

## Genetic diversity of the Ostreid Herpesvirus type 1

**Camille Pelletier<sup>1\*</sup>, Germain Chevignon<sup>1</sup>, Maude Jacquot<sup>1</sup>, Serge Heurtebise<sup>1</sup>, Nicole Faury<sup>1</sup>, Lionel Degremont<sup>1</sup>, Jean-Michel Escoubas<sup>2</sup>, Jean Delmotte<sup>2</sup>, Elise Maurouard<sup>1</sup>, Tristan Renault<sup>3</sup>, Benjamin Morga<sup>1</sup>.**

<sup>1</sup> Ifremer, Unité Adaptation Santé des Invertébrés Marins, Avenue du Mus de Loup 17390 La Tremblade, France

<sup>2</sup> IHPE, Univ. Montpellier, CNRS, Ifremer, UPVD, 34095 Pl. Eugène Bataillon Bâtiment 24, 34090 Montpellier, France

<sup>2</sup> Ifremer, Département Ressources Biologiques et Environnement, 44311 Cedex 03, Rue de l'Île d'Yeu, 44980 Nantes, France

camille.pelletier@ifremer.fr

The use of next generation sequencing (NGS) is essential for studying and monitoring pathogens in bivalve mollusks in order to anticipate the emergence of new genotypes or species. The improvement of knowledge and approaches to characterize their genome allows for a better understanding of their life cycle, host interactions, and capacity for adaptation or evolution.

Ostreid Herpesvirus 1 (OsHV-1), a pathogen of the Pacific oyster *Crassostrea gigas*, is responsible for significant mortality of larval and juvenile oysters each year. The study of its genome is complicated by the inability to culture the virus in vitro. Currently, 52 OsHV-1 genomes are available in public databases. This emphasizes the need for the development of diversity and phylodynamic analyses, which are key elements in understanding the spatial and temporal viruses diffusion.

Through the use of "ultra-deep" short-read sequencing on individual moribund oysters, combined with a new bioinformatics pipeline, 440 de novo OsHV-1 genomes were assembled. By combining the genetic variations quantification, phylogenetic analysis, and ancestral state reconstruction of discrete traits, the connectivity of OsHV-1 viral populations between oyster farming areas was assessed. The results suggest that some oyster aquaculture areas have higher OsHV-1 diversity than others. The phylogenetic study indicates samples clustering according to host, location, and time. This work demonstrates that phylodynamic approaches can be applied to aquatic DNA viruses to determine how epidemiological, immunological, and evolutionary processes act and interact on viral diversity.