Genetic Variation in The Great South Bay and Long Island Sound Oyster Species

Authors: Ava Dawydiak and Isabel Roccaro
Mentor: Frank Diehl
Westhampton Beach High School

Abstract

The Great South Bay (GSB) and the Long Island Sound (LIS) are both areas that exhibit degraded water quality, with the oyster (C. virginica) being a commonly used bivalve to restore it (Shusman 1). This study was conducted to evaluate the biodiversity present in both locations and to determine if genetic diversity occurred more in the wild oysters than farm-raised (inbred). Ten farm-raised (GSB) and ten wild (LIS) oysters were extracted of their DNA, which was amplified using PCR. During the research, only two samples were strong enough to be analyzed. The research proved that that farm-raised sample NTA-010 was most closely related to the marine fish Cod (relativity of 57) and that it contained DNA similar to the fungus species sepsis sepsi (Relativity of 41). The wild bred sample NTA-020 was most closely related to the fly species chovela elongata (Relativity of 46).

Introduction

- Oysters are used for water quality restoration because of their water filtration capabilities, removing organic and inorganic particles from the water column (Zhang 1).
- Currently, extensive oyster farming is being conducted in the GSB and LIS to replenish the water quality, with the oyster populations exposed to pathogens and abiotic environmental stressors.
- The GSB is a lagoon that cultivated an average of 750,000 oysters a year, and in 1976, the annual harvest fell by 99% (Kassner 1).
- The LIS is a tidal estuary located on the east side of the Atlantic Ocean that has the highest levels of nitrogen towards the West (Gobler 1).
- In a previous study of the genomes of oyster in harsh conditions, it was revealed that the wild oyster had a 44% higher polymorphism rate than the farm-raised (inbred) oyster. An abundance of repetitive adaptations was also present in genes when responding to environmental stressors (Zhang 1).

Purpose

- The oyster biodiversity on Long Island is yet to be determined. This study will reveal the present oyster species diversity and serve as a record and comparison between the LIS and GSB oyster genetic variance.

Hypothesis

- It is expected that when GSB farm-raised and LIS wild-grown oyster are genetics are compared, than the genomes will reveal equally extensive biodiversity in both locations.
- This hypothesis is based off of previous research proving that adaptation occurs in the prescence of environmental stressors (Zhang 1).

Methodology

- Modifications: Oyster samples were originally labeled as F1-10 and W1-10. F1-10 represented farm-raised samples 1-10 and W1-10 represented wild samples 1-10.
- 10 oysters of varying location were collected from the LIS and GSB (Figure 1).
- The 10 from the GSB were farm-raised (inbred) and collected offshore in various breeding cages near the Fire Island Inlet by a commercial source in Sayville, NY (Figure 2).
- The 10 samples from the LIS were wild grown for a genetic variance evaluation. They were collected from their distributor in Port Jefferson, NY (Figure 3).
- Each oyster was opened and the 20 bellies were put into separate containers to be frozen for the barcoding process (figure 4).

DNA Barcoding Process

- DNA Extraction- DNA was extracted and purified from each processed oyster sample.
- PCR Amplification-Each DNA extraction was barcoded for a portion of the COI and was amplified by PCR.
- Gel Electrophoresis- All PCR products were analyzed after being run through 130 V of power. All successful products were then submitted for sequencing in both directions.

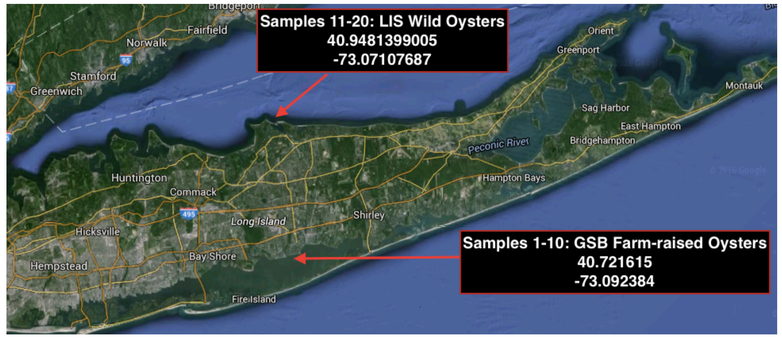

Figure 1. GSB and LIS collection coordinates

Figure 2. Farm-raised oyster-Sample F1 front/back

Figure 3. Wild oyster- Sample W1

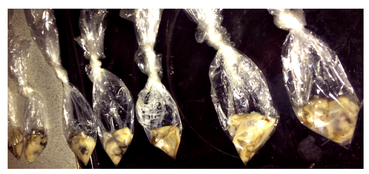

Figure 4. Oyster belly extraction

Acknowledgements

We would like to thank the Cold Spring Harbor Laboratory for funding this research, as well as the Westhampton Beach High School for allowing us to take part in the DNA Barcoding program. We would also like to thank Frank Diehl for introducing us to this research, assisting us throughout, and being a supportive mentor along the way. Lastly, we would like to thank our oyster supply company for giving us the materials needed to carry out this research.

References

Zhang, Guofan. "The oyster genome reveals stress adaptation and complexity of shell formation." Nature. N.p., 19 Sept. 2012. Web. 17 Dec. 2015. <http://www.nature.com/nature/journal/v490/n7418/full/nature11413.html>.

Gobler, Christopher J., et al. "Nitrogen and silicon limitation of phytoplankton communities across an urban estuary: The East River-Long Island Sound system." ScienceDirect. N.p., n.d. Web. 13 May 2016. <http://www.sciencedirect.com/science/article/pii/S0272771406000485>.

Kassner, Jeffrey. "A HISTORY OF OYSTERS AND HARD CLAMS IN THE GREAT SOUTH BAY." Long Island Traditions. N.p., n.d. Web. 17 May 2016. <http:www.longislandtraditions.org/southshore/sights_sounds/fishing/pdf/ kassner_essay.pdf>.

Results

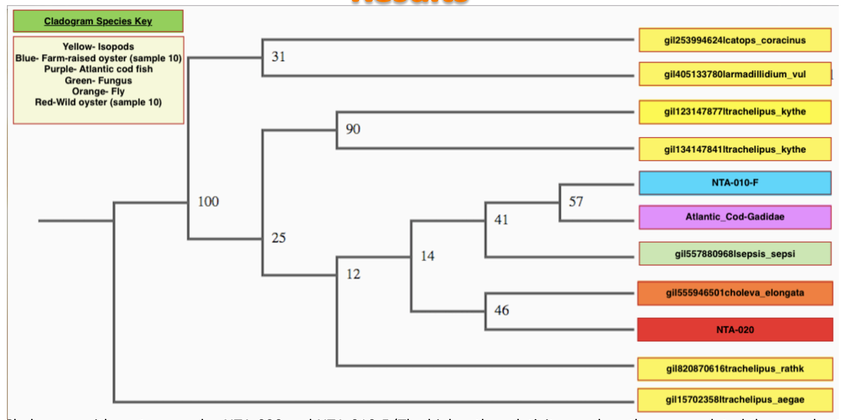

Figure 5. Cladogram with oyster samples NTA-020 and NTA-010-F (The higher the relativity number, the more related the samples are)

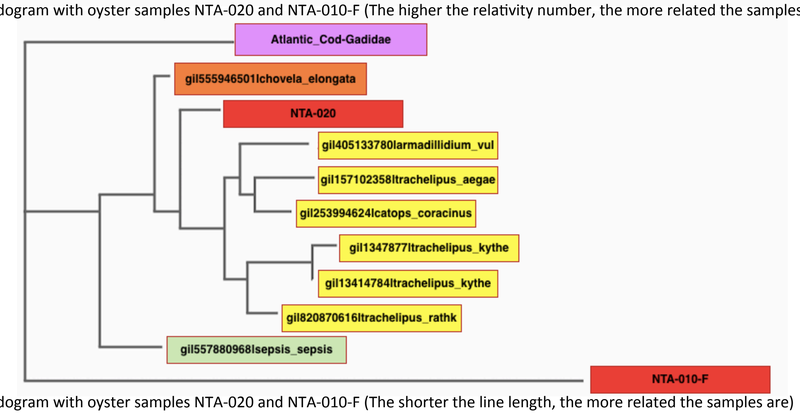

Figure 6. Cladogram with oyster samples NTA-020 and NTA-010-F (The shorter the line length, the more related the samples are)

- Out of the 20 samples, sample NTA-020 (W10) and NTA-010-F (F10) were the only two samples with strong enough DNA sequences for species analysis. Sample NTA-010-F (F10) only had amplified DNA from the forward direction of the strand.
- Figure 5 proves that sample NTA-010-F (F10) was most closely related to the marine fish Cod (relativity of 57) and that sample NTA-010-F (F10) contained DNA similar to the fungus species sepsis sepsi (Relativity of 41).
- NTA-020 (W10) was most closely related to the fly species chovela elongata (Relativity of 46).
- Figure 5 and 6 prove that both samples contained DNA similar to many isopods.
- Figure 5 and 6 prove that the isopod trachelipus rathk had very little DNA similarity to sample NTA-020 (Relativity of 12).

Discussion

- When the gel electrophoresis was run the first time, there was no banding showing up in gel, most likely due to an insufficient DNA sample, or an error during the PCR process.
- The two oyster samples were not determined to have relevance to other oyster species, most likely due to sample NTA-010 not being analyzed in the reverse direction, or possibly not having enough of the samples PCR product for analyzing.
- Due to the lack of samples being analyzed, there was no observation that compared farm-raised and wild-raised oysters.
- Future research may be conducted, using oysters from a few locations in both bays to ensure a greater possibility for more adequate DNA samples.
- Future research may include an improved methodology to enhance the consistency and comparability in oyster genome research.