Vivaldi Project

Data management plan

Infected/healthy oysters in field and lab condition (Italy)
Crassostrea gigas, OsHV-1, RNA-seq

14/10/2018

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*UNIPD*
Data category	*Transcriptome (host)*
Concerned WP	***WP2*** *WP1* *WP4*
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/Subtask 2.1.1/Dual RNA-seq/P12*
Description of the data	*Raw RNA-seq data*
Type	*Sequences*
Period and frequency of data collection	*2016: Goro-deployed oyster sampling with storage at -80°C;* *2017: OsHV-1 diagnosis, sampling oysters farmed offshore Goro (May), surnatant preparation and time-course challenge (May)* *2018-2019: Illumina RNA-seq of both challenged oysters and oysters deployed in the Goro lagoon (analysis in progress)* *;*
Geographical site of data collection (if applicable)	*Native oysters collected offshore the Goro lagoon (Po river delta, Italy) and in the Goro lagoon (deployed C. gigas oyster spat)*
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***	*Transcriptome data expected from* ***IZSBIO17_OffGORO1-14****: C. gigas (OsHV-1 negative) oysters farmed and sampled offshore the Goro lagoon in the Po river delta (see geographical coordinates in Domeneghetti et al 2014), injected with a surnatant batch prepared from C. gigas oyster spat deployed to the Goro lagoon in 2016 and detected positive in May 2016 without evidence or mortality.* ***IZSBIO16_GORO1-12****: oysters deployed in the Goro lagoon and sampled (May 2016)* *RNA extraction from gills of individual oysters (samples at different time after injection with surnatant or SW; samples from oysters deployed into the Goro lagoon).* *Illumina technology (HiSeq/TrueSeq)*

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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***	*Data in .fastqc*
Coverage (if applicable) *Example: random genomic regions covered at 50 X* ***Please refer to the DMP table* for more examples***	*2x125 paired end seq, expected ~30,000,000/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***	*Data will be stored in local computer and back-up hard discs, reliable data will be recorded in public repositories*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*Associated data refer to the origin of the material, conditions of preparation of libraries and sequencing, conditions of sequence treatment (work in progress)*
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:

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1. **Be sent to the referent(s) identified above for a final check**
2. **Be uploaded on the [VIVALDI online platform]**

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