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First report of meiofauna biodiversity from the Tennessee River

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WHAT'S LIVING IN THE TENNESSEE RIVER?

Background

The term meiofauna broadly defines small-sized animals (<1mm), widely distributed phylogenetically and ecologically. These organisms play fundamental trophic and ecological roles in all aquatic ecosystems. The biodiversity of marine meiofauna and its links to anthropogenic activities is routinely investigated, with most results supporting marine meiofauna as a valuable bioindicator of environmental changes. However, research on freshwater communities is rare and scattered. **This flaw is particularly evident in the Southeastern United States, which is a well-investigated area and collectively known as a hotspot of biodiversity for bigger species (Fig. 1), but also a hotspot of imperilment.** Almost nothing is known about freshwater meiofauna from the Southeast U.S. This work shows results obtained between 2019 and 2021 thanks to the contribution of research students working in Leasi's lab and students enrolled in Meiofauna Biodiversity (4770-5770 with Lab).

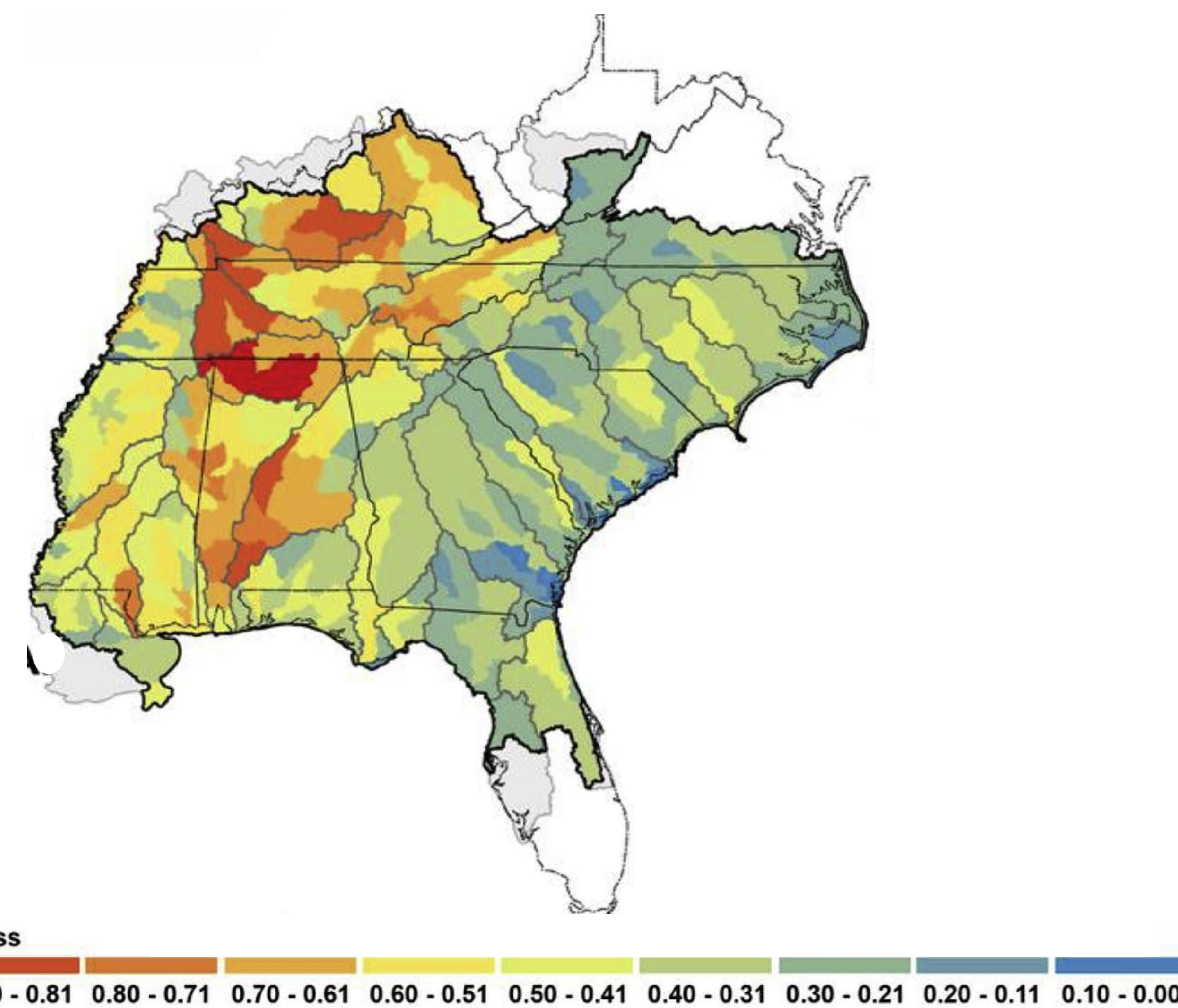


Fig. 1 - Normalized species richness scores for macrofauna (fishes, mussels, and crayfishes) in the Southeast U.S. (modified from Elkins et al., 2019). Nothing was known about meiofauna...UNTIL NOW!

Methods

Water and sediment samples were collected from different sites located along the Tennessee River. The diversity of meiofaunal taxa was estimated through two separated protocols: observations under microscopes (Fig. 2a) or using a metagenomic approach (Fig. 2b). Results are used to estimate biodiversity as richness (number of taxa in each sample), community composition (distribution of taxa among samples), and phylogenetic diversity (relatedness among taxa).



Fig. 2a - Meiofauna identification using a morphological-based approach.

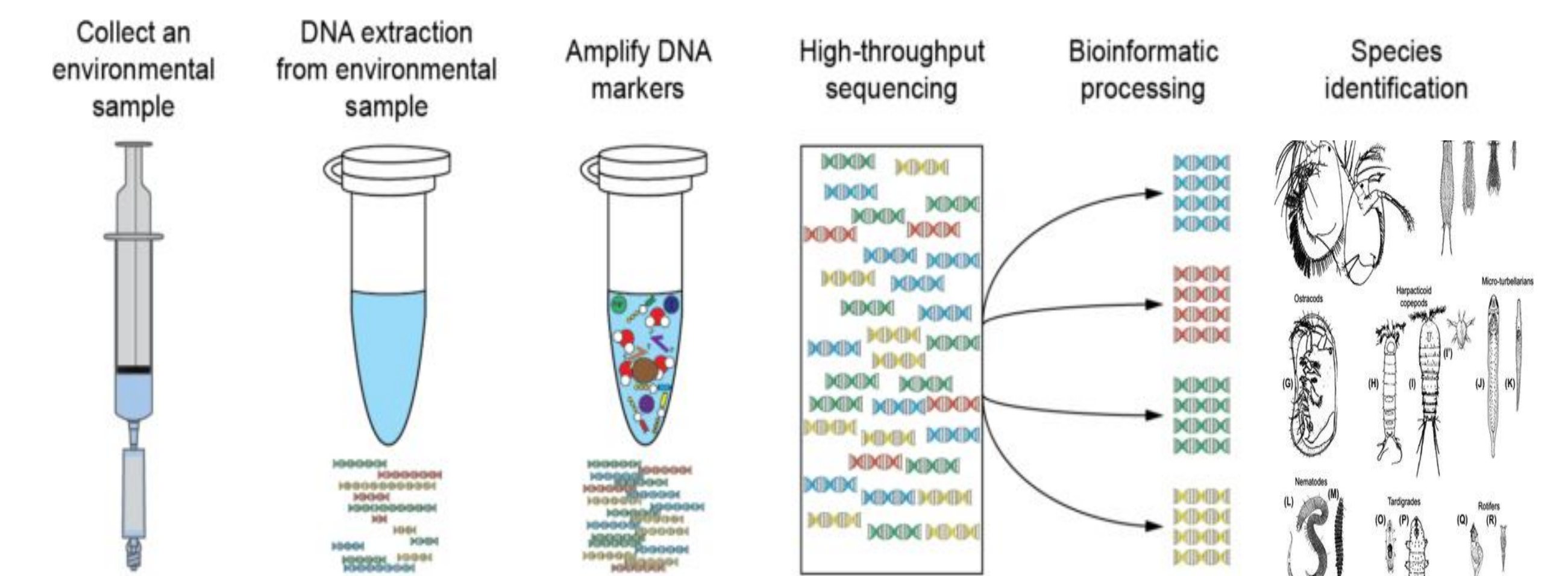


Fig. 2b - Meiofauna identification using a metagenomic-based approach.

Results

The fast and cost-effective metagenomic approach allowed us to identify 10 animal phyla distributed in more than 200 species. The most common phylum was Arthropoda, including copepods, water fleas, ostracods, water mites, etc.

Arthropods were represented with over 80 species (Fig. 3a), making up more than 40% of the total meiofaunal diversity (Fig. 3b). The second most diverse phylum was Rotifera, with 40 species (Fig. 3a) making up almost 20% of the meiofaunal total diversity (Fig. 3b).

Observations using microscopy helped understanding phenotypic and functional traits among taxa, such as size, maturity stage, locomotion, diet, etc. (Fig. 4). Single specimens are preserved for additional genetic and genomic analyses as well as to investigate their gut microbiome. Some taxa (e.g., bryozoans) have yet to be discovered using a morphological-based identification.

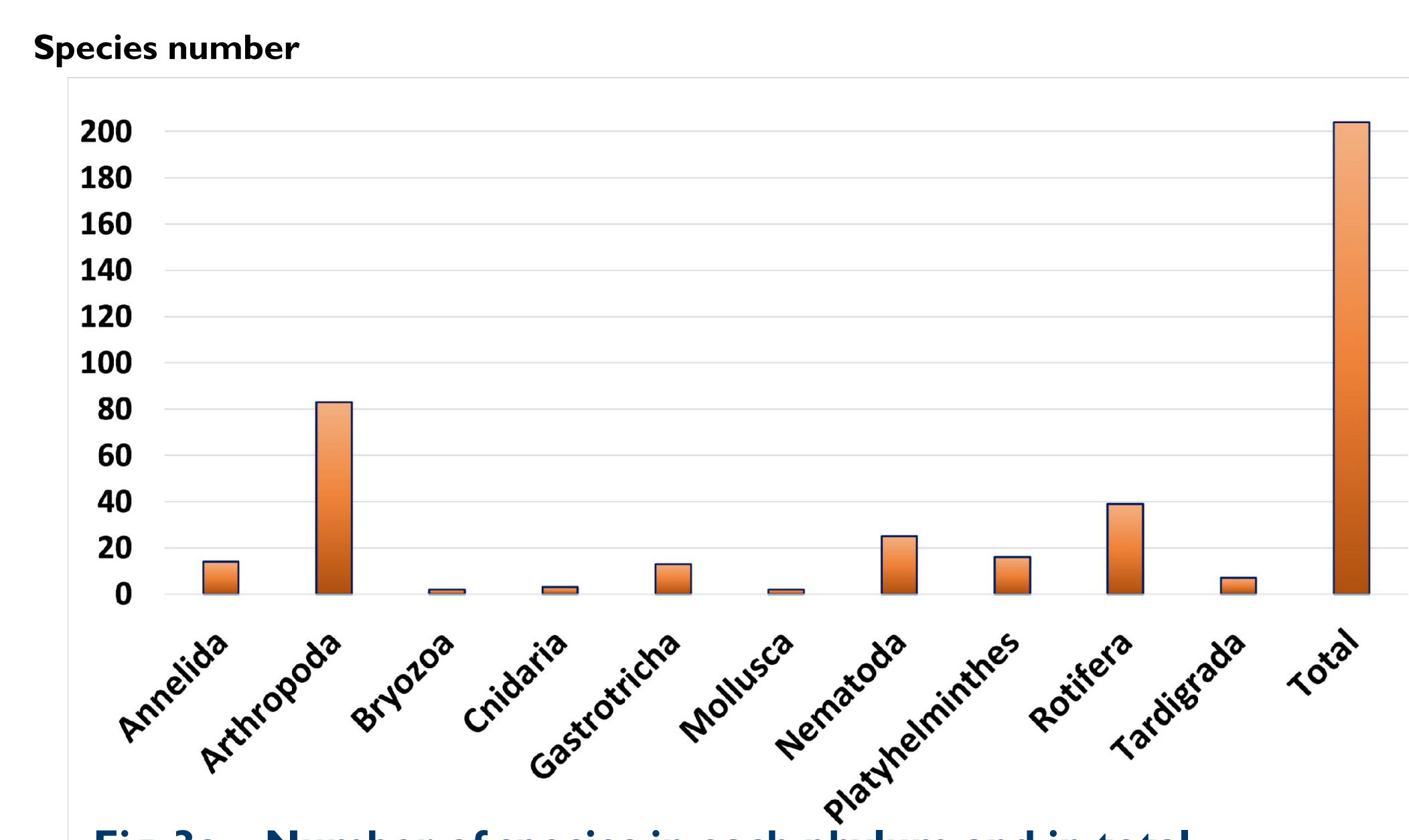


Fig. 3a - Number of species in each phylum and in total.

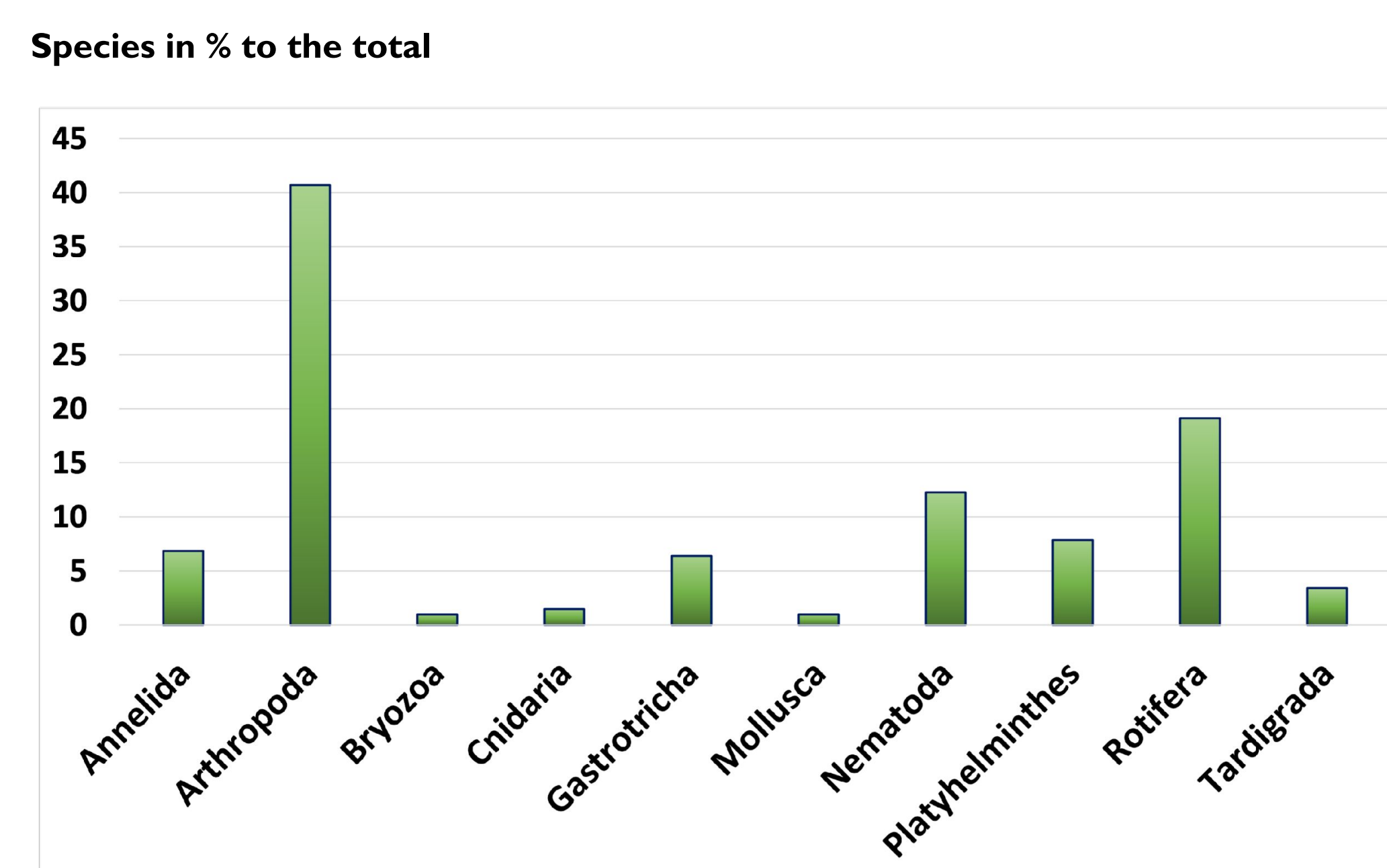


Fig. 3b - Percentage of species found in each phylum.



Fig. 4 - Representative specimens found in the Tennessee River. Scale bar = 100µm

Conclusions

We present for the first time Meiofauna from the Tennessee River. With at least 10 phyla and over 200 species, we support that the Tennessee River is a hotspot of biodiversity for small-sized animals as well. Metagenomics allows the detection of taxa in a cost-effective and timely manner. However, additional morphological and genetic analyses are needed to better explore biodiversity and functional traits in changing environments.

Acknowledgements

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