

7.2 Identification of major pathogens and epidemiological dynamics

Across intensive systems, Pacific Oyster Mortality Syndrome (POMS) associated with Ostreid herpesvirus 1 microvariants (OsHV-1 μ Var) is the dominant cause of recurrent mass mortalities of *Crassostrea gigas* since 2008, often followed by opportunistic bacterial infections (Pernet et al., 2016). Epidemiological surveys also frequently implicate *Vibrio* spp., particularly *Vibrio aestuarianus* and other pathogenic vibrios, as co-factors or primary agents in some mortality events, with pathogen diversity contributing to variable clinical outcomes (Alfaro et al., 2019). Outbreak dynamics often follow a sequence in which OsHV-1 titres rise in oyster tissues before visible signs, peak around the mortality maximum, and are accompanied by shifts in bacterial communities towards known pathogenic genera (Richard et al., 2021). Environmental factors such as temperature thresholds and confinement influence both virus activation and bacterial proliferation, while host age, size, and genetic background modulate susceptibility, creating complex interaction patterns in intensive farms.

7.3 Evaluation of control measure effectiveness and economic losses

Because curative treatments and vaccination are not feasible, control in intensive oyster systems relies on risk-based husbandry, spatial planning and biosecurity, including movement restrictions and zoning, which can reduce infection pressure but have not prevented the global spread of OsHV-1 μ Var (Pernet et al., 2016). Adjustments in farming practices, such as optimizing stocking density, modifying culture structures or immersion regimes, and timing seeding to avoid high-risk temperature periods, have demonstrated reductions in mortality in some intensive settings. Economically, OsHV-1 microvariants have challenged the viability of Pacific oyster industries in both hemispheres, driving sector consolidation, loss of smaller farms, and shifts towards compensatory production strategies rather than purely technical disease solutions (Pernet et al., 2016; Fuhrmann et al., 2019). At a broader scale, marine diseases of farmed oysters and other aquaculture species impose economic burdens measured in billions of dollars annually, through direct losses, control costs, and regulatory compliance, underscoring the need for integrated, economically informed disease management in intensive oyster systems (Freitag et al., 2022).

8 Integrated Disease Management Strategies for Sustainable Oyster Farming

Ecologically informed farm placement and water-quality management can reduce disease risk. Spatial epidemiology of OsHV-1 shows that mortality is highest in inshore, high-biomass intertidal farming zones and decreases offshore, where better food quality and lower turbidity align with improved oyster health, indicating that maintaining good ecological status of coastal waters is a practical disease-mitigation strategy. Broader ecosystem-based perspectives argue that sustainable aquaculture must explicitly integrate organism health, environmental integrity, and human health, embedding disease control in wider ecosystem and food-system planning. Well-designed oyster culture can also act as a regulating service, filtering pathogens and reducing disease pressure on wild stocks when harvests occur before infected farmed oysters shed large quantities of parasites. At the farm scale, healthy-farming models emphasize carrying-capacity assessment, climate-change adaptation, and use of habitat features (e.g. mangroves, ecological floats) to buffer environmental stress and disease risk.

Selective breeding provides a powerful tool to reduce disease impacts where environmental control is limited. Reviews of breeding programmes show significant gains in resistance to major oyster pathogens (OsHV-1, *Haplosporidium nelsoni*, *Roseovarius crassostreae*, *Marteilia sydneyi*) after only a few generations, demonstrating that resistance is heritable and can be exploited to stabilize production. Family-based experiments in Pacific oysters confirm a strong genetic basis for resistance to OsHV-1 across life stages and show that improving OsHV-1 resistance does not compromise resistance to *Vibrio aestuarianus*, supporting multi-trait resistance breeding. Field mass-selection programmes have achieved dramatic survival improvements under OsHV-1 pressure, with selected lines of *Crassostrea gigas* reaching about 69% survival compared with 7% in controls after four generations, while also improving growth and yield. More recently, genomic selection has been shown to further accelerate gains in resistance to vibriosis, with genomic breeding values enabling discrimination between resistant and susceptible oysters and producing double-digit increases in survival and survival time in progeny, indicating a route to faster development of robust seedstock.