

# Short-term Dynamics of Dissolved Organic Matter and Bacterial Communities

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## INTRODUCTION

Dissolved organic matter (DOM) in the ocean is one of the largest carbon pools on earth, similar in size to atmospheric CO<sub>2</sub>. Due to its richness in energy and nutrients it is fundamental for marine food webs and for microbial life. The microbial loop is an essential compartment in the global carbon cycle and is important for the transformation and recycling of organic matter and nutrients in the oceans.

Microbial communities shape the molecular composition of DOM and vice versa. Earlier studies have shown that seasonal dynamics in DOM composition and microbial communities exist. A central aim of the study was to explore and characterize variations in composition of bacterial communities and DOM over much shorter periods of time, ranging from hours to days.

## RESULTS I

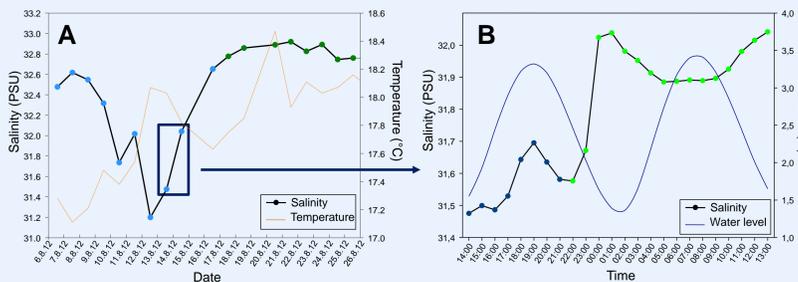


Fig. 2 A and B Salinity variation over daily (A) and hourly (B) sampling periods. Additionally, Figure A depicts the water temperature and figure B the water level.

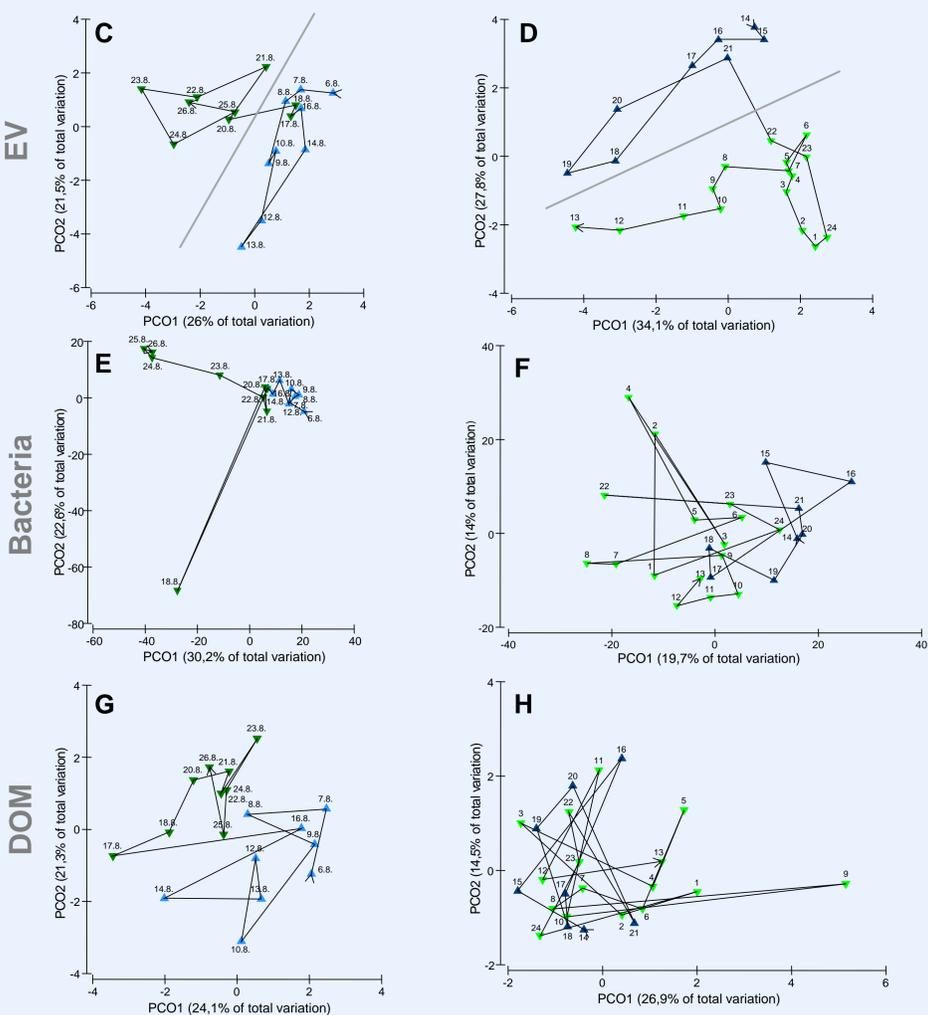


Fig. 2 C-H Principal coordinates analyses (PCO) of environmental variables (EV) based on Euclidean distance referring to daily (C) and hourly sampling (D), of bacterial community fingerprints based on Jaccard index referring to daily (E) and hourly sampling (F) and of molecular DOM composition based on Bray Curtis similarity referring to daily (G) and hourly sampling (H). Gray line separates groups of samples.

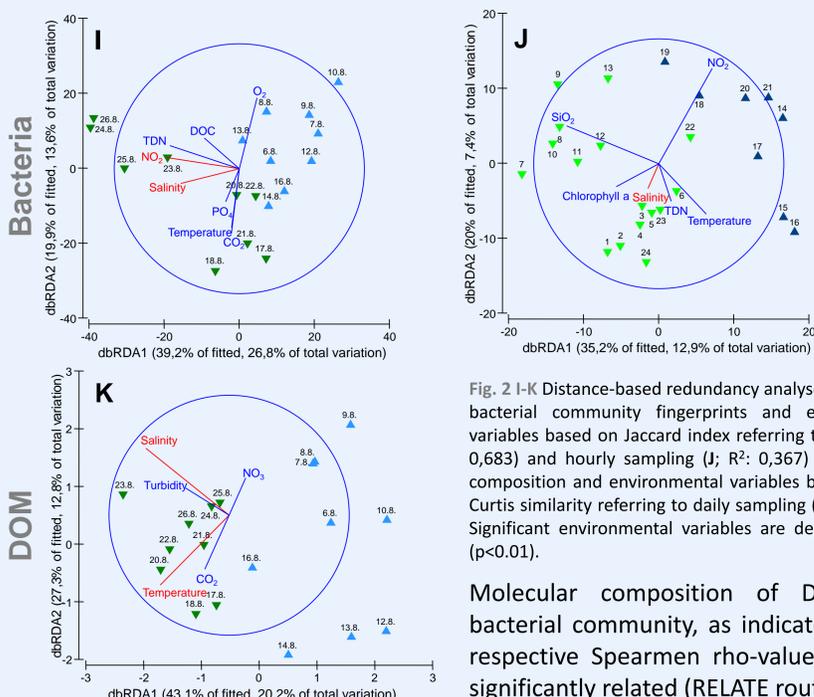


Fig. 2 I-K Distance-based redundancy analyses (dbRDA) of bacterial community fingerprints and environmental variables based on Jaccard index referring to daily (I; R<sup>2</sup>: 0,683) and hourly sampling (J; R<sup>2</sup>: 0,367) and of DOM composition and environmental variables based on Bray Curtis similarity referring to daily sampling (K; R<sup>2</sup>: 0,468). Significant environmental variables are depicted in red (p<0.01).

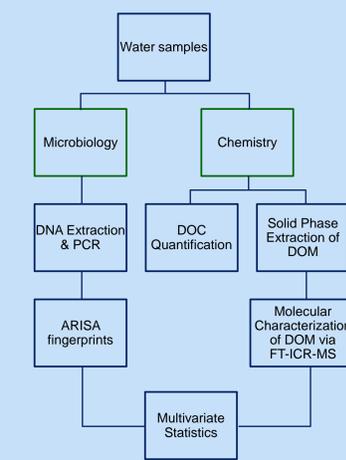
Molecular composition of DOM and bacterial community, as indicated by the respective Spearman rho-values are not significantly related (RELATE routine).

## SAMPLING AND METHODS

Water samples were taken daily over a period of 20 days and hourly (over 24 hours) in the open North Sea off Helgoland Island (Fig. 1).



Fig. 1 Helgoland Island is located in the German Bight in the North Sea. Sampling for time series took place at the Ferry-Box site.



- Bacterial community structure: Automated Ribosomal Intergenic Spacer Analysis (ARISA)
- Molecular DOM composition: several thousands of molecular formulas as determined by Fourier-Transform Ion Cyclotron Resonance Mass Spectrometry (FT-ICR-MS)
- Concentration of dissolved organic carbon (DOC)
- Environmental variables: Ferry-Box
- Statistical analyses: PRIMER 6 with the add-on package PERMANOVA+

## RESULTS II

Distance-based redundancy analysis (dbRDA) of DOM composition and environmental variables referring to daily sampling reveal that salinity and temperature are significant parameters (Fig. 2 K). Univariate correlations (Pearson) between these two parameters and the molecular composition of the daily sampling were calculated.

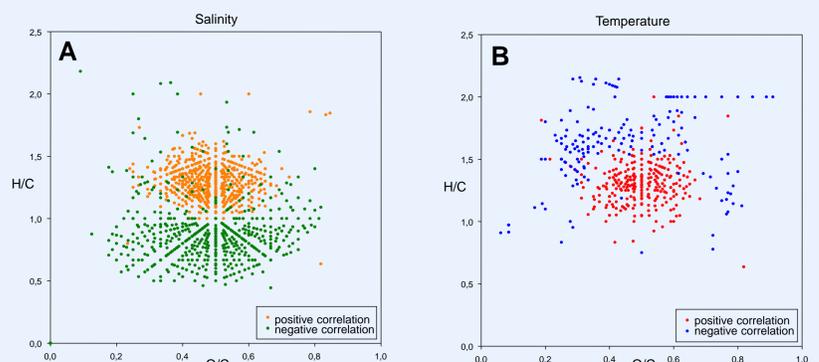


Fig. 3 Van Krevelen plots for molecular formulae of DOM of daily sampling which correlate significantly with salinity (A) and temperature (B).

Molecules, which are positively correlated with salinity are characteristic for marine DOM. Negatively correlated molecules are characteristic for terrestrial DOM (Fig. 3 A).

Most of the molecules, which are negatively correlated with temperature have a higher H/C ratio. This might indicate recent production of labile DOM (Fig. 3 B).

## CONCLUSION

- There was no relation between the composition of DOM and the bacterial community neither in daily sampling nor in hourly sampling.
- Two significantly different sample groups can be distinguished in both daily and hourly taken sets of samples of bacterial communities and molecular DOM composition (PERMANOVA, p<0.1). DOM samples taken hourly do not group significantly.
- Multivariate statistics (dbRDA) reveal that variations in bacterial community and DOM composition are mainly driven by salinity changes.
- Salinity and molecules typical for marine and terrestrial organic matter are significantly correlated.

## OUTLOOK

- Further information on bacterial community structure will be available through sequencing of bacterial DNA.

## Acknowledgement

We thank Prof. Dr. Karen H. Wiltshire (BAH, AWI Helgoland) for providing environmental data. We also thank Helena Osterholz for support during sampling of the 24h-time series, Matthias Friebe and Ina Ulber for technical assistance and Katrin Klaproth for help with FT-ICR-MS analysis.