

# A Mutant Microbial Species alters Interspecies Interactions in the Zebrafish Gut

Jade Kast<sup>1</sup>, Deepika Sundarraman<sup>2</sup>, Raghuveer Parthasarathy<sup>2</sup>

<sup>1</sup>University of Oregon, Department of Biology

<sup>2</sup>University of Oregon, Department of Physics

Phil and Penny Knight  
Campus for Accelerating Scientific Impact



UNIVERSITY OF OREGON  
Office of the Vice President  
for Research and Innovation

## Introduction

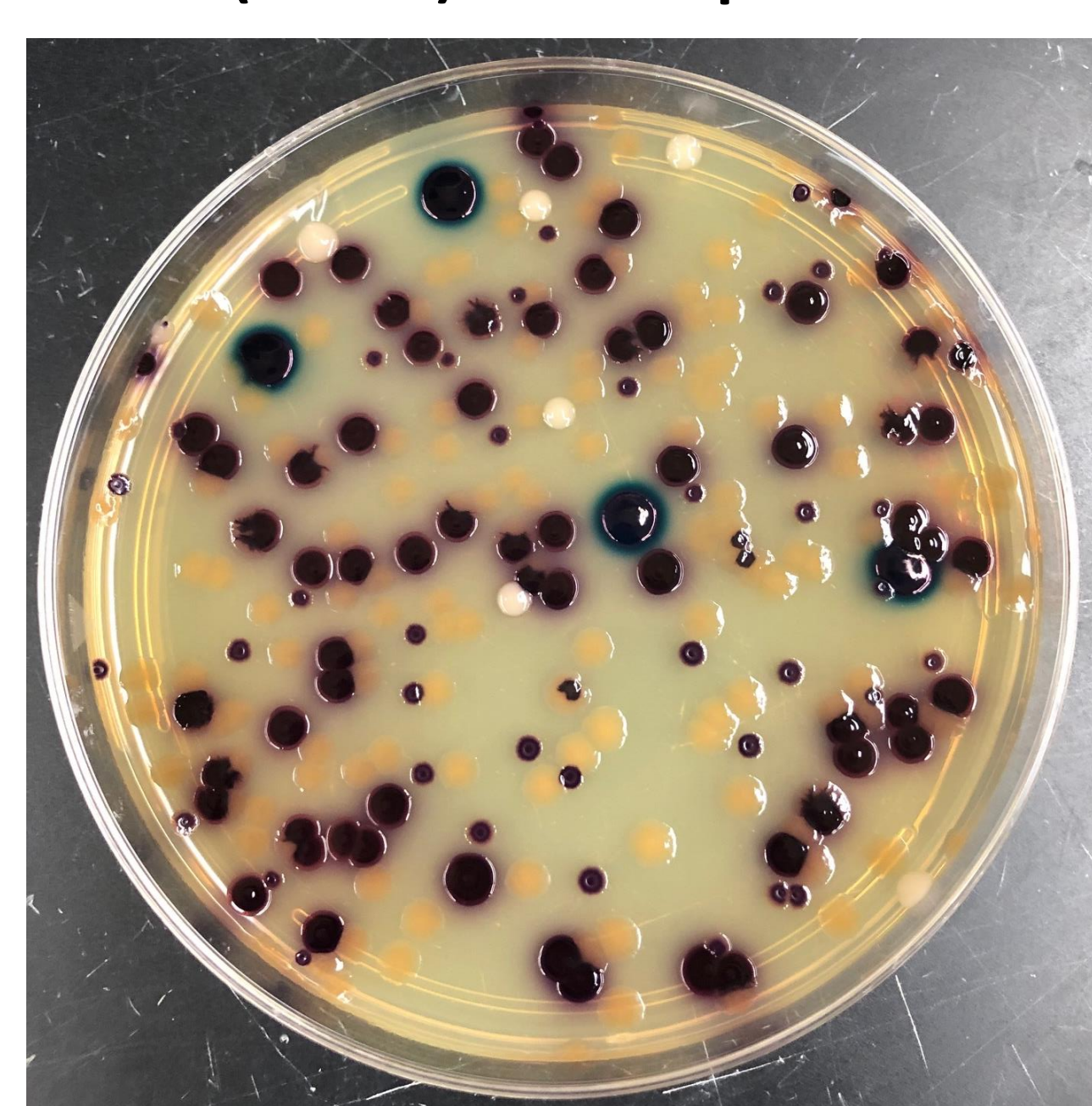
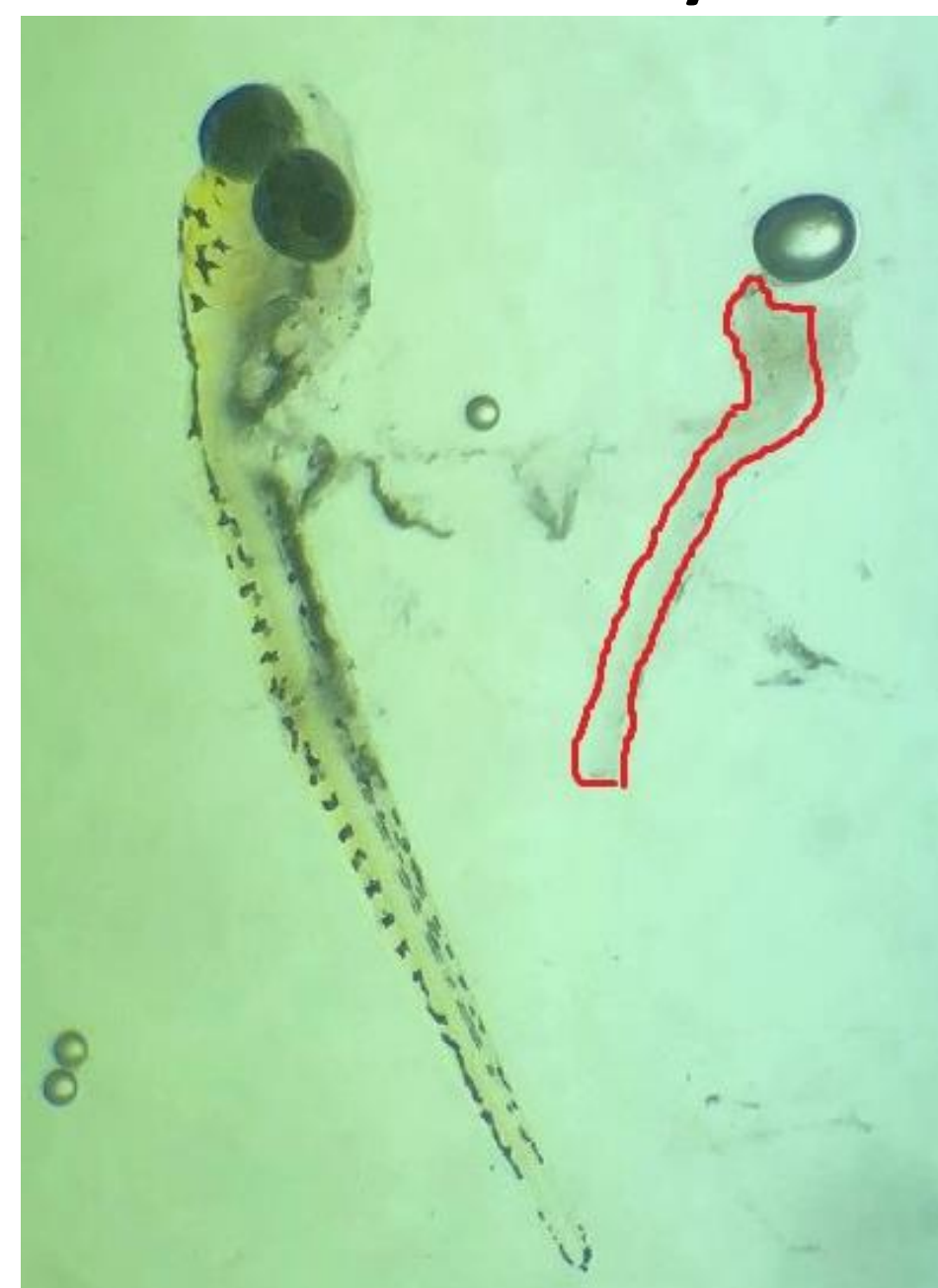
- The gut microbiome is important for health, but hard to study in vivo due to its complexity and variability.
- Model organisms can be used to study interactions between microbial species by building specific communities in initially germ-free organisms.
- Previous work in the zebrafish gut determined interactions between bacterial species pairs dampen in a multispecies community (Sundarraman et al., 2020).
- One pair studied was *Aeromonas* (AE) and *Enterobacter* (EN) which have a strong negative interaction.
- We have seen that a mutant *Aeromonas* strain (AEmb) has a different spatial structure in the gut than AE.

## Research Questions

- How does a mutant microbial species with a different spatial structure alter interspecies interactions?
- How is the interaction between the AEmb and EN pair different in a multispecies community?

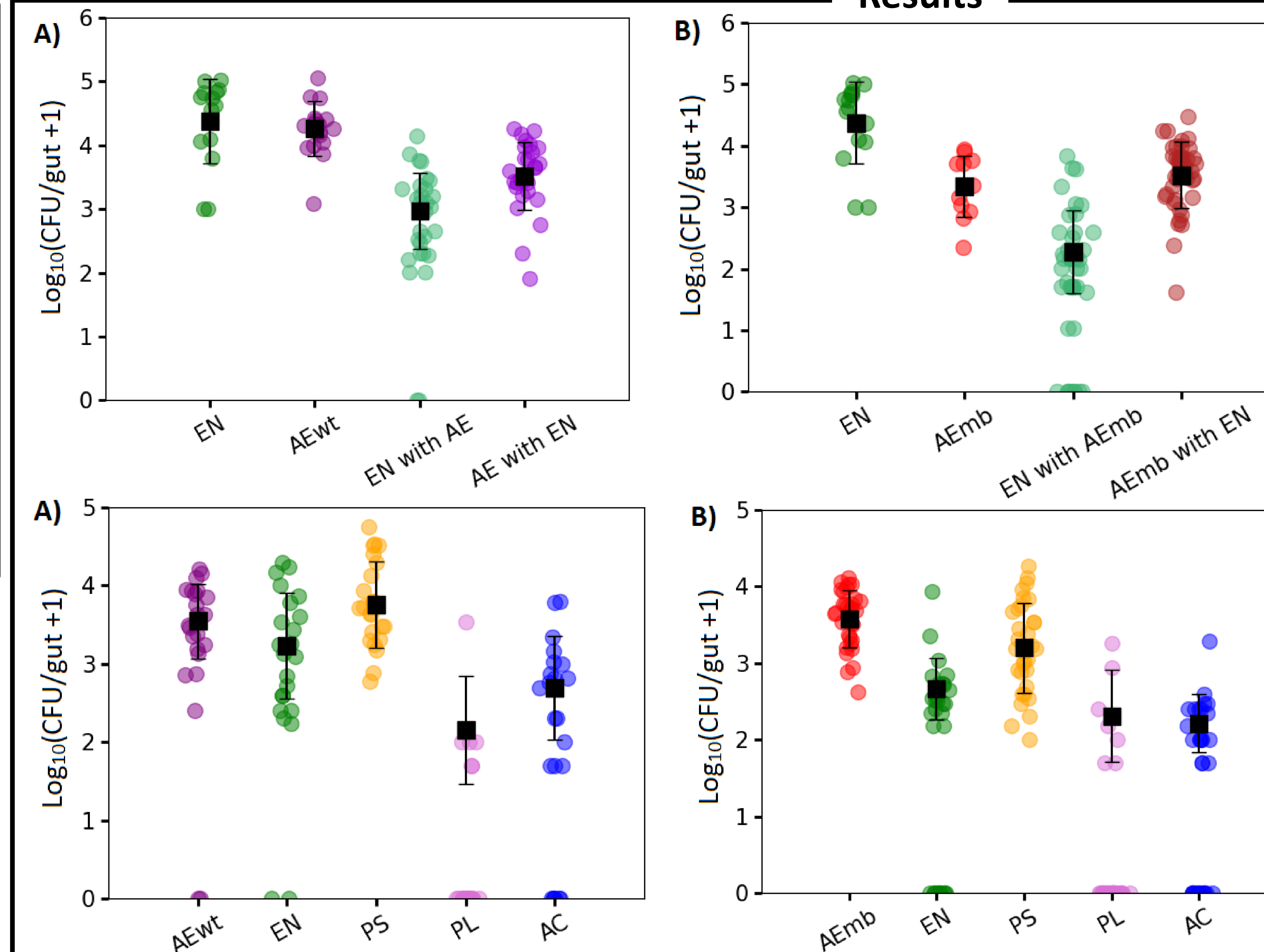
## Methods

- Inoculate germ-free fish with a set of 2 or 5 commensal bacterial species at 5 days post fertilization (dpf).
- Dissect out the gut and plate contents on agar plates to count colony forming units (CFU) at 7dpf.



**Figure 1.** The gut is dissected out (red outline) under a microscope (left). Average fish length is 2mm. On the agar plate (right) each species is a different color.

## Results



**Figure 2.** The 1-species and 2-species log abundances per fish for **(A)** EN (green), AE (purple), and **(B)** AEmb (red). Black squares indicate the average log abundances and standard deviation.

**Figure 3.** The 5-species log abundances per fish with **(A)** AE or **(B)** AEmb included. Black squares indicate the average log abundances and standard deviation.

## Conclusions

- AEmb has a stronger negative interaction with EN than AE does.
- In contrast to previous work, this strong interaction is seen in a five-species community as well.
- Spatial distribution of species in the gut can influence interspecies interactions.

## Future Directions

- Determine the mechanism of the strong negative interaction between AEmb and EN.
- Determine how multispecies communities alter interactions between pairs of species to affect community composition.

## References

Sundarraman, D., Hay, E. A., Martins, D. M., Shields, D. S., Pettinari, N. L., & Parthasarathy, R. (2020). Higher-Order Interactions Dampen Pairwise Competition in the Zebrafish Gut Microbiome. *MBio*, 11(5). <https://doi.org/10.1128/mBio.01667-20>

## Acknowledgments

Thank you to Deepika Sundarraman, Dr. Raghuveer Parthasarathy, and everyone else in the Parthasarathy lab for their guidance and support. Thank you to friends and family who have supported me as well. Additionally, I want to thank the Knight Campus Undergraduate Scholars Program for giving me the opportunity work on this project.