Vivaldi Project

Data management plan

Phenotypic markers (host)

Keyword : field experiments, Manilla clams, *Ruditapes Philippinarum*, biometry, *V. tapetis*, *Perkinsus olseni*

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 *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	*Phenotypic-Marker-Host/3.2.2/Ruditapesphilippinarum/SYSAAF*

Description of the data	Individual data collected on Manilla clams after growing in 3 field sites (Venice lagoon, Marennes, Chausey) up to commercial size.

Type	Tabular files

Period and frequency of data collection	Data were collected from to 10/09/2018 to 13/09/2018 for Venice lagoon batch, from 26/11/2018 to 28/11/2018 for Marennes batch and from 11/03/2019 to 14/03/2019 for Chausey batch.

Geographical site of data collection (if applicable)	Measurements took place in Chioggia, Italy, for Venice lagoon batch (LAT 45.223382 ; LONG 12.284471) and in Rennes, France, for Marennes and Chausey batches (LAT 48.118032 ; LONG -1.640493).

Description of the material from which the dataset is generated *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.*	Measured animals were produced with 56 males and 53 females in May 2016. They were transferred to the field in Marennes and Chausey in June 2016, then in Venice lagoon in September 2016. Biometries (lengths, weight, picture, shell weight, flesh weight) and DNA sampling were performed from 2.5 to 3 years old depending on site. For Venice lagoon batch, gill samples were collected in addiction to quantify *Perkinsus olseni*. For Chausey batch, extra-palleal fluids were collected for DNA extraction and quantification of *V. tapetis*. 1051, 1016 and 1048 were analysed from Venice lagoon, Marennes and Chausey respectively.
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS* **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	Tabular files

data *Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed datas set will be .vcf/.bed formats.* ***Please refer to the DMP table* for more examples***	
Coverage (if applicable) *Example: random genomic regions covered at 50 X* ***Please refer to the DMP table* for more examples***	N/A
What are the prerequisites allowing to use the data as such? *Example: Any person able to use .fastqc file and .fasta file* ***Please refer to the DMP table* for more examples***	Anybody that is able to use xls files.
Sharing of main data	Saved and shared after publication Please specify
Archiving and preservation *Example: data will be stored on a hard drive + online back up and then will be released on public database (Sinoe, Dryad) after publication.* ***Please refer to the DMP table* for more examples***	Data is stored in the the Infaqua database from the SATMAR. One copy is stored in the SYSAAF's server.
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	Pedigree is stored in the the Infaqua database from the SATMAR. One copy is stored in the SYSAAF's server.
Sharing of metadata (if relevant)	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**