Dataset name: **Prokaryotic diversity**

|  |  |
| --- | --- |
| Parameters: | * **Table of Operational Taxonomic Units (OTUs) in Excel file** * **List of genes present in metagenomes** |

PROJECT TITLE: **MOBYDICK**

Oceanographic cruise: **MOBYDICK**

Start date: **18/02/2018**

End date: **27/03/2018**

Project manager: **Bernard Quéguiner** [bernard.queguiner@mio.osupytheas.fr](mailto:bernard.queguiner@mio.osupytheas.fr)

Address: **Mediterranean Institute of Oceanolography**

**Institut Pytheas - Observatoire des Sciences de l'Univers**

**Bâtiment OCEANOMED, Campus de Luminy, case 901**

**F-13288 Marseille Cedex 09, France**

Chief scientist: **Ingrid Obernosterer** [ingrid.obernosterer@obs-banyuls.fr](mailto:ingrid.obernosterer@obs-banyuls.fr)

Address: **Laboratoire d’Océanographie Microbienne**

**Observatoire Océanologique de Banyuls sur mer**

**66650 Banyuls sur mer, France**

Geographic information: **Indian sector of the Southern Ocean**

Latitude: **49.5°S – 52.5°S**

Longitude: **67,0°E – 74.5°E**

Parameter supervisor: **Ingrid Obernosterer**

LOMIC

Observatoire Océanologique de Banyuls sur mer

66650 Banyuls sur mer, France

+33 (0)4 68 88 73 44

+33 (0)7 89 63 93 00

[ingrid.obernosterer@obs-banyuls.fr](mailto:ingrid.obernosterer@obs-banyuls.fr)

Dataset contact: **Ingrid Obernosterer**

LOMIC

Observatoire Océanologique de Banyuls sur mer

66650 Banyuls sur mer, France

+33 (0)4 68 88 73 44

+33 (0)7 89 63 93 00

[ingrid.obernosterer@obs-banyuls.fr](mailto:ingrid.obernosterer@obs-banyuls.fr)

# OPERATIONS

## Sampling device(s)

Water samples were collected from Niskin bottles at every station (surface: 10 or 15 m, and deep levels: 100 to 4000 m).

## List of stations sampled

**Table 1 : Sampled stations, cast numbers and sampling depths**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **station** | **cast #** | **depth** |  | **station** | **cast #** | **depth** |
| M2\_1 | CTD-009 | 10 m |  | M4\_2 | CTD-046 | 10 m |
| M2\_1 | CTD-009 | 50 m |  | M4\_2 | CTD-046 | 60 m |
| M2\_1 | CTD-009 | 100 m |  | M4\_2 | CTD-046 | 125 m |
| M2\_1 | CTD-009 | 300 m |  | M4\_2 | CTD-046 | 300 m |
| M3 | CTD-021 | 10 m |  | M2\_3 | CTD-049 | 10 m |
| M3 | CTD-021 | 60 m |  | M2\_3 | CTD-049 | 60 m |
| M3 | CTD-021 | 125 m |  | M2\_3 | CTD-049 | 125 m |
| M3 | CTD-021 | 300 m |  | M2\_3 | CTD-049 | 300 m |
| M2\_2 | CTD-027 | 10 m |  | M3\_3 | CTD-058 | 10 m |
| M2\_2 | CTD-027 | 60 m |  | M3\_3 | CTD-058 | 60 m |
| M2\_2 | CTD-027 | 125 m |  | M3\_3 | CTD-058 | 125 m |
| M2\_2 | CTD-027 | 300 m |  | M3\_3 | CTD-058 | 300 m |
| M1 | CTD-036 | 10 m |  |  |  |  |
| M1 | CTD-036 | 60 m |  |  |  |  |
| M1 | CTD-036 | 125 m |  |  |  |  |
| M1 | CTD-036 | 300 m |  |  |  |  |

# INSTRUMENTS

Instrument Type: **Peristaltic pump**

Manufacturer: **Cole Parmer**

Model: **Masterflex L/S Easy-Load II**

Instrument Features / Calibration: **N/A**

# DESCRIPTION of PARAMETERS

## Measurement details

Seawater samples were passed through a 60 µm mesh and then sequentially filtered through a 0.8 µm polycarbonate filter (47 mm) and a 0.2 µm Sterivex cartridge (6 L each).

## Analytical procedure

The filters and cartridges were stored at –80°C. Back in the home lab, DNA will be extracted for metagenomic and 16S rRNA analysis (Landa *et al.,* 2016). The diversity will be determined by high throughput sequencing of the 16S rRNA genes and total DNA sequencing for Metagenomes (Illumina MiSeq). Metagenomic analysis will be used as a database for selected contrasting stations.

## Units

N/A

## Sensor precision

N/A

## Post-cruise data analysis/treatment required

N/A

## Estimated Date of Delivery

End of 2018.

# BIBLIOGRAPHY

Landa M., Blain S., Christaki U., Monchy S., Obernosterer I., 2016. Shifts in bacterial community composition associated with increased carbon cycling in a mosaic of phytoplankton blooms. *The ISME Journal*, **10**(1), 39-50.

Delmont T.O., Quince C., Shaiber A., Esen Ö.C., Lee S.T.M., Rappé M.S., MacLellan S.L., Lücker S., Eren A.M., 2018. Nitrogen-fixing populations of Planctomycetes and Proteobacteria are abundant in surface ocean metagenomes. *Nature Microbiology*, **3**(7), 804-813.