

Global phylogeography of *Gammarus lacustris* G.O. Sars, 1864, the most widespread freshwater amphipod species

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ABSTRACT

A phylogeographic analysis of *Gammarus lacustris* G.O. Sars, 1864 across its Northern Holarctic range reconfirms a subdivision into two main lineages, which meet in Eastern Europe.

KEY WORDS

Gammarus lacustris; phylogeography; systematics.

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Gammarus lacustris G.O. Sars, 1863 (Gammaridae) is the most widespread of all freshwater amphipods, with a range extending from northwestern Europe eastwards across the Holarctic, up to north-eastern North America. It mostly inhabits mountain lakes in the central parts of the continents but also lowland waters towards the north. Much of this range must have been colonized post-glacially. Several other Central European *Gammarus* taxa have recently been split into complexes of local, deeply diverged cryptic species, but inferences from studies of *G. lacustris* have been confounding. Adding two new broad datasets from across Northern Europe and North America to the previously available mtDNA COI sequence data, we reconfirm a basic subdivision of *G. lacustris* into two major lineages, which correspond to the W and E allozyme races of Vainio & Väinölä (2003). One is distributed

in Central and North-West Europe (e.g. the Alps, the British Isles, and Scandinavia up to northern Norway: this is the typical *lacustris* clade, encompassing the “*G. alpinus*” of Alther et al. (2016), which needs to be synonymised). The other one reaches from NE Fennoscandia and Eastern Europe through Eurasia and the entire North American distribution, including the range of the putative *G. limnaeus* Smith, 1874 in NE North America (the *limnaeus* clade). The sequence divergence between the clades is 6 %, which is less than differences among regional cryptic species of other gammarids. The ranges of the main clades also overlap, and mtDNA alone might not suffice for determining their taxonomic rank. There is further phylogeographic structuring within each clade (differences of 1–2%), informative of wide dispersal from a number of Pleistocene refugia.