



Vivaldi Project

Data management plan

Phenotypic markers (host)

Keyword : field experiments, oysters, *Crassostrea gigas*,
biometry, OSHV-1

20/05/2019

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	SYSAAF
Data category	Phenotypic markers (host)
Concerned WP	WP3
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>	<i>Phenotypic-Marker-Host/3.2.1/Crassostreagigas/SYSAAF</i>
Description of the data	Individual data collected on oysters after growing in 1 field sites exposed to OsHV-1 (Vendée batch) and 1 site less impacted by OsHV-1 (Normandy batch) up to commercial size.
Type	Tabular files
Period and frequency of data collection	Data were collected from to 19/11/2018 to 23/11/2018 for Vendée batch and from 08/04/2019 to 12/04/2019 for Normandy batch.
Geographical site of data collection (if applicable)	Measurements took place in Bouin, France (LAT 46.949417 ; LONG -2.050798).
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>	Measured animals were produced with 70 males and 70 females in April 2016. They were transferred to the field in Vendée and Normandy in July 2016. Biometries (lengths, weight, picture, shell weight, flesh weight) and DNA sampling were performed from 2.5 to 3 years old depending on site. 1253 and 1401 individuals were analysed from Vendée and Normandy respectively.
Protocols <i>Example: 16S ribosomal RNA gene sequencing by NGS</i> Please refer to the DMP table* for more examples	Animals were brought from the field a few days before sampling days and stocked in tanks. All measures were performed one after the others and were collected in the software Infaqua. Traceability has been ensured by individual electronic identification.
Nature of the collected/generated data <i>Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic</i>	Tabular files

<p>information, and processed data set will be .vcf/.bed formats. Please refer to the DMP table* for more examples</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>	N/A
<p>What are the prerequisites allowing to use the data as such? <i>Example: Any person able to use .fastq file and .fasta file</i> Please refer to the DMP table* for more examples</p>	Anybody that is able to use xls files.
<p>Sharing of main data</p>	Saved and shared after publication Please specify
<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>	Data is stored in the Infaqua database from the Vendée Naissain. One copy is stored in the SYSAAF's server.
<p>List, description and storage of associated data (metadata) <i>Examples: environmental data, mortality monitoring, genotyping...</i></p>	Pedigree is stored in the Infaqua database from the SATMAR. One copy is stored in the SYSAAF's server.
<p>Sharing of metadata (if relevant)</p>	Saved and shared after publication Please specify

*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](#)

