

Ossetra Caviar Microbiome

■ Domain Bacteria

■ Brochothrix sp.

Zymomonas mobilis

Meadow Hansen & Irene Faizi

Faculty Advisors: Benjamin J. Reading and Scott A. Salger

North Carolina State University, Department of Applied Ecology; University of San Francisco; University of Tulsa



Introduction

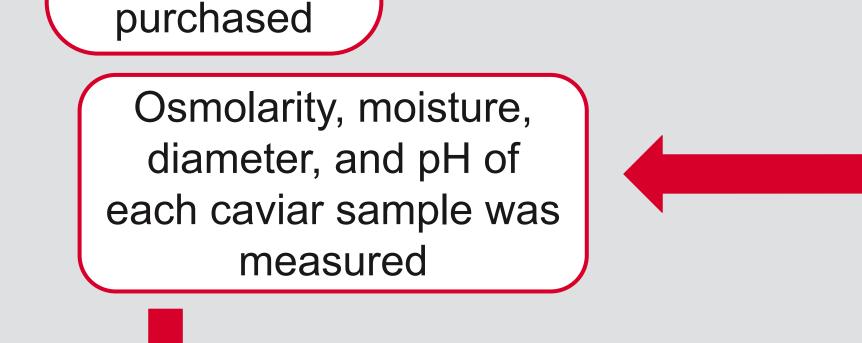
Russian sturgeon Acipenser caviar from gueldenstaedtii is one of the most sought-after caviars in the world. Wild Russian sturgeon populations have been vastly depleted due to overexploitation and habitat degradation. In fact, importation of caviar from their native areas has become illegal in many countries. Sturgeons are now raised in aquaculture to overcome this challenge. As a result, aquaculture has become more popular as it farms sturgeon, and thus caviar, without putting them at risk. The purpose of this study was to investigate the microbiome of caviar and identify key differences among prokaryotic taxa. This model may be used to infer the impact of microorganisms on the quality of caviar and explain how they may be used to improve the value and appeal of caviars produced in aquaculture.

Hypothesis/Objective

- There is a difference in prokaryotic microbial communities between Ossetra caviar samples.
- Characterize the microbiome present on the caviar and infer its role in quality and price (grades 1 through 4).

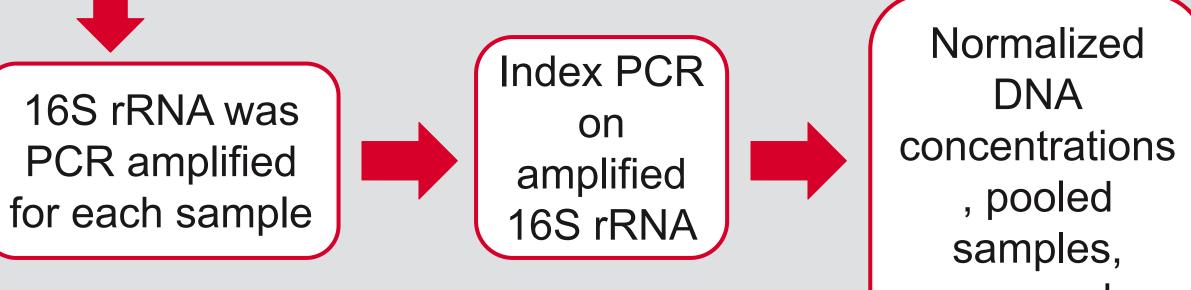
Fifteen caviars of varying Brine was removed

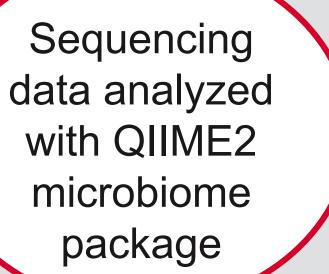
from the caviar tins

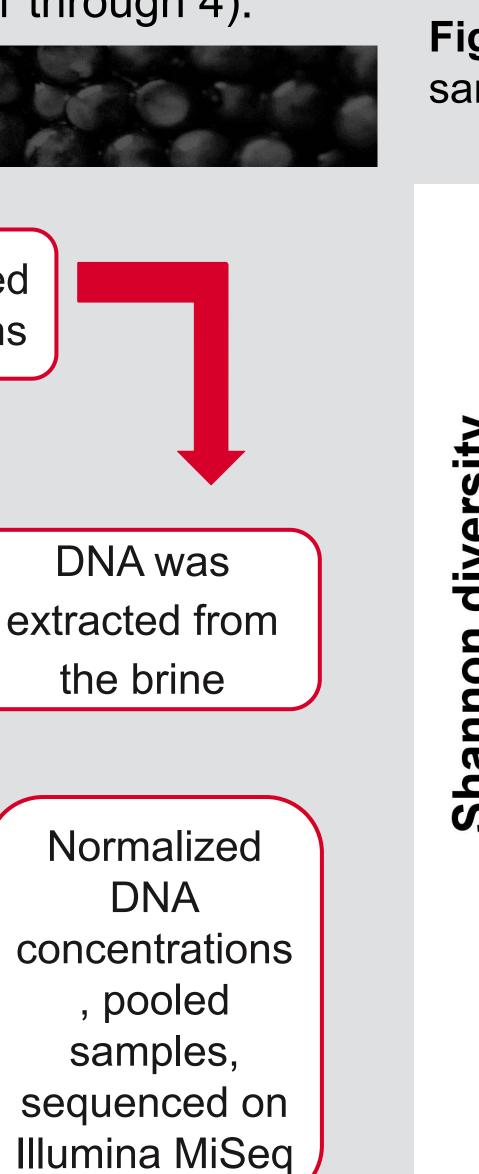


price (\$60 to

\$595/oz.) were







Results 100% 90% 80% 70% 60% 10% 20% 10%

Figure 1. Relative abundance of prokaryotes found in varying samples of Ossetra caviar.

■ Salinibacter sp.

Psychrobacter sp.

■ Family Moraxellaceae

Order Bacillales

■ Flavobacterium sp.

Psychrobacter aquimaris

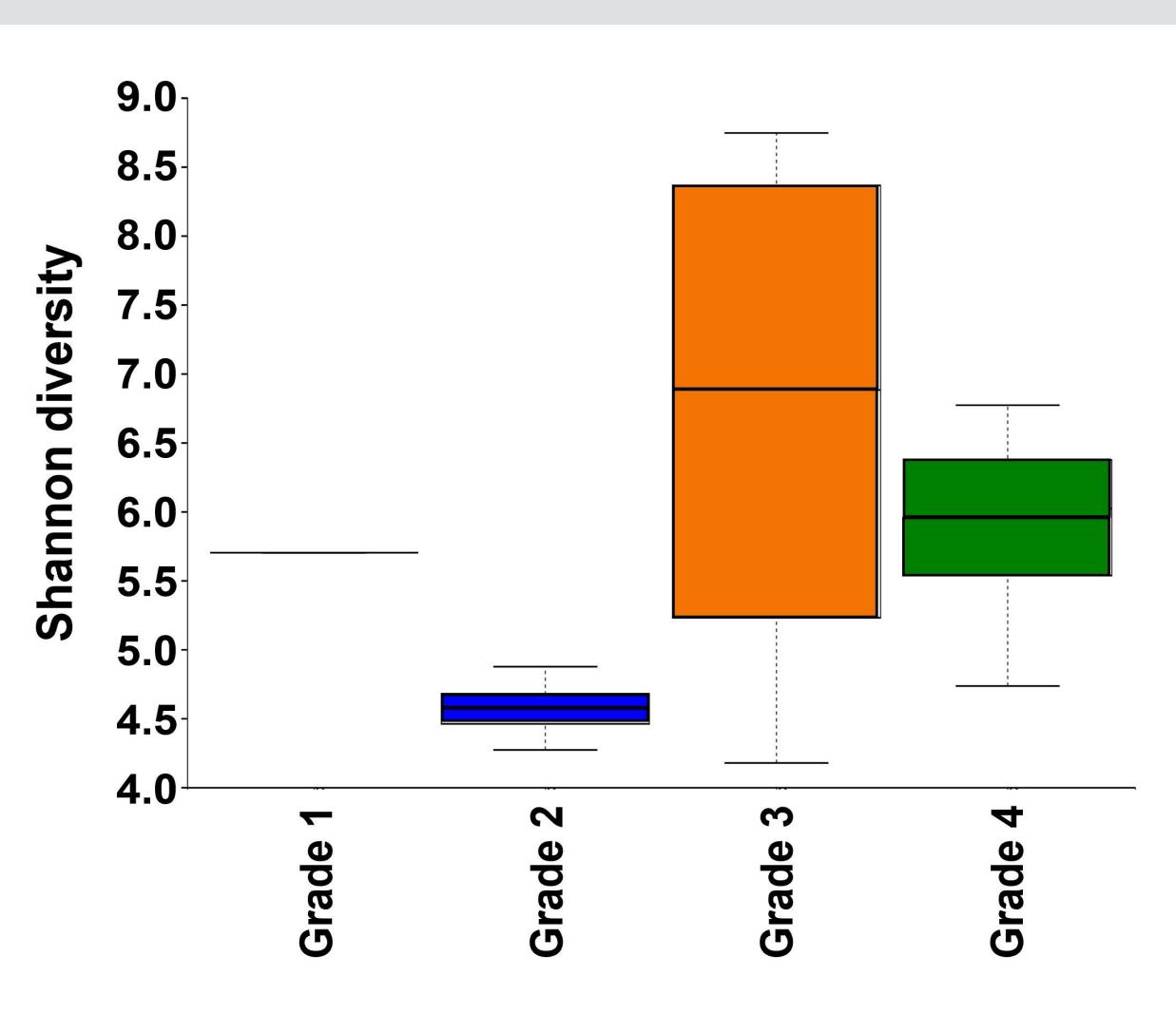


Figure 2. Shannon diversity of prokaryotes found in samples of Ossetra caviar. There is a significant difference between caviar grades 2 and 4 (p = 0.043)

Results (continued)

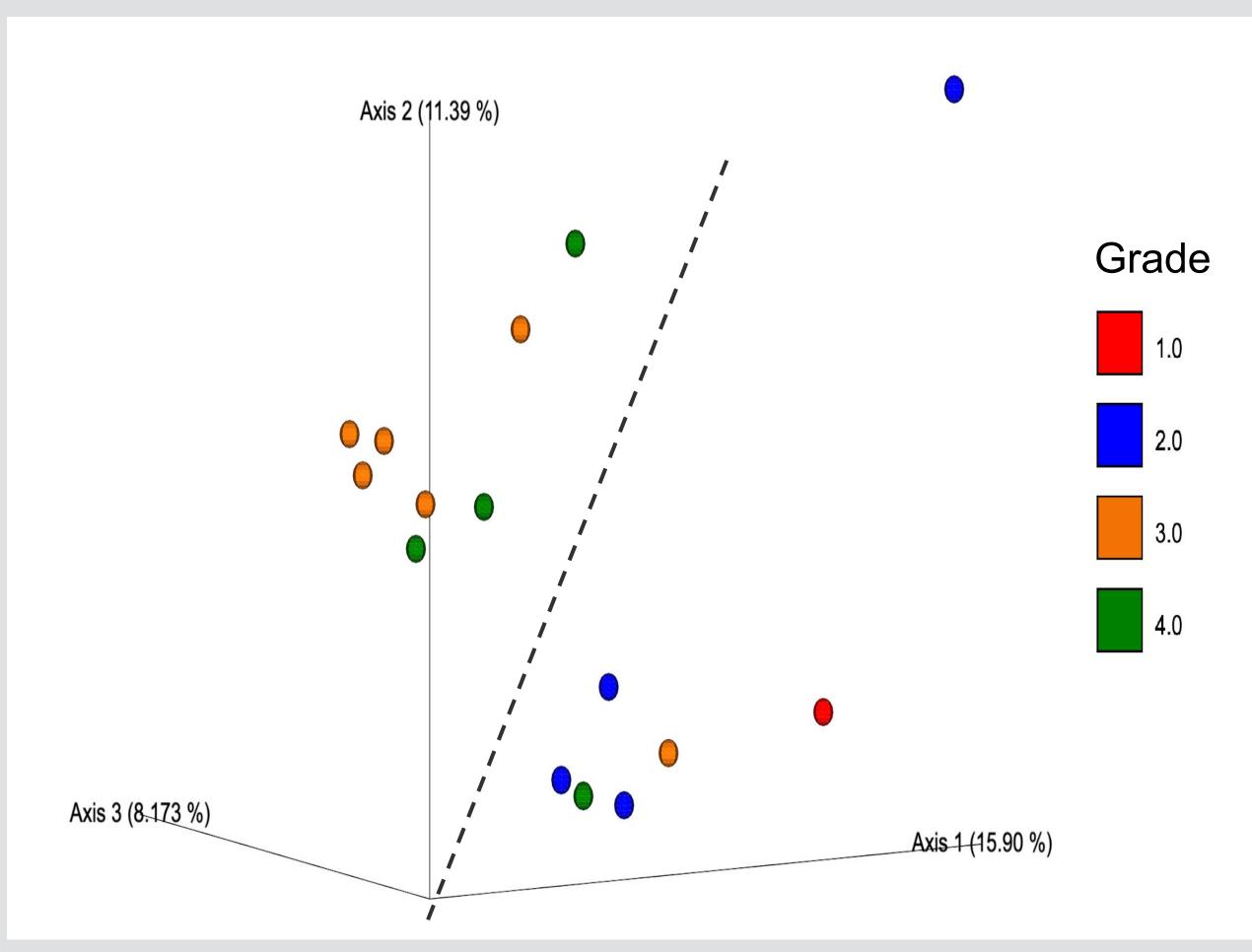


Figure 3. PCoA plot of microbial community diversity between sample grades. The closer the samples, the more similar the microbial communities. There is overlap between each grade, however grades 2 and 4 can generally be differentiated by the dashed line.

Conclusions

- Key taxa were present generally in caviars were from *Psychrobacter*, *Brochothrix*, *Salinibacter*, and *Flavobacterium*.
- Significant differences were found in Shannon diversity of prokaryotic organisms between different caviar grades (grades 2 and 4).
- No differences in diversity were discovered when comparing the osmolarity, salt content, pH, presence of sodium tetraborate, container type, diameter, or moisture content of the roe.

Future Directions

- Understanding the microbiome of caviars can help to improve caviar quality as well as shelflife and food preservation.
- Beneficial microbes may be used to enhance food safety and quality.

Acknowledgements

Drs. Benjamin J. Reading and Scott Salger for their mentorship, and support, and Dr. Carlos Goller for allowing us to be a part of the NSF BITSURE REU. Award #1659225