Preventing and mitigating farmed bivalve diseases

Vivaldi Project

Data management plan

Phenotypic markers on Mytilus galloprovincialis

Key words:
Mytilus galloprovincialis
Hemocytes
Flow cytometry
Apoptosis

05/02/2019

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*CSIC*
Data category	*Phenotypic markers (host)*
Concerned WP	*WP2*
Name of the VIVALDI referent(s)	*Phenotypic markers (host): Florian Enez & Christine Paillard*
Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	Phenotypic-Marker-Host/2.2.1/Mussel hemocytes/CSIC
Description of the data	*Differential characteristics in control vs Vibrio infected mussels: hemocytes population structure and apoptosis*
Type	*Tabular files*
Period and frequency of data collection	*Mussels were challenged with Vibrio and after 24h hemolymph from individual mussels was withdrawn to perform the experiments.*
Geographical site of data collection (if applicable)	*Mussels origin was the Ría de Vigo (raft mussels). The experiment was carried out in lab controlled conditions.*
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***	*Eight individual mussels (M. galloprovincialis), 8-10 cm shell length, purchased on September 2016 from local mussel farmers were experimentally infected with V. splendidus, reference strain, and after 24 hours hemolymph was individually recovered from the posterior adductor muscle. Hemocytes count was adjusted to 10e6 to perform further experiments:* *Hemocytes population distribution and apoptosis were evaluated by flow cytometry in a FACS Calibur Flow Cytometer. The analyses were carried out using CellQuest software. The hemocytes populations were analysed directly. For the apoptosis measurement hemocytes were treated with Annexin V.*
Nature of the collected/generated data *Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed datas set*	*The raw data is a excel file exported from the CellQuest analysis software.*

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will be .vcf/.bed formats. ***Please refer to the DMP table* for more examples***	
Coverage (if applicable) *Example: random genomic regions covered at 50 X* ***Please refer to the DMP table* for more examples***	*Unique measurement of each 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 excel files*
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 our hard disks and it would be shared after publication upon request.*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*NA*
Sharing of metadata (if relevant)	*No relevant* Cliquez ici pour taper du texte.

*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**

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