

Metabolic Modeling of a Novel *Mycoplasma* Identified from Eastern Oyster Microbiome

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Bacteria of the genus *Mycoplasma* are commonly known for having pathogenic or symbiotic relationships with their hosts. They generally have a relatively small genome that lacks pathways for the synthesis of essential biomass components. As a result, survival of the *Mycoplasma* species is dependent on the accessibility of rich nutrient resources from their environment. In our prior study, a specific *Mycoplasma* strain was identified from oyster gut samples, and its draft genome was assembled from metagenomic sequencing. Here, we construct a genome-scale metabolic model of this strain and use the model to provide insights into its potential roles in the gut microbiome of oyster. A draft model was first generated using ortholog mapping to the KEGG database. Manual curations were then performed using references from other *Mycoplasma* species and using sequence comparisons with annotated transporters from the Transporter Classification Database. The model was then used to identify a list of essential nutrients that would be required for growing the oyster-associated *Mycoplasma* strain. Overall, this project represents a first metabolic model of a bacterial species in the oyster gut microbiome. In the next step, we will attempt to isolate this bacterial strain from live oysters and continue to investigate the roles of this bacteria in oyster health and ecology.