Vivaldi Project

Data management plan

Crassostrea gigas response to Vibrio tasmaniensis and Vibrio crassostreae

Dual RNAseq
Oyster response to vibrios

30/05/2019

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*CNRS*
Data category	*Transcriptome (host)*
Concerned WP	*WP2*
Name of the VIVALDI referent(s)	*Transcriptome: Beatriz Novoa & Paola Venier*
Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	*Transcriptome-host/2.1.1/oyster/CNRS_IHPE*
Description of the data	*The response of oysters C. gigas to virulent/non-virulent vibrios of the Splendidus clade was evaluated by RNAseq on oysters infected with two virulent and two non-virulent strains of the Vibrio spendidus clade. Material was one full-sib family of oysters susceptible to wild infections and to pathogenic vibrios of the Splendidus clade. The oyster and bacterial responses to infection were compared before mortalities occurrence and 8h after infection.*
Type	*Sequences*
Period and frequency of data collection	Control and treated oysters sampled at 8 h after infection
Geographical site of data collection (if applicable)	*France*
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.*	*A biparental family of oysters (Decipher #14). Whole tissues.*
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS* **Please refer to the DMP table* for more examples**	*NGS sequencing of polyA extracted from infected and non-infected oysters. Illumina, Paired end. Fasteris.*
Nature of the collected/generated data	*fastq*

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***	*25 millions reads per 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 .fastqc file and .fasta file*
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***	*SRA database:* *BioProject accession number PRJNA515169* *SRA accessions SRR8551076-SRR8551093*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	
Sharing of metadata (if relevant)	*No relevant*

*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**