

Introduction & Objectives

The Issue

Mine drainage exposing contaminants, like sulfate and heavy metals at mine sites.

The Solution

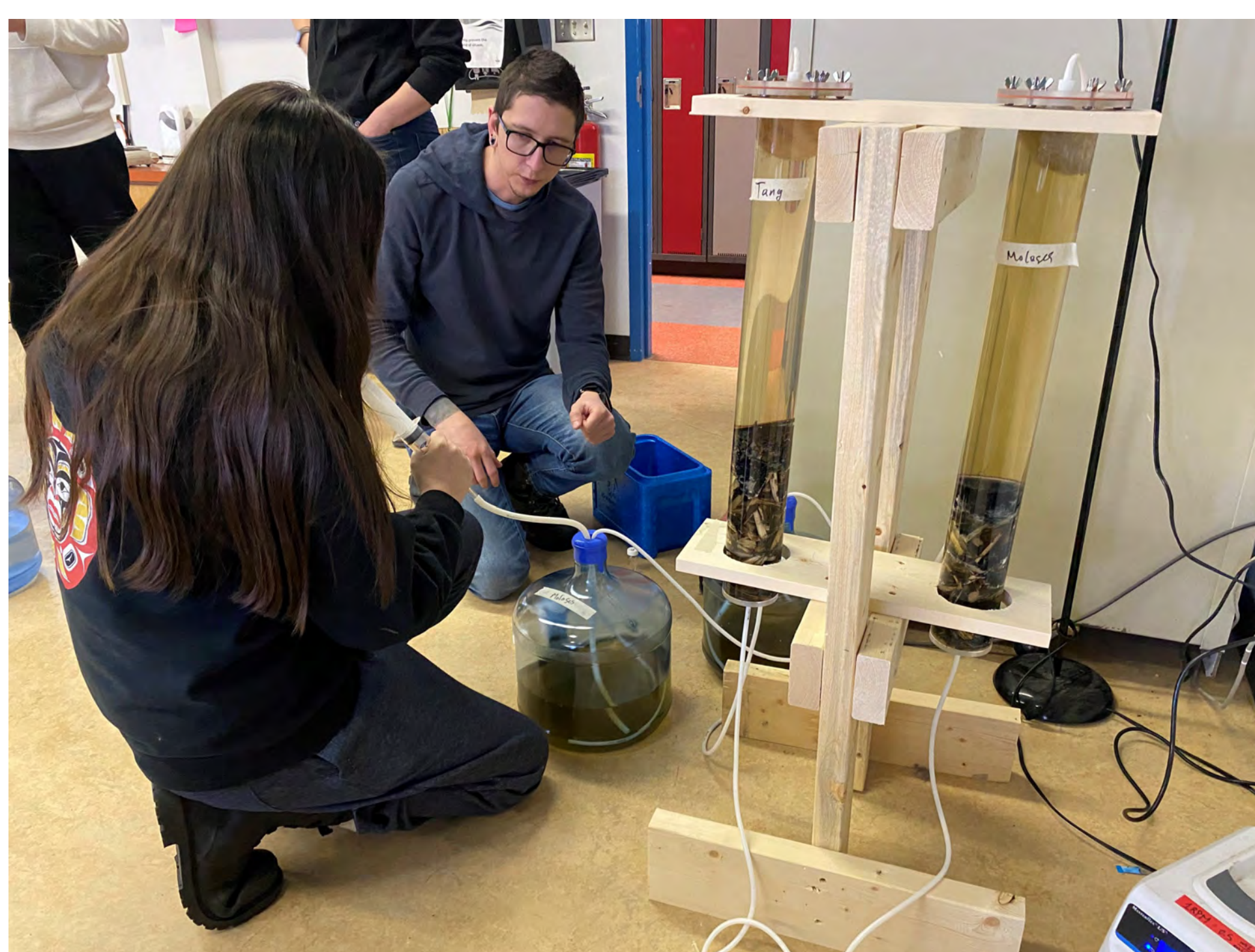
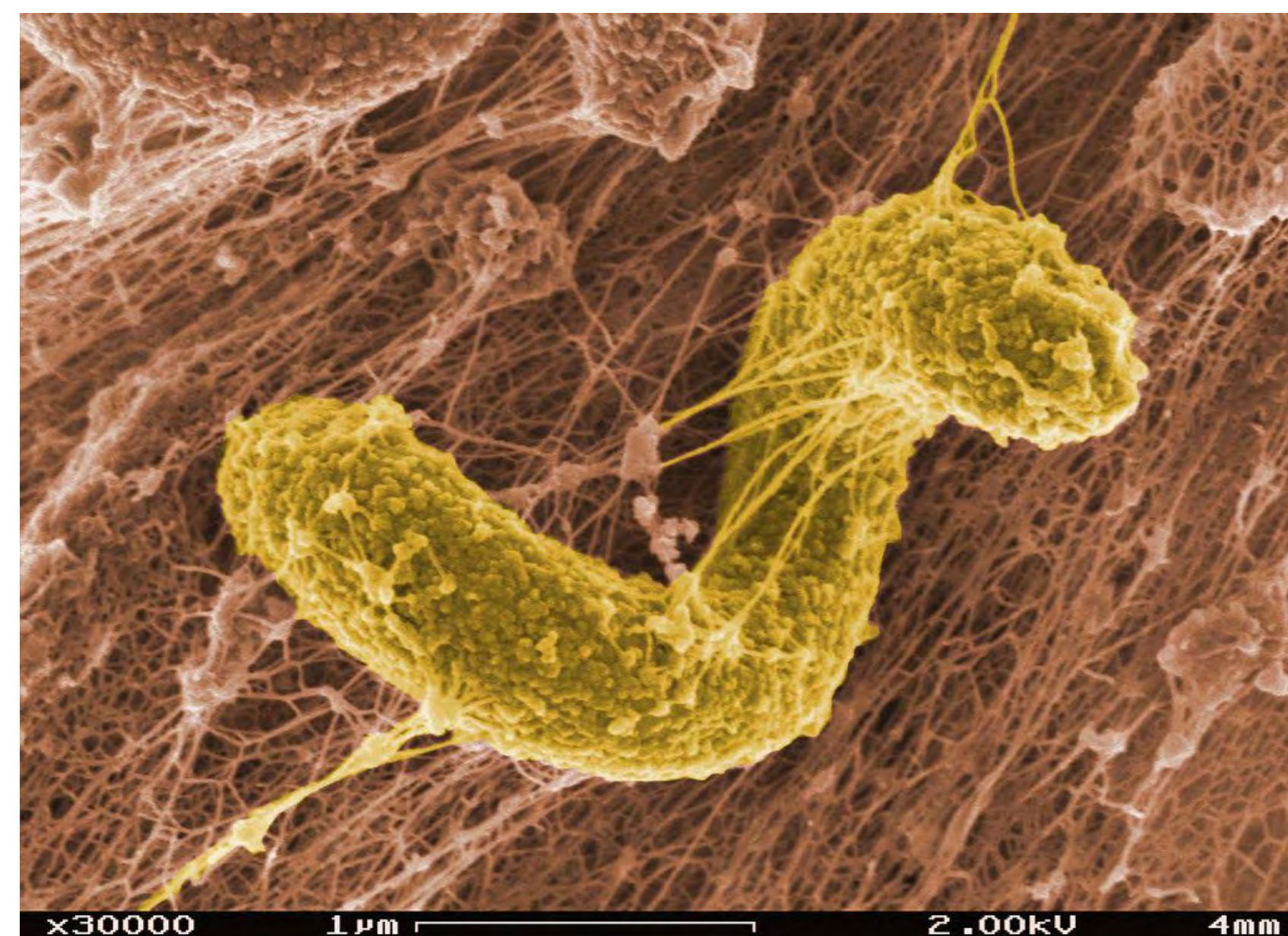
Semi-Passive treatment using sulfate reducing bacteria native to the Yukon soil.

Objectives

- To determine and demonstrate that bioreactors using sulfate reducing bacteria can remove sulfate and heavy metals, specifically copper and zinc, from synthetic mine impacted water (MIW).
- To demonstrate analytical procedures for MIW analysis during laboratory visit at YukonU Research Centre (YRC).

Color-enhanced photograph from a scanning electron microscope (SEM) image of sulfate reducing bacteria.

Image courtesy of Pacific Northwest National Laboratory.



Column bioreactors BR1 (right) and BR2 (left) set up and monitored by Eliza Van Bibber School students.

Figure 1: Physical appearance of column bioreactors BR1 and BR2 containing Sulfate Reducing Bacteria.

Experimental protocol



Figure 2: Eagle Gold Mine visit by the students.

Procedure

- Built two column bioreactors (BR1, BR2) using sulfate reducing bacteria previously collected at Minto Mine.
- Used the bioreactors to remove contaminants from synthetic mine impacted water.
- Monitored different parameters in the effluent water (color, smell, pH, sulfate, copper, zinc).

Variables

Bioreactors BR1 and BR2 were similar (bacteria, wood chips) except for the sources of carbon. BR1 was set up with Molasses. BR2 was set up with Tang.



Figure 3: YRC lab visit by the students.

Results

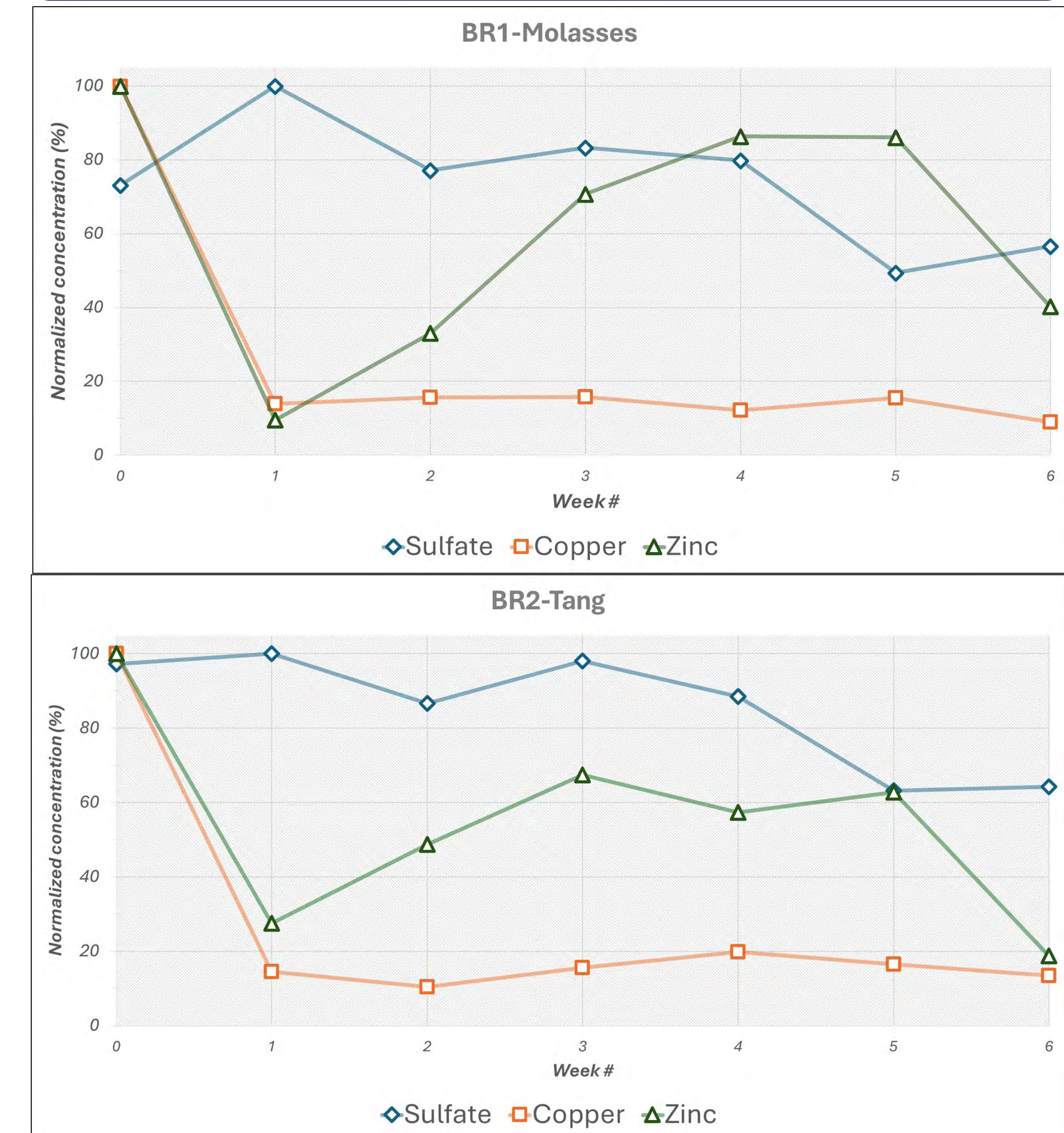


Figure 4: Changes to the concentrations of Sulfate, Copper and Zinc in the two bioreactors over time.

Conclusions

- Both bioreactors saw a gradual reduction in sulfate concentration over time, indicating bacterial activity.
- Both bioreactors successfully removed ~90% of copper.
- Both bioreactors were able to remove zinc initially, however, became less efficient at zinc removal over time.
- Both carbon sources (Molasses and Tang) performed similarly, as both contain sugar which is food for bacteria.

Acknowledgements

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