

Barcoding of Kuril-Kamchatka (NW Pacific) deep-sea amphipods

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Background: The amphipod fauna of the deep sea is poorly known with only 400 benthic species found below 2000 m worldwide of which 50 were recorded from the abyssal of NW Pacific. Deep-sea invertebrates, especially crustaceans, are very fragile and can be easily destroyed already during sampling. Thus, obtaining proper morphological material is difficult. This makes DNA barcoding a precious tool for biodiversity assessment of deep-sea organisms. We studied diversity of deep-sea amphipods from the Kuril-Kamchatka Trench and adjacent abyssal plain. The material was collected using epibenthic sled at 28 stations, along ca. 1000 km transect, at the depth range 4830-8745 m.

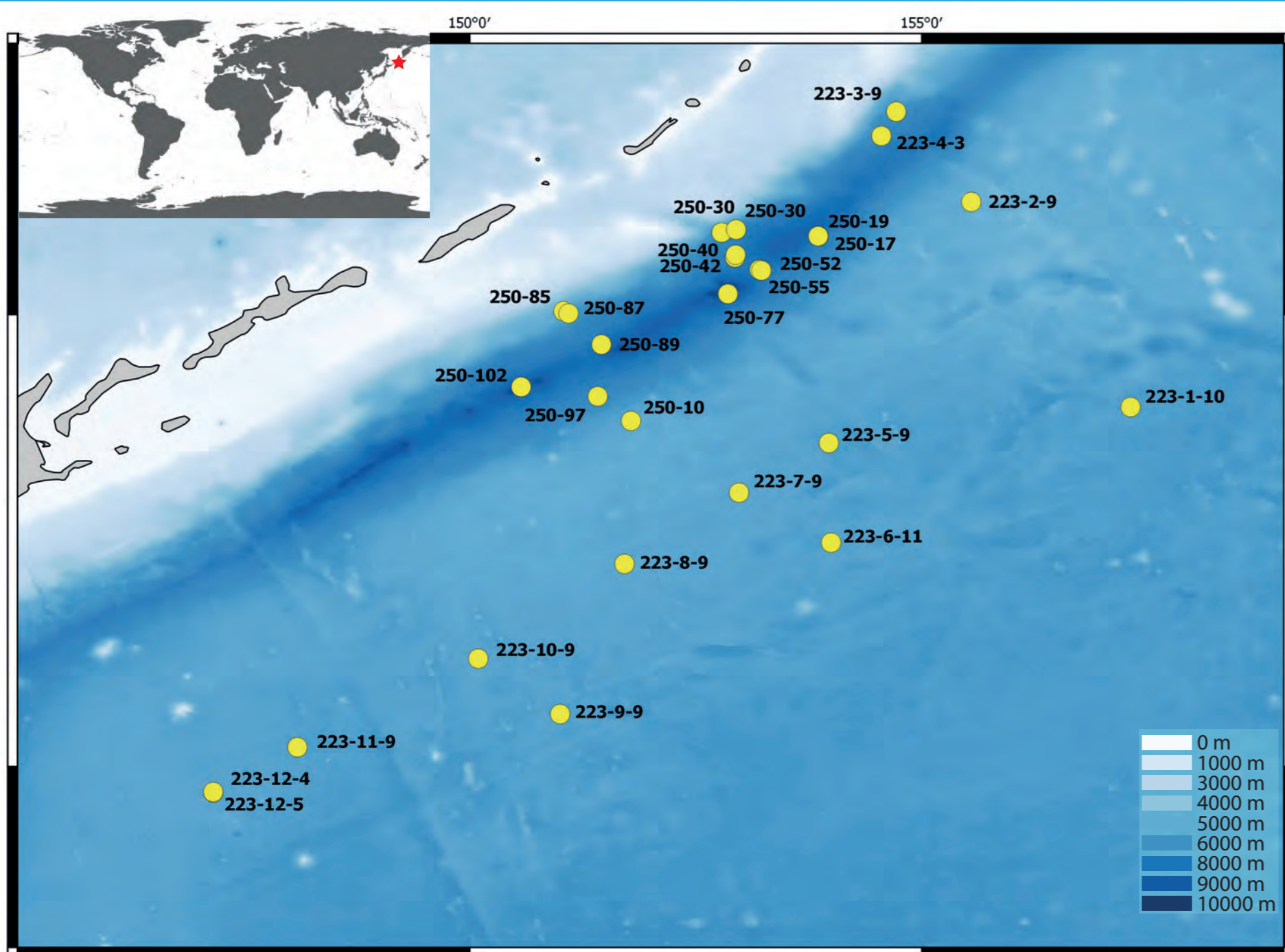


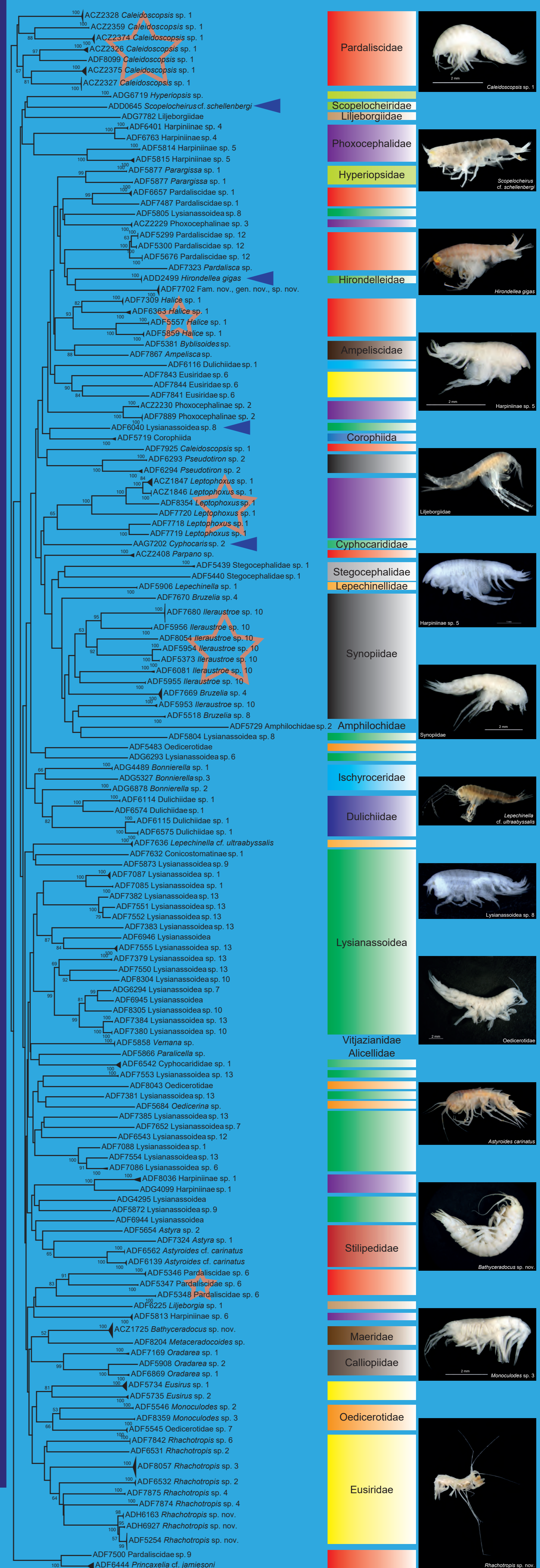
Fig. 1 Top: map presenting sampling sites in the Kuril-Kamchatka Trench area. Bottom: pictures from the German-Russian KuramBio II Expedition.

Results: The identified amphipods belong to 24 families and were preliminary assigned to 65 morphospecies. Most importantly, almost half of the species are potentially new to science. So far, we obtained 504 DNA barcodes divided into 143 Barcode Index Numbers (BINs). Up to 7 BINs were recognized within a morphospecies, indicating existence of potential cryptic species.

Significance: This is the first such a wide study dealing with biodiversity of deep-sea Amphipoda at the molecular level. Taking into account that, after Polychaeta and Isopoda, amphipods are among the most abundant abyssal invertebrate groups, the knowledge upon their real diversity is a first step towards understanding the functioning of deep-sea ecosystem.

Fig. 2 Neighbour-Joining tree based on COI K2p distances for sequences of studied species. 1000 bootstrap replicates were performed, only bootstrap supports above 50% are reported. Each family is represented by rectangle of unique color. Pictures are given for selected specimens representing genera.

▲ previously existing BINs ★ potential cryptic diversity observed



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