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Vivaldi Project

Data management plan

***Vibrio tasmaniensis* and *Vibrio crassostreae response to C. gigas colonization***

***Dual RNAseq***

***Bacterial response to oyster colonization.***

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* |
|  |  |
|  | *The response of virulent  vibrios of the Splendidus clade to colonization was evaluated by RNAseq on oysters infected with V. tasmaniensis LGP32 and V. crassostreae J2-9. 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.* |
| **Description of the data** |  |
|  |  |
| **Type** | *Sequences* |
|  |  |
| **Period and frequency of data collection** | One time point (8 h 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.* | *A biparental family of oysters (Decipher #14)**Vibrio tasmaniensis LGP32**Vibrio crassostreae J2-*9*The strain RNAs were sequenced within the host tossues (whole tissue extracts)* |
| **Protocols***Example: 16S ribosomal RNA gene sequencing by NGS****Please refer to the DMP table\* for more examples*** | *NGS sequencing of host and bacterial RNAs depleted from ribosomal RNAs (before and after oyster infection). Illunia sequencing, paired end; Fasteris, Switzerland.* |
|  |  |
| **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*** | *fastq* |
|  |  |
| **Coverage (if applicable)***Example: random genomic regions covered at 50 X****Please refer to the DMP table\* for more examples*** | *100 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 PRJNA521688* *SRA accessions SRR8567597-SRR8567602 (V. crassostreae J2-9)* *BioProject accession number PRJNA521693**SRA accessions SRR8573808- SRR8573813 (V. tasmaniensis LGP32).* |
|  |  |
| **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](https://share.ifremer.fr/share/proxy/alfresco/api/node/content/workspace/SpacesStore/565d871b-1934-44b7-8260-6e248da8d70a/Data%20Management%20Plan%20preparatory%20table), 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**](https://share.ifremer.fr/)