**Spatial and temporal dynamics of the bacterial community in the German Bight**

Judith Lucas, Antje Wichels, Gunnar Gerds

Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, Helgoland, Germany

**Introduction**

Temporal and spatial diversity and variability of BCC in marine systems have been investigated separately in many studies during the past few decades. Bearing in mind that conditions in the marine environment are influenced by a large-scale hydrographic regime, exploring these structures by Eulerian approaches is merely adequate. The current study is aiming to assess the dynamics of the BCC in the German Bight on both, spatial and temporal scales at the same time and to link observations with hydrodynamic simulations. Water samples have been taken on monthly transects in the German Bight (Fig. 1) over a period of one year. Different habitats have been taken into account by sampling surface and bottom water and by separation of water samples via fractionated filtration (10 µm, 3µm, 0.2µm). To reveal seasonal and spatial patterns of the bacterial community, ARISA (automated ribosomal intergenic spacer analyses) fingerprints are being analysed currently, referring to various abiotic environmental parameters. A selection of preliminary results actually represents the 0.2 µm fraction of surface water samples.

**Results**

- **BCC and environmental data** appear very dynamic over time and space
- **Between-group variation** superimposes within-group variation (PERMANOVA and PERMDISP)
- **Partitioning (DISTLM)** revealed physico-chemical parameters to explain most of the variation
- **Temporal variation** seems to be dominated by temperature, spatial variation by CDOM
- **Multi-linearity**: temperature/DO (-0.9) and CDOM/DOC, turbidity, salinity (±0.8)

**Outlook**

- Analyses of bottom water, particle and plankton attached fractions
- 16S rRNA tag sequence analyses
- Linkage with hydrodynamic simulations

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* Nutrient data kindly provided by Prof. Dr. Karen Wiltshire and analysed by Kristine Carstens.

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**Fig. 1:** Sampling sites along transects in the German Bight

**Fig. 2:** Comparison of PERMANOVA and PERMDISP results. ARISA* fingerprints (jaccard) and environmental data (euclidean distance) have been analysed for the three transects P8 (A), Elbe (B), Eider (C). No significant variation (a), significant variation in PERMANOVA (b), significant variation in PERMANOVA and PERMDISP (c) (P < 0.05).

**Fig. 3:** Intersample distances (Jaccard index) of bacterial community fingerprints based on ARISA* using contextual data (dbRDA plot). Samples from march 2012 representing all three transects were chosen to demonstrate spatial variation (A) whereas all samples taken on transect PB serve to demonstrate temporal variation (B). Significant factors are depicted in red (P < 0.05). CDOM: colored dissolved organic matter, DO: Dissolved Oxygen, Sal: Salinity, Turb: Turbidity.

**Tab. 1:** Conditional effects of environmental parameters** on temporal and spatial variation. Distance-based linear model (DISTLM) analyses using jaccard dissimilarity and stepwise selection of explaining variables. Significant numbers are red (P < 0.05). Numbers showing the highest proportion of explanation are underlined.