Assessment of natural and man-made pressures on microbial communities

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Background

The ability to assess and predict the effects of human activities against a background of natural change is largely dependent on understanding and integrating the response of organisms at all levels of organisation. Although microorganisms play crucial roles in all marine ecosystems, they are currently excluded from routine marine monitoring and assessment programmes. However, investigating the diversity and structure of microbial communities as well as their relationship to the environment and other organisms hold promise as a potential tool to monitor ecosystem health.

The diversity of benthic bacterial and archaeal communities is being studied at Cefas, utilising different fingerprinting methods. These are combined with multivariate statistics to investigate the community response to environmental changes induced naturally or by human activity. Non-metric multidimensional scaling (MDS) and Canonical Correspondence Analysis (CCA) are applied to clarify how communities and specific microbial phylotypes respond to changes in their environment.

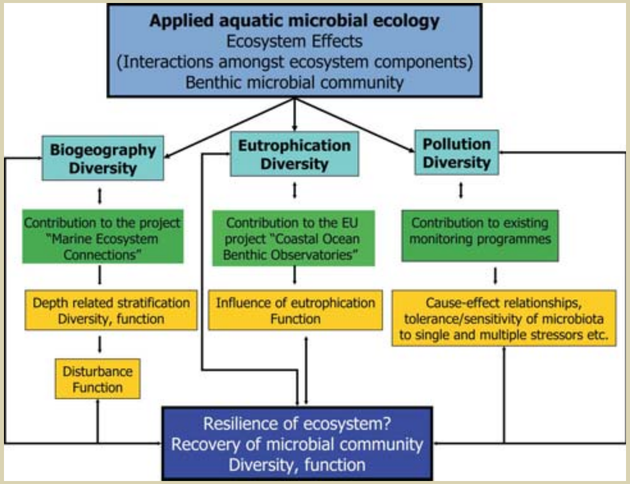

Figure 1. Overview of current and future research in microbial ecology at Cefas. Light blue = major topic; turquoise = research themes; green = planned research integrated into existing projects; yellow = future research topics based on data analyses of planned research ; dark blue = overall aim of all future studies.

Advancing understanding of biogeography-diversity relationships of microorganisms in the North Sea

Sediment

- Heterogeneous environment, local habitat characteristics
- Prevention of dispersal ➥Biogeography
- Physical environmental conditions ➥large scale patterns
- Food sources, local disturbances (natural or man-made) ➥small scale patterns

Benthic microbial communities

Diversity of communities and distribution of species
➥Ecological roles
➥Impact consequences

Influence of ecological factors on assemblages and scale of variation
➥Prediction of community change between areas

Study site: Oyster Ground, North Sea, 54°4'N / 4°'E;

- Small scale variation of bacterial and archaeal communities
- Link to variation in multicellular ecosystem components and habitat characteristics
- Prediction of community patterns by quality and quantity of carbon sources?

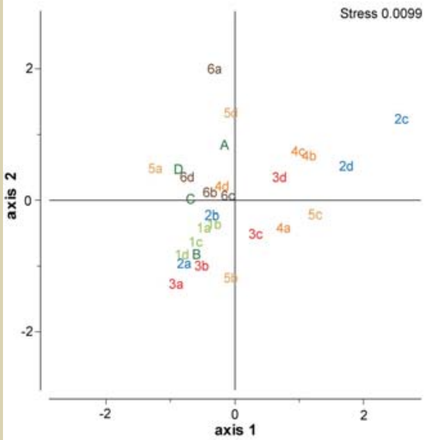

Figure 2. MDS plot based on Bray–Curtis similarities of bacterial communities (RISA fingerprints). Samples were collected at a replicated centre station (A-D) and 6 replicated surrounding stations (1-6). The ordination shows no strong separation of bacterial communities on the basis of stations as confirmed by the analysis of similarities (ANOSIM) with sample statistic R=0.241 (P=0.002).

Advancing understanding of eutrophication-diversity relationships

Eutrophication

- Increased rate of organic matter supply to an ecosystem due to inorganic nutrient enrichment
- Input of allochthonous organic carbon or pollutants (e.g. Fish farming)
- Decrease in water turbidity
- Decline in grazing pressure

➥ Proliferation and toxicity increase of harmful algal blooms
➥ Hypoxia and anoxia
➥ Altered routes/fluxes of organic and inorganic matter cycling
➥ Disruption of food webs
➥ Impacts on biogeochemical cycling and trophic relationships

Benthic microbial communities

Unique transformations in biogeochemical cycles
Community structure and function affected by eutrophication
Study site: Scotland, fish farm; contribution to EU funded project: Coastal Ocean Benthic Observatory

- Linkage of changes in microbial communities (bacterial and archaeal) including appearance of certain phylotypes and enrichment gradient
- Specific responses to impact by specific phylotypes or functional groups?

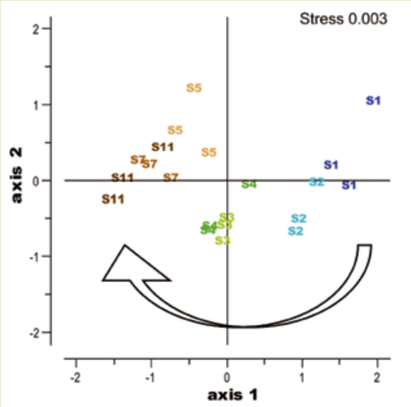

Figure 3. MDS plot based on Bray–Curtis similarities of bacterial communities (RISA fingerprints). The seven replicated stations sampled covered a gradient from unimpacted conditions (S1) to high organic carbon impact (S11). The ordination shows a clear shift of communities in response to the eutrophication impact (see arrow). This is confirmed by the analysis of similarities (ANOSIM) with sample statistic R=0.77 (P=0.001).

Acknowledgements

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