



Vivaldi Project

Data management plan

Microbiome (bivalve)

Key words: Crassostrea gigas, DNA, bacterial diversity, vibriome

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	IRTA
Data category	Microbiome (bivalve)
Concerned WP	WP1 WP4 Choisissez un élément.
Name of the VIVALDI referent(s)	Microbiome: Alberto Pallavicini
Reference of the dataset <i>Please refer to the DMP table to find the appropriate reference.</i> <i>Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°</i>	Microbiome-bivalve/SubTaskN°1.2.1/Oyster/PartnerN°6-11-13
	16S sequencing from contrasting animals
Description of the data	
Type	Sequences
Period and frequency of data collection	Samples has been collected along one complete year between April 2016 and May 2017 during 3 risk periods for OsHv-1 associated mortalities (April 2016, November 2016 and May 2017)
Geographical site of data collection (if applicable)	Samples were collected in Alfacs and Fangar Bays in the Ebro Delta, in Catalanian Mediterranean Coast.
Description of the material from which the dataset is generated <i>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,</i>	Bacterial diversity and/or vibriome information is obtained from the analysis of DNA extracted from <i>C. gigas</i> individuals (juveniles and spat) collected during mortality episodes and no mortality episodes in the Ebro Delta (Spain). The data set is generated from DNA samples (different lots of n=30 individuals) Bacterial diversity and/or vibriome information will be obtained from the analysis of DNA extracted from <i>C. gigas</i> collected in selected aquaculture sites and periods Samples were preliminary screened for the presence of Ostreid herpesvirus 1 (OsHV-1) and <i>Vibrio aestuarianus</i> by real-Time PCR based methods (Webb et al, 2007; IFREMER, 2013)



<i>tissue.</i>	
Protocols <i>Example: 16S ribosomal RNA gene sequencing by NGS</i> Please refer to the DMP table* for more examples	16S ribosomal RNA (V4 region) gene sequencing by NGS
Nature of the collected/generated data <i>Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed data set will be .vcf/.bed formats.</i> Please refer to the DMP table* for more examples	Raw dataset in .fastqc format
Coverage (if applicable) <i>Example: random genomic regions covered at 50 X</i> Please refer to the DMP table* for more examples	N/A
What are the prerequisites allowing to use the data as such? <i>Example: Any person able to use .fastqc file and .fasta file</i> Please refer to the DMP table* for more examples	Any person able to use .fastqc file
Sharing of main data	Saved and shared after publication
	<i>Please specify</i>
Archiving and preservation <i>Example: data will be stored on a hard drive + online back up and then will be released</i>	Data saved on hard drive and cloud service. Stored in at least two different sites in Trieste and Genova.

on public database (Sinoe, Dryad) after publication. Please refer to the DMP table* for more examples																																																																																																									
List, description and storage of associated data (metadata) <i>Examples: environmental data, mortality monitoring, genotyping...</i>	<p>Samples provided by IRTA, DNA extracted and amplicons libraries produced by UNIGE DNA sequencing performed by UNITS</p> <table border="1"> <thead> <tr> <th>Date</th> <th>Code</th> <th>C. gigas (age)</th> <th>Mortality (%)</th> <th>OshV-1 (PCR results)</th> <th>V. aestuarianus (PCR results)</th> <th>Microbiome analysis (analysed samples)</th> <th>Vibriome analysis (analysed samples)</th> </tr> </thead> <tbody> <tr> <td colspan="8">Ebro Delta (Spain)</td> </tr> <tr> <td>13_04_2016</td> <td>EFCgAbr16 (extr.)</td> <td>adult</td> <td>23% (Up to 50%)</td> <td>0+/30</td> <td>22+/30</td> <td>5 Va infect-5 controls</td> <td>1 va infected</td> </tr> <tr> <td>26_04_2016</td> <td>ACgAbr16</td> <td>juvenile</td> <td>76% (Up to 90 %)</td> <td>17+/30</td> <td>0+/30</td> <td>5 OshV infect-5 controls</td> <td></td> </tr> <tr> <td>26_04_2016</td> <td>FCgAbr16</td> <td>juvenile</td> <td>46,6% (Up to 80%)</td> <td>21+/30</td> <td>4+/30</td> <td>5 OshV infect-5 controls</td> <td></td> </tr> <tr> <td>19_07_2016</td> <td>ACgJl16</td> <td>juvenile</td> <td>3% (ligh mortality)</td> <td>1+/30</td> <td>0+/30</td> <td>5 controls</td> <td></td> </tr> <tr> <td>19_07_2016</td> <td>FCgJl16</td> <td>juvenile</td> <td>no mortality</td> <td>0+/30</td> <td>0+/30</td> <td></td> <td></td> </tr> <tr> <td>24_11_2016</td> <td>FCgNov16_b</td> <td>juvenile</td> <td>30% recent mortality</td> <td>7+/30</td> <td>1+/30</td> <td></td> <td></td> </tr> <tr> <td>25_01_2017</td> <td>ACgGen17</td> <td>juvenile</td> <td>no mortality</td> <td>0+/30</td> <td>0+/30</td> <td>5 controls</td> <td></td> </tr> <tr> <td>26_01_2017</td> <td>FCgGen17</td> <td>juvenile</td> <td>no mortality</td> <td>0+/30</td> <td>0+/30</td> <td></td> <td></td> </tr> <tr> <td>05_05_2017</td> <td>E-AmCgMa17(extr)</td> <td>juvenile</td> <td>87.83% mortality</td> <td>10+/18</td> <td>0+/18</td> <td>5 OshV infect-5 controls</td> <td></td> </tr> <tr> <td>05_05_2017</td> <td>E-ACgMa17 (extr)</td> <td>juvenile</td> <td>no mortality</td> <td>0+/30</td> <td>0+/30</td> <td></td> <td></td> </tr> <tr> <td>31_05_2017</td> <td>E-FmCgMa17 (extr)</td> <td>adult</td> <td>85% mortality</td> <td>0+/30</td> <td>9+/30</td> <td></td> <td></td> </tr> </tbody> </table>	Date	Code	C. gigas (age)	Mortality (%)	OshV-1 (PCR results)	V. aestuarianus (PCR results)	Microbiome analysis (analysed samples)	Vibriome analysis (analysed samples)	Ebro Delta (Spain)								13_04_2016	EFCgAbr16 (extr.)	adult	23% (Up to 50%)	0+/30	22+/30	5 Va infect-5 controls	1 va infected	26_04_2016	ACgAbr16	juvenile	76% (Up to 90 %)	17+/30	0+/30	5 OshV infect-5 controls		26_04_2016	FCgAbr16	juvenile	46,6% (Up to 80%)	21+/30	4+/30	5 OshV infect-5 controls		19_07_2016	ACgJl16	juvenile	3% (ligh mortality)	1+/30	0+/30	5 controls		19_07_2016	FCgJl16	juvenile	no mortality	0+/30	0+/30			24_11_2016	FCgNov16_b	juvenile	30% recent mortality	7+/30	1+/30			25_01_2017	ACgGen17	juvenile	no mortality	0+/30	0+/30	5 controls		26_01_2017	FCgGen17	juvenile	no mortality	0+/30	0+/30			05_05_2017	E-AmCgMa17(extr)	juvenile	87.83% mortality	10+/18	0+/18	5 OshV infect-5 controls		05_05_2017	E-ACgMa17 (extr)	juvenile	no mortality	0+/30	0+/30			31_05_2017	E-FmCgMa17 (extr)	adult	85% mortality	0+/30	9+/30		
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*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](#)

