

Feature Review

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Characteristics of Disease Occurrence in Oyster Farming

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Abstract Oyster aquaculture is an important component of global marine fisheries, yet disease outbreaks have become a major constraint on its sustainable development. This paper systematically analyzes the characteristics of disease occurrence in oyster farming by integrating biological susceptibility, pathogen diversity, environmental drivers, transmission pathways, host immune responses, and epidemiological patterns. The results indicate that oysters are highly vulnerable to pathogenic infections due to their filter-feeding behavior and limited adaptive immune capacity. Bacterial diseases, particularly those caused by *Vibrio* species, are the most frequently reported, followed by viral, parasitic, and fungal infections. Environmental stressors such as elevated water temperature, salinity fluctuation, dissolved oxygen depletion, and eutrophication significantly increase disease incidence by weakening host immunity and promoting pathogen proliferation. High stocking density further accelerates disease transmission through waterborne pathways and aquaculture facility-mediated spread. In addition, microbial community dysbiosis plays a critical role in disease development and progression. A case study of intensive farming systems demonstrates that poor environmental management and inadequate biosecurity measures can lead to rapid disease outbreaks and substantial economic losses. Based on these findings, integrated disease management strategies combining ecological regulation, pathogen monitoring, and improved farming practices are proposed to enhance disease prevention and control in oyster aquaculture.

Keywords Oyster aquaculture; Disease occurrence; Pathogen dynamics; Environmental stress; Disease management

1 Introduction

Oyster aquaculture has become one of the most important components of global seafood production, expanding rapidly as demand for sustainable animal protein grows. Oysters are now among the most widely farmed molluscs, with several commercial species cultivated worldwide, and global output has climbed into the multi-million-tonne range as producers respond to rising consumer interest in nutritious seafood (Okon et al., 2023). Within this expanding sector, the Pacific oyster *Crassostrea gigas* dominates production and underpins the economies of many coastal regions; yet the industry remains highly vulnerable to disease, environmental change and management constraints that limit producers' ability to fully exploit growing markets (Botta et al., 2020; Petton et al., 2021). Over the past decade, infectious diseases have emerged as a central constraint on oyster farming, with repeated mass mortality events reported from major producing regions. In Pacific oysters, outbreaks associated with Ostreid herpesvirus 1 and *Vibrio* bacteria have intensified since 2008, increasing in both severity and geographic extent and making disease a particularly sensitive issue for producers (Alfaro et al., 2019). Pacific oyster mortality syndrome (POMS), driven by OsHV-1 μ Var and subsequent bacterial dysbiosis, has become panzootic and now affects juvenile oysters in multiple countries, illustrating how complex host-pathogen-environment interactions can produce recurrent, large-scale losses (Petton et al., 2021). The economic and social consequences of these disease events are profound, with massive mortalities sometimes causing near-total stock losses and threatening the viability of farms and coastal communities. For POMS alone, annual juvenile mortality in France has been estimated to exceed 35% of cultivated and natural oysters, illustrating the scale at which disease can erode production and income. At the broader aquaculture scale, diseases across species are estimated to cost billions of dollars annually, yet economic assessments remain sparse, underscoring the need for more systematic evaluations of losses and of the benefits of control strategies in oyster systems (Maezono et al., 2025). Against this backdrop, there is a pressing need to better characterize the patterns and drivers of disease occurrence in real farming contexts so that risk can be