Outlook

Metadata Cambodia meiofauna study

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Date Tue 02/04/2024 12:22

To Tânia Campinas Bezerra <Tania.CampinasBezerra@UGent.be>

Cc torrey.gorra@imbrsea.eu <torrey.gorra@imbrsea.eu>

2 attachments (8 MB)

02_Meiofauna.xlsx; Gorra_Torrey_02106860.pdf;

Dear Tania,

I have put Torrey in cc since it is her who built the dataset and did the field work in 2023. I am also attaching her thesis manuscript for some extra context for the student and yourself.

In attachment finally you may find the complete meiofauna metadata file with the various sheets.

I have made a Nematode_genus sheet to be filled by your student. The headers have the sample number as you will find written on the little sample bottles. The genus names will need to be filled by your student and maybe you can add a list you have to start with. It would be nice to have both Family and Genus there, as you see.

I think we could start with picking out 100 nematodes per replicate. She could start with 6 samples and then progress (6+3+4+2 = 15 total ; see below)

In green I highlighted the samples that should have priority, and I would suggest having the following hierarchical processing strategy:

Step 1: 2 x replicate per habitat (BB_01, CANTS_01, IS_01, a total of 6 samples). This is the most basic and smaller dataset, and it will already give us an idea. If the student is done with this he/she can move to

Step 2: 3 x replicate per habitat (one extra replicate for BB_01, CANTS_01, IS_01, total 3 extra samples). This completes the habitat dataset;

Step 3: 2 x replicate per Station_ID (2 replicate of BB_02, IS_02, total 4 extra samples).

Step 4: 3 x replicate for Station_ID one extra replicate for BB_02, IS_02 total 2 extra samples. This completes the Station_ID dataset.

See whether it is clear and let's go in steps.

thanks and cheers

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