

Vivaldi Project

Data management plan

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





family produced in hatchery. Animals can

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	UNITS
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 ^v /Pathogen/Partn erN ^o	Microbiome-bivalve/SubTaskN°1.2.1/MusselClamOyster/PartnerN°12-13
	16S sequencing from contrasting animals
Description of the data	
Туре	Sequences
Period and frequency of data collection	Samples has been collected the 10 th July (mortalities) and 5 th October 2017
	Samples were collected in different Italian seas after an alert of bivalve mortality.

Bacterial diversity and/or vibriome information will be obtained from the analysis of DNA **Description of the** extracted from bivalves collected in italian aquaculture sites. The samples from the material from abnormal mortality in Italy where initially analysed by total bacterial count, then cultured on TSA2% plates and colonies analysed by MALDI-TOF The histology analysis was done on which the dataset is generated digestive glands looking for bacteria and parasites. DNA was extracted from the whole Information will be homogenate.. no common difference could be noticed between dying and non-dying obtained from populations individuals, which can come from natural/hatchery population and/or from





Preventing and mitigating farmed biva

be infected (naturally or experimentally). DNA 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
Natura of the	Paw datasat in fastor format
Collected/generat ed 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	Any person able to use .fastqc file
Sharing of main data	Saved and shared after publication
	Please specify
Archiving and preservation	Raw sequences will be preserved in the server devoted for data storage at the Department of Life Sciences (UNITS). In case of publication data will be submitted to public sequence





DMP table* for more examples	
Samples provided by UNIPD, DNA extracted and amplicons libraries produced by UNITS DNA sequencing performed by UNITS	
List, description Species No. Location Date T Salinity Estimat and storage of [%]	ed ty
associated data Mytilus 180 La Spezia 06/03/201 13.5° 36-38/1000 80%	
(metadata) Examples: <i>Crassostrea gigas</i> ≈100 Scardovari 18/05/201 21°C 27-28/1000 70-809	6
environmental data, Tappes 180 Laguna di 28/05/201 19.6° 10.52/1000 - philippinarum Barbamarco 5 C	
genotyping Tappes 180 Laguna di 09/07/201 28°C 33% 15%	
Chamelea gallina 90 Transetto 7 11/07/201	
Chamelea gallina 90 Transetto 4 San 11/01/201	
Chamelea gallina [†] 90 Cupra Marittima 11/01/201	
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 <u>VIVALDI online platform</u>

