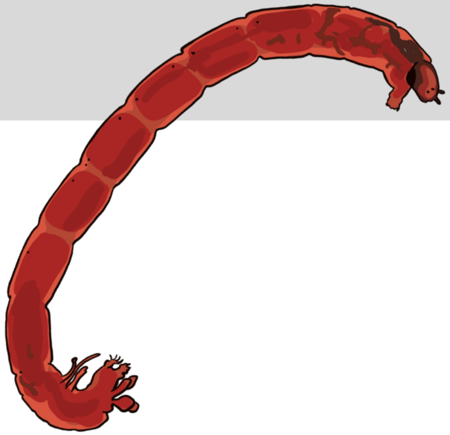
Univeristy of Niš, Serbia
Faculty Of Science and Mathematics
Department of Biology and Ecology

Characterization of Gut Microbiota in *Chironomus riparius* Under Natural and Laboratory Conditions



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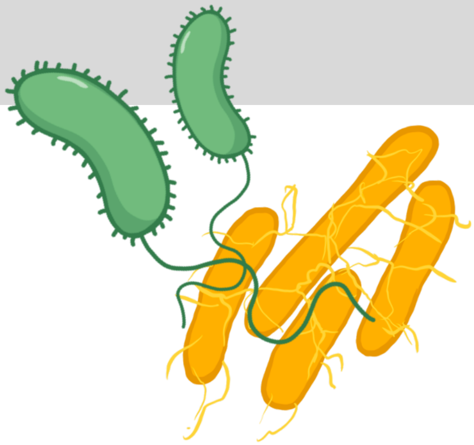

Characterization of Gut Microbiota in *Chironomus riparius* Under Natural and Laboratory Conditions

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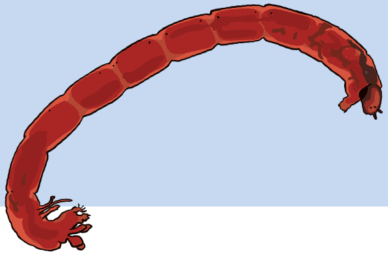
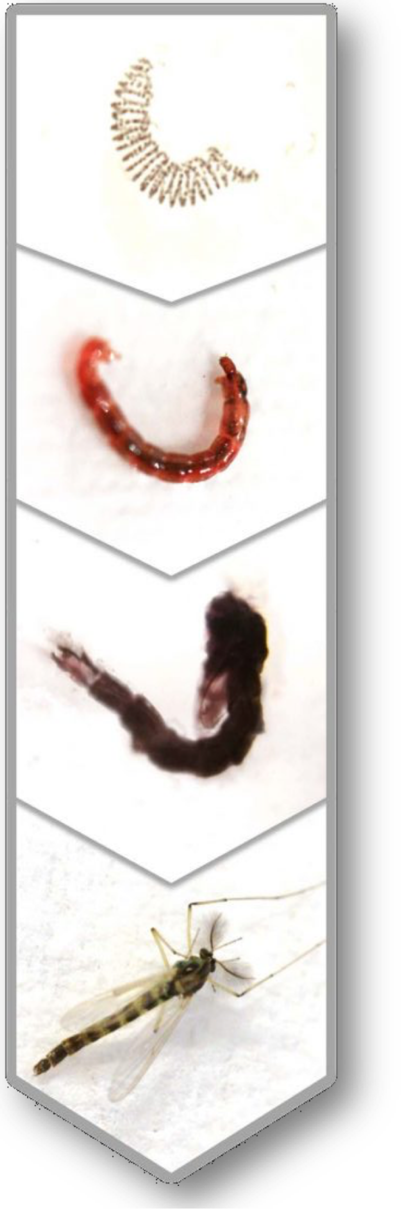
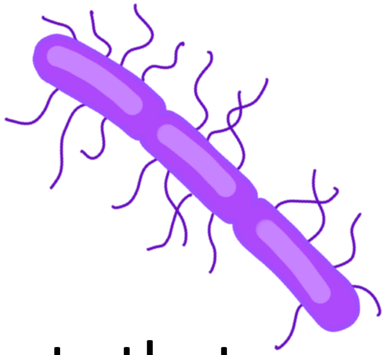


Chironomus riparius

- sediment-dwelling and non-selective feeder invertebrates in freshwater ecosystems.
- routinely used in bioassays and toxicity tests as an important tool to evaluate the level of response to environmental pollution stressors at the biochemical and physiological levels.



Gut microbiota



One of the most important components that enable Chironomids to survive in harsh conditions is their **microbiota**, which plays an important role in the defense of insects under various stress conditions.

Chironomids often inhabit polluted environments and their gut microbiota aids in detoxifying harmful substances.

Gut microbiota

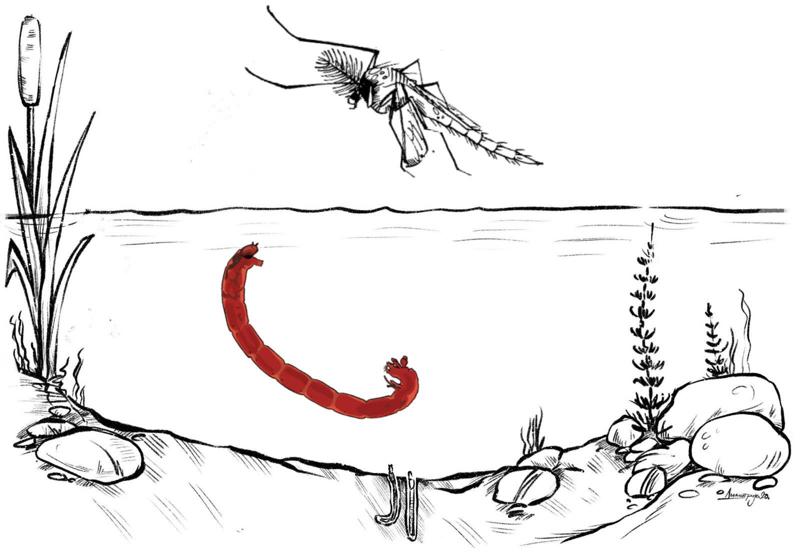
- Endosymbiotic microorganisms are often essential for the growth and development of insect species as they are involved in the reproduction, supply of essential nutrients and digestion.
- Chironomid habitat is threatened by high levels of contaminants such as microplastics and organic matter.

OBJECTIVE

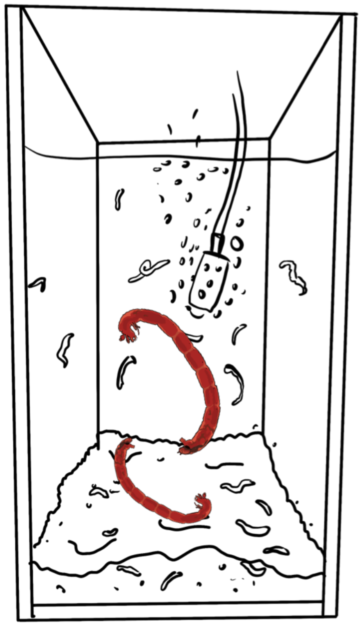
Our study aims to characterize for the first time bacteriobiota associated with the gut of *C. riparius* larvae from **nature** and **laboratory** samples.

The characterized strains are promising candidates for the development of environmentally friendly strategies to degrade organic pollution and microplastics in freshwater ecosystems.

Nature



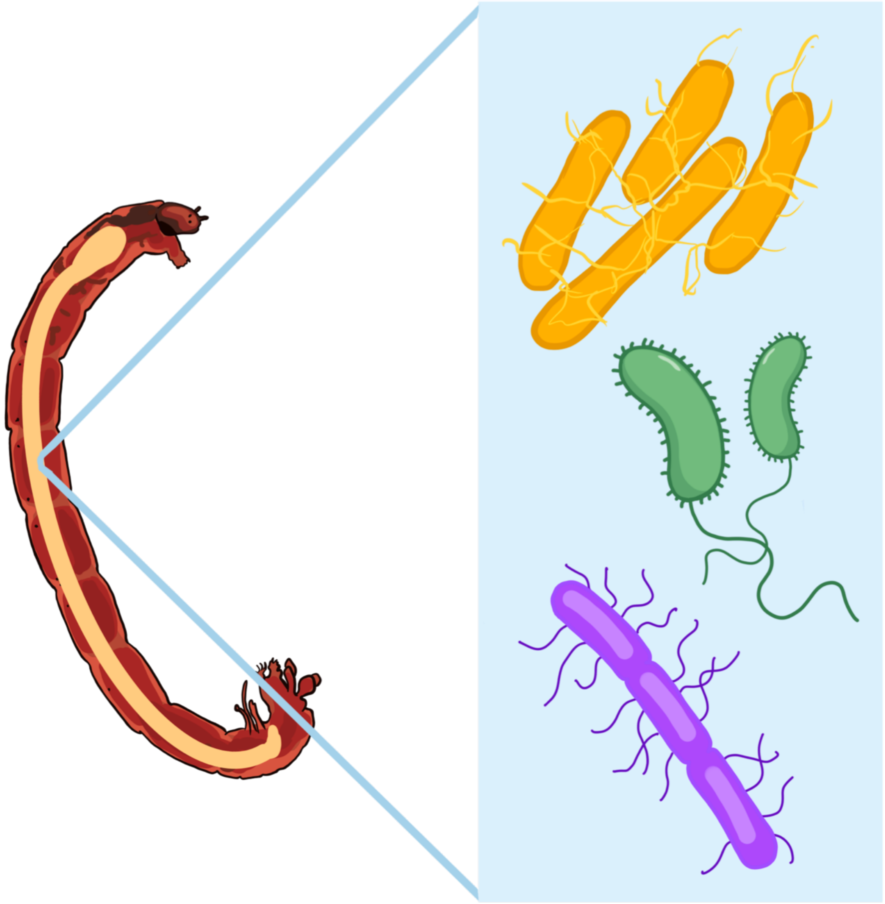
Laboratory



RESULTS AND DISCUSSION

Isolation and molecular analysis

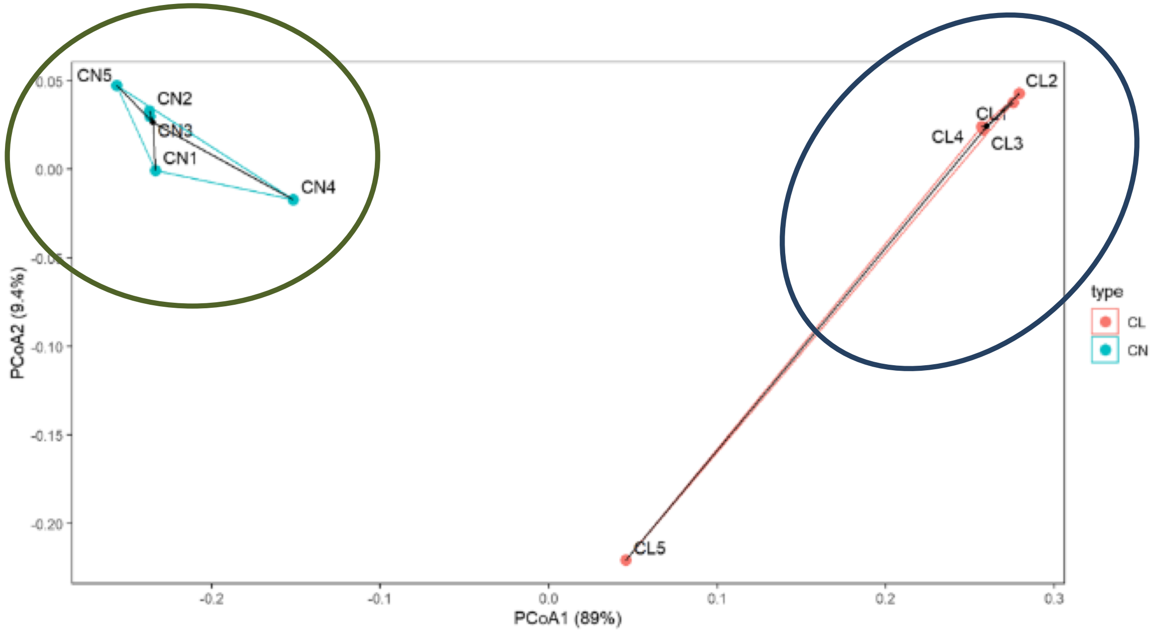
- ***Bacillus*** (including 13 species, such as *B. subtilis* and *B. thuringiensis*) and ***Paenibacillus*** were predominant in samples from **natural habitat.**
- *Peribacillus frigoritolerans*, *Lysinibacillus fusiformis* and *Gottfriedia solisilvae* were characteristic of **laboratory samples**.
- Five bacterial species, including *Metabacillus idriensis*, *Peribacillus simplex*, *Neobacillus cucumis*, *Bacillus thuringiensis/toyonensis* and *Fictibacillus phosphorivorans*, were identified in **both environments**.

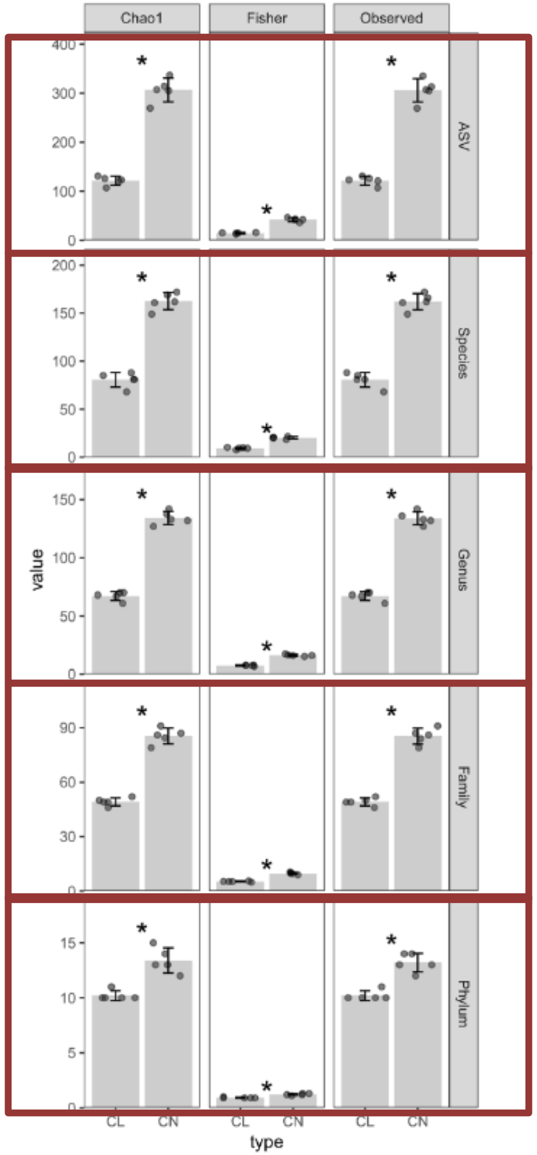


Total Bacteriobiota of *C. riparius* Larvae

Estimation of **alpha diversity** using Chao1 and Fisher indices and observed features (OBS) detected statistically significantly higher diversity in the **nature samples (CN)** compared with **laboratory culture (CL)** at all taxonomic levels assessed.

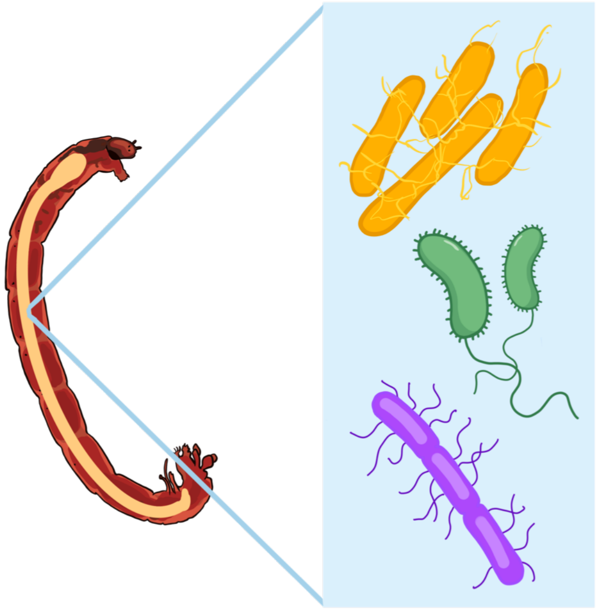
Beta diversity analysis was performed using DPCoA at the ASV level where the samples from nature and from the laboratory showed significant difference (P = 0.004).

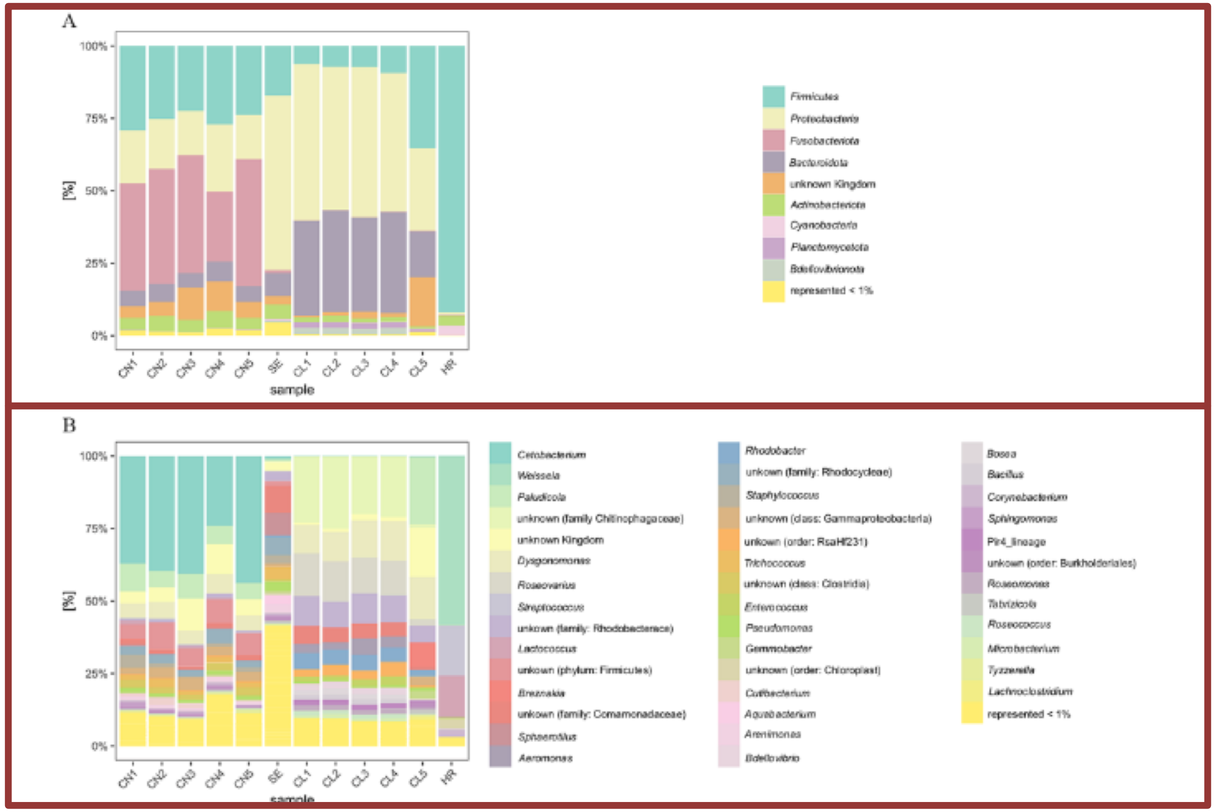




The Composition of Total Bacteriobiota

According to the analysis of the 16S rRNA gene sequences obtained from larval gut samples in both habitats studied, a total of **31 phyla** were detected. Mainly, Proteobacteria, Firmicutes, Bacteroidota and Actinobacteriota were detected in both gut samples. In the CN samples, the phylum Fusobacteriota was additionally detected.



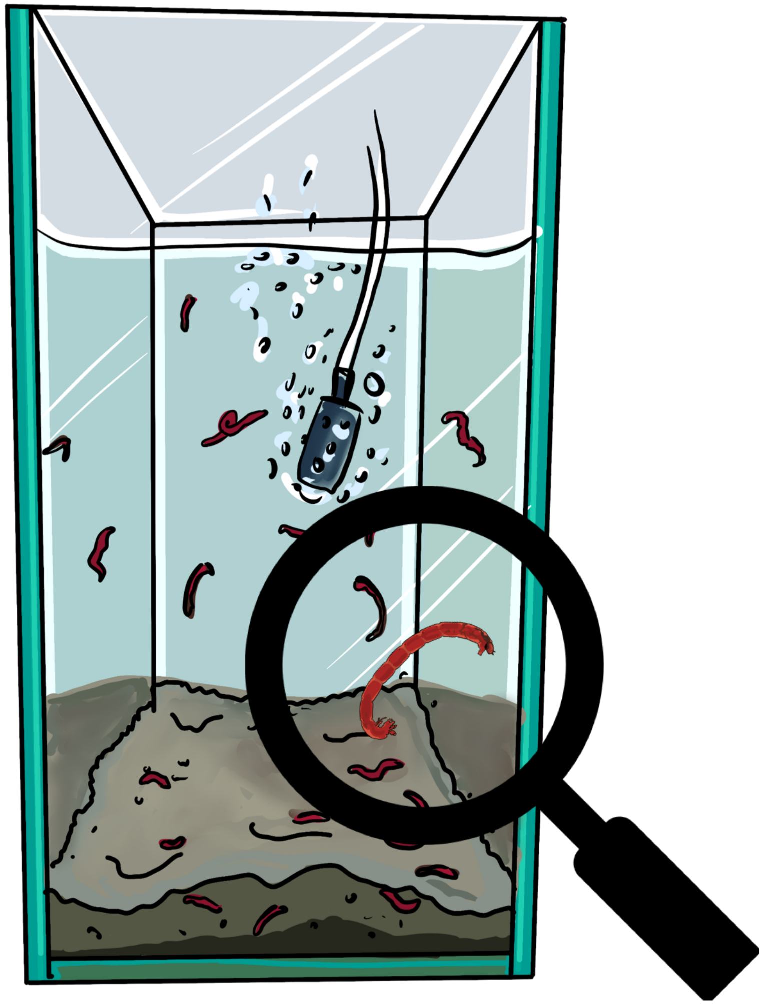


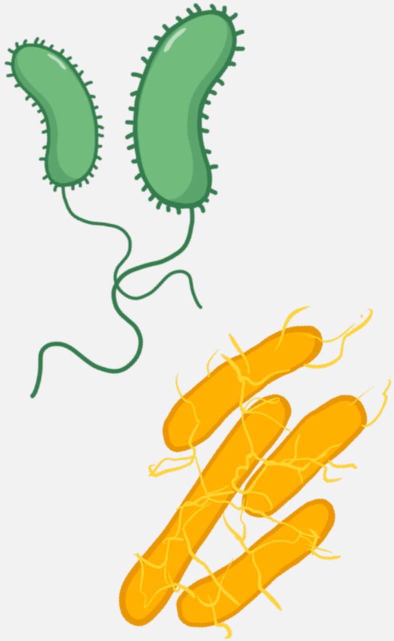
CONCLUSIONS

The study demonstrates that natural habitat samples of *C. riparius* larvae exhibit higher microbiome diversity and unique bacterial species compared to laboratory-reared larvae, underscoring the influence of complex natural environments on microbiome composition.

These findings highlight the critical importance of characterizing microbiota at the time of collection from natural habitats and tracking subsequent shifts during laboratory acclimation. Understanding these changes is essential for assessing their impact on the species and its role as a model organism.

Future research should focus on uncovering the mechanisms driving microbiome shifts in *C. riparius* and their implications for the species' adaptability. Such studies could optimize the rearing of *C. riparius* in laboratory conditions, potentially benefiting environmental protection applications.





Any questions?

You can find me at

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THANK YOU

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Ana Samardžić

University of Niš
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