DGGE fingerprinting for microbial community monitoring as a new tool for anthropogenic impact assessment on the Belgian part of the North Sea

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Human activities at sea, such as sand extraction, may have an effect on the health status of the marine ecosystem. The assessment of the microbial communities on sediments will provide additional information on the potential impact of disturbances on biodiversity. A new assay for the evaluation of microbial diversity on sediments on the Belgian Part of the North Sea (BPNS) in relation to physical impact, based on the clustering of DGGE (denaturing gradient gel electrophoresis) profiles, will be presented.

Sediment samples were collected at 6 different locations on the BPNS using a Van Veen grab. DNA was extracted from the sediments and specific primers for bacterial (V3 region), protist (V8 region) and Archaea (V3 region) communities were used for the amplification with various PCR-techniques. These PCR products were loaded on a DGGE gel using an optimized protocol, which resulted in a clear DGGE fingerprint. Clustering of the genetic fingerprints was performed using Bionumerics.

The developed DGGE fingerprinting assay allows differentiating between sediment type, location on BPNS and used PCR technique based on the bacterial communities living on sediment. Since the used PCR techniques clearly influences the DGGE profile, it is important to develop a standard operating protocol for sampling and analysis. The standardized fingerprinting assay is a useful tool to integrate in monitoring programmes for the assessment of anthropogenic impact.

The genetic fingerprints revealed a higher bacterial diversity on muddy sediments compared to sandy sediments. To improve the taxonomical knowledge on the achieved bacterial profiles, bacterial species present on sediment could be identified using V3-V4 16S rDNA amplicon sequencing.

In 2015, the microbial diversity on sediment samples of the different marine sand extraction areas on the BPNS will be further evaluated using the DGGE fingerprinting clustering assay. Impact versus reference sites will be evaluated for each extraction area.

References:

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