Vivaldi Project

Data management plan

Genetic markers
Key words*: *C. gigas, SNP panel

07/08/2018

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*IFREMER*
Data category	*Genetic markers*
Concerned WP	*WP3* *Choisissez un élément.* *Choisissez un élément.*
Name of the VIVALDI referent(s)	*Genetic markers: Mathias Wegner & JB Lamy*
Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	Genetic-Marker/WP3.1.2/Crassostreagigas/Ifremer
Description of the data	Optimized list of SNP used in SNP panel (parentage assignation) in Crassostrea gigas (removed loci with high linkage disequilibrium and mendelian error).
Type	*Sequences*
Period and frequency of data collection	*N/A*
Geographical site of data collection (if applicable)	*N/A*
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***	This original dataset and sequences (transcriptomics and sanger sequencing) are from a publication by Lapègue, S., Harrang, E., Heurtebise, S., Flahauw, E., Donnadieu, C., Gayral, P., Ballenghien, M., Genestout, L., Barbotte, L., Mahla, R., Haffray, P. and Klopp, C. (2014), Development of SNP-genotyping arrays in two shellfish species. Mol Ecol Resour, 14: 820–830. doi:10.1111/1755-0998.12230 All the details about the software used and the filtrer applied to data are detailed in the D3.1 *These panels SNP have been developed in infimum technology (Illumina) by Labogéna http://www.labogena.fr/.*
Nature of the collected/generated data *Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed datas set*	*.txt format with header.*

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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***	*N/A*
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***	*N/A*
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 the list and sequences are available from Labogéna Laboratory. They could sell and provide any information regarding this parentage panels.* *In addition, External hard-drive DISKII_G:\IFREMER\02-PROJETS\GENOYSTER\11_GigaDNA_Ifremer_samples\04_mask_label_loci\keep_noSD_*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	*See above-mentioned paper and for an extensive description see D3.1. We also provide all the codes and raw data upon request.*
Sharing of metadata (if relevant)	*Choisissez un élément.* *Please specify*

Commentaire [IAILTP1]: Je ne crois pas que ça colle avec les metadata

*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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