Analysis of Trophic Transfer, Bioaccumulation, and Microbiome Alterations of Chinese Mystery Snails Exposed to Arsenic

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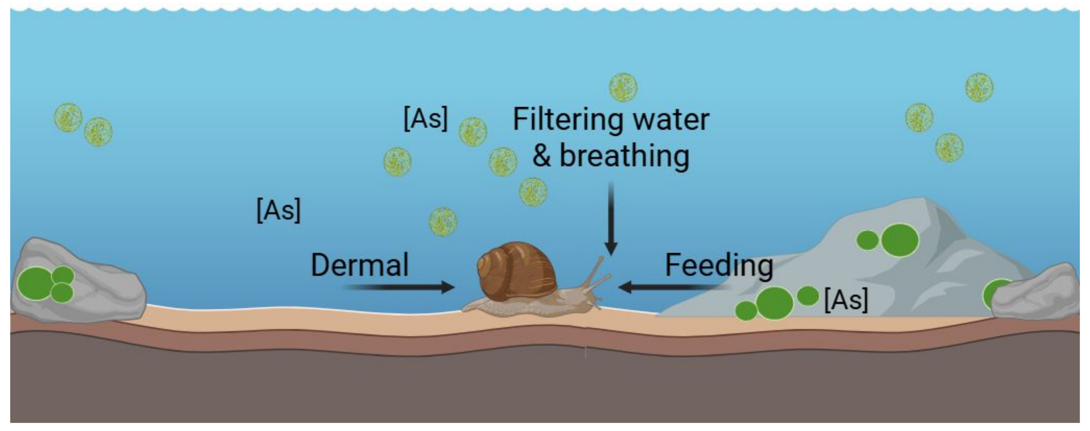
Introduction

- South Puget Sound lake ecosystems have been impacted by industrial legacy arsenic contamination[1].
- The lower trophic standing of the ubiquitous Chinese Mystery Snail (CMS), *Cipangopaludina chinensis*, can provide insight to the transfer of legacy arsenic contaminants.



Objective: (1) Compare routes of exposure that lead to arsenic bioaccumulation in CMS, (2) and observe microbiome alterations that occur between treatment groups.

Hypothesis: Waterborne arsenic exposure is an important route of bioaccumulation in CMS, with arsenic concentration correlating with gut microbiome changes.

Preliminary Feeding Based Exposure:

- Performed to observe bioaccumulation capabilities using a feeding based route of exposure

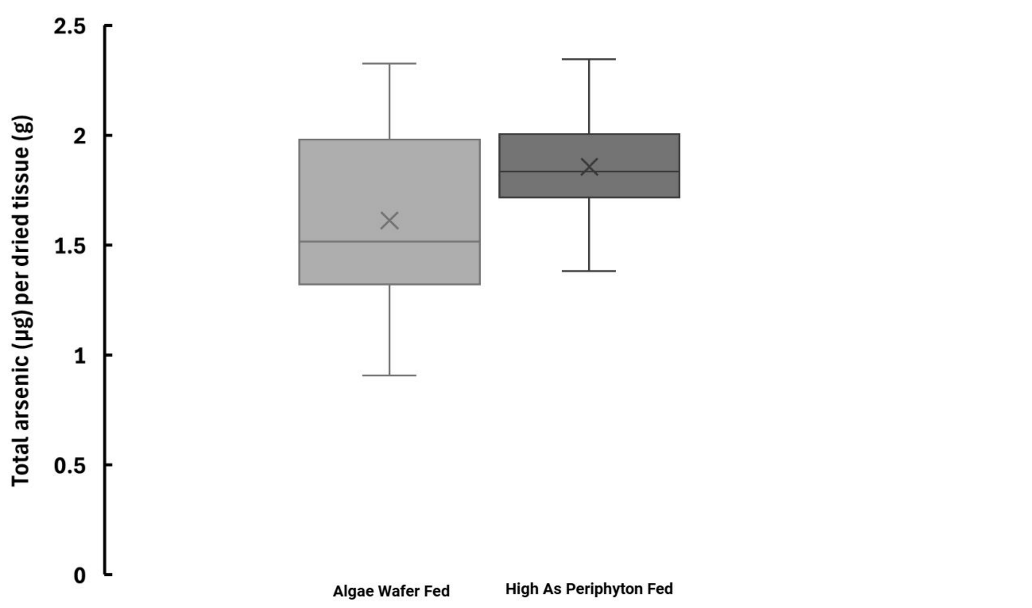
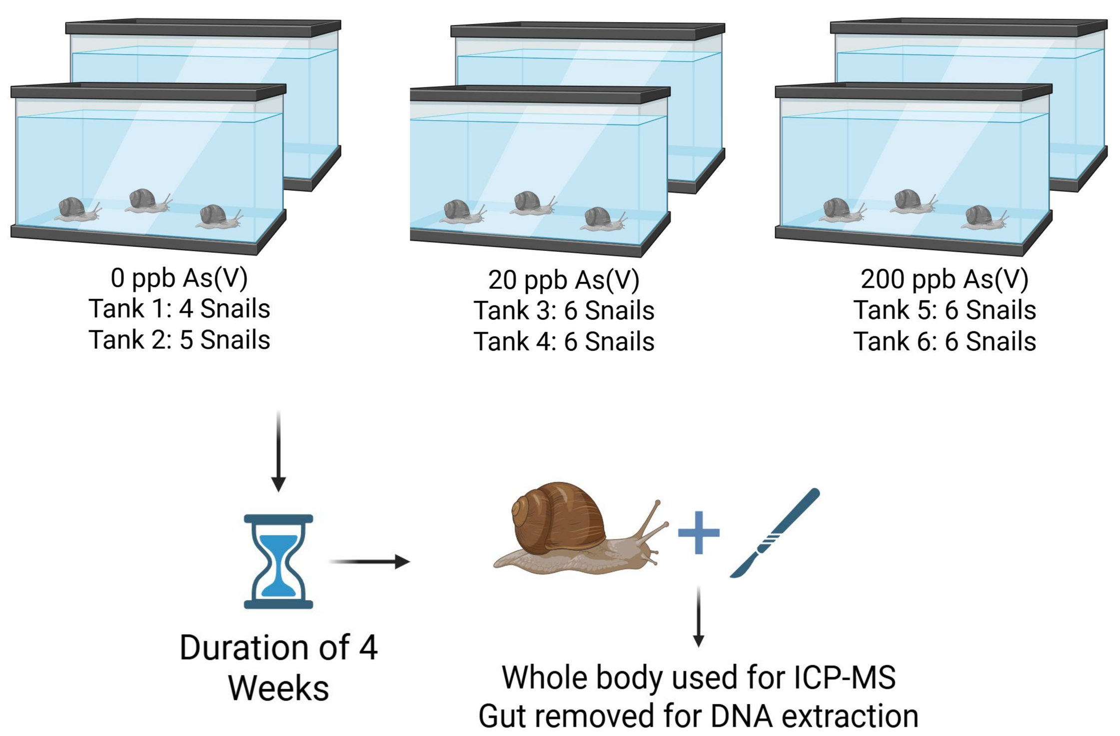
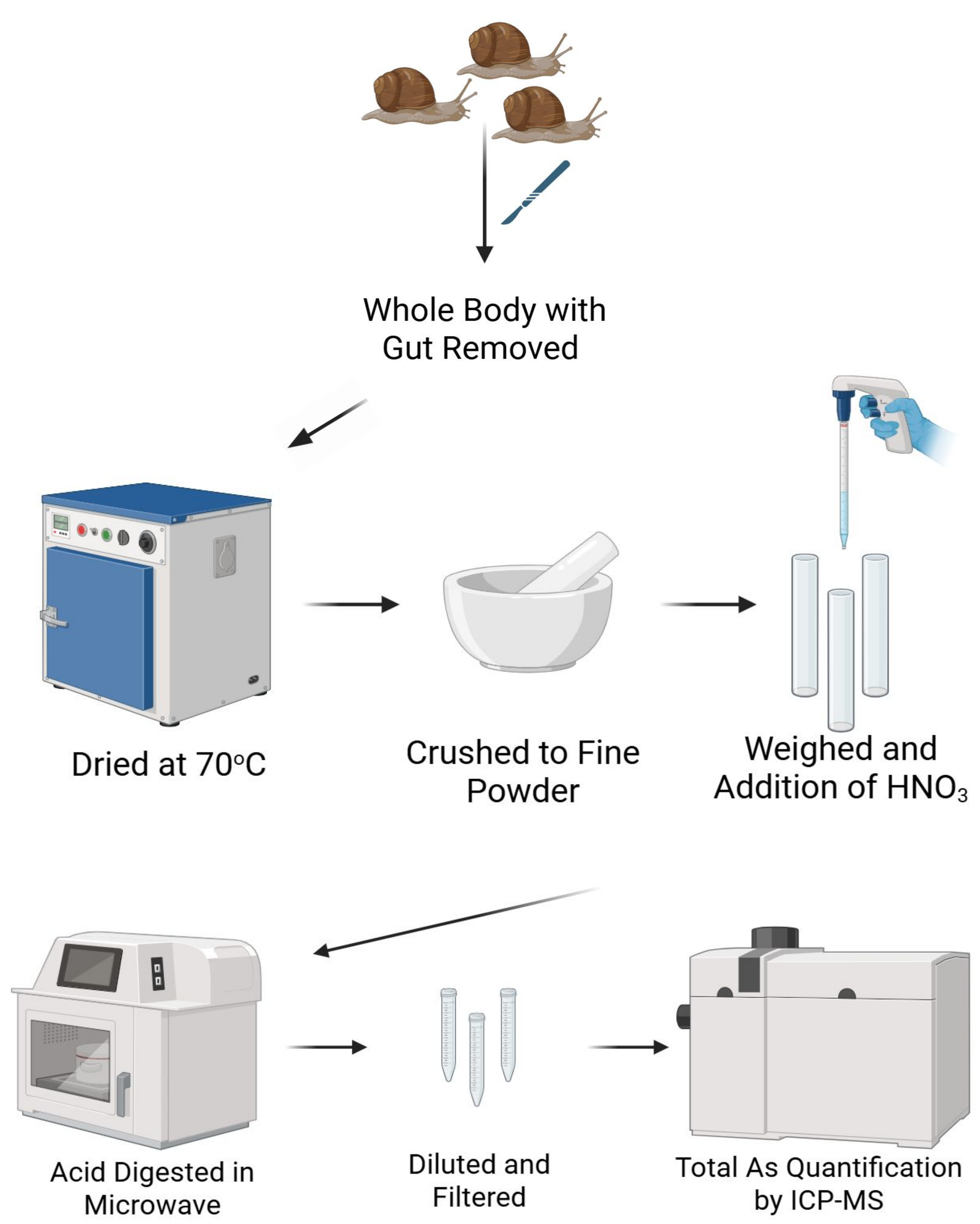


Figure 1. Comparison of total arsenic concentrations in Chinese Mystery snails fed high As containing periphyton and algae wafer (control) indicate no significant difference in As bioaccumulation. Twenty-four adult Chinese Mystery snails were fed algae wafers (n = 12) or high arsenic containing periphyton, 627 ± 92 µg/g, (n = 12) for a duration of 4 weeks. Snails were dissected to remove the guts and the remaining soft tissue was processed for ICP-MS total arsenic quantification. A T-test in GraphPad: Prism was performed and no significance difference between groups was determined ($p > 0.05$).

Waterborne Exposure



Bioaccumulation Analysis



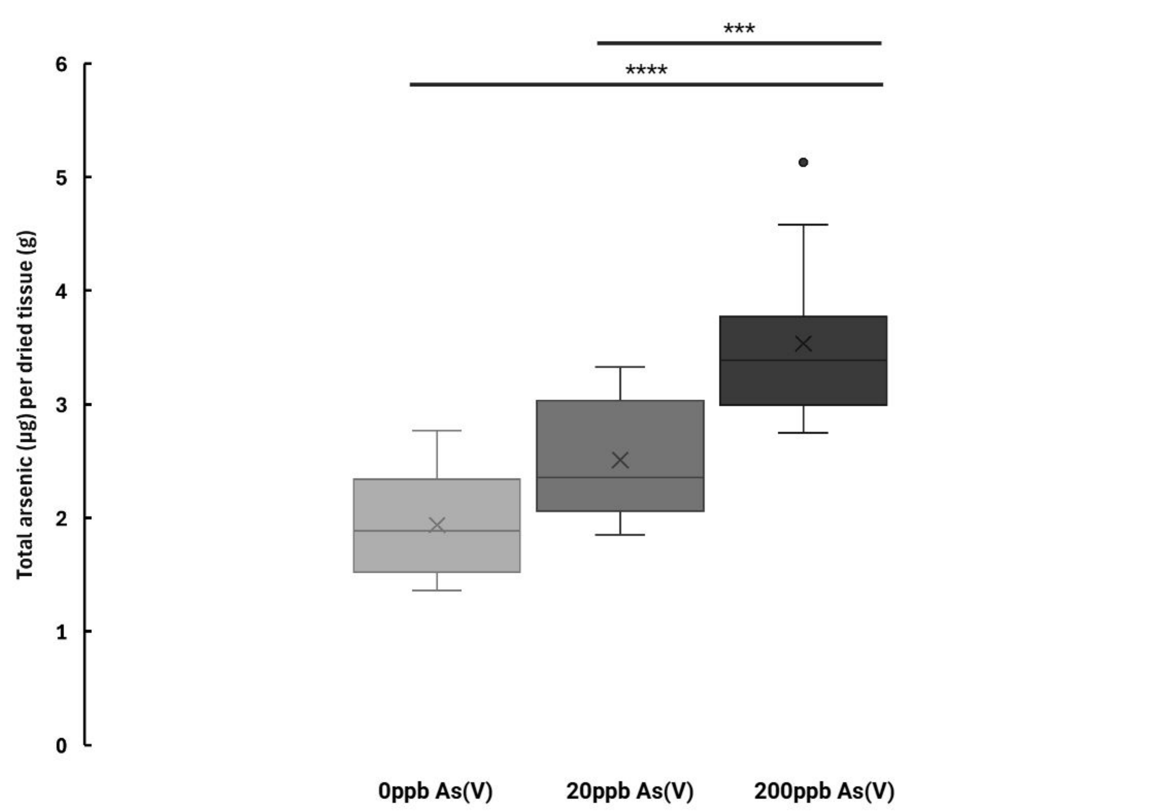
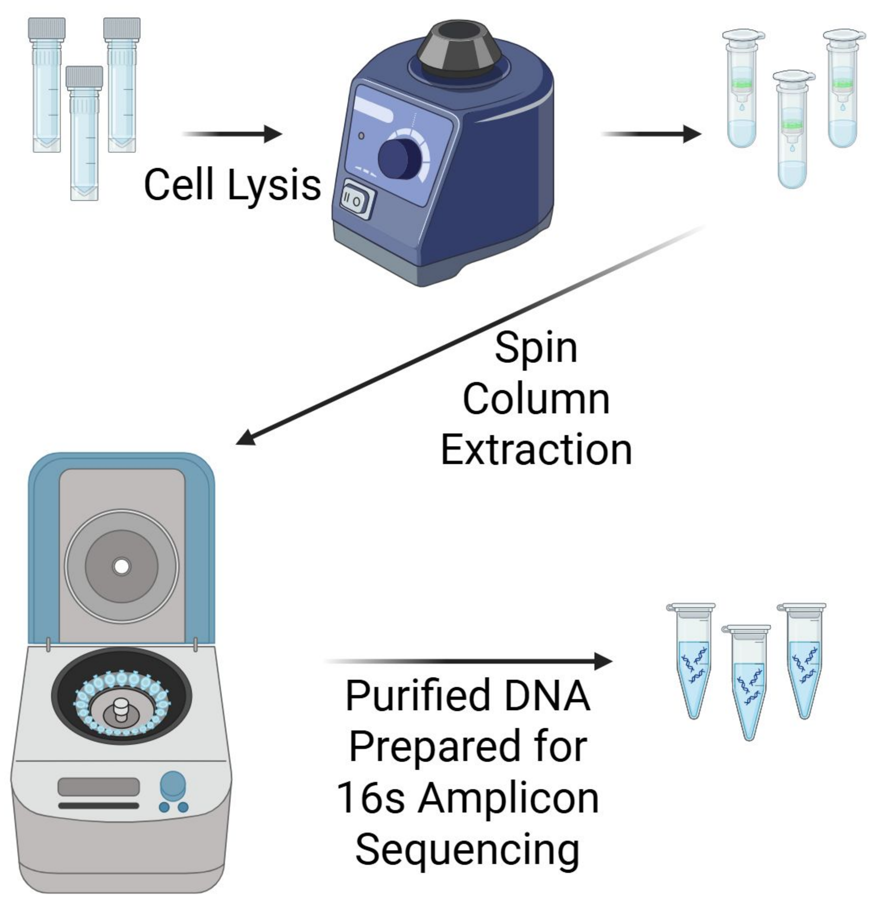


Figure 2. Comparison of total arsenic concentrations in Chinese Mystery snails exposed to waterborne arsenate indicate a significant difference in uptake between 0ppb and 200ppb As(V), and 20ppb and 200ppb As(V) concentrations. Thirty-three adult Chinese Mystery snails were exposed to waterborne arsenate at concentrations of 0 ppb (n = 9), 20 ppb (n = 12), and 200 ppb (n = 12) for a duration of 4 weeks. Snails were dissected to remove the guts and the remaining soft tissue was processed for ICP-MS total arsenic quantification. A one-way ANOVA with a Post-Hoc Tukey's test in GraphPad: Prism was performed to compare treatment groups (***$p<0.01$, ****$p<0.0001$).

Preliminary Microbiome Analysis



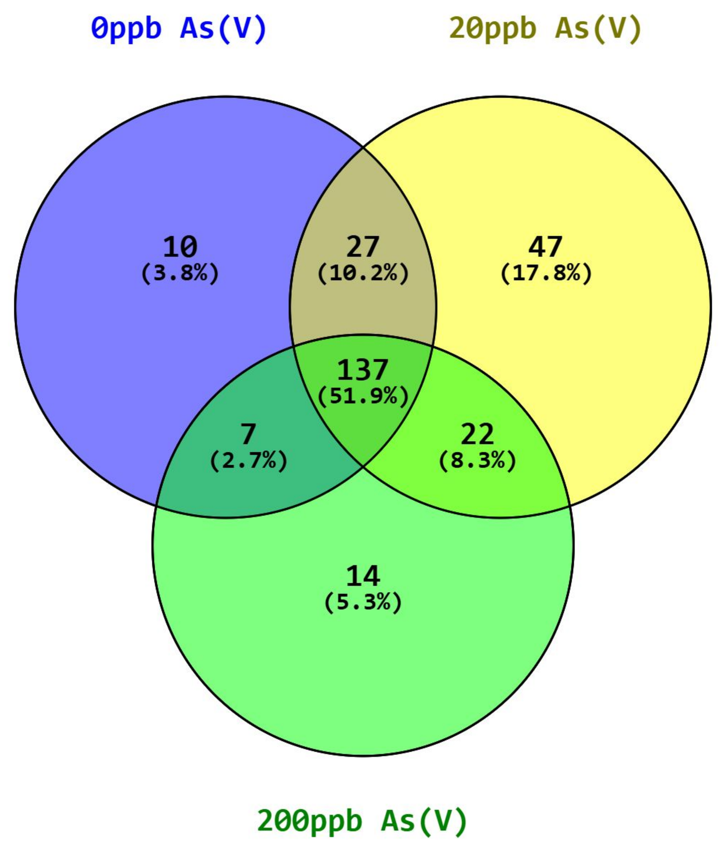


Figure 3. Venn Diagram comparing taxonomy on the family level shows initial diversity in microbial makeup within gut samples of Chinese Mystery Snails exposed to waterborne arsenate. The gut region of thirty-three Chinese Mystery Snails was removed after undergoing a four week water-borne arsenic exposure at concentrations of 0 ppb (n = 9), 20 ppb (n = 12), and 200 01 ppb (n = 12). The gut tissue was processed for 16S rRNA gene sequencing from which the family data was extracted using QIIME2 and visualized in a Venn diagram using Venny 2.01. Venn diagram displays the unique and shared family found between samples from each exposure concentration.

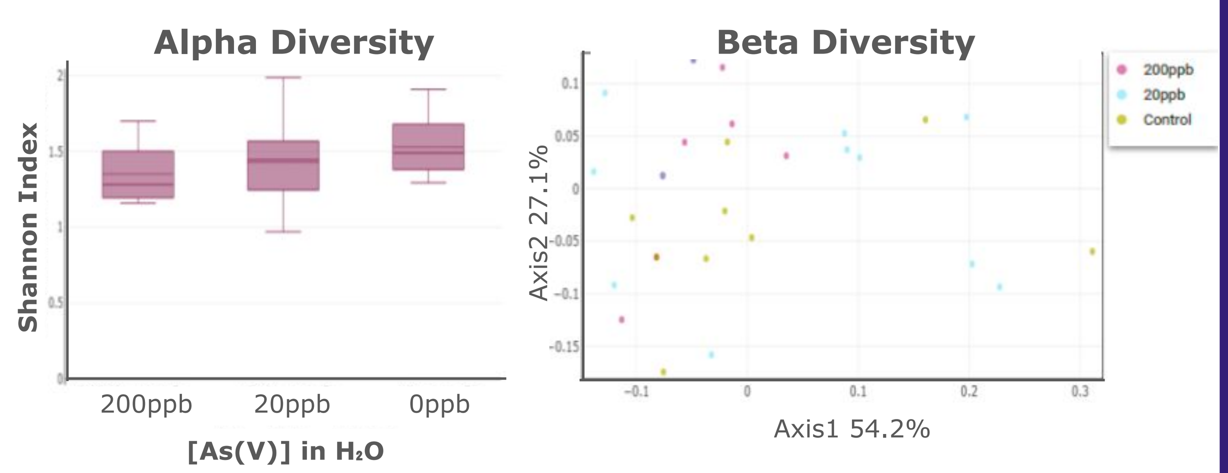


Figure 4. Alpha diversity did not change with As(V) exposure and Bray-Curtis dissimilarity analysis showed no obvious clustering by treatment group. The gut region of thirty-three Chinese Mystery Snails was removed after undergoing a four week water-borne arsenic exposure. The gut tissue was processed for 16S rRNA gene sequencing from which the family data was extracted using QIIME2 and visualized in MicrobiomeDB on the phylum level.

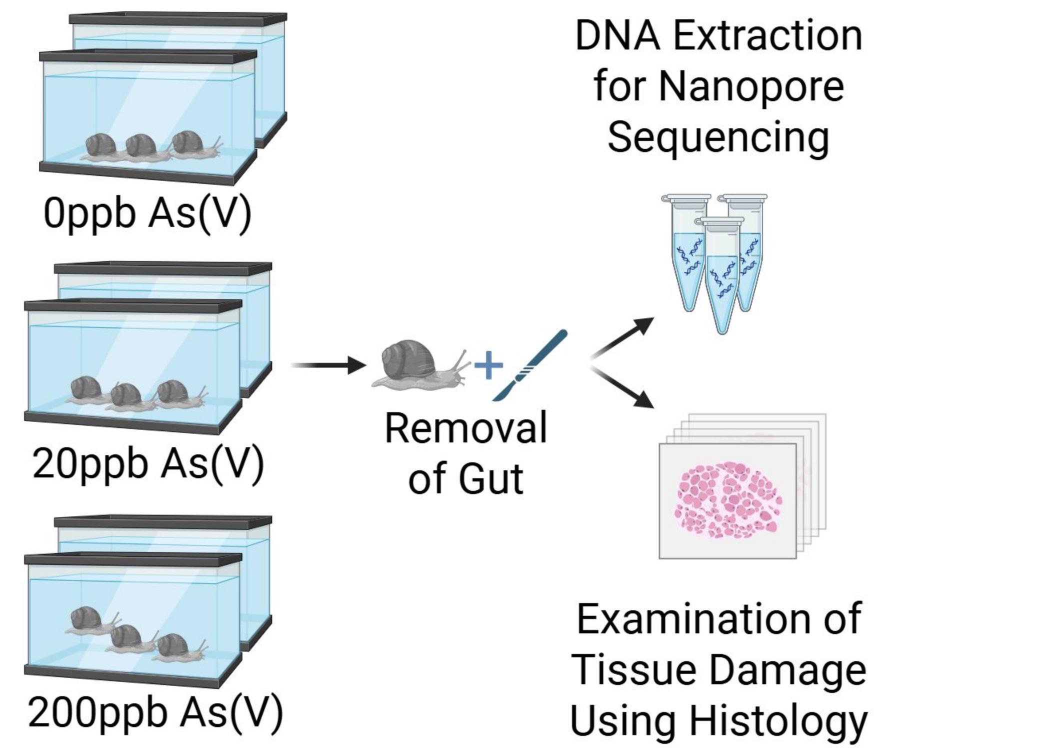
Discussion

A dietary As exposure did not result in a significant increase of As bioaccumulation, however exposing CMS to waterborne As did cause significant uptake. These findings suggest water-based routes of exposure contribute greater to bioaccumulation in CMS than dietary exposure. Breathing through gills, filtering water, and dermal contact could all be contributing factors to CMS uptaking this arsenic. Water with higher amounts of arsenic also correlate with an increased bioaccumulation in CMS, suggesting that the amount of arsenic CMS intakes is dependent on the amount present.

Preliminary microbiome analysis showed a majority of core family were consistent in all treatments along with 20ppb As being a possible concentration to hold intermediate families. Further analysis will be done to determine specific species present in samples along with abundance, this can give insight into possible As biotransformation microbiota.

Continued Research

In light of the preliminary microbiome analysis results, our lab performed a second exposure under the same conditions utilizing juvenile CMS. We investigated how juvenile development impacts the uptake and bioaccumulation of arsenic, how drastically a juvenile microbiome can be altered, and if alterations to gut morphology are observed histologically.



Acknowledgments

These accomplishments were made possible by the mentorship of Dr. Alaei, Dr. Gardell, and the accomplishments of former undergraduate researchers who conducted the feeding-based exposure. We thank Dr. Jim Gawel for his support in the arsenic quantification analysis. Funding was provided by the UW Royalty Research Fund, UW Tacoma Founders Endowment, and the Clare Booth Luce Foundation.

Citations

[1]Hull EA, Stiling RR, Barajas M, Neumann RB, Olden JD, Gawel JE. 2023. Littoral sediment arsenic concentrations predict arsenic trophic transfer and human health risk in contaminated lakes. PloS one. 18(10):e0293214–e0293214. doi:https://doi.org/10.1371/journal.pone.0293214.