Vivaldi Project

Data management plan

Name of the dataset
FASTQ_Generation_2019-04-03_01_50_33Z-172143005
101_L001-ds.c49d2ff2360e44f49123068bd729f97b

Bacteriome . Crassostrea gigas . Biotic interactions . Macroalgae . Oyster survival

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	UNIGE

Data category	Microbiome (bivalve)
	Microbiome (env)

Concerned WP	WP1
	WP4
	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/SubTaskN°/BivalveHostSpecies/PartnerN° Microbiome-Env/SubTaskN°/EnvironmentalData/PartnerN°

Description of the data	Sequencing of bacterial diversity in bivalves, water and macroalgae.

Type	Sequences

Period and frequency of data collection	DNA extraction performed from October 2018 to February 2019 for 292 samples. Sequencing carried out in March 2019.

Geographical site of data collection (if applicable)	Oyster came from the IFREMER experimental station of Bouin (France, 46°57' N, 2°02 O).

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.	Bacterial diversity information was obtained from the analysis of DNA extracted from samples collected during a survival monitoring experiment. The dataset generated comes from bacterial DNA extraction in water samples, algal samples and oyster samples. Four months old oyster, produced in hatchery, have been acclimated to different types of algae to test the potential effect on their survival facing the virus OsHV-1. Natural populations of algae have been gathered on the field in Anse du Roz (France, Logonna-Daoulas, 48°19'N, 4°19'W). Water used in the experiment was directly sampled from the experimental tanks.
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 (bivalve associated microbiome and environmental microbiome).

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. **Please refer to the DMP table* for more examples**	Raw dataset in .fasta format for genomic information suitable for metabarcoding analyses.

Coverage (if applicable) *Example: random genomic regions covered at 50 X* ***Please refer to the DMP table* for more examples***	
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 in VIVALDI able to use .fasta files.*
Sharing of main data	*Saved and shared after publication*
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 by each partner and then will be released on genebank once it will have been published.*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*Any data associated with the main generated/collected data, such as environmental data, mortality rates, genotyping… These can be data that are obtained on the same biological material, but not used in the context of the project.*
Sharing of metadata (if relevant)	*Saved and shared after 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**