

## Ocean Sampling Day – Data now available!

Press release 09/09/22

Marine Biodiversity Observation Networks (MBON) are a growing global initiative consisting of regional networks of scientists, resource managers and end users, working to integrate data from existing long-term programmes. The aim is to improve our understanding of changes and connections between marine biodiversity and ecosystem functions. Within ASSEMBLE Plus's Joint Research Activity 1 (JRA1) there are two genomic observation networks: Ocean Sampling Day (OSD) and Autonomous Reef Monitoring Structures (ARMS-MBON).

OSD is a simultaneous worldwide research campaign where marine biologists around the globe participate in sampling of the world's oceans to produce contextual genomic data. OSD was launched by the [MicroB3 project](#) in the summer, on the solstice, 21 June 2014, with ASSEMBLE Plus taking on the OSD coordination in 2018. Through MBONs collecting cumulative samples, related in time, space and environmental parameters, researchers can gain invaluable insights into the marine environment, including insights into the changes in biodiversity as a result of climate change and the introduction of non-native species by shipping, etc. DNA analysis with chosen marker genes allows us to identify all prokaryotic and eukaryotic microbial species in the water samples obtained, while analysis of metagenomic data allows us to assess the functional content and potential of bacterial communities. Among the many questions that the data can answer, the basic ones include "what organisms are found where" and "what functions they can fulfil, under the assessed environmental conditions". All the samplings were carried out in a standardised way to allow comparability among samples and an accurate tracking of changes in the marine environment over time. The data collected will be a reference data set for generations of experiments to follow in the coming decades. One particular project that has benefitted from OSD data is the European Marine Omics Biodiversity Observation Network (EMO BON), an EMBRC project aiming to enhance the European contribution to global genomic observation efforts.

Since 2018, the ASSEMBLE Plus partner, the Hellenic Centre for Marine Research (HCMR) in Heraklion, Crete, have coordinated OSD, received and processed all the samples as well as extracted the DNA and sequenced 16S and 18S rRNA. Shotgun metagenomics data have also been produced by GENOSCOPE, France.

An important effort was necessary to find the best ways to make the data open access and FAIR (Findable, Accessible, Interoperable and Reusable), this was achieved by collaboration between the Flanders Marine Institute (VLIZ), the German Federation for Biological Data (GFBio) and HCMR. There is no one best route to data FAIRification, and there is still room for improvement in the interoperability between databases hosting biodiversity and environmental data and databases hosting molecular data. OSD data FAIRification has inspired collaborative projects between the European infrastructures European Marine Biological Resource Centre (EMBRC ERIC), ELIXIR Europe, and LifeWatch ERIC, within the context of the European Open Science Cloud (EOSC).

The cost of sequencing has been covered by EMBRC. The value of FAIR data will increase with time, as any new environmental dataset can be compared to it, to add insights on marine biodiversity structure, function and dynamics. As the quantity of genomic data on single species will increase with

time, and high quality genomic and biological annotations will be added, OSD data can be revisited and reanalysed delivering more knowledge.

HCMR has carried out a preliminary analysis on the DNA metabarcoding of the OSD 16S rRNA data, to gain insights into the value of the data. These analysis results (species identifications) and the raw sequence data are published, to be shared for exploration with experts around the world. The OSD 2018 and 2019 sampling, environmental, and raw sequence data are published as a metadata record via VLIZ's Integrated Marine Information System (IMIS); the OSD 2014 data have long been published on PANGAEA. Species identifications obtained from all three years of OSD will also shortly be submitted to biodiversity archives (OBIS, GBIF).

- [OSD metadata record for 2014 in PANGAEA](#)
- [OSD metadata record for 2018 in IMIS](#)
- [OSD metadata record for 2019 in IMIS](#)

The datasets and metadata are also available via the [OSD GitHub Repository](#) which also provides the data in machine-accessible formats, ensuring the data is in compliance with H2020's Open Research Data Pilot, following the principles of FAIR (Findable, Interoperable, Accessible and Reusable).

For any questions, information, or assistance, contact the OSD team by sending an email to [osd-contact@embrc.eu](mailto:osd-contact@embrc.eu). For more information, please visit the [OSD webpage](#). You can also watch previous videos at the [OSD YouTube channel](#).

### **Notes for Editors**

ASSEMBLE Plus's Joint Research Activity 1 (JRA1) Genomics Observatories, fosters the application of genomics technologies at Long Term Ecological Research Network (LTER) sites. Research encompasses populating and verifying databases of taxonomic reference barcodes, harmonisation of metabarcoding standard operating procedures (SOPs) across the consortium so that the resulting data can be compared across the partnership, and inter-calibration of classical biodiversity data and genomics data (metabarcoding, meta-transcriptomics, etc.). The results will be the establishment of a distributed Genomics Observatory across the partnership and beyond of which the data are available for virtual access. The project began in October 2017 and will run until September 2022. The project is coordinated by Sorbonne Université.

### **About ASSEMBLE Plus**

For more information about the project, please visit [assembleplus.eu](http://assembleplus.eu) or email [assembleplus\\_ta@embrc.eu](mailto:assembleplus_ta@embrc.eu). Follow [@ASSEMBLE\\_Plus](#) on Twitter for regular updates from the project.

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