Arsenic Bioaccumulation Leads to Behavioral Impairment in Chinese Mystery Snails

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Introduction

Arsenic (As) is a naturally occurring, toxic, and widely used heavy metal. High levels of arsenic were found in a cluster of lakes within the former ASARCO smelter plume zone in south king county. The periphyton, a biofilm composed of bacteria, algae, invertebrates that attaches to submerged surfaces, is enriched with arsenic and subsequently consumed by grazers, including Chinese Mystery Snails (CMS). However, little is known about how arsenic exposure affects the gut microbiome and what other extended effects it has on CMS. Understanding this relationship is important for assessing the ecological consequences of arsenic pollution in aquatic ecosystems.

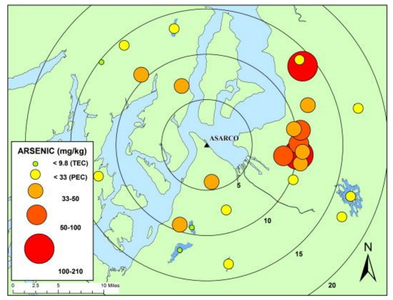

Figure 1: Distribution of arsenic concentrations (µg/g) in surfaces sediments from lakes in the South Puget Sound region. (adapted from Gawel et al., 2014)

Hypothesis

There are known bacteria with the ability to metabolize arsenic, and because the CMS feeds on arsenic-enriched biofilms, we hypothesized that **Arsenic exposure is a selective pressure that contributes to microbial shifts in CMS gut, which alter their behavior and possibly impact their nervous system.**

Figure 2: Photo of Chinese Mystery Snails

Scan QR code for full abstract

Methods

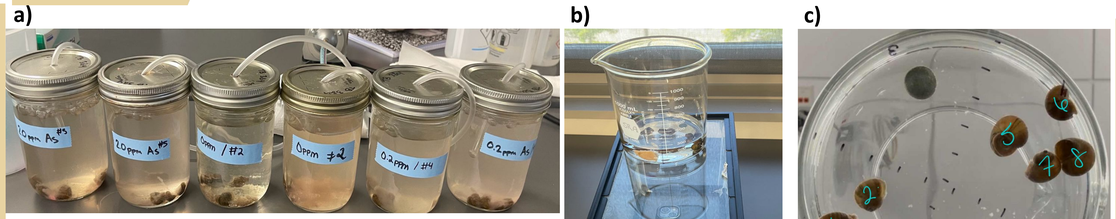

Figure 3: Laboratory Setup for Snail Exposure, Assay Recording, and Individual Tracking. A) Initial experimental setup showing paired jars for each treatment group (0 ppm, 0.2 ppm, and 2 ppm As), with approximately four snails per jar. B) Observation tank arrangement used to film and quantify mobility and feeding behavior. C) Numbered snails used to differentiate individuals during behavioral analysis. (All photos taken by students in the course.)

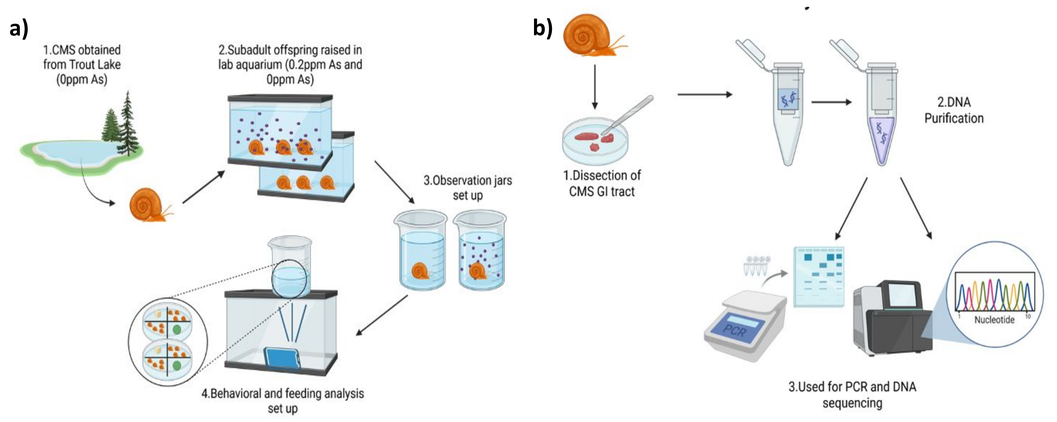

Figure 4: a) Experimental Setup for Behavioral and Feeding Assays of Chinese Mystery Snails. Chinese mystery snails were collected from Trout Lake (low arsenic). Subadults were raised under two treatments: control (0 ppm As) and arsenic-exposed (0.2 ppm As), and tested in observation tanks. Snails and food were alternated across quadrants to assess differences in feeding and movement between treatments.**b) Attempted experimental Setup for CMS Gut Microbiome Analysis.** Gastrointestinal tracts of Chinese mystery snails were dissected for DNA extraction, PCR amplification, and sequencing to characterize gut microbial communities. Low DNA yield and time constraints limited full analysis, leading to preliminary screening for arsenic metabolic genes.

Results

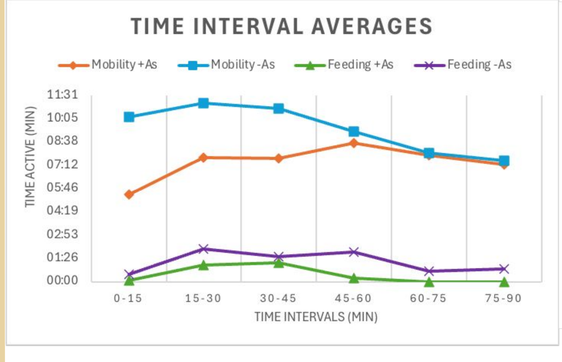

Figure 5: Average Mobility and Feeding Activity Across 15-Minute Intervals. Mean mobility and feeding time for control (0 ppm As) and arsenic-exposed (0.2 ppm As) over six 15-minute intervals. Arsenic-exposed snails showed reduced early mobility and consistently lower feeding activity compared to controls. Activity on exposed snails gradually approached control levels over time.

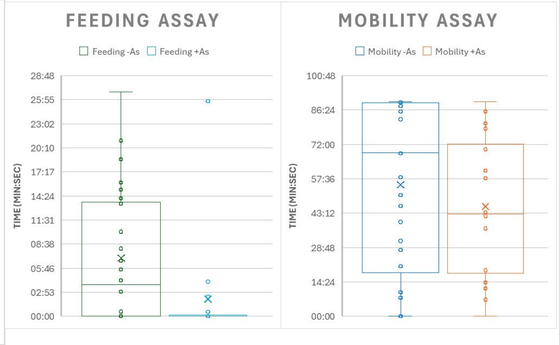

Figure 6: Total Mobility and Feeding Duration for Control vs. Arsenic-Exposed Snails. Boxplots showing total time spent moving and feeding over the full 90-minute assay for control (0 ppm As) and arsenic-exposed (0.2 ppm As) snails. Arsenic-exposed individuals displayed substantially lower feeding durations and greater variability in mobility.

Conclusion

Our results show that arsenic exposure significantly reduces feeding behavior in Chinese mystery snails, indicating clear behavioral effects at sublethal levels. The connection between these behaviors and potential gut microbiome changes remains inconclusive due to limited DNA data. Overall, this work highlights behavioral sensitivity to arsenic and supports continued research to clarify microbial and neurological mechanisms.

Future Steps

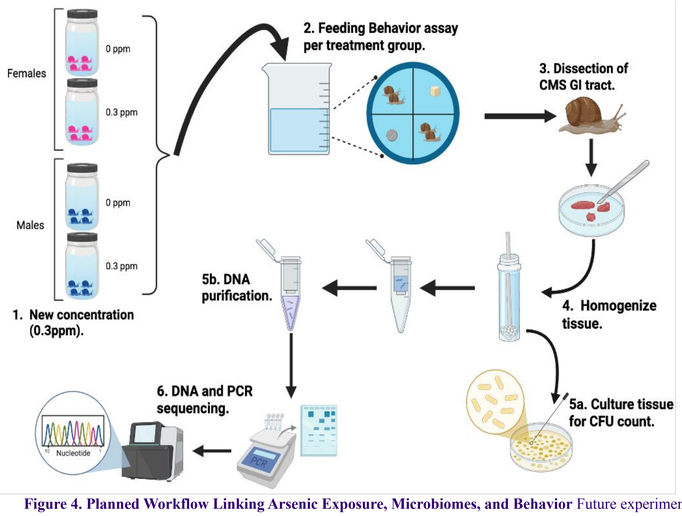

Figure 4. Planned Workflow Linking Arsenic Exposure, Microbiomes, and Behavior Future experiments will separate Chinese mystery snails by sex and expose them to a higher arsenic concentration (0.3 ppm). Feeding assays and gut dissections will be conducted per treatment. Homogenized gut tissue will be used for CFU counts, DNA extraction, and PCR amplification, followed by gel electrophoresis and Nanopore sequencing to characterize microbial communities.

Acknowledgements

Thank you to Dr. Marc Nahmani and Dr. Sarah Alaei for their mentorship and support. We also want to acknowledge fellow classmates in BIOMD 495 and the UW Tacoma Biomedical Sciences program for their collaboration, help with experiments, and contributions to data collection.

References

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