Disease on the Half-Shell: Prevalence and impact of the protistan pathogen MSX on oyster population health throughout the Gulf of Maine

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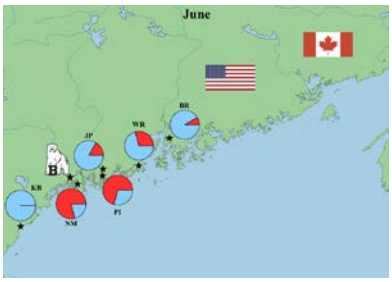
The Gulf of Maine (GoM) encompasses thousands of miles of coastline characterized by numerous bays and estuaries that have historically supported abundant shellfish populations. A keystone species in this environment is the American oyster, *Crassostrea virginica*, whose structurally complex reef systems provide habitat and substrata for other GoM organisms like juvenile cod, act as biogenic breakwaters, filter algae and microorganisms from large amounts of water, and are a sustainable commercial food source.

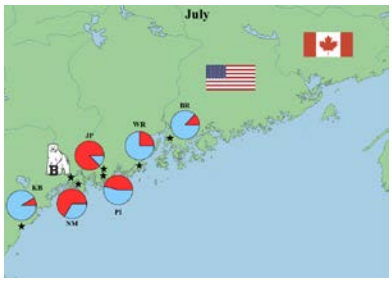
As a suspension-feeding bivalve, oysters come into direct contact with many pathogens that can cause numerous diseases. One such pathogen is the protistan parasite *Haplosporidium nelsoni*, which is widely considered to be the most pertinent pathogen affecting GoM oyster farming at the present moment. *H. nelsoni* is highly infective and induces a disease called MSX (multinucleated sphere unknown) that results in reduced fecundity and high mortality rates. MSX has caused massive die-offs across the Eastern coast of the US and in Maine, specifically in the Damariscotta River Estuary (DRE), which is coincidentally also the foremost site of oyster aquaculture in Maine. The result has been a quarantine of the river such that no oysters larger than three millimeters can be moved from the DRE to other waters.

Despite this, little is known about the life prevalence and impact of MSX in oysters. Thus, this project's aim was to increase the body of knowledge regarding MSX infection by quantifying the prevalence of infection, abundance of the pathogen within the infected oysters, and temporal and geographic spread of *H. nelsoni* within farmed oysters of the GoM.

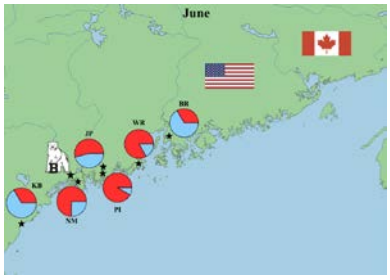
In order to do this, I employed a new technique called quantitative polymerase chain reaction (qPCR). This allows me to detect not only the presence of the pathogen in samples, but also to quantify the starting amount of the pathogen within each sample. The results indicate that site, year, and month, were all significant predictors of variance in *H. nelsoni* prevalence for the period tested. Presence/absence results of oysters as each site are shown below. In 2017, the DRE (sites JP and PI) also experienced a strong increase in severity of infection.

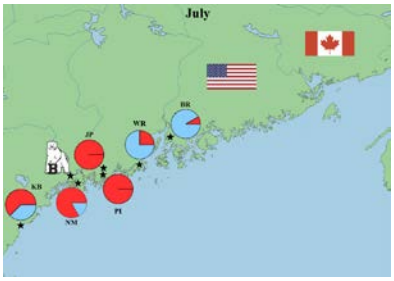
2016





2017





Oysters tested at sites located within the DRE (JP and PI), illustrated noticeably consistently higher levels of prevalence as well as seasonally patterned spikes. The high concentration of *H. nelsoni* in and around the DRE suggests that current quarantine measures may be successful in reducing the speed and potentially the geographic spread of the pathogen. The lack of prevalence of infection at BR and WR demonstrate the potential for infection to be influenced by salinity, temperature, and thus current patterns, concurring with other studies in the Delaware Bay. The cold temperatures, highly tidal, and highly saline waters that flow into the Penobscot Bay (BR and WR sites) are a result of the Eastern Maine Coastal Current that brings cold water from the Bay of Fundy into the Maine's Downeast bioregion.

Changes in frequency and severity of MSX infection may also be attributable to changes in weather patterns of the previous season. Moreover, the genomic architecture of oysters under selection, either naturally or in a laboratory setting, play an important part in understanding the severity of MSX infection in individual oysters and across reefs. In summation, this study exemplifies the need for further research into the pathogens life cycle and performing tests in order to draw a threshold of severity of infection such that the information afforded by qPCR can be better understood.

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