Dataset name: **Active prokaryotes diversity and activity rates**

|  |  |
| --- | --- |
| Parameters: | * **Abundance of active cells**
* **Thymidine uptake**
* **Méthionine uptake**
 |

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

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 **Observatoire Océanologique de Banyuls sur mer**

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

 Latitude: **49.5°S – 52.5°S**

 Longitude: **67,0°E – 74.5°E**

Parameter supervisor: **Eva Sintes**

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# OPERATIONS

## Sampling device(s)

Water samples were collected from the rosette bottles.

## List of stations sampled

**Table 1 : Details of sampled stations,** **casts, and number of samples collected for the different parameters (see text § 3 below for acronyms)**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Station** | **Cast** | **BrdU** | **Bulk Thy/Met** | **Micro-CARD-FISH** | **Click-FISH** | **Resp. cells** | **SAGS** |
| M2\_1 | 5 | 6 | 3 | 3 | 6 | 6 | 6 |
| M4\_1 | 17 | 5 | 3 | 3 | 5 | 5 | 5 |
| M4\_1 | 18 | 2 | 2 | 2 | 2 | 2 | 2 |
| M3 | 26 | 9 | 3 | 3 | 9 | 9 | 9 |
| M2\_2 | 29 | 7 | 3 | 3 | 7 | 7 | 7 |
| M1 | 35 | 8 | 3 | 3 | 8 | 8 | 8 |
| M4\_2 | 44 | 8 | 5 | 5 | 8 | 8 | 8 |
| M2\_3 | 52 | 9 | 3 | 3 | 9 | 3 | 9 |
| M3\_3 | 57 | 8 | 3 | 3 | 8 | 2 | 8 |

# INSTRUMENTS

Instrument Type: **Liquid scintillation counter TRICARB 2100**

Manufacturer: **Perkin Elmer**

Model: **Tri-Carb® 2100TR**

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

Instrument Type: **Flow cytometer**

Manufacturer: Becton Dickinson

Model: **FACSAria II**

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

# DESCRIPTION of PARAMETERS

## Measurement details

Active bacterial and archaeal community composition and metabolic potential will be analyzed based on the incorporation of Bromodeoxyuridine (BrdU, an analog of thymidine) into the DNA of dividing cells (Hamasaki *et al.*, 2007), bacterial reductase activity, uptake of 3H-labeled thymidine and methionine and of fluorescent analogs of thymidine and methionine after click-chemistry reaction (Samo *et al.*, 2014). Additionally, single cell amplified genomes (SAGs) will be sequenced at Bigelow Laboratory Single Cell Genomics Center (Stepanauskas & Sieracki, 2007).

## Analytical procedure

Next generation sequencing will be performed on the 16S rRNA gene and at the metagenome level on BrdU-labeled (Hamasaki *et al.*, 2007). MICRO-CARD-FISH samples will be processed in the lab will (Sintes & Herndl, 2006). Microscopic evaluation following click-chemistry of methionine and thymidine analogs will be conducted at the home laboratory (Samo *et al.*, 2014). Respiring prokaryotes will be analyzed by flow cytometry at the home lab.

## Units

* Abundance of active cells cells mL-1
* Thymidine uptake nmol Thymidine L-1 h-1
* Méthionine uptake nmol Methionine L-1 h-1

## Sensor precision

N/A

## Post-cruise data analysis/treatment required

N/A

## Estimated Date of Delivery

* 16S rRNA gene sequencing: 2–3 years after cruise end,
* MICRO-CARD-FISH: 1–2 years after cruise end,
* microscopical analyses: 1–2 years after cruise end,
* Flow cytometry: 1 years after cruise end.

# BIBLIOGRAPHY

Hamasaki K., Taniguchi A., Tada Y., Long R.A., Azam F., 2007. Actively growing bacteria in the inland sea of japan, identified by combined bromodeoxyuridine immunocapture and denaturing gradient gel electrophoresis. *Applied and Environmental Microbiology*, **73**, 2787–2798.

Samo T.J., Smriga S., Malfatti F., Sherwood B.P., Azam F., 2014. Broad distribution and high proportion of protein synthesis active marine bacteria revealed by click chemistry at the single cell level. *Frontiers in Marine Science*, **1**, 48.

Sintes E., Herndl G.J., 2006. Quantifying substrate uptake by individual cells of marine bacterioplankton by catalyzed reporter deposition fluorescence *in situ* hybrid- ization combined with microautoradiography. *Applied and Environmental Microbiology*, **72**, 7022–7028.

Stepanauskas R., Sieracki M.E., 2007. Matching phylogeny and metabolism in the uncultured marine bacteria, one cell at a time. *Proceedings of the National Academy of Sciences of the United States of America*, **104**, 9052-9057.