Preventing and mitigating farmed bivalve diseases

Vivaldi Project

Data management plan

Transcriptome (host) Transcriptomic analysis of clam extrapallial fluids reveals immunity and cytoskeleton alterations in the first week of Brown Ring Disease development

Key words:
Transcriptome
Ruditapes philippinarum
Extrapallial fluids

20/01/2020

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*CNRS*
Data category	*Transcriptome (host)*
Concerned WP	*WP2* *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 pathogen microbiote/2.1.1./R.philippinarum /CNRS**
Description of the data	Illumina MiSeq sequenced reads of mRNA harvested from collection of extrapallial fluids of *R. philippinarum* challenged by *V. tapetis*
Type	*Sequences*
Period and frequency of data collection	*Collection of data after 1 week of infection by V. tapetis*
Geographical site of data collection (if applicable)	CNRS Ifremer Brest
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.*	*Extrapallial fluids of Ruditapes philippinarum* after infection with *V. tapetis*
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS* ***Please refer to the DMP table* for more examples***	*We performed two rRNA depletion steps, the first one targeting bacterial rRNA and the second one targeting eukaryotic ones (by using the Ribo-Zero rRNA Removal Kits, bacteria and Human/Mouse/Rat, respectively, from Illumina). The RNAs from seven clams, 3 healthy and 4 infected, were subjected to cDNA libraries creation according to standard Illumina procedures (TruSeq Stranded mRNA Library Prep Kit). All the libraries were sequenced, by Illumina Miseq PE300, at the Federal University of Rio de Janeiro, Brazil.*

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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 fastq format (RNA sequences reads)
Coverage (if applicable) *Example: random genomic regions covered at 50 X* ***Please refer to the DMP table* for more examples***	*5,62X* *Could you please include the obtained millions of reads per sample?* *C1_R1 : 1 809 464* *C1_R2 : 1 818 386* *C2_R1 : 2 776 550* *C2_R2 : 2732099* *C3_R1 : 780088* *C3_R2 : 787782* *T1_R1 : 2333575* *T1_R2 : 2339455* *T2_R1 : 1972834* *T2_R2: 1930156* *T3_R1 : 2340146* *T3_R2 : 2348446* *T4_R1 : 2703227* *T4_R2 : 2703341*
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 are saved on external storage + ABIMS galaxy platform (SB ROSCOFF) The sequencing data have been made available at the European Nucleotide Archive (project PRJEB23385).
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*BRD diagnostic, Vibrio load, temperature, nutrition, reproduction, lipid content*
Sharing of metadata (if relevant)	*C : control* *T : Infected*

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