

Drivers of Assembly in the Developing Zebrafish (*Danio rerio*) Embryo Microbiome

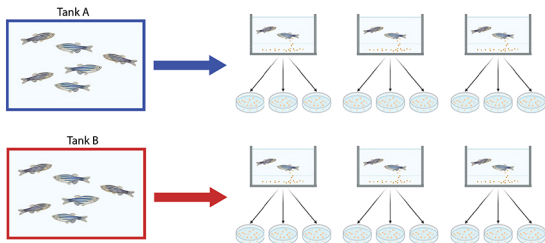
SMITH, Caitlin A.*; ADAIR, Karen L.; BOHANNAN, Brendan J. M.

Institute of Ecology and Evolution, University of Oregon; Eugene OR, USA * Contact: csmith29@uoregon.edu

Research Questions

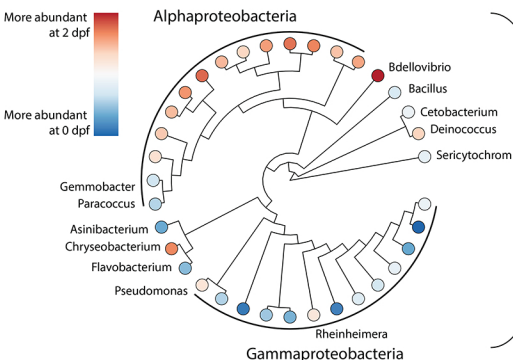
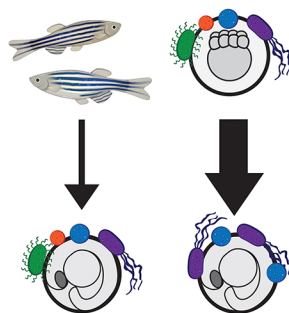
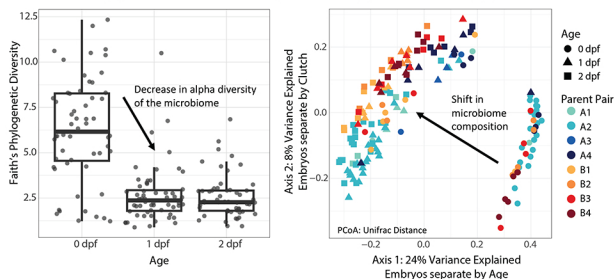
- How do parentals influence the microbiomes of their offspring?
- How does age influence the microbiome of a developing embryo?

To address these questions, we sampled wildtype zebrafish embryos from multiple pairs of parents from two stock tanks at the UO Huestis Zebrafish Facility.



Related embryos are more similar in their microbiomes than unrelated embryos. However, age has a stronger effect on microbiome composition than relatedness.

Changes in phylogenetic diversity may indicate clades of bacteria being lost or changing in abundance between ages 0 and 1 day post fertilization (dpf).



What genera change in abundance during development?

Differential abundance analysis reveals phylogenetic patterns in abundance of bacterial genera from age 0 to age 2 dpf.

With few exceptions, genera in the class Alphaproteobacteria grow in abundance between ages 0 and 2 dpf, while Gammaproteobacteria decrease.

Acknowledgments: This research was supported by the US National Institutes of Health, grant P01GM125576. This content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. I would like to thank the UO Zebrafish Facility for their assistance in rearing the zebrafish and providing training for animal care and handling, the UO Genomics and Cell Characterization Core Facility, and the Bohannan Lab for feedback and advice on experimental design, statistics and this poster presentation.