Vivaldi Project

Data management plan

Phenotypic markers on Crassostrea gigas

Key words: biometry, pathogen analysis & Environmental data, Crassostrea gigas at adult stage, Thau Lagoon

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*IFREMER*
Data category	*Phenotypic markers (host)*
Concerned WP	*WP5*
Name of the VIVALDI referent(s)	*Phenotypic markers (host): Florian Enez & Christine Paillard*
Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	Phenotypic-Marker-Host/ WP5-1.2/C.gigas-Adults/Ifremer
Description of the data	Biometry measures: Length, total, shell & flesh weights, condition index (AFNOR) + V. aestuarianus and V. splendidus DNA concentration
Type	*Tabular files*
Period and frequency of data collection	2016 (8 June to 8 August: oyster on ropes: 2 sites, 5 dates, 10 ind (n= 100) + oysters in shellfish farmer tanks: N=10) + 2017 (8 June to 13 September: oyster on ropes: 1 site, 7 dates, 10 ind (n = 70), 21 June to 5 July 2017: oysters in bags: 1 site, 6 dates, 3 bags, 3 ind (n = 54)) Oysters were collected weekly in 2016 & 2017 at the exception of the sampling done in bags during which sampling frequency was higher
Geographical site of data collection (if applicable)	2016: Two rearing tables in the Thau lagoon, France (TT, TL noted N and S respectively in the D5-2 delivrable) 2017: one rearing table (TT, ie. N) + stocking table (B in D5-2) where bag were suspended (named “poche” in data file)
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.*	Oysters (3n) *Crassostrea gigas* of commercialized size originated from farming site. Oysters have been individually frozen at -80°C for qPCR analysis. DNA extraction has been carried out on gills and mantle from some oyster samples to determine *V. aestuarianus* and *V. splendidus* DNA concentration in tissues (2016: ropes N=96 + 15 oysters from shellfish farmer tanks (N=10), 2017: Bag: 1 site, 3 dates, 3 replicats (n=9). DNA samples were stored at -80°C in LDV34, flesh were stored at -80°C at the Sete Ifremer
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS*	*Protocols will be described in the publications*

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Please refer to the DMP table* for more examples	
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 data set (.xls)*
Coverage (if applicable) *Example: random genomic regions covered at 50 X* ***Please refer to the DMP table* for more examples***	*Unique measurement of each 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 tabular file*
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***	*the data are archived in the Q hard drive of the Ifremer Institute. When data will be published, database could be public via Sinoe.*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*V. aestuarianus* and *V. splendidus* DNA concentration in tissues Environmental data (2016 & 2017: Temperature, Salinity, oxygen, chlorophyll a,b,c biomass at TT (N), TL (S) and C (outside farms, see D5-2)
Sharing of metadata (if relevant)	*Saved and shared after publication*

*To access the DMP table, please login on the VIVALDI online platform

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