Vivaldi Project

Data management plan

Responses of vibrios (Harveyi clade) to C. gigas colonization

Dual RNAseq
Bacterial response to oyster colonization in the presence/absence of OsHV-1 virus

30/05/2019

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*CNRS*

Data category	*Transcriptome (pathogen)*

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-pathogen/2.1.1/vibrio/CNRS_IHPE*

Description of the data	*The response of vibrios to colonization was evaluated by RNAseq on oysters infected with 18 strains of the Harveyi clade (both virulent and non virulent) and in the presence/absence of OsHV-1. Material was one full-sib family of oysters susceptible to wild infections. The oyster and bacterial responses to infection were compared before mortalities occurrence at 0, 4, 24 and 48h after infection.*

Type	*Sequences*

Period and frequency of data collection	*0, 4, 24 and 48h after infection.*

Geographical site of data collection (if applicable)	*n/a*

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.* **Protocols** *Example: 16S ribosomal RNA gene sequencing by NGS* **Please refer to the DMP table* for more examples**	*A biparental family of oysters (La Tremblade H12)* Strain from the Harveyi clade *V. harveyi* O-A01, O-G11, O-D03 *V. rotiferianus* O-G05, O-E12, O-G10, O-B06, O-F05 *V.owensii* O-D04, Z-B04, F1-D04, O-A03, ZG08 *V. jasicida* F5-G08, F5-H11, F5-A12, F1-C08 *The strain RNAs were sequenced within the host tissues (whole tissue extracts)* *NGS sequencing of ribo-depleted RNA (Nugen technology) extracted from infected and non-infected oysters. Sequencing Novaseq 2x50 bp. 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**	*100 millions paired-end 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*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	Cliquez ici pour taper du texte.
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**