

Key outcomes from VIVALDI on preventing and mitigating bivalve diseases

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The European shellfish industry is a major contributor to global production of marine bivalves. Its success depends a great deal on high environmental quality and susceptibility to mortality events, often linked to pathogenic organisms such as viruses, bacteria and parasites (protozoa).

In this context, the European project VIVALDI has developed tools and approaches with a view to better preventing and controlling marine bivalve diseases. 21 partners, research institutes, universities and SMEs, from 10 countries in Europe and beyond, have been cooperating in VIVALDI with the common objective of improving the competitiveness and sustainability of the shellfish industry.



Improved knowledge of pathogens:



OsHV-1 diversity informs us about its host range, geographic distribution and origin.

New pathogens characterised (e.g. *Rickettsia*-like Endozoicomonas).

Passive sensors or Magnetic Beads improve **pathogen detection**.

Interactions with the environment :



Environmental parameters influence disease development (e.g. temperature, acidification, UV-B, presence of macro algae...).

Plankton organisms involved in transmission and outcome of bacterial diseases in oysters.

Disease **transmission models** established in key sites monitored in VIVALDI.

Host defence mechanisms:



Identification of key **biological pathways** (e.g. autophagy pathway and Warburg effect) and **antimicrobial peptides** involved in bivalve defence mechanisms.

Description of **tissular distribution of pathogens** and associated **lesions** during an infection.

Stimulating **bivalve immunity** is possible by exposure to different immuno-stimulant molecules.

Disease management measures :



Optimal **husbandry practices** locally adapted have been identified.

Efficiency of **UV-based technology** to inactivate pathogens and remove oyster gametes from the wastewater.

Risk-ranking shellfish farm models are helpful to implement risk-based surveillance of shellfish diseases.

Breeding programmes:



Oyster and clam families produced and challenged regarding their susceptibility to pathogens.

Massive **genotyping approach** to identify genomic regions associated with resistance/tolerance to OsHV-1. Effective **optimisation of breeding programmes** using parentage assignation tools and simulation studies.

Sharing information:



Mapping stakeholders and analysing their relationships.

Sociological interviews and focus discussion groups to **understand their perception**.

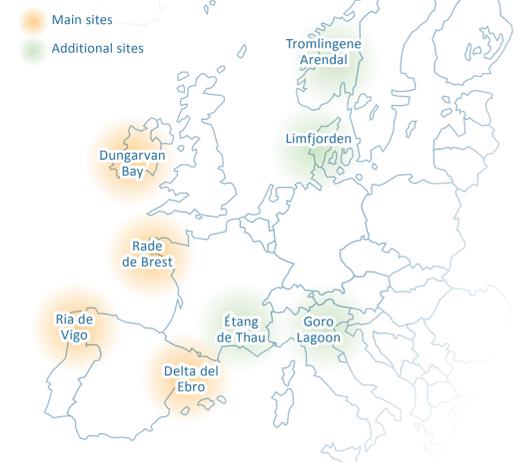
Co-building a biosecurity manual with stakeholders.

VIVALDI Consortium



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Study sites



www.vivaldi-project.eu

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