Vivaldi Project

Data management plan

Genome (pathogen)

Key words: OsHV-1, *Crassostrea gigas,* Illumina sequencing

07/08/2018

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*UNIPD*

Data category	*Genome (pathogen)*

Concerned WP	*WP1* *WP2* *WP3*

Name of the VIVALDI referent(s)	*Genome (OsHV-1): Benjamin*

Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	*Genome-Patho/subtask 1.2.1/Pathogen/P12*

Description of the data	Whole genome sequence of the viral isolate OsHV-1-PT (PT means virus isolated from *C. gigas* farmed in the Porto Tolle area)

Type	*Sequences*

Period and frequency of data collection	Oysters sampled during late Spring 2016

Geographical site of data collection (if applicable)	North Adriatic Sea, Po river delta, P. Tolle area

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**	The infection propagation trial started from a tissue homogenate surnatant obtained from farmed oysters resulted to be OsHV-1 positive: -total DNA from gills/mantle tissue fragments of oysters ($\leq$4-5 months age, Porto Tolle area, North Adriatic Sea, Italy); -q-RT-PCR diagnosis with the HVDP-F /HVDP-R primers targeting the catalytic subunit of the viral DNA polymerase: ORF100, nucleotides 147655-153291 of the reference OsHV-1 genome (AY509253); - 2.5-2.8x10^8 virus DNA copies/100 µl (see Tab. 1 Abbadi et al. 2018). All protocols, including whole genome shotgun sequencing and de novo assembly, are detailed in Abbadi et al. 2018 (DOI 10.1099/jgv.0.001042). See the technical summary at NCBI (PRJNA398466 and SRS2433575).

Nature of the collected/generated	About the OsHV-1-PT genome, raw data are in the SRA archive under

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**	accession number SRR5936879 whereas the consensus sequence is recorded in GenBank under accession number MG561751). The OsHV-1-PT genome organization, equal to that of OsHV-1 μVar, can be represented as $TR_L–U_L–IR_L–X–IR_S–U_S–TR_S–X'$ or $X'–TR_L–U_L–IR_L–X–IR_S–U_S–TR_S$.
Coverage (if applicable) *Example: random genomic regions covered at 50 X* **Please refer to the DMP table* for more examples**	**200-fold base pair sequence coverage** and a **279-fold physical coverage** of the OsHV-1 genome. Illumina sequencing was directly performed on a virus-rich oyster sample and yielded 3 436 820 paired-end reads (2×300 bp), which allowed the recovery of 87 582 high-quality reads truly belonging to the order Herpesvirales (2.6 % OsHV-1 DNA to exogenous DNA ratio).
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**	Anyone interested in the molecular OsHV-1-oyster interactions and in the mitigation of OsHV-1-related pathogenicity
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**	*Please refer to the public repositories SRA and GenBank as they represent a reference for the whole scientific community.*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	See SSampling table to Fill-in.xls (IZSVE16_PT OsHV1 pos CG) See publicly available data (SRR5936879 and MG561751) See Abbadi et al 2018 (DOI 10.1099/jgv.0.001042)
Sharing of metadata (if relevant)	*Choisissez un élément.* *Please specify*

*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**