

Title:

Introduction:

Infectious diseases pose major threats to not only human health but economic sustainability and wildlife conservation [1]. Within the realm of infectious disease, is co-infection, which is prevalent in the wild [2]. *Magallana gigas*, commonly known as the Pacific Oyster, contends with Ostreid Herpesvirus (OsHV-1) every summer during what are called summer mortality events or Pacific Oyster Mortality Syndrome (POMS) that cause up to 90% mortality in farmed populations every year [3-5]. These summer mortality events are caused by a co-infection of OsHV-1 and varying *Vibrio* species. Without bacteria, OsHV1 does not allow for full expression of the disease [5]. The purpose of this study is to address the gap in research that is host-microbiome-pathogen interactions during a co- infection by comparing the abundance of bacteria on SEM micrographs of infected and healthy oyster gill tissues.

Methods:

*M. gigas* were collected from two locations- one known to have OsHV-1 present (Tomales Bay, CA) and one that does not (Humboldt Bay, CA). Oysters were dissected and transported in 70% ethanol to Cal Poly Humboldt. qPCR was done to determine presence of OsHV-1 in Tomales Bay samples. To photograph OsHV-1, oyster tissues were fixed, set in resin, and observed at 13,000x magnification using a transmission electron microscope. To compare bacterial abundance of infected and healthy oysters tissue was fixed, dried, mounted, sputter coated, and was observed under — using a scanning electron microscope.

Results:



Fig 1- OshV-1 found in *M. gigas* gill tissue at 13,000x

Sources:

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oyster microbiomes across oyster families exhibiting different levels of susceptibility to OsHV-1  $\mu$ var disease. *Frontiers in microbiology*, 10, p.473.