

VIVALDI: A year of research for preventing and mitigating farmed bivalve diseases

Arzul I¹, Feist S², Figueras A³, Lapègue S¹, Paillard C⁴, Furones D⁵

¹Ifremer, SG2M-LGPMM, La Tremblade, France, ²CEFAS, Weymouth Laboratory, Weymouth, UK, ³Instituto Investigaciones Marinas, CSIC, Vigo, Spain, ⁴LEMAR, UMR CNRS 6539, IUEM, Technopôle Brest-Iroise, Plouzané, France, ⁵IRTA, Sant Carles de la Ràpita, Spain

The European shellfish production, which mostly relies on mussels, oysters and clams, is a promising and dynamic sector, whose growth has unfortunately been hindered over the recent years by mortality events, linked to pathogen organisms. The EU project VIVALDI is a 4-years Horizon 2020 project, involving 21 partners, and aiming at better preventing and controlling marine bivalve diseases. VIVALDI will bring new knowledge on the interactions between shellfish, environment and pathogens. It will develop practical tools and approaches to better prevent and control the pathogens affecting the main European farmed shellfish species: oysters (*Crassostrea gigas* and *Ostrea edulis*), mussels (*Mytilus edulis* and *M. galloprovincialis*), clams (*Venerupis philippinarum*) and scallops (*Pecten maximus*). The project addresses the most harmful pathogens affecting these species: the virus Ostreid herpesvirus 1 (OsHV-1), *Vibrio* species (e.g. *V. aestuarianus* and *V. tapetis*) as well as micro-eukaryotes such as the parasites *Perkinsus olseni* and *Bonamia ostreae*.

Key sampling sites in VIVALDI: The main sampling sites have been chosen for their contrasted features and with a view to represent at best the diversity of the EU shellfish production, allowing the partners to gather samples from the main bivalves studied in the project: Dungarvan Bay (IE), Ria de Vigo and Delta del Ebro (ES) and Rade de Brest (FR).

Progress achieved in 2016: The project started in April 2016, first results have been achieved in understanding the diversity of pathogens in bivalve populations and in their detection thanks to the elaboration of passive sensors. These tools are currently being tested for the detection of OsHV-1 in the natural environment. Genes involved in some key pathways including the Warburg metabolism and autophagy have been identified in *C. gigas* in response to an infection with OsHV61. Novel TIR-DC protein families known to play a key role in the regulation of the inflammatory response and the production of antimicrobial effectors have also been identified in *M. galloprovincialis*. Finally, in order to improve the dialogue among the parties affected by shellfish diseases and to disseminate results of the project, a mapping of stakeholders is currently under way.

Funding of presentation:

European Union's Horizon 2020 Research and innovation programme under grant agreement N°678589.