. Presence of the species in the Barents Sea may explain multi-modal length distributions previously obtained in the region. Potential implications for future identification of *Calanus* spp. in this region are discussed.

KEY WORDS: *Calanus marshallae* · *Calanus finmarchicus* · *Calanus glacialis* · Mitochondrial DNA · 16S ribosomal RNA · Molecular species identification

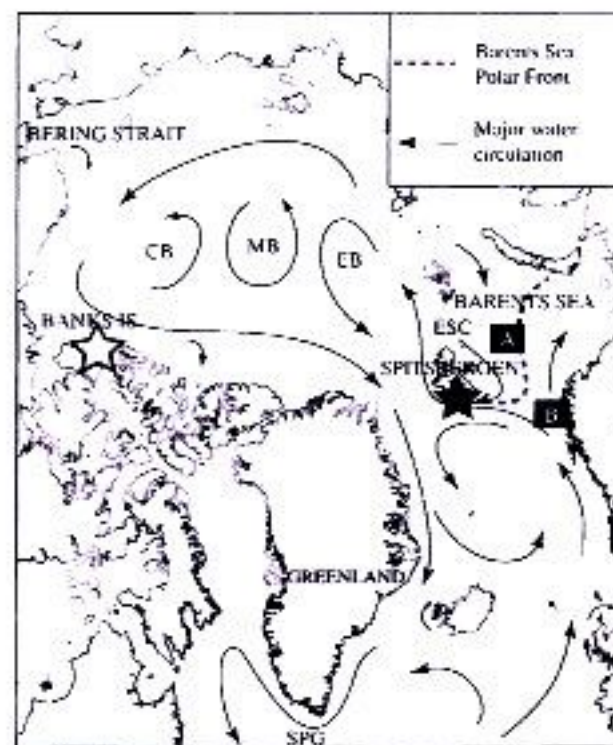


Fig. 1 Major circulation in the Atlantic and Arctic Oceans [after Grotefend et al. (in press); coastlines from GMT (Generic Mapping Tools), Wessel & Smith (1995)] (★) Present observation of *Calanus marshallae*; (☆) observations from Frost (1974). CB: Canadian Basin; MB: Mekarov Basin; EB: Eurasian Basin; ESC: East Spitsbergen Current; SPG: Subpolar Gyre. Rectangles A and B denote sampling areas for stations presented in Fig. 3



Where do they come from?



A biological consequence of reducing Arctic ice cover: arrival of the Pacific diatom *Neodenticula seminae* in the North Atlantic for the first time in 800 000 years

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MICHEL POULIN[§] and PAULI SNOEIJIS[¶]

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Abstract

The Continuous Plankton Recorder survey has monitored plankton in the Northwest Atlantic at monthly intervals since 1962, with an interregnum between 1978 and 1990. In May 1999, large numbers of the Pacific diatom *Neodenticula seminae* were found in Continuous Plankton Recorder (CPR) samples in the Labrador Sea as the first record in the North Atlantic for more than 800 000 years. The event coincided with modifications in Arctic hydrography and circulation, increased flows of Pacific water into the North-west Atlantic and in the previous year the exceptional occurrence of extensive ice-free water to the North of Canada. These observations indicate that *N. seminae* was carried in a pulse of Pacific water in 1998/early 1999 via the Canadian Arctic Archipelago and/or Fram Strait. The species occurred previously in the North Atlantic during the Pleistocene from ~1.2 to ~0.8 Ma as recorded in deep sea sediment cores. The reappearance of *N. seminae* in the North Atlantic is an indicator of the scale and speed of changes that are taking place in the Arctic and North Atlantic oceans as a consequence of regional climate warming. Because of the unusual nature of the event it appears that a threshold has been passed, marking a change in the circulation between the North Pacific and North Atlantic Oceans via the Arctic. Trans-Arctic migrations from the Pacific into the Atlantic are likely to occur increasingly over the next 100 years as Arctic ice continues to melt affecting Atlantic biodiversity and the biological pump with consequent feedbacks to the carbon cycle.

Keywords: Arctic, biological pump, continuous plankton recorder, CPR, deep sea cores, *Neodenticula seminae*, North Atlantic, North Pacific, phytoplankton, Pleistocene, subpolar gyre

Received 4 May 2006; revised version received 29 March 2007 and accepted 3 April 2007

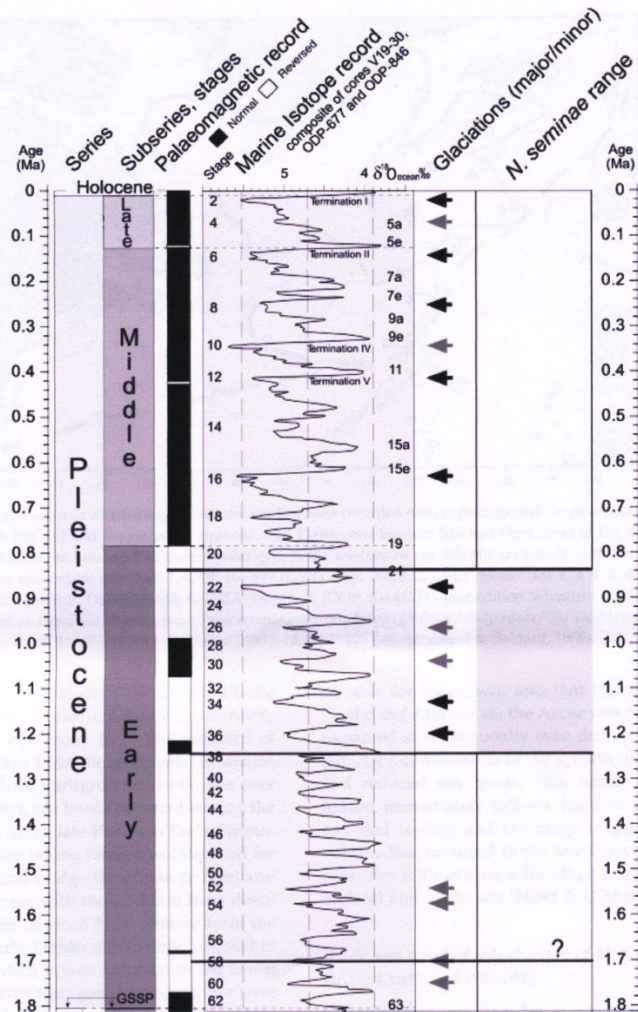
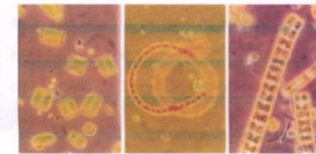


Fig. 3 Stratigraphic range of *Neodenticula seminiae* in North Atlantic cores plotted against the palaeomagnetic and marine isotope record with an indication of the timing of glaciations as arrows (Figure in part redrawn from Fig. 2 in Head & Gibbard, 2005).

Mudelsee & Stattegger (1997) as a possible precursor of the later colder Pleistocene climate state when ice sheets spread beyond polar regions and outside mountains. The LO of *N. seminiae* in MIS 21 follows immediately after the first evidence for severe cooling (MIS 22, approximately 880–870 ka). As can be seen from Fig. 2

in Head & Gibbard (2005), this localized extinction coincides with a large number of other events in the marine and terrestrial realm. Head & Gibbard (2005) deduced that the apparent large growth of ice in MIS 22 must be associated with a complimentary reduction in sea level.

Breached barrier



Neodenticula seminiae may be the first species for thousands of years to become established in the Atlantic via the trans-Arctic pathway. © Lyse Bérard-Therriault; Maurice Lamontagne Institute, Fisheries and Oceans Canada.

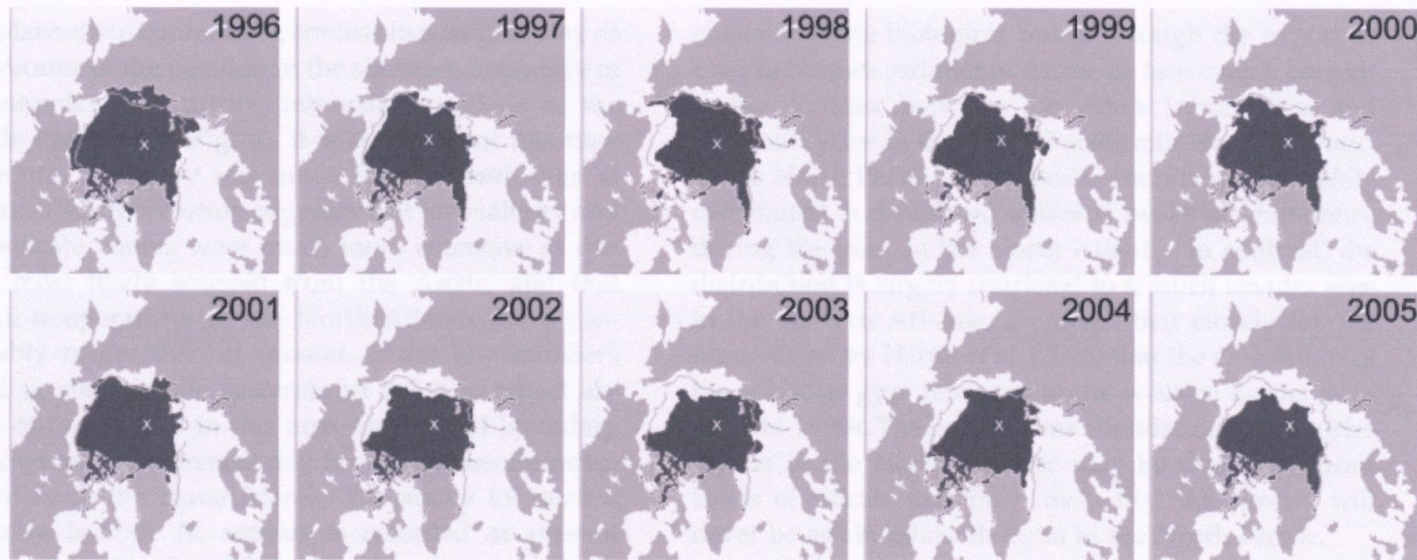


Fig. 5 Annual maps of Arctic summer (September) ice extent (1996–2005). A white cross marks the position of the North Pole (Data sourced from Fetterer & Knowles, 2002, updated to 2005).

from ~ 1.2 to ~ 0.8 Ma as recorded in deep sea sediment cores. The reappearance of *N. seminae* in the North Atlantic is an indicator of the scale and speed of changes that are taking place in the Arctic and North Atlantic oceans as a consequence of regional climate warming. Because of the unusual nature of the event it appears that a threshold has been passed, marking a change in the circulation between the North Pacific and North Atlantic Oceans via the Arctic. Trans-Arctic migrations from the Pacific into the Atlantic are likely to occur increasingly over the next 100 years as Arctic ice continues to melt affecting Atlantic biodiversity and the biological pump with consequent feedbacks to the carbon cycle.

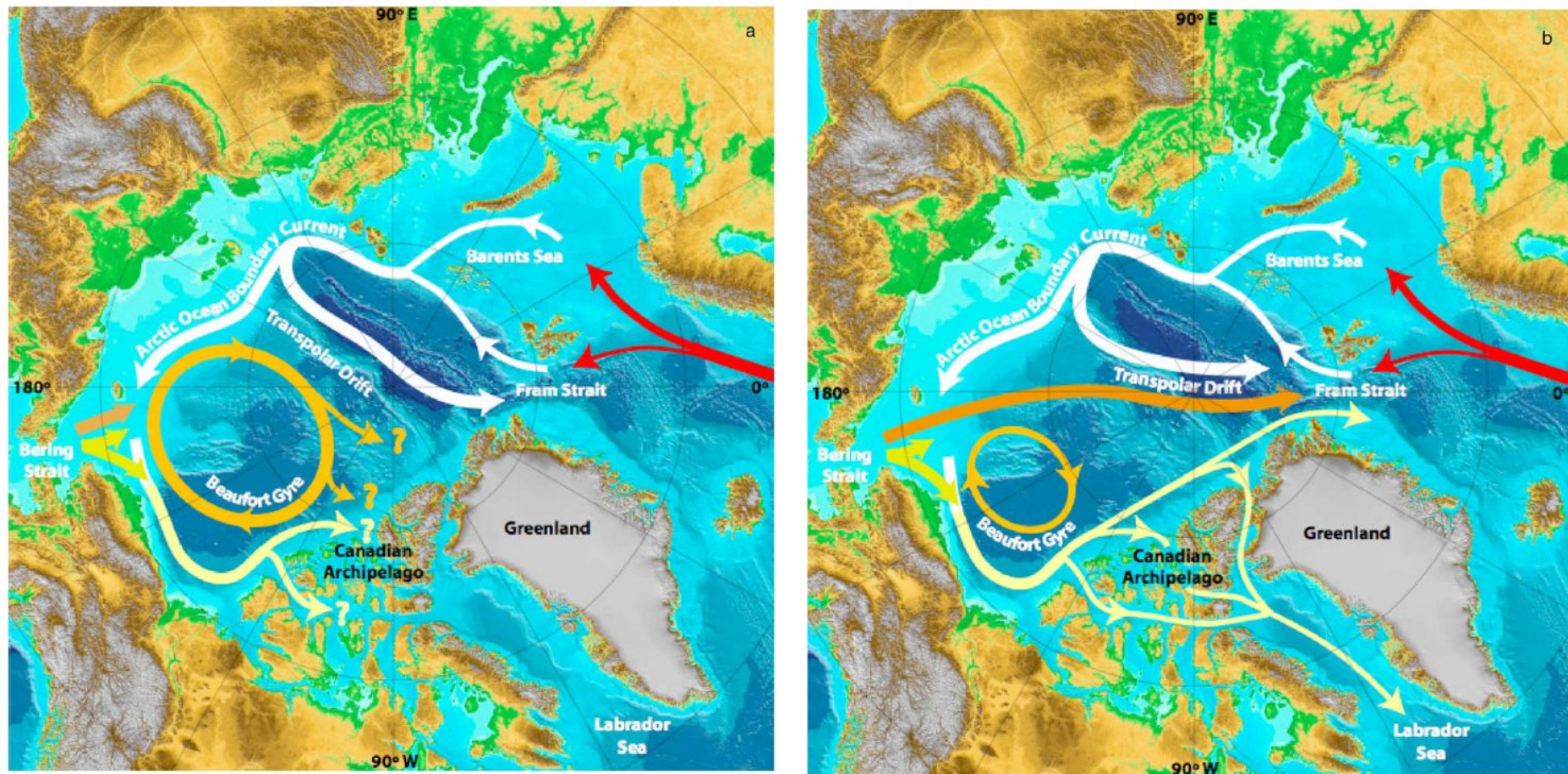
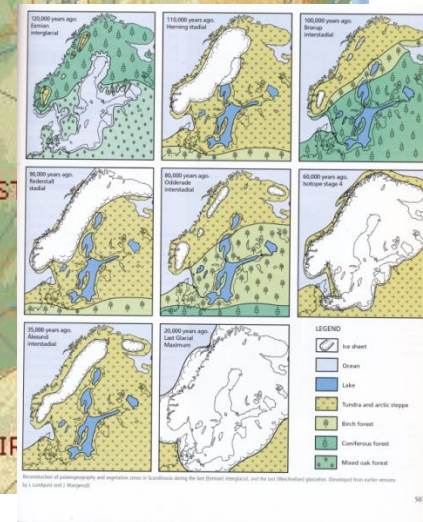
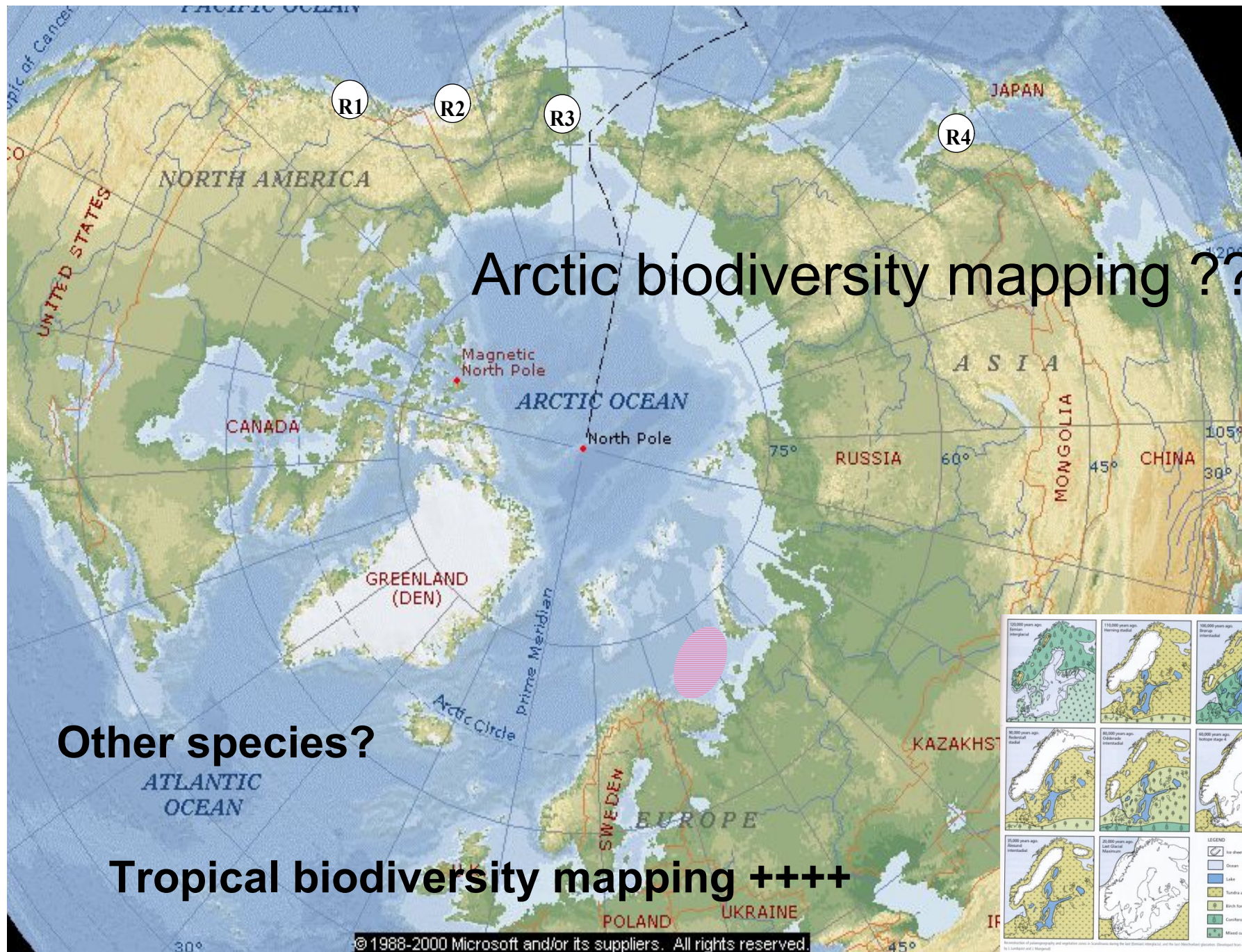


FIG. 2. Upper ocean circulation patterns in the Arctic Ocean (a) before and (b) after the shift to a strongly cyclonic atmospheric circulation regime. Red arrows indicate inflow of Atlantic water into the Arctic Ocean through the Barents Sea and Fram Strait. White arrows indicate surface flows of polar water. Yellow and orange arrows indicate inflow of Pacific water into the Arctic Ocean through the Bering Strait. Pale yellow and orange arrows indicate mixtures of polar- and Pacific-derived waters.

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ARCTIC CLIMATE CHANGE AND ITS IMPACTS ON THE ECOLOGY OF THE NORTH ATLANTIC

CHARLES H. GREENE,^{1,4} ANDREW J. PERSHING,^{1,2} THOMAS M. CRONIN,³ AND NICOLE CECI¹



Genomics and the future of conservation genetics

Fred W. Allendorf^{‡}, Paul A. Hohenlohe^{§||} and Gordon Luikart^{¶#}*

Abstract | We will soon have complete genome sequences from thousands of species, as well as from many individuals within species. This coming explosion of information will transform our understanding of the amount, distribution and functional significance of genetic variation in natural populations. Now is a crucial time to explore the potential implications of this information revolution for conservation genetics and to recognize limitations in applying genomic tools to conservation issues. We identify and discuss those problems for which genomics will be most valuable for curbing the accelerating worldwide loss of biodiversity. We also provide guidance on which genomics tools and approaches will be most appropriate to use for different aspects of conservation.

MOLECULAR ECOLOGY

Molecular Ecology (2014) 23, 1661–1667

NEWS AND VIEWS

MEETING REVIEW

Recent novel approaches for population genomics data analysis

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Next-generation sequencing (NGS) technology is revolutionizing the fields of population genetics, molecular ecology and conservation biology. But it can be challenging for researchers to learn the new and rapidly evolving techniques required to use NGS data. A recent workshop entitled 'Population Genomic Data Analysis' was held to provide training in conceptual and practical aspects of data production and analysis for population genomics, with an emphasis on NGS data analysis. This workshop

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A defining decade in DNA sequencing

John D McPherson

A revolution in DNA sequencing technology has enabled new insights from thousands of genomes sequenced across taxa.

The tenth anniversary of *Nature Methods* offers an excellent occasion to reflect on protocols and technologies that are rapidly shaping research methodology. A major advance has undoubtedly been the massive increase in DNA and RNA sequencing capabilities that fall under the general term of next-generation sequencing (NGS). The death in 2013 of Frederick Sanger, who pioneered methods for deciphering amino acid and nucleic acid sequences, for which he was awarded two Nobel Prizes (1958 and 1980), also affords the opportunity to look back at recent events and the extraordinary progress that has come from the sequencing metamorphosis. Many new sequencing platforms have matured while others have failed to gain a market share, but the result has been an extraordinary increase in sequencing capabilities (Fig. 1).

For many years, Sanger DNA sequencing—a method that utilizes dideoxynucleotide analogs to halt template elongation, resulting in a ladder of fragments separable on a gel matrix—dominated the DNA analysis field. Its dominance was ensured by the introduction of fluorescent markers, which enabled the automation of sequence data collection. Incremental improvements on this basic concept produced a fully automated platform capable of generating 500,000 bases per day, enabling the first sequencing of the human genome in less than a decade. The Sanger sequenc-

Invasive hybridization in a threatened species is accelerated by climate change

Clint C. Muhlfeld^{1,2*}, Ryan P. Kovach², Leslie A. Jones^{1,3}, Robert Al-Chokhachy⁴, Matthew C. Boyer⁵, Robb F. Leary⁶, Winsor H. Lowe³, Gordon Luikart² and Fred W. Allendorf³

Climate change will decrease worldwide biodiversity through a number of potential pathways¹, including invasive hybridization² (cross-breeding between invasive and native species). How climate warming influences the spread of hybridization and loss of native genomes poses difficult ecological and evolutionary questions with little empirical information to guide conservation management decisions³. Here we combine long-term genetic monitoring data with high-resolution climate and stream temperature predictions to evaluate how recent climate warming has influenced the spatio-temporal spread of human-mediated hybridization between threatened native westslope cutthroat trout (*Oncorhynchus clarkii lewisi*) and non-native rainbow trout (*Oncorhynchus mykiss*), the world's most widely introduced invasive fish⁴. Despite widespread release of millions of rainbow trout over the past century within the Flathead River system⁵, a large relatively pristine

Session: "Circumpolar marine biodiversity in the Arctic"

Conveners:

Hein Rune Skjoldal, Institute of Marine Research, Bergen, Norway

Knut Eirik Jørstad, Jørstad marin AS / Institute of Marine Research), Bergen, Norway

Jørgen Schou Christiansen, The Arctic University of Norway, Tromsø

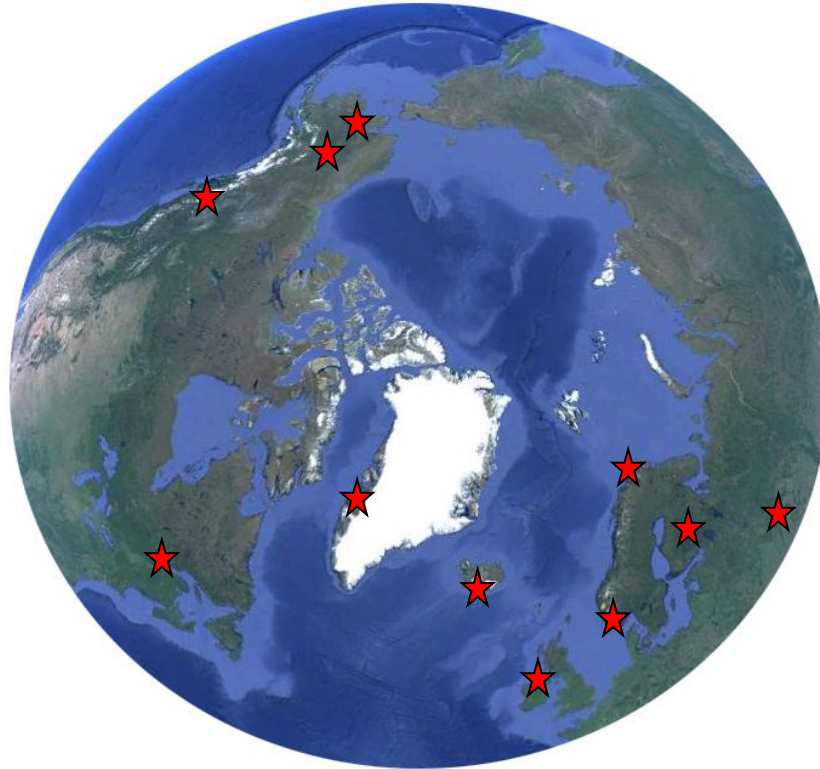
Svein-Erik Fevolden, The Arctic University of Norway, Tromsø

Session description:

The ongoing warming of the sub-arctic and arctic seas presently shifts the distributional range for a number of boreal and arctic species and, at the same time, opens up for human activities in previously inaccessible areas. Recent studies also show genetic linkages between marine species in sub-arctic Pacific and Euro-arctic waters and new invasions are pending. Therefore, the arctic marine fauna must be viewed in a circumpolar context to develop proper monitoring and management policies. This calls for more comprehensive studies of phylogeography and taxonomical and functional biodiversity to meet the conservation aims raised in the Arctic Biodiversity Assessment report.

Proposal for international workshop

CIRCUMPOLAR MARINE BIODIVERSITY - GENETIC LINKAGE BETWEEN ATLANTIC AND PACIFIC SPECIES



Conveners:

Hein Rune Skjoldal, Institute of Marine Research,
Bergen

Knut Eirik Jørstad, Jørstad marin AS, Bergen

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- Review existing knowledge about marine biodiversities in the Arctic with particular focus on the genetic relationship between Atlantic and Pacific species
- Discuss new challenges to arctic marine biodiversities due to future climate changes
- Develop a circumpolar scientific network for collected samples of selected species for biological and genetic profiling, as baselines for evaluating future effects due to climate changes

THANK YOU!

Arctic biodiversity mapping ???

Other species?

Tropical biodiversity mapping +++++

