

In the last week we finished our work in areas A6 and A5 and have started to work in area A4 in 8700 m depth. In the late evening of the 31. of August we had to interrupt our station work and return to Tomakomai due to a case of illness of a crew member who had to be brought to hospital. However, since Sunday morning 4 a.m. we are back in our study area and already map the seafloor of the Kuril-Kamchatka Trench on our way to area A4, in order to obtain more precise bathymetric information of the topography of our next research area A7 in roughly 9500 m depth. Due to our d-tour to Tomakomai (about 3.5 days) and additionally due to winch problems which caused and will continue to cause some loss of time during heaving of each gear deployment, we have to think

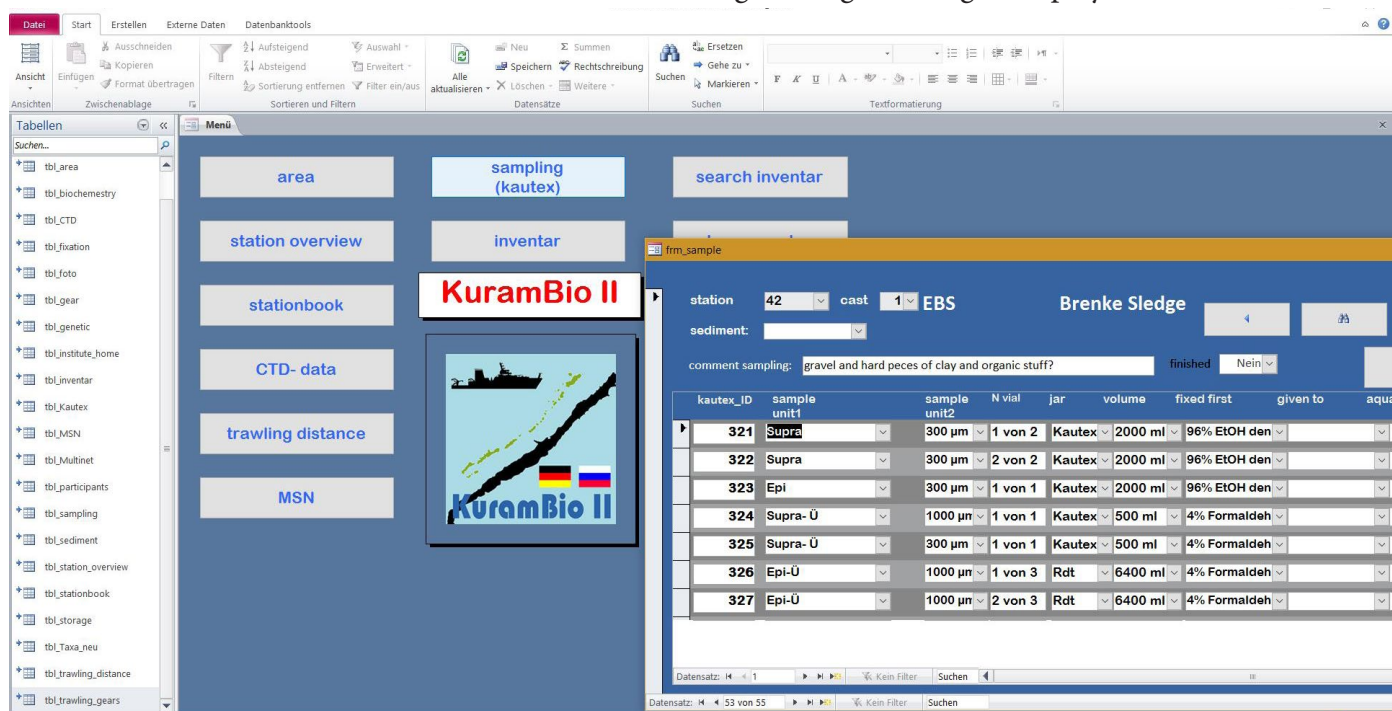


Fig.1: User interface of the on-board database when entering sample data for a sample of the epibenthic sledge (EBS) during the KuramBio II campaign..

Table 1: Summary of EBS catches sorted to higher taxon levels so far during the expedition KuramBio II.

Taxa \ Area	Area A8 ca. 5100m	A6 ca. 6000m	A5 ca. 7200m	A1 ca. 8200m
Cnidaria	14	11	1	7
Mysida	11		15	27
Cumacea	40	16	11	27
Tanaidacea	105	3	11	6
Ostracoda	128	1		25
Copepoda Harpacticoida	232	43		86
Nematoda	180	89	1	211
Amphipoda	273	34	85	150
Echinodermata	138	59	14	356
Copepoda Calanoida	564	38	2	281
Isopoda	703	63	37	192
Mollusca	653	154	17	397
Polychaeta	1083	1261	224	978
<b>Gesamtergebnis</b>	<b>4124</b>	<b>1772</b>	<b>418</b>	<b>2743</b>

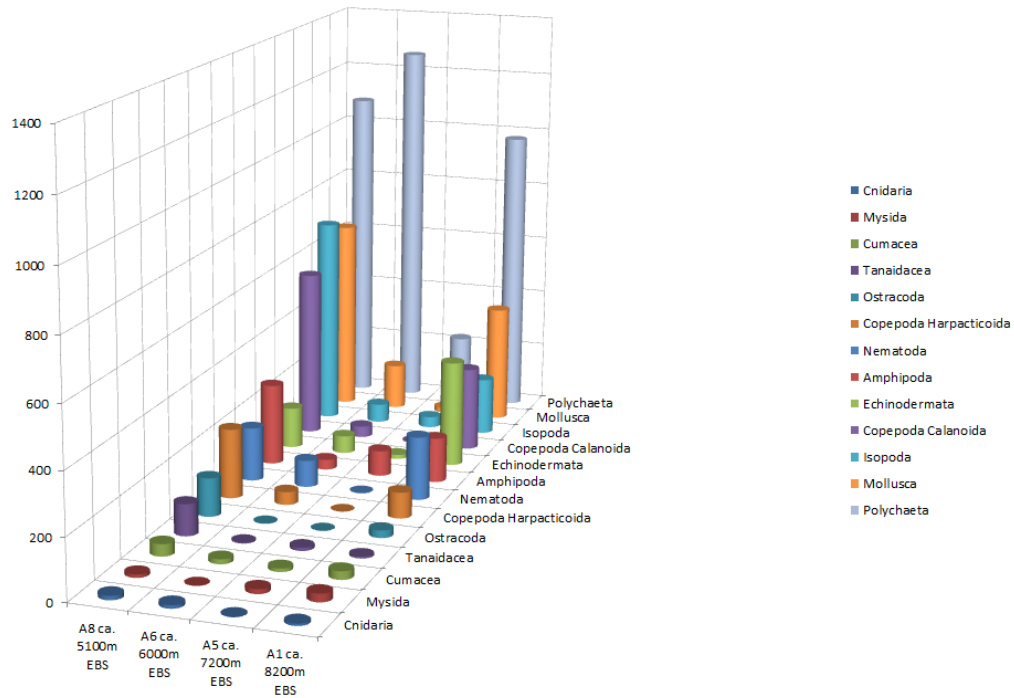


Fig. 2: Taxa composition of the epibenthic sledge catches made and sorted so far during the KuramBio II cruise.

of where and how to save on station time during the second half of the campaign. Until now we have decided to sacrifice the complete station work in area A2 in about 5000 m depth because this area is situated at the southeastern slope of the Kuril-Kamchatka Trench, where we already sampled a few stations during KuramBio I in 2012. This has already saved us about 2.5 days, but we will continue as planned with the other stations for now. In about 1.5 weeks we will have to decide again where and how we will have to save on time again.

Meanwhile we have used the steaming time to process and sort our samples further. In the last weekly report we explained which gear we used to answer our scientific questions. Today we want to focus on our samples and a few first results, because we have had three out of six working weeks so far and it is important to make an inventory now showing what we have managed to sample so far and whether we can be satisfied with our material obtained. For this purpose we want to shed some more light on our



Fig. 3: One of the highlights of this week: *Gigantocypris* is by far the largest genus of Ostracoda. It belongs to the family Cypridinidae. This specimen was caught with a multi-closing plankton net from the mesopelagial. Scale: 2 mm. (c) T. Riehl



Abb. 4: *Mesocletodes* is a genus of typical deep-sea harpacticoid copepods. This crustacean group is an abundant and diverse representative of the marine interstitial fauna. (c) P. Martínez Arbizu

KuramBio II Access database. After the third week of sampling our database contains 1180 entries, which is reflected by the number of vials filled with organisms. We think this is quite a good number, as this number is based on only four completed working areas until now and considering that by far not all samples could be sorted on board.

The main purpose of this database is cataloguing all collected animals. Our inventory will then allow us to keep track of the samples, where they are stored on board and which scientist will take care of them. We can also use the database for an extraction of some first results.

By the end of our expedition this database will be furthermore very valuable when writing the final cruise report, as we can use it to document and visualize the results obtained on

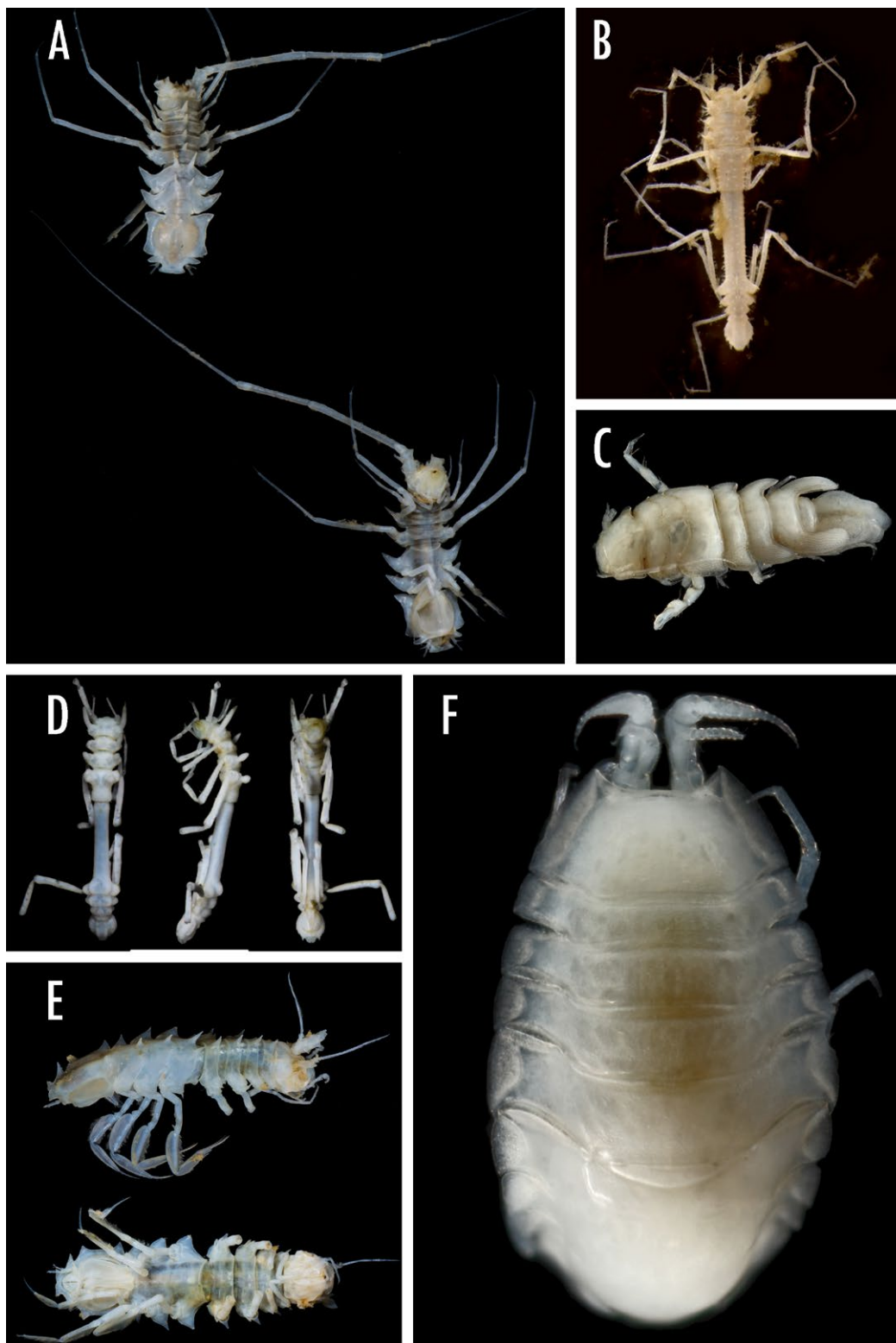


Fig. 5: Isopod crustaceans of abyssal and hadal depths of the Kuril- Kamchatka Trench. A, E: Munnopsidae; B, D: Ischnomesidae; C: Macrostyliidae; F: Haplonesicidae. Specimens are not shown to scale. (c) A.V. Lavrenteva (A, D, E), S. Brix (B), T. Riehl (C, F).

board during KuramBio II.

Until now we have sorted 15.988 invertebrates from the various samples and gears (GKG, EBS, AGT), most of these are polychaetes (4551 individuals). Bivalvia, however, also occur in the samples frequently (1290 ind.), as well as isopods (1241 ind.) and other taxa of crustaceans. Moreover, we already extracted DNA (COI gene) of 61 copepods, 60 ophiuroids, 40 tanaids, 40 amphipods as well as 20 isopods.

All participants are well and we greet you and our families!

Angelika Brandt, Center for Natural History (CeNak), (chief scientist SO250) and the cruise participants