

# First molecular data of the parasitic crustaceans genus *Salmincola* (Copepoda: Lernaepodidae)

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## from Asian part of Russia

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Parasitic copepods genus *Salmincola* are among the more widely-reported ectoparasites of salmonid fishes. They are recognized as surveillance-worthy pathogens among wild and cultured salmonid stocks. As a result, a lot of research has been devoted to them (Kabata, 1969, Kabata and Cousens, 1973, Hoffman, 1999, Roon and al. 2015, Burdukovskaya and Pronin, 2016 etc. ), but at the moment there is an obvious lack of molecular data on this genus. The present study is the first attempt to identify several parasitic crustaceans from Siberia and Kamchatka regions using 28S rDNA gene sequence.

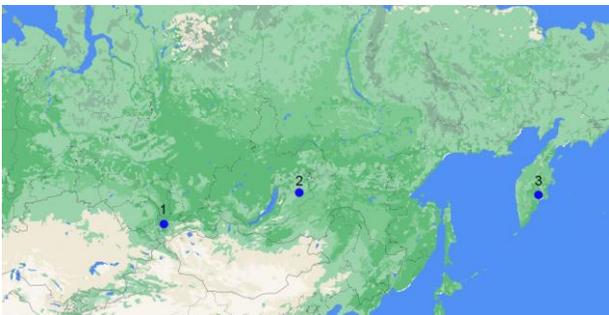


Fig. 1. The sampling localities. 1 – Teletskoye Lake, Altay region, 2 – Baunt Lake, Buryatia, 3 – Kronotskoye Lake, Kamchatka.

**Material and Methods.** Ectoparasitic crustaceans were collected from fins, skin, gill, and nasal fossae of whitefishes (genus *Coregonus*) in the area of Teletskoye and Baunt lakes (Siberia) and from mouth of charr (genus *Salvelinus*) and kokanee salmon (genus *Oncorhynchus*) from Kronotskoye Lake (Kamchatka). The 28S gene region was amplified using the primers described by Reumont et al. (2009). Phylogenetic reconstruction was performed using the Bayesian inference approaches with MrBayes v.3.2.1. The 28S sequences available in the GeneBank were used to reconstruct phylogenetic relationships within the genus .

**Results.** A total of 21 specimens of *Salmincola* spp. from studied salmonids of Siberia and Kamchatka were examined. The newly obtained sequences were distributed among five species-level clades: *S. carpionis* (charr), *S. edwardsii* (kokanee salmon), *S. extumescens* (whitefish from Baunt Lake), *S. lavaretus* (whitefish from Teletskoye Lake), and *S. extensus* (whitefish from Baunt Lake). The two *S. californiensis* sequences obtained from the GeneBank formed a separate clade. The sequences from *S. edwardsii* were distributed into two non-sister clades, which at least indicates the difficulty of species identification, but as a maximum the heterogeneity of this species.

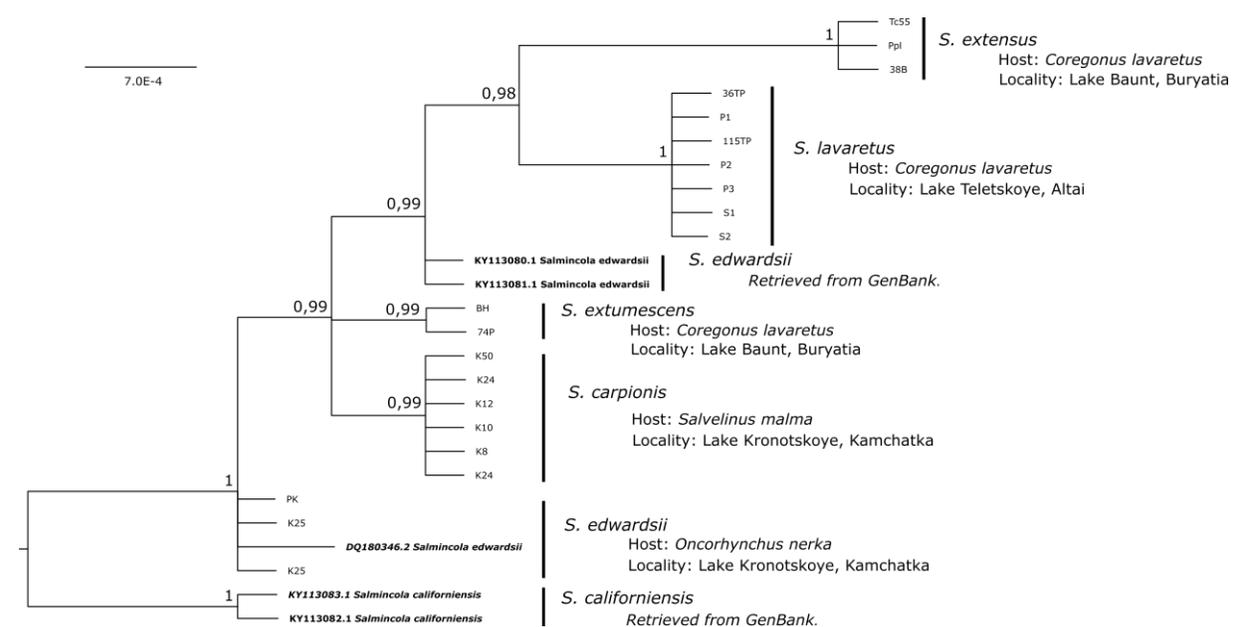


Fig. 2. Bayesian inference phylogram reconstructed using partial 28S rDNA sequences based on JC nucleotide substitution model. Species of host fish and sampling locations are indicated..



Fig. 3. *S. carpionis* in the oral cavity of the white charr (*Salvelinus malma*).

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