Jan 09, 2020

Handling of genomics samples

In 1 collection

Adriana Alberti[1], Julie Poulain[1], Stefan Engelen[1], Karine Labadie[1], Sarah Romac[2,3], Isabel Ferrera[4], Guillaume Albini[1], Jean-Marc Aury[1], Caroline Belser[1], Alexis Bertrand[1], Corinne Cruaud[1], Corinne Da Silva[1], Carole Dossat[1], Frédéric Gavory[1], Shahinaz Gas[1], Julie Guy[1], Maud Haquelle[1], E'krame Jacoby[1], Olivier Jaillon[1,5,6], Arnaud Lemainque[1], Eric Pelletier[1], Gaëlle Samson[1], Marc Wessner[1], Genoscope Technical Team[1], Silvia G. Acinas[4], Marta Royo-Llonch[4], Francisco M. Cornejo-Castillo[4], Ramiro Logares[4], Beatriz Fernández-Gómez[4,7,8], Chris Bowler[9], Guy Cochrane[10], Clara Amid[10], Petra Ten Hoopen[10], Colomban De Vargas[2,3], Nigel Grimsley[11,12], Elodie Desgranges[11,12], Stefanie Kandels-Lewis[13,14], Hiroyuki Ogata[15], Nicole Poulton[16], Michael E. Sieracki[16,17], Ramunas Stepanauskas[16], Matthew B. Sullivan[18,19], Jennifer R. Brum[19,20], Melissa B. Duhaime[21], Bonnie T. Poulos[22], Bonnie L. Hurwitz[23], Stéphane Pesant[24,25], Eric Karsenti[9,13,26], Patrick Wincker[1,5,6]

[1]CEA - Institut de Biologie François Jacob, Genoscope, Evry, France, [2]CNRS, UMR 7144, Station Biologique de Roscoff, France, [3]Sorbonne Universités, UPMC Univ Paris 06, UMR 7144, Station Biologique de Roscoff, France, [4]Departament de Biologia Marina i Oceanografia, Institute of Marine Sciences (ICM), CSIC, Barcelona, Spain, [5]CNRS, UMR 8030, Evry , France, [6]Université d'Evry, UMR 8030, Evry, France, [7]FONDAP Center for Genome Regulation, Santiago, Chile, [8]Laboratorio de Bioinformática y Expresión Génica, Instituto de Nutrición y Tecnología de los Alimentos (INTA), Universidad de Chile, El Libano Macul, Santiago, Chile, [9]Ecole Normale Supérieure, PSL Research University, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS UMR 8197, INSERM U1024, Paris, France, [10]European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genomes Campus, Hinxton, Cambridge , UK, [11]CNRS UMR 7232, BIOM, Banyuls-sur-Mer, France, [12]Sorbonne Universités Paris 06, OOB UPMC, Banyuls-sur-Mer , France, [13]Directors' Research European Molecular Biology Laboratory, Heidelberg, Germany, [14]Structural and Computational Biology, European Molecular Biology Laboratory, Heidelberg, Germany, [15]Institute for Chemical Research, Kyoto University, Gokasho, Uji, Kyoto, Japan, [16]Bigelow Laboratory for Ocean Sciences, East Boothbay, Maine, USA, [17]National Science Foundation, Arlington, Virginia, USA, [18]Departments of Microbiology and Civil, Environmental and Geodetic Engineering, Ohio State University, Columbus, Ohio, USA, [19]Department of Microbiology, The Ohio State University, Columbus, Ohio, USA, [20]Present address: Department of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, Louisiana, USA, [21]Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan, USA, [22]University of Arizona, Tucson, Arizona, USA, [23]Department of Agricultural and Biosystems Engineering, University of Arizona, Tucson, Arizona, USA, [24]MARUM, Center for Marine Environmental Sciences, University of Bremen, Germany, [25]PANGAEA, Data Publisher for Earth and Environmental Science, University of Bremen, Germany, [26]Sorbonne Universités, UPMC Université Paris 06, CNRS, Laboratoire d'oceanographie de Villefranche (LOV), Observatoire Océanologique, Villefranche-sur-mer, France

1 Works for me dx.doi.org/10.17504/protocols.io.qwfdxbn

Adriana Alberti
CEA, Genoscope, France

ABSTRACT

This protocol describes the handling of genomics samples for the *Tara* Oceans expedition and is part of Viral to metazoan marine plankton nucleotide sequences from the *Tara* Oceans expedition.

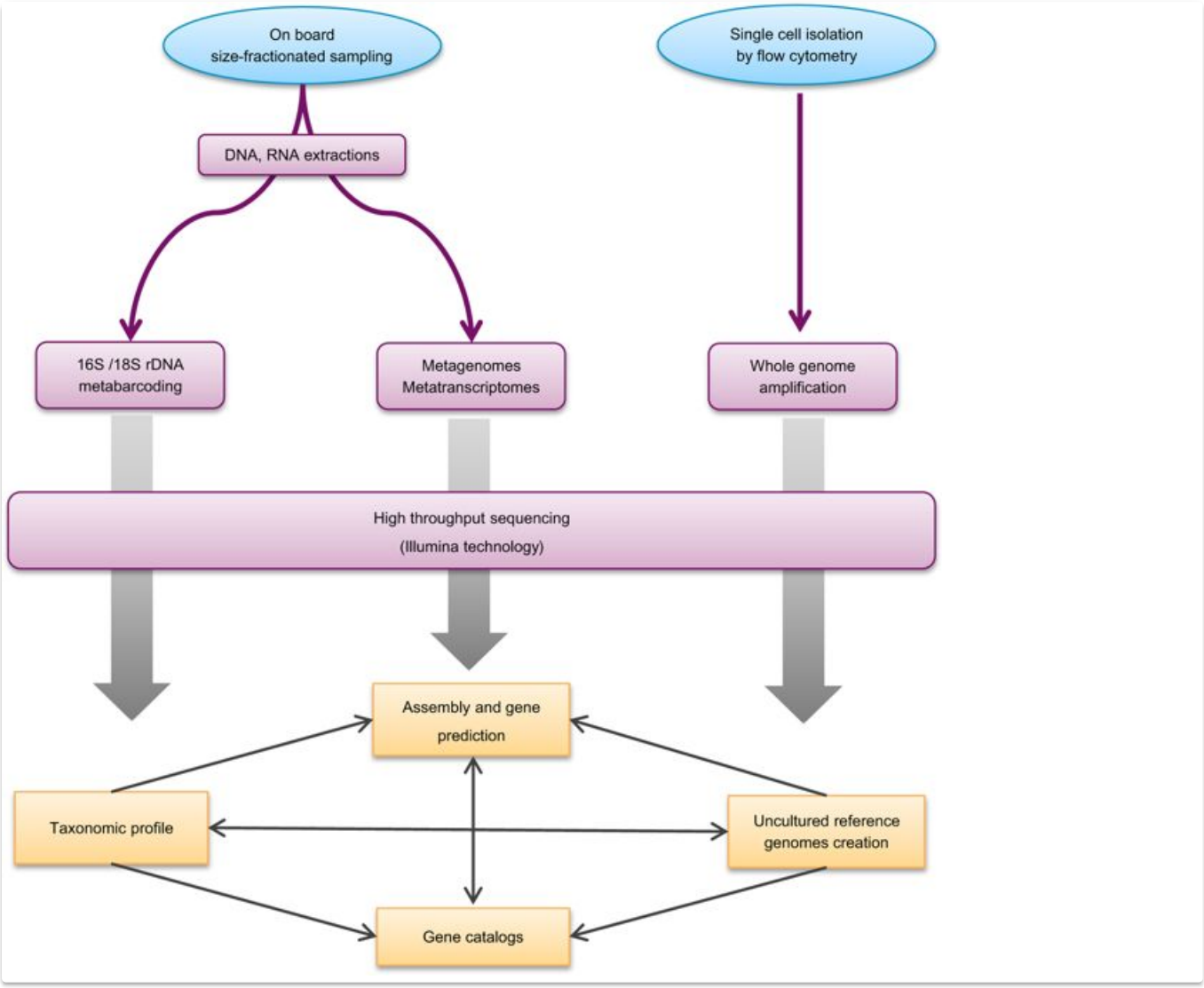

Figure 1: Overview of -omics analysis strategy applied on Tara Oceans samples.

EXTERNAL LINK

https://www.nature.com/articles/sdata201793#methods

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Alberti, A. (2017). Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. *Scientific Data* **4**, 170093 (2017)
doi: 10.1038/sdata.2017.93

ATTACHMENTS

Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition.pdf

GUIDELINES

Genomics samples were transferred on average every 6 weeks from a port of call to the European Molecular Biology Laboratory (EMBL, Heidelberg) in Germany. Transportation was organized by experts from World Courier (www.worldcourier.com) who ensured that the chain of cold was never broken. At EMBL, samples were sorted, repackaged according to their final destination, and transported again by World Courier to the different laboratories responsible for their analysis (Table 1).

Table 1: Summary of libraries generated from Tara Oceans DNA and RNA samples and sequencing experiments performed on each type of library.

Size fractions (µm)	Mainly targeted organisms	Targeted genomic analysis	Sample storage laboratory	Sequencing laboratory	Method ID Nucleic acids preparation (Section)	Method ID Amplicons generation (Section)	Method ID Library preparation (Section)
< 0.2 µM	Viruses	Metagenomics	M. Sullivan lab (University of Arizona, AZ, US)	CEA, Genoscope, France	Virus_DNA_ext (2.4)		MetaG_virus (4.2)
0.2–1.6, 0.1–0.2, 0.45–0.8, 0.2–0.45	Giruses	Metagenomics	N. Grimsley lab (CNRS, Banyuls-sur -Mer, France)	CEA, Genoscope, France	Girus_DNA_ext (2.5)		MetaG (4.1)
0.2–1.6, 0.2–3	Viruses, Giruses, Prokaryotes, small Eucaryotes	16S metabarcoding	S.G. Acinas lab (ICM-CSIC, Barcelona, Spain)	CEA, Genoscope, France	Acinas_Prok_DNA_ext (2.2)	16S_PCR (3.2)	MetaBar_16S (4.6)
		Metagenomics			Acinas_Prok_DNA_ext (2.2)		MetaG (4.1)
		Metatranscriptomics by random priming			Acinas_Prok_RNA_ext Genoscope_Prok_RNA_ext (2.2)		RiboZero_SMART_strand (4.4)
0.8-inf, 3-inf, 0.8–5 (0.8–3), 5–20 (3–20), 20–180, 180–2,000	Protists and metazoa	18S metabarcoding	C. De Vargas lab (CNRS/UPMC, Roscoff, France)	CEA, Genoscope, France		18S_PCR (3.1)	MetaBar_18S (4.5)
		16S metabarcoding				16S_PCR (3.2)	MetaBar_16S (4.6)
		Metagenomics	P. Wincker lab (CEA, Genoscope, France)		Euk_ DNA_RNA_ext (2.1)		MetaG (4.1)
		Metatranscriptomics on poly(A)$^+$ RNA			Euk_ DNA_RNA_ext (2.1)		TS_RNA (4.4) TS_strand (4.4) SMART_dT (4.4)
Samples for SAGs	Protists	*De novo* sequencing	N. Poulton lab (Bigelow lab, ME, US)	CEA, Genoscope, France	SAGs_amplif (2.6)		MetaG_SAGs (4.3)

*Number of libraries with available readsets in public databases at the date of publication of the paper

In the respective laboratories, samples were immediately identified by scanning/reading their barcode label and were stored in cryo boxes or in −80 °C freezers. During all these steps, samples were manipulated on dry ice. Each laboratory used its own sample management system to record the storage location and to monitor sample usage.