



Marine environmental DNA workshop:

Defining best practices for oceanic eDNA studies from coastal to deep sea ecosystems, from micro- to macro-organisms and from past to present times

A joint event of Ifremer, Fondation Tara Océan and EMBL

26-28 April 2021
Ifremer, Brest, France

Organizing committee

Ifremer: Bruno Ernande, Philippe Gouletquer
Tara Océans: Chris Bowler, Damien Eveillard, Lionel Guidi
EMBL: Detlev Arendt, Peer Bork

Program

26 April

14:00-14:20 *Opening and welcome (Chair: Bruno Ernande)*

François Houllier, Chief Executive Officer of IFREMER, Brest, France
Romain Troublé, Executive Director of Tara Océan, Paris, France, & Chris Bowler, Scientific Coordinator of Tara Océan, ENS, Paris, France
Edith Heard, Director General of EMBL, Heidelberg, Germany

Session 1: Best practices/State-of-the-art (Chair: Chris Bowler)

14:20-14:40 *Keynote: Ancient Environmental Metagenomics: Exploit the Full Potential*, Yucheng Wang

Department of Zoology, University of Cambridge, Cambridge, UK

Abstract: Shotgun metagenomics is widely applied in modern microbial community studies, but its application on ancient eDNA is rarely reported. In this presentation I will summarise recent advances and applications of ancient eDNA metagenomics, and discuss the potential directions of it for near future.

14:40-15:00 *Keynote: Next-generation marine biodiversity research using environmental DNA*, Philip Francis Thomsen (no streaming)

Aarhus University, Aarhus, Denmark

Abstract: Aquatic environmental DNA (eDNA) – DNA obtained directly from water – has become a rapidly growing research field and proven a successful avenue for biodiversity monitoring encompassing analyses of single species, population genetics and communities from mass sequencing data. Aquatic eDNA may thus be a strong supplementary approach for obtaining data on species compositions and interactions in marine ecosystems – from microbes to mammals, and from polar to

tropical environments. Furthermore, eDNA analyses may provide a better understanding of the yet unknown biodiversity in the oceans. In this talk, I will give examples of the achievements of marine macro-organismal eDNA research and address the challenges and perspectives of eDNA for fundamental and applied marine research.

15:00-15:20 *Keynote:* Best practices in metabarcoding, Pierre Taberlet
CNRS, UMR LECA, Grenoble, France

15:20-15:30 Questions and discussion

15:30-16:00 Brainstorming session

Subgroup 1: Yucheng Wang, Detlev Arendt, Kiley Seitz

Subgroup 2: Philip Francis Thomsen, Bruno Ernande, Céline Reisser

Subgroup 3: Pierre Taberlet, Chris Bowler, Flora Vincent

16:00-16:30 Coffee break

Session 2: Sampling methodologies (Chair: Lionel Guidi)

16:30-16:50 *Keynote:* In-situ Autonomous Acquisition and Preservation of Environmental DNA Using the Environmental Sample Processor, Kevan Yamahara (no streaming)
MBARI, Moss Landing, California, USA

Abstract: Over the past decade environmental DNA (eDNA) assessments have increasingly been applied to detect aquatic organisms. While there is great promise in using eDNA to identify organisms from multiple trophic levels in a single sample of water, acquiring that sample can be surprisingly difficult. For instance, appropriately scaling sample acquisition to the spatial and temporal scales needed for effective biodiversity monitoring in aquatic environments would require prohibitively large investments in ship time and human resources. In this presentation we demonstrate how the use of an autonomous eDNA collection and preservation system, the Environmental Sample Processor (ESP), can help alleviate those limitations.

16:50-17:10 *Keynote:* The use of eDNA in the field of biogeochemistry, Alexandra Z. Worden
GEOMAR, Kiel, Germany

17:10-17:20 Sampling eDNA in deep sea ecosystems, Sophie Arnaud Haond
Ifremer, UMR MARBEC, Sète, France

17:20-17:30 Questions and discussion

17:30-18:00 Brainstorming session

Subgroup 1: Kevan Yamahara, Lionel Guidi, Manon Boosten

Subgroup 2: Alexandra Z. Worden, Damien Eveillard, Daniela Zeppilli

Session 3: Analysis methodologies (Chair: Peer Bork)

18:00-18:20 *Keynote:* Interpretations of eDNA in the context of community ecology, Jerome Chave
CNRS, UMR LEDB, Toulouse, France

27 April

Session 3: Analysis methodologies (continued; Chair: Peer Bork)

14:00-14:20 **Keynote:** Exploring the unknown: Linking past, present and future through metagenomics, Antonio Fernandez-Guerra

Centre for GeoGenetics, University of Copenhagen, Copenhagen, Denmark

14:20-14:40 **Keynote:** Community analyses, Pier Luigi Buttigieg

Helmholtz Metadata Collaboration, GEOMAR, Kiel, Germany

14:40-14:50 Network analysis of eDNA, Damien Eveillard

Tara Oceans, Université de Nantes, UMR LSNN, Nantes, France

14:50-15:00 Analysis of microbiomes, Peer Bork

EMBL, Heidelberg, Germany

15:00-15:10 Semi-quantitation in fish communities, Verena Trenkel

Ifremer, EMH, Nantes, France

15:10-15:20 Functional Metagenomics, Patrick Wincker

Tara Oceans, Génomscope, Evry, France

Abstract: Direct sequencing of DNA or RNA from microbial communities can in theory allow to access the functional information present in microbiomes. However, this information is difficult to leverage, due to high heterogeneity in genome abundances and frequent lack of homology of metagenomic genes to databases. These two main issues are particularly problematic for microbial eukaryotes, for which few reference genomes exist, and also because many species of ecological importance are evolutionary distant from model organisms. In this talk, we will consider how metatranscriptomics, single-cell genomics and genome-centered metagenomics can be used in combination to decipher the functional potential of eukaryotes in microbial communities.

15:20-15:30 Questions and discussion

15:30-16:00 Brainstorming session

Subgroup 1: Jerome Chave, Chris Bowler, Tobias Gerber

Subgroup 2: Antonio Fernandez-Guerra, Damien Eveillard, Fabienne Wiederkehr

Subgroup 3: Pier Luigi Buttigieg, Peer Bork, Agostino Leone

16:00-16:30 Coffee break

Session 4: Distinguishing DNA in living and from dead organisms (Chair: Philippe Gouletquer)

16:30-16:50 **Keynote:** eDNA stability in the marine environment, Grant Burgess

Newcastle University, Newcastle, UK

16:50-17:10 **Keynote:** Marine eDNA transport and diffusion, Elizabeth Andruszkiewicz Allan

University of Washington, USA

17:10-17:30 **Keynote:** Deposition and burial of eDNA in marine sediments, Michal Kucera

MARUM, Bremen, Germany



Abstract: Environmental DNA deposited in marine sediments consists of a cocktail of molecules settling from the water column, derived mainly from the pelagic community, mixed with "domestic" cellular and eDNA from benthic organisms that live on the sea surface and beneath. Since marine sediments are a potentially powerful archive of long-term changes in the composition of benthic and pelagic communities, it is important to decipher the nature of this eDNA cocktail. To this end, we studied the composition of eDNA metabarcodes of foraminifera on the sediment surface and several decimeters beneath. These abundant and diverse microscopic protists possess distinctive barcodes and contain benthic as well planktonic clades, the latter having a near complete barcode coverage. The analyses of foraminifera sedimentary metabarcodes indicate that the planktonic community composition is preserved in the eDNA settling on the seafloor and that this signature persists during burial in the sediment. We also show that key process affecting the composition of the sedimentary eDNA is rapid degradation of a labile portion of the total DNA, biasing the surface eDNA towards the youngest and freshest part of the settling flux. This process also leaves a strong imprint on the composition of benthic DNA, which is dominated by the living community until the depth of the inhabited zone. Collectively, these results show how eDNA on the seafloor could be used for monitoring of temporally averaged community composition, for the assessment of historical baselines and tracking of marine diversity changes on geological timescales.

17:30-17:40 Ancient DNA from phytoplankton, Chris Bowler
Tara Oceans, ENS, Paris, France

17:40-17:50 Sedimentary ancient DNA (sedaDNA) reveal shifts in marine protist communities after World War II and agricultural pollution, Raffaele Siano
Ifremer, DYNECO, Brest, France

*Abstract: To evaluate the stability and resilience of coastal ecosystem communities to perturbations occurred during the Anthropocene, pre-industrial biodiversity baselines inferred from paleo-archives are needed. The study of ancient DNA (aDNA) from sediments (sedaDNA) has provided valuable information about past dynamics of specific taxa, including Harmful Algal Bloom (HABs) species, and protist communities in relation to ecosystem variations. Here, sediment cores collected from different sites of the Bay of Brest (Northeast Atlantic, France) allowed ca. 1400 years of retrospective analyses of the effects of human pollution on marine protists and HABs. Comparison of sedaDNA extractions and metabarcoding analyses with different barcode regions (V4 and V7 18S rDNA) revealed that protist assemblages in ancient sediments are mainly composed of species known to produce resting stages. Heavy metal pollution traces in sediments were ascribed to the World War II period and coincided with community shifts within dinoflagellates and stramenopiles. After the war and especially from the 1980s to 1990s, protist genera shift followed chronic contaminations of agricultural origin, showing an increase in the HAB species *Alexandrium minutum* across the XXth century. Community composition reconstruction over the time showed that there was no recovery to a Middle-Age baseline composition. This demonstrates the irreversibility of the observed shifts after the cumulative effect of war and agricultural pollutions. Developing a paleoecological approach, this study highlights how human contaminations irreversibly affect the marine microbial compartments, which contributes to the debate on coastal ecosystem preservation and restoration.*

17:50-18:00 Questions and discussion

18:00-18:30 Brainstorming session

Subgroup 1: Chris Bowler, Mathilde Bourreau

Subgroup 2: Elizabeth Andruszkiewicz Allan, Bruno Ernande, Babett Gunther

Subgroup 3: Michal Kucera, Philippe Gouletquer, Leslie Pan

28 April

Session 5: Examples of applications and flagship projects (Chair: Lucie Zinger)

- 14:00-14:20 *Keynote:* Quantitation of macro-organisms, Ian Salter
Faroe Marine Research Institute, Faore Islands, Denmark
- 14:20-14:40 *Keynote:* Detection and monitoring of invasive species, Frédérique Viard
CNRS, UMR ISEM, Montpellier, France
- 14:40-15:00 *Keynote:* Global biodiversity observatory based on eDNA, Loic Pellissier (no streaming)
ETH Zürich, Switzerland
- 15:00-15:20 *Keynote:* Lakes as accumulators of large-scale biodiversity information, Kristy Deiner
ETH Zürich, Switzerland
- 15:20-15:30 Detection and monitoring of pathogens, Benjamin Morga
Ifremer, SG2M, La Tremblade, France
- 15:30-15:40 Protist biodiversity, Colombar de Vargas
Tara Oceans, CNRS, UMR ADMM, Roscoff, France
- 15:40-15:50 Questions and discussion
- 15:50-16:20 Brainstorming session
- Subgroup 1: Ian Salter, Detlev Arendt, Paola Bertucci
- Subgroup 2: Frédérique Viard, Philippe Gouletquer, Benjamin Morga
- Subgroup 3: Loic Pellissier, Peer Bork, Josipa Bilic
- Subgroup 4: Kristy Deiner, Damien Eveillard, Xavier Capet

16:20-16:50 Coffee break

Final discussion and wrap up

- 16:50-17:40 Wrap-up of the brainstorming sessions by rapporteurs
- Brainstorming session 1
- Brainstorming session 2
- Brainstorming session 3
- Brainstorming session 4
- Brainstorming session 5
- 17:40-18:30 Discussion of overarching topics