



Vivaldi Project

Data management plan

*Tolerance and resistance to OsHV-1 infection in
Crassostrea gigas*

30/03/2020

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	IFREMER
Data category	Phenotypic markers (host)
Concerned WP	WP3 <i>Choisissez un élément.</i> <i>Choisissez un élément.</i>
Name of the VIVALDI referent(s)	Phenotypic markers (host): Florian Enez & Christine Paillard
Reference of the dataset <i>Please refer to the DMP table to find the appropriate reference.</i> <small>Ex: Genome-Patho/SubTaskN*/Pathogen/PartnerN*</small>	Phenotypic-Marker-Host/3.2.1/Crassostreagigas/IFREMER
Description of the data	<i>DNA OsHV-1 copies in live oysters sampled in 2016 and 2017 and survival of the families produced in 2016 and 2017</i>
Type	Tabular files
Period and frequency of data collection	<i>Survival data were collected from May to July in 2016 and in 2017. The detection and quantification occurred in June/July 2016 and 2017</i>
Geographical site of data collection (if applicable)	<i>All oyster families were produced at our hatchery in La Tremblade. Experimental infection was done in a quarantine room at the Ifremer laboratory in La Tremblade, while field testing occurred in our experimental oyster farms in La Floride (France),</i>
Description of the material from which the dataset is generated <i>Information will be obtained from individuals, which can come from natural/hatchery population and/or from family produced in hatchery. Animals can be infected (naturally or experimentally). DNA extraction can be done from the whole animal, tissue.</i>	<i>All families were produced from previously selected oyster lines developed by Ifremer La Tremblade (from 2009 to 2015). Experimental infection by OsHV-1 was done at Ifremer in La Tremblade. All individuals used for the detection and the quantification of OsHV-1 were sampled during a mortality outbreak in our oyster farms in La Floride.</i>
Protocols <i>Example: 16S ribosomal RNA gene sequencing by NGS</i> Please refer to the DMP table* for more examples	<i>Oysters production in hatchery Experimental infection by OsHv-1 Field evaluation during the summer when OsHV-1 mortality outbreaks occurs Biopsy of oysters for selection on resistance/tolerance to OsHV-1 infection, and production of a new generation to evaluate the response to selection</i>



<p>Nature of the collected/generated data <i>Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed data set will be .vcf/.bed formats.</i> Please refer to the DMP table* for more examples</p>	<p><i>Excel spreadsheets</i></p>
<p>Coverage (if applicable) <i>Example: random genomic regions covered at 50 X</i> Please refer to the DMP table* for more examples</p>	<p><i>N/A</i></p>
<p>What are the prerequisites allowing to use the data as such? <i>Example: Any person able to use .fastqc file and .fasta file</i> Please refer to the DMP table* for more examples</p>	<p><i>None</i></p>
<p>Sharing of main data</p>	<p><i>Saved and shared after publication</i> <i>Please specify</i></p>
<p>Archiving and preservation <i>Example: data will be stored on a hard drive + online back up and then will be released on public database (Sinoe, Dryad) after publication.</i> Please refer to the DMP table* for more examples</p>	<p><i>All data are saved on Ifremer servers</i></p>
<p>List, description and storage of associated data (metadata) <i>Examples: environmental data, mortality monitoring, genotyping...</i></p>	<p><i>Pedigree is stored on Ifremer servers.</i></p>
<p>Sharing of metadata (if relevant)</p>	<p><i>Saved and shared after publication</i> <i>Please specify</i></p>