Vivaldi Project

Data management plan

Hemomicrobiote from the oyster Crassostrea gigas

02/07/2018

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*CNRS*

Data category	*Microbiome (bivalve)*

Concerned WP	*WP4* *Choisissez un élément.* *Choisissez un élément.*

Name of the VIVALDI referent(s)	*Microbiome: Alberto Pallavicini*

Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°	*Microbiome-bivalve/4.1.1/Crassostrea_gigas/2*

Description of the data	NGS; Metabarcoding 16S and 18S and metagenomics

Type	*Sequences*

Period and frequency of data collection	Three sets of data were collected

Geographical site of data collection (if applicable)	Ifremer facilities Argenton and Thau lagoon (2 periods).

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.*	Oyster hemolymph
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS* **Please refer to the DMP table* for more examples**	16S ribosomal RNA gene sequencing by NGS 18S ribosomal RNA gene sequencing by NGS MiSeq (paired ends) metagenomics

Nature of the collected/generated data *Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed datas set will be .vcf/.bed formats.*	Raw dataset (*fastq* format).

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***	*large*
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***	Any person able to use *fastq* 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 will be stored and released on public database (NCBI BioProject PRJNA381401) after publication
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	Metadata files contain all available information related to: the oysters used in this study (genitors origins, families production and ages, etc.), the environmental conditions (location, water temperature, time of transplantation, mortality monitoring, etc.), material and methods used for the production and analyses of metadata (metabarcoding and metagenomics). All these metadata will be available in both the SRA bioproject (to be released after publication) and the associated publication (in preparation).
Sharing of metadata (if relevant)	*Saved and shared after publication* *All data will be available with the publication*

*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**