Vivaldi Project

Data management plan

Microscopical description of OsHV-1 lesions

18/02/2019

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*IFREMER*
Data category	*Microscopical description*
Concerned WP	*WP2* *Choisissez un élément.* *Choisissez un élément.*
Name of the VIVALDI referent(s)	*Microscopical description: Noelia Carrasco & Steve Feist*
Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	*2.2.1/C.gigas/OsHV-1/P01*
Description of the data	*Images of the different tissue lesions induced by the virus OsVH-1 in the oyster Crassostrea gigas and descriptive text of the lesions present.*
Type	*Photos* *text*
Period and frequency of data collection	*Images and descriptive text were performed during the observation of histological slides in 2018 and 2019.*
Geographical site of data collection (if applicable)	*Experimental infection*
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.*	*The histological slides came from a hatchery oyster population infected experimentally by the OsHV-1 virus. Each histological slide corresponds to one individual. 208 individuals were analysed.*
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS* **Please refer to the DMP table* for more examples**	*Each oyster was cut in two parts; one was fixed in Davidson's fixative for histological examination and the other one was fixed in Carson's fixative for further electron microscopic analysis. After 48 h in Davidson's fixative, tissues were maintained in 70% ethanol until dehydrated and embedded in paraffin for histology according to standard procedures. Sections of 2–3 µm thickness were stained by hematoxylin and eosin.*
Nature of the collected/generated	*Images in TIFF format*

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**	*Descriptive text of the lesions present in text format*
Coverage (if applicable) *Example: random genomic regions covered at 50 X* **Please refer to the DMP table* for more examples**	*Main organs of Crassostrea gigas (gills digestive gland mantle, muscle, labial palps).*
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 image software allowing the image viewing on TIFF format.*
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**	*All slides and blocks are kept in the laboratory. The images and text were kept on a local computer server. The references of the blocks and slides are 2016FRE116 1 to 208.*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*The oyster mortality was followed during the experiment. DNA analyses were performed on all individuals.*
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 VIVALDI online platform**