

Project information

Keywords

Pseudocalanus, congeners, phylogeography, connectivity, N-Migrate model

Project title

Pan-Arctic phylogeography and population connectivity of species of Pseudocalanus (Copepoda, Calanoida)

Year

2017

Project leader

Claudia Halsband

Geographical localization of the research project in decimal degrees (max 5 per project, ex. 70,662°N and 23,707°E)

panarctic, e.g. 70.9, -166.01; 79.67, 9.77; 68.0, -18.49; 78.81, -169.46; 83.23, -168.35

Participants

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International:

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Flagship

Fjord and Coast

Funding Source

Flagship F&C

Summary of Results

Existing and new DNA sequence information for *Pseudocalanus* (Copepoda, Calanoida) congeners were combined across the Atlantic and Pacific sectors of the Arctic Ocean (Fig. 1) in a multi-national effort between Norwegian, Polish, US-American and Russian collaborators.

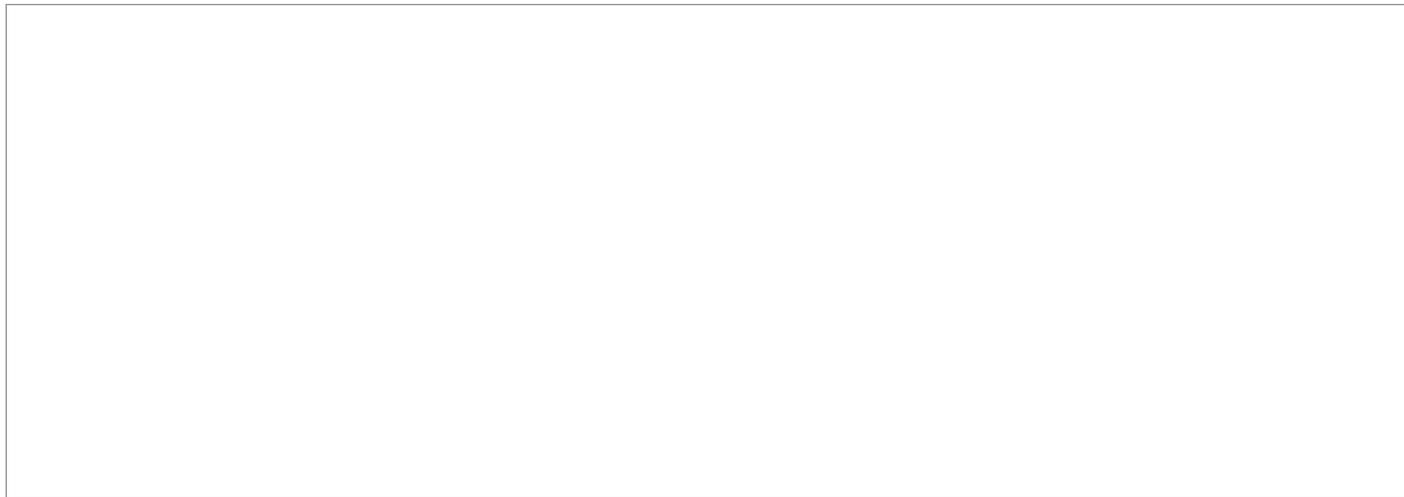


Fig. 1: Sample sizes for the three Pseudocalanus congeners

Haplotype analyses showed three different patterns: *P. minutus* has two very commonly occurring haplotypes, shared among all 10 populations (Fig. 2), indicating high levels of connectivity between all of their populations. *P. acuspes*, in contrast, has only one and very

dominant haplotype throughout all 7 populations, but the Norwegian Sea has a unique set of divergent haplotypes (Fig. 3). The moderate haplotype diversity in both species is a direct reflection of the relatively small inherent population size typical for Arctic populations (compared to temperate populations). Finally, *P. newmani* has two almost equally frequently occurring haplotypes shared only among the North Pacific/Pacific Arctic populations, with strong connectivity among all sampled populations. The Northwest Atlantic populations have a unique set of haplotypes that radiates from haplotypes in the Bering Sea (Fig. 4). High haplotype diversity reflects a larger population size in this temperate species than in the previous two.



Fig. 2: Haplotype network of *P. minutus*

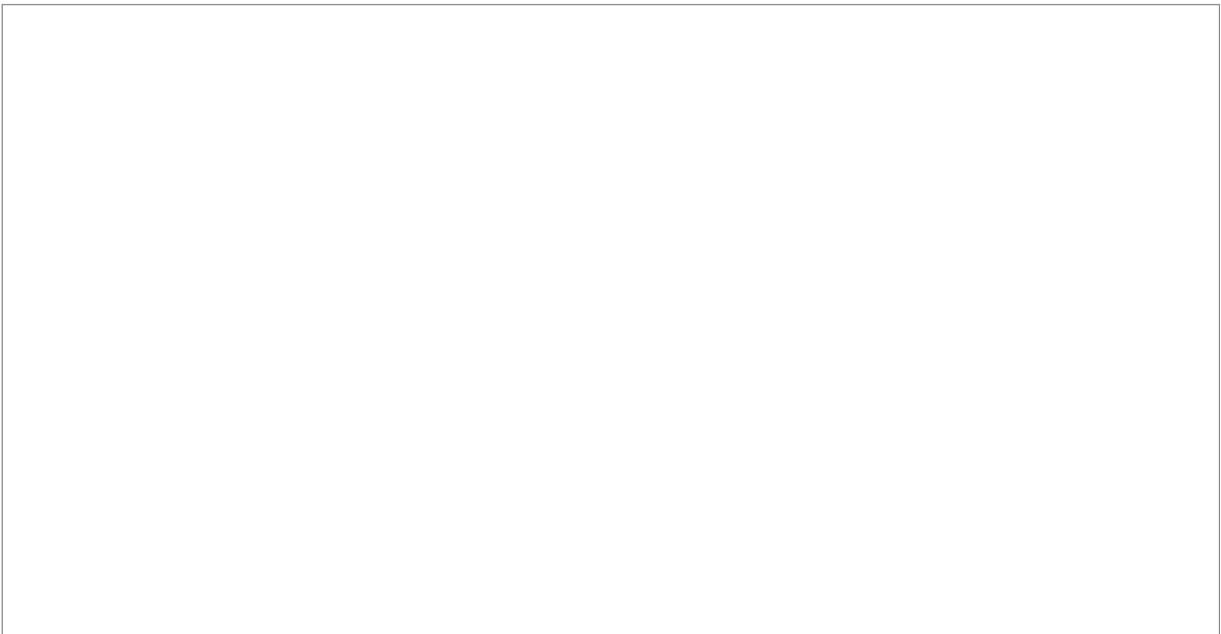


Fig. 3: Haplotype network of *P. acuspes*

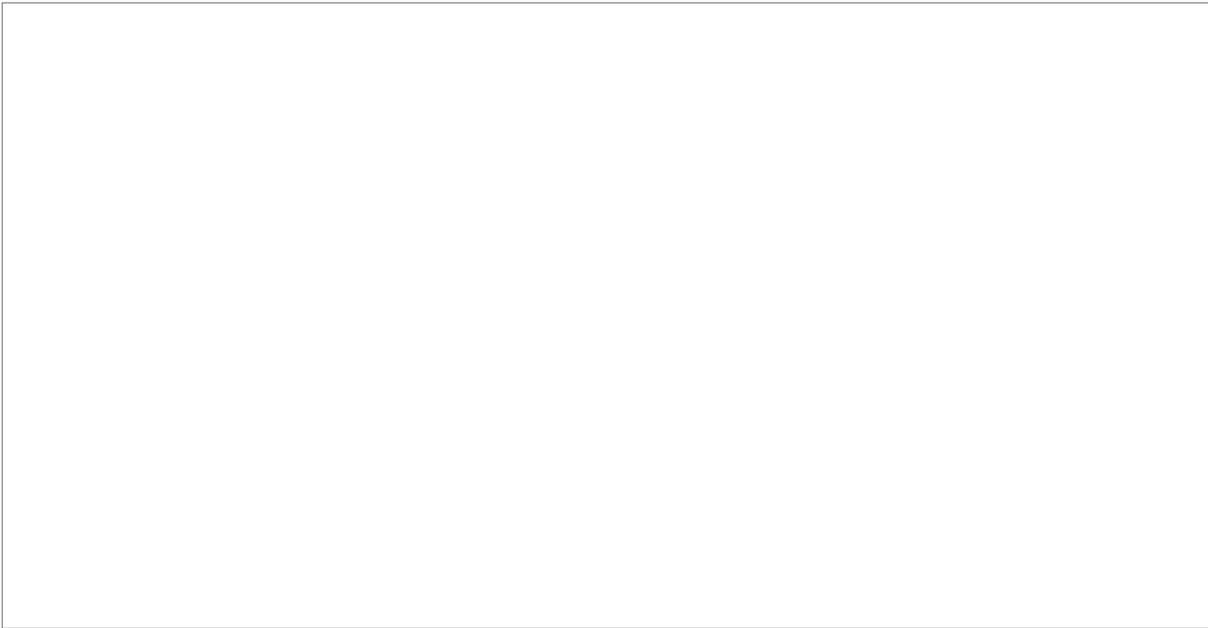


Fig. 4: Haplotype network of *P. newmani*

A pan-Arctic phylogeographic analysis with the help of N-Migrate models revealed differing patterns and pathways of population connectivity, indicating that even sibling species of copepods exhibit disparate tolerances to ecological and environmental pressures structuring zooplankton populations. With the updated data set, filling in populations over the entire geographic region, the gene-flow models showed that both *P. newmani* and *P. minutus* are panmictic, while *P. acuspes* is showing a strong directional gene-flow pattern from the Pacific Arctic to the Atlantic Arctic (Table 1). These differences demonstrate the potential for differential distribution changes of congeners depending on ocean current changes under climate change.

Table 1: N-Migrate model results for *Pseudocalanus* gene flow patterns

	<i>P. minutus</i>	<i>P. acuspes</i>	<i>P. newmani</i>
N-Migrate model with highest rank probability	Panmictic	Pacific to Atlantic Arctic	Panmictic

Master and PhD-students involved in the project

NA

For the Management

Together with predictions of expected ocean current alterations in the Arctic Ocean, the data obtained here can help to describe future *Pseudocalanus* habitat expansions or contractions, especially in the light of climatic warming scenarios, to facilitate estimations of changes in energy flow through Arctic food-webs.

Published Results/Planned Publications

The results are written up as a manuscript to be submitted to *Polar Biology* by the end of 2017.

Communicated Results

The results have been presented at Arctic Frontiers (January) and the ESSAS meeting (June) in Tromsø, as well as the International Conference on Copepoda in Los Angeles (July).

Interdisciplinary Cooperation

NA

Budget in accordance to results

The budget has been used for salaries and travel costs in accordance with the original budget.

Could results from the project be subject for any commercial utilization

No

Conclusions

Four species of the copepod genus *Pseudocalanus* exhibit widespread distributions over polar and sub-polar latitudes of the northern hemisphere: *Pseudocalanus minutus*, *P. acuspes*, *P. moultoni* and *P. newmani*. This project provides a pan-arctic phylogeographic analysis for three of these, with a view to provide new insight into how reduction in sea-ice cover due to climate change may reduce existing barriers to gene flow and modify connectivity among Arctic and sub-Arctic populations.