

Vivaldi Project

Data management plan

Diversity and stability of bacterial microbiota associated to healthy and diseased *Crassostrea gigas* oysters

02/07/2018



DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	CNRS
raither name	CNAS
Data category	Microbiome (bivalve)
C	14/DA
Concerned WP	WP4 Choisissez un élément.
	Choisissez un élément.
Name of the VIVALDI referent(s)	Microbiome: Alberto Pallavicini
Reference of the dataset	Microbiome-bivalve/4.2/Crassostrea_gigas/2
Please refer to the DMP table to find	Wilciobioffie-bivarve/4.2/Crassostrea_gigas/2
the appropriate reference.	
Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°	
	NGS; Metabarcoding 16S
Description of the data	
Туре	Sequences
.,,,,	
Period and frequency of data	5 datasets were collected (controled condition Argenton facilities –
collection	Thau lagoon (infectious and non-infectious periods) – Atlantic ocean
	(infectious and non-infectious periods)
Geographical site of data	Ifremer facilities Argenton, Thau lagoon (2 periods) and Atlantic
collection (if applicable)	ocean (2 periods)
Description of the material from	16S bacterial microbiota sequencing for 12 individual oysters for 5
which the dataset is generated	families (contrasted susceptibilities to summer mortalities) and for 5
Information will be obtained from	sites/periods – samples of filtered seawater
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.	
done from the whole diffinal, tissue.	
Protocols	Standards/protocols = Standard protocol for 16S
Example: 16S ribosomal RNA gene sequencing by NGS	ribosomal RNA gene (V3V4) amplicon sequencing by NGS (MiSeq illumina 2x250)
Please refer to the DMP table* for	NGS (MISEY IIIUIIIIII 2X2SO)
more examples	
Nature of the collected/generated	Raw datasets paired-end sequencing (fastq format R1+R2)
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	30000 seq / sample
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	Archiving Raw sequence data have been deposited in the SRA database (BioProject ID PRJNA419907) and will be released after publication
List, description and storage of associated data (metadata) Examples: environmental data, mortality monitoring, genotyping	The metadata file contains all available information related to the animals used in this study: family of origin, origin of genitors (Atlantic or Mediterranea, farming or non-farming area), experimental/environmental condition at the time of microbiota analysis (hatchery or site of transplant, infectious or non-infectious period, seawater temperature). All these metadata will be available in both the SRA bioproject (to be released after publication) and the associated publication (currently submitted to PCI Ecology) Associated metadata will be available after publication. The metadata file contains all available information related to the environmental data for this study: sample type, season, GPS data. All these metadata will be available in both the SRA bioproject (to be released after publication) and the associated publication (currently submitted to PCI ECOLOGY)
Sharing of metadata (if relevant)	Saved and shared after publication
	All data will be available with the publication

^{*}To access the <u>DMP table</u>, 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