

THE WAYS OF FORMATION OF FRESHWATER COPEPOD GENETIC DIVERSITY IN THE ARCTIC SUBAREA OF PALAEARCTIC

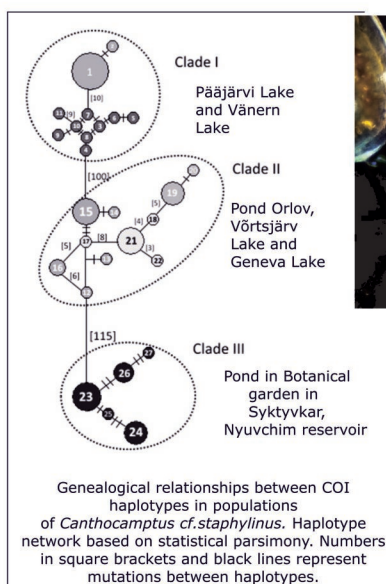
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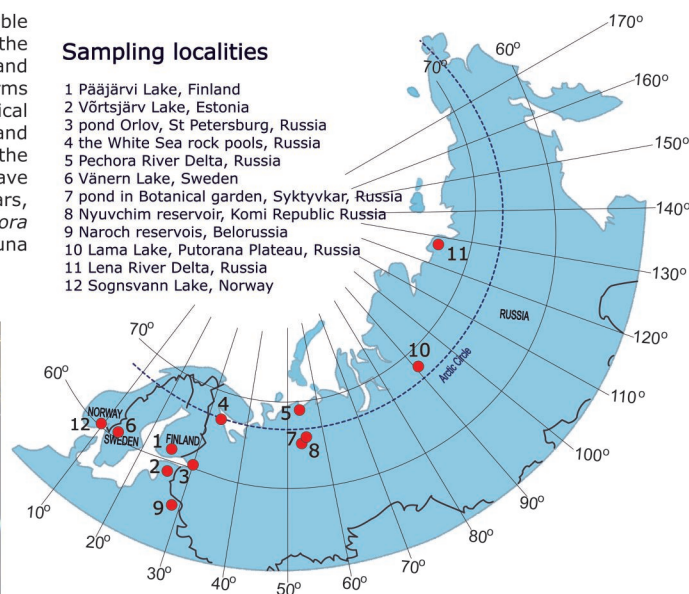
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The Arctic copepods manifest all signs of biological progress: they show remarkable species richness in comparison with the temperate zone, often dominate on the abundance and biomass in zooplankton and meiobenthos, have wide geographical and ecological distribution, and high differentiation and a variety of adaptive forms (Chernov, 2008). Due to their developmental history from the ancient geological periods, they demonstrate a high degree of biochemical (Makhutova et al., 2014) and genetic variety. In the geological past the biodiversity of them was formed under the influence of tectonic processes and movements of the glacier. These processes have caused the genesis of glacial relicts among copepods – *Limnocalanus macrurus* Sars, *L. johanseni* Marsh, *Senecella siberica* Vyshkvartzeva, species of *Eurytemora* (Sushchenya et al., 1986; Dubovskaya, Glushenko, 2018), and endemic copepod fauna of Baikal Lake (Boxshall, Evstigneeva, 1994; Mayor et al., 2010). Glacial relicts were found by us in lakes Pääjärvi, Lama and in the Lena River Delta.



Sampling localities

- 1 Pääjärvi Lake, Finland
- 2 Võrtsjärv Lake, Estonia
- 3 pond Orlov, St Petersburg, Russia
- 4 the White Sea rock pools, Russia
- 5 Pechora River Delta, Russia
- 6 Vänern Lake, Sweden
- 7 pond in Botanical garden, Syktyvkar, Russia
- 8 Nyuvchim reservoir, Komi Republic, Russia
- 9 Naroch reservoirs, Belorussia
- 10 Lama Lake, Putorana Plateau, Russia
- 11 Lena River Delta, Russia
- 12 Sognsvann Lake, Norway

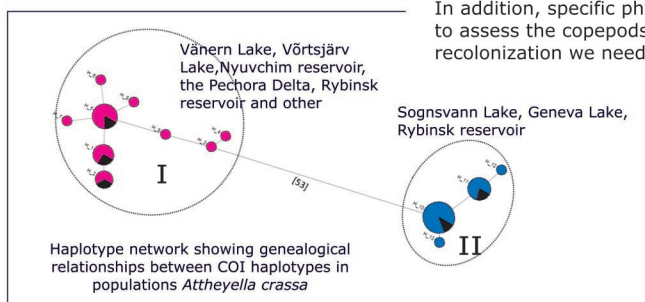


As a result of mtDNA (COI gene) sequencing of harpacticoid copepods (*Canthocamptus cf. staphylinus* (Jurine) and *Attheyella crassa* (G.O. Sars)) populations, several clades with the high level of divergence (0.3–27.1%) in each of taxa have been obtained.

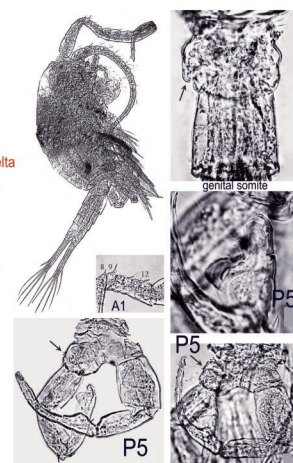
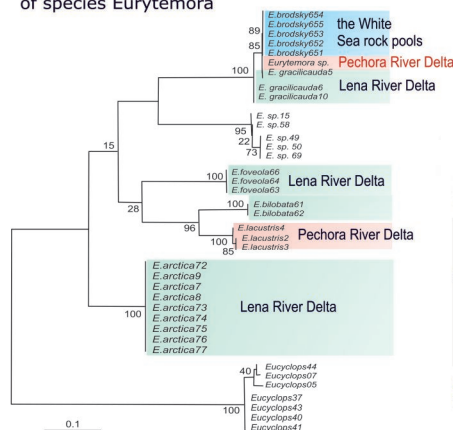
Canthocamptus cf. staphylinus complex was presented by three geographically separated clades. The first consisted of Fennoscandian populations (lakes Pääjärvi and Vänern), the second formed by populations from Northeast of the European part of Russia (the waterbodies in the basin of the Vychegda River) and third mixed clade, presented by populations from the Lake Võrtsjärv (Estonia), a pond in St. Petersburg and the lake Geneva (Switzerland).

The pattern of population structure which is observed in *C. staphylinus* is defined by the present-day gene flow as well as the historical processes, related to development of water basins in post-glacial period (Kochanova et al., 2018).

In addition, specific phylogenetic structure of *Attheyella crassa* populations was added to the analysis. However, to assess the copepods cryptic diversity, trace refugial areas of diversification and routes of post-glacial recolonization we need more data on genetic diversity of the taxon.



Preliminary phylogenetic tree, constructed according to the data of mitochondrial sequences of the COI gene of species Eurytemora



Male morphology of *Eurytemora* sp. from the Pechora River Delta, 2016

Copepods generally comprise the most abundant and diverse taxonomic group within ship ballast water, and thus are transported worldwide in extremely large numbers (Chu et al., 1999). Ballast water transfer is the main factor of *Eurytemora* species distribution (Sabia et al., 2015).

There are 16 species of *Eurytemora* in the inland and costal water of the Arctic subarea of Palaearctic. Recently, several new for the Arctic regions species have been identified: *Eurytemora arctica* M. Wilson and Tash, *E. gracilicauda* Akatova and *E. foveola* (Johnson M. W.) have been registered in the Lena River Delta since 2000 (Abramova, Zhulay, 2016; Abramova et al., 2017). We have found a *Eurytemora* species in the Pechora River Delta in 2016 and 2017. It is very close to *Eurytemora americana* Williams by morphology. However, molecular analysis showed similarity of the species with *Eurytemora brodskyi* Kos from the Baltic Basin waterbodies and *Eurytemora gracilicauda* from the Lena River Delta.

Invasive copepods provide particularly valuable models for exploring fundamental mechanisms of niche evolution (Bron et al., 2011).

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