



Vivaldi Project

Data management plan

Phenotypic markers on Crassostrea gigas

Key words: biometry, OsHV-1 analysis & Environmental data, Crassostrea gigas at juvenile stage, Thau Lagoon

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	IFREMER
Data category	Phenotypic markers (host)
Concerned WP	WP5
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/ WP5-1.2/C.gigas-Juveniles/Ifremer
Description of the data	Biometry measures: Length, total, shell & flesh weights, condition index (AFNOR), OsHV-1 concentrations
Type	Tabular files
Period and frequency of data collection	2017: 1 Site, 9 dates, 3 lanterns, 10 ind: N= 270 Oysters were collected weekly
Geographical site of data collection (if applicable)	2017: at the Marseillan Ifremer table in Thau lagoon
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>	Oysters (2n) <i>Crassostrea gigas</i> juveniles originated from Marrennes Oléron (settling in august 2016). Oysters have been individually frozen at -80°C for qPCR analysis. DNA extraction has been carried out on total flesh from some oyster samples to determine <i>OsHV-1</i> DNA concentration in tissues (9 dates, 3 lanterns, 1 pool of three oysters, n = 27). DNA samples were stored at -80°C in LDV34, flesh were stored at -80°C at the Sete Ifremer
Protocols <i>Example: 16S ribosomal RNA gene sequencing by NGS</i> Please refer to the DMP table* for more examples	<i>Protocols will be described in the publications</i>
Nature of the collected/generated data <i>Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed datas set will be .vcf/.bed formats.</i> Please refer to the DMP table* for	Raw data set (.xls)



more examples	
Coverage (if applicable) <i>Example: random genomic regions covered at 50 X</i> Please refer to the DMP table* for more examples	<i>Unique measurement of each sample</i>
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	<i>Any person able to use tabular file</i>
Sharing of main data	<i>Saved and shared after publication</i>
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	<i>the data are archived in the Q hard drive of the Ifremer Institute. When data will be published, database could be public via Sinoe.</i>
List, description and storage of associated data (metadata) <i>Examples: environmental data, mortality monitoring, genotyping...</i>	<i>OsHV1 DNA concentration in tissues and in filters (0.2, 3 & 20 µm) Environmental data (Temperature, Salinity, Chlorophyll a,b,c biomass inside and outside farms, see D5-2)</i>
Sharing of metadata (if relevant)	<i>Saved and shared after publication</i>

*To access the [DMP table](#), please login on the VIVALDI online platform

Once completed, this sheet has to:

1. Be sent to the referent(s) identified above for a final check
2. Be uploaded on the [VIVALDI online platform](#)

