Vivaldi Project

Data management plan

Microbiome (bivalve)
Key words: Crassostrea gigas gigas, DNA, Bacterial diversity, vibriome

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	MI

Data category	Microbiome (bivalve)

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°1.2.1/Oyster/PartnerN°8-11-13

	Microbiota and Pathobiota (vibriome) NGS analysis
Description of the data	16SrDNA sequence (Microbiota) and phylogenetic and virulence markers *sequences (Pathobiota-Vibriome)*
Type	Sequences
Period and frequency of data collection	Samples has been collected the 5th July 2016 (20% mortalities), 3rd October 2016 (end of mortalities), 10th January 2017 (control)
Geographical site of data collection (if applicable)	Samples were collected in Dungarvan Bay.
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*	Bacterial diversity and/or vibriome information will be obtained from the analysis of DNA extracted from C gigas collected in selected aquaculture sites and periods Contrasted (eg healthy and diseased) bivalve samples (*Crassostrea gigas*) were collected in different seasons before, during and after the occurrence of abnormal mortality episodes in Dungarvan Bay, Ireland. DNA from single animals was extracted from whole homogenate of the bivalve tissues using commercial kit with a protocol agreed by VIVALDI partner Samples were preliminary screened for the presence of Ostreid herpesvirus 1 (OsHV-1) and *Vibrio aestuarianus* by real-Time PCR based methods (Webb et al, 2007; IFREMER, 2013)

extraction can be done from the whole animal, tissue.	
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS* **Please refer to the DMP table* for more examples**	*16S ribosomal RNA (V4 region) gene sequencing by NGS (Microbiota)* *Target Enrichment next generation sequencing protocol for the analysis of the Bivalve Pathobiota (TEBP protocol) (Pathobiota-Vibriome)*
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 .fastqc format*
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**	*Any person able to use .fastqc file*
Sharing of main data	Saved and shared after publication
	Please specify
Archiving and preservation *Example: data will be stored on a hard drive*	*Hard drive and cloud service. We maintain at least 2 copies of the files in different locations (Trieste and Genova).*

+ online back up and then will be released on public database (Sinoe, Dryad) after publication. **Please refer to the DMP table* for more examples**	
List, description and description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*Samples provided by MI,* *DNA extracted and amplicons libraries produced by UNIGE* *DNA sequencing performed by UNITS*
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**