

University of Montana

ScholarWorks at University of Montana

University of Montana Conference on Undergraduate Research (UMCUR)

Apr 21st, 3:00 PM - 4:00 PM

Metabolic Versatility in Melainabacteria, a Close Relative of Cyanobacteria

Sophia Marie Miller

The University Of Montana, sm171634@umconnect.umt.edu

Kathryn Alexandra Bick

The University Of Montana, Kb172085@umconnect.umt.edu

Heidi E. Abresch

The University Of Montana, heidi.abresch@umconnect.umt.edu

Follow this and additional works at: <https://scholarworks.umt.edu/umcur>

Let us know how access to this document benefits you.

Miller, Sophia Marie; Bick, Kathryn Alexandra; and Abresch, Heidi E., "Metabolic Versatility in Melainabacteria, a Close Relative of Cyanobacteria" (2023). *University of Montana Conference on Undergraduate Research (UMCUR)*. 15.

<https://scholarworks.umt.edu/umcur/2023/posters/15>

This Poster is brought to you for free and open access by ScholarWorks at University of Montana. It has been accepted for inclusion in University of Montana Conference on Undergraduate Research (UMCUR) by an authorized administrator of ScholarWorks at University of Montana. For more information, please contact scholarworks@mso.umt.edu.

Metabolic Versatility in Melainabacteria, a Close Relative of Cyanobacteria

Kate Bick and Sophia Miller, Heidi Abresch, Scott Miller

Microbial Evolution and Ecology Lab, Division of Biological Sciences, University of Montana

Background

- Melainabacteria is the closest non-photosynthetic relative to Cyanobacteria prior to the evolution of photosynthesis
- No known representatives of this phylum are currently being successfully grown and maintained in labs
- DNA sequencing revealed that a strain of Melainabacteria was growing in a culture of diatoms from the Clark Fork River

Goals

- Identify close relatives of cultured strain
- Determine how Melainabacteria “makes a living” metabolically
- Begin isolation process from co-culture

Methods

- Assembled Melainabacteria genomes from metagenomic sequencing data
- Constructed phylogenies to understand evolutionary history
- Examined predicted genes to understand metabolic capacity
- Began efforts to grow Melainabacteria by itself

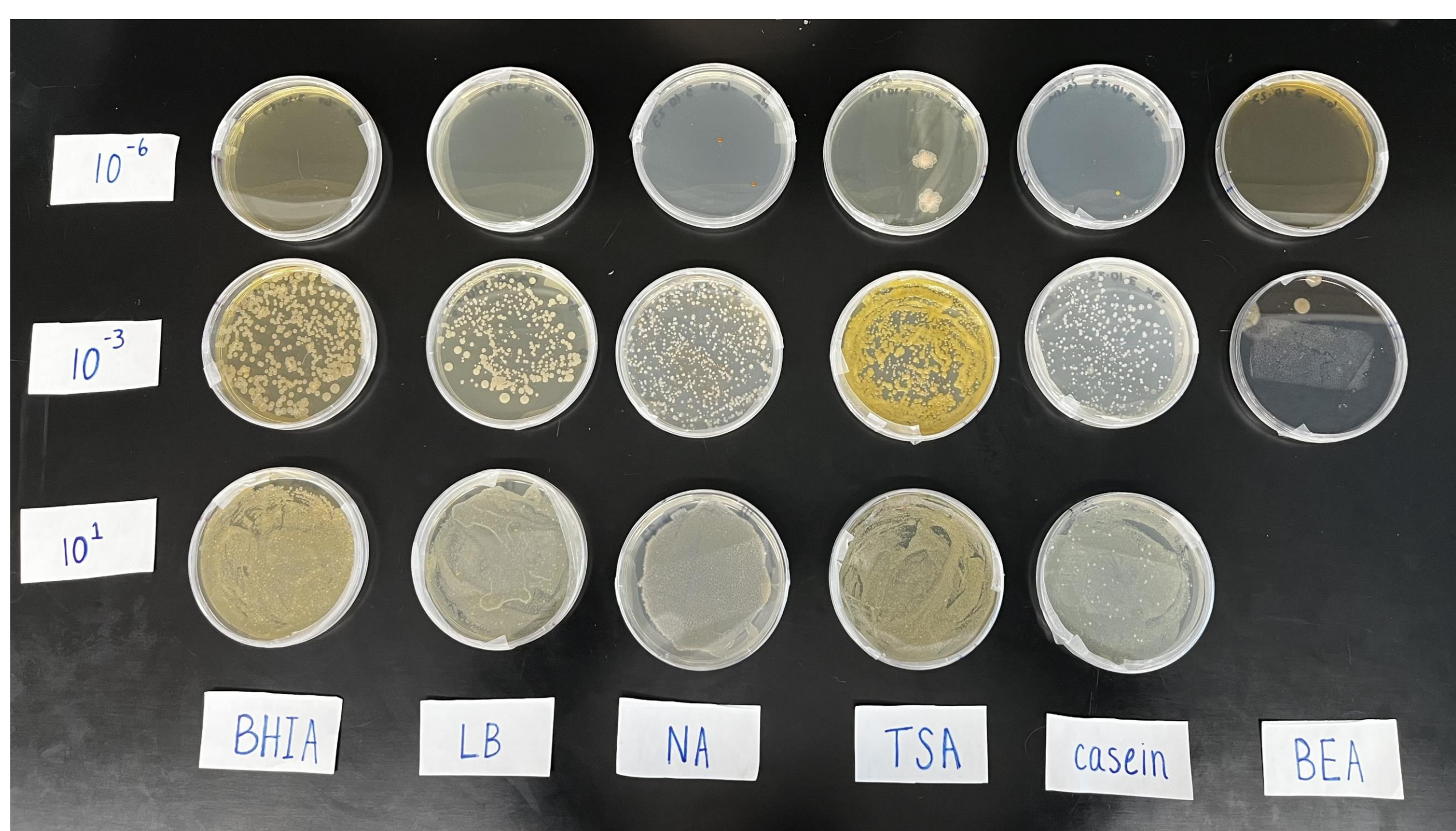


Figure 1. Bacterial growth at separate dilutions on selected media after two weeks incubation (20°C). Sixteen bacterial colonies were selected for 16S amplification using polymerase chain reaction (PCR).

Results

Tree Scale: 0.1

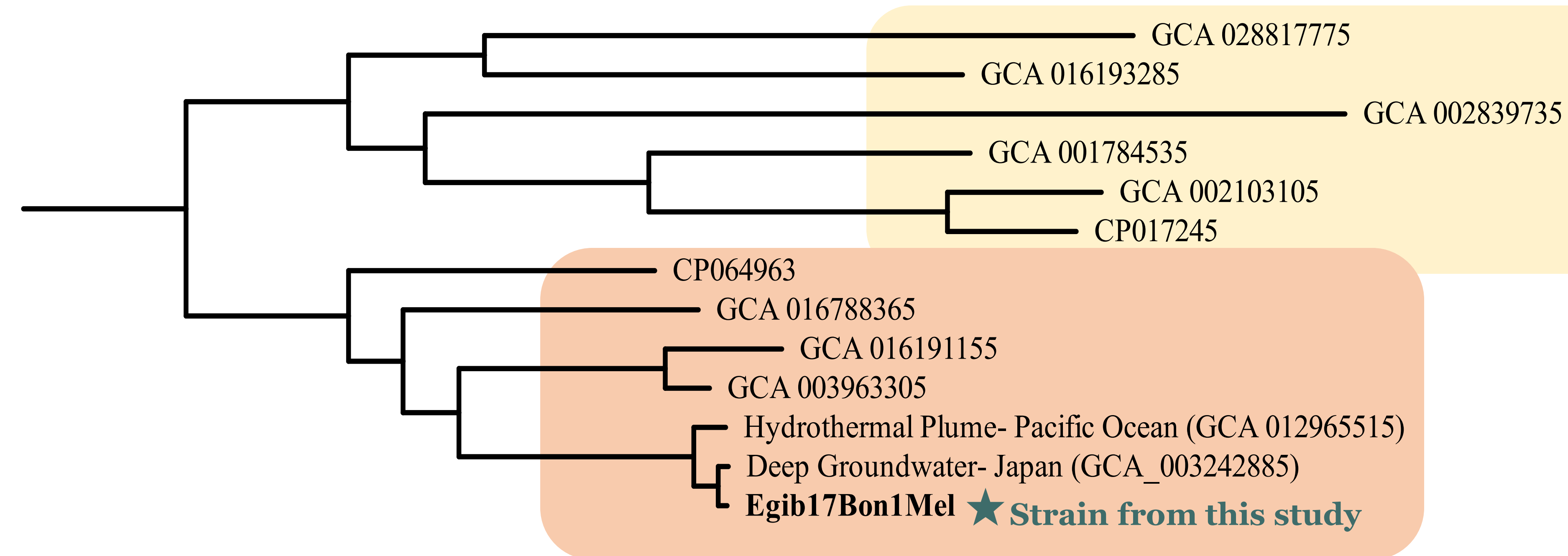


Figure 2. A maximum likelihood phylogeny of 80 single-copy amino acid sequences in Melainabacteria metagenomes. Constructed in IQTree using the LG+F+I+G4 model and 1000 bootstrap replicates. Bootstrap values at all nodes = 100.

- Gut-associated (genomes <3 Mb)
- Environmental (genomes >5 Mb)

Metabolic Versatility

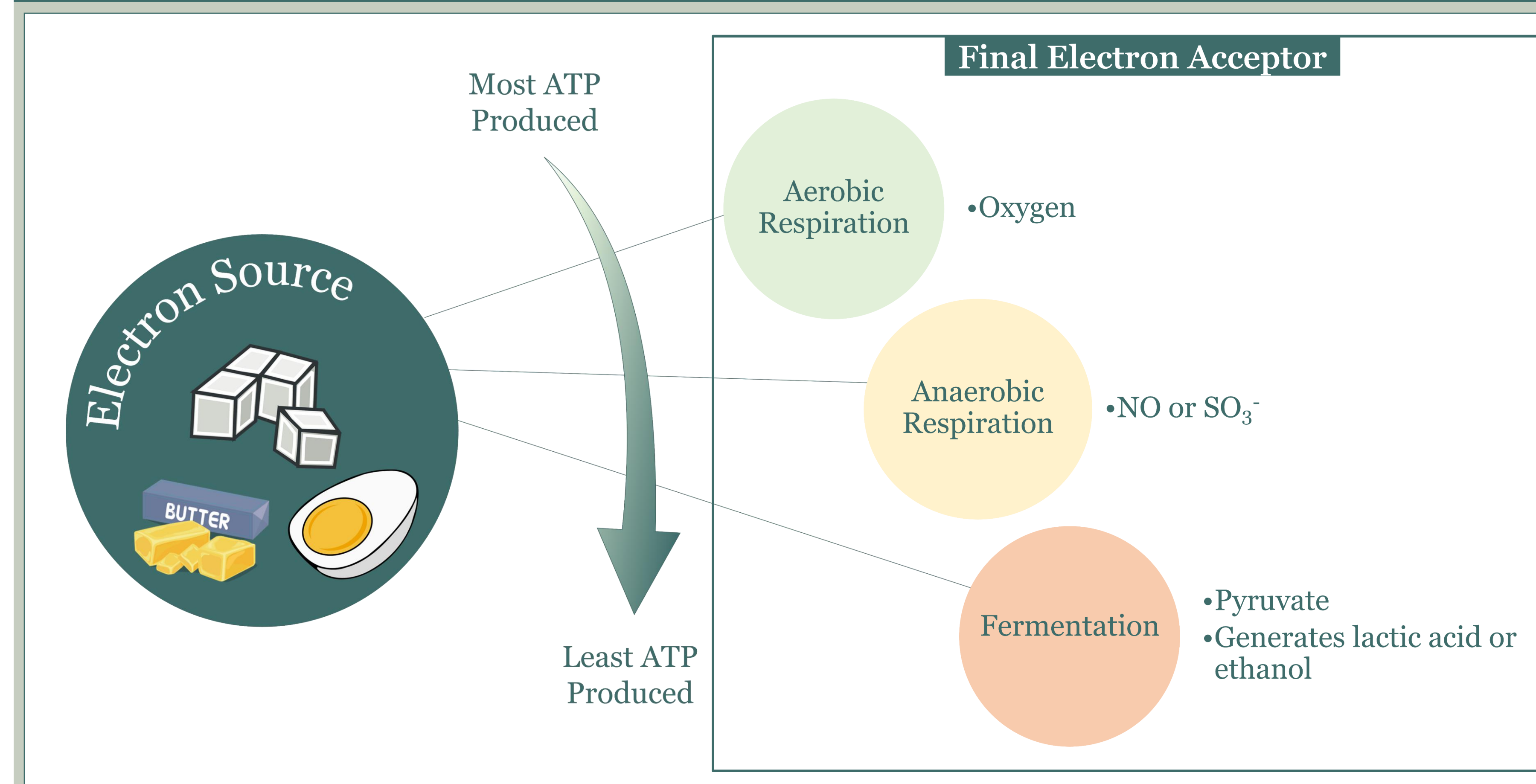
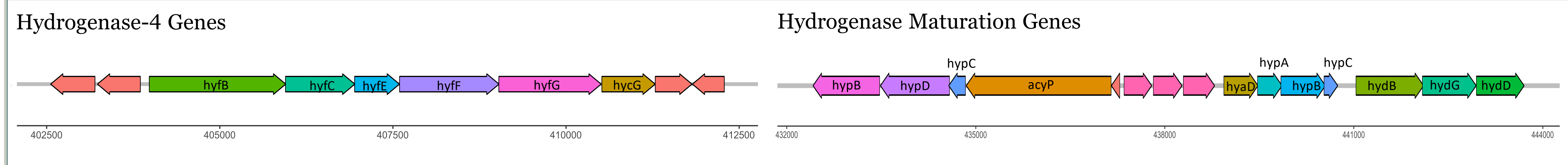


Figure 3 (left). *Melainabacteria sp. 17Bon1* genome encodes genes that allow it to obtain energy from a variety of inorganic and organic molecules, in oxic and anoxic environments.

Figure 4 (below). *Melainabacteria sp. 17Bon1* also encodes for multiple hydrogenases, including a group 4 hydrogenase, which is proposed to be used in formate fermentation. However, this strain does not appear to have the genes for formate fermentation, suggesting it may be used for another purpose.



Conclusions

- *Melainabacteria sp. 17Bon1* is most closely related to those collected from Japanese deep groundwater
- Environmental *Melainabacteria* have highly versatile metabolisms which may contribute to its presence in diverse and extreme environments
- Hydrogenases in some *Melainabacteria spp.* may link important nutrient cycles in microbial driven ecosystems

Significance

- *Melainabacteria sp. 17Bon1* is the **only known strain from this phylum currently growing in culture in the world**
- Lab strains of Melainabacteria are needed to study its function and role in nature
- Melainabacteria are critical to understand how photosynthesis evolved in Cyanobacteria

Acknowledgments

Initial culturing and sequencing efforts were supported by award NNA15BB04A from the National Aeronautics and Space Administration.

UMGC
University of Montana Genomics Core

