

PATTERNS IN MICROBIAL DIVERSITY IN NORTH SEA SEDIMENTS; CORRELATIONS WITH SPECIFIC SEDIMENT CHARACTERISTICS AND HEAVY METAL POLLUTION

Pede Annelies¹, David Gillan², Yue Gao³, Gabriel Billon⁴, Ludovic Lesven⁴, Martine Leermakers³, Willy Baeyens³, Wim Vyverman and Koen Sabbe¹

¹ Ghent University, Department of Biology, Lab. Protistology and Aquatic Ecology, Krijgslaan 281-S8, 9000 Ghent, Belgium
E-mail: ajpede.pede@ugent.be

² Université Libre de Bruxelles, Marine Biology Laboratory, 50 Av Roosevelt, 1050 Brussels, Belgium

³ Vrije Universiteit Brussel, Department of Analytical and Environmental Chemistry, Pleinlaan 2, 1050 Brussels, Belgium

⁴ Université des Sciences et Technologies de Lille, UMR-CNRS 8110, France

Very little information is available on the diversity and structure of microbial communities in marine subtidal sediments, especially for micro-eukaryotes. In the framework of the Belgian MICROMET project, we investigated spatial (9 subtidal stations, top 0-1cm vs bottom 9-10cm) and seasonal (February vs July) variation patterns in the molecular diversity of archaeal, bacterial and eukaryotic communities in the Belgian Continental Plate (BCP) in relation to sediment granulometry, geochemistry and metal contamination. Microbial diversity was determined using DGGE and clone libraries based on the SSU rDNA gene; metals were determined using DET/DGT. Sediments ranged from sandy and well oxygenated to muddy, anoxic and heavily metal contaminated. Eukaryotic diversity was surprisingly high (20-50 phylotypes per station) and was dominated by Stramenopila (mainly diatoms), unidentified (or ambiguously identified) marine Eukaryotes, Metazoa and Fungi. Protozoa (Alveolata, Cercozoa, Foraminifera) were found in a lesser degree. While no clear trends in eukaryotic diversity between stations or seasons were found, community composition showed pronounced differences between sandy and muddy stations; spatial variation in diversity is much more pronounced in sandy stations. Seasonal differences were less marked. Archaeal diversity was very low to non-detectable in all stations. Bacterial diversity was dominated by γ - and δ -Proteobacteria and CFB bacteria; eubacterial diversity was significantly reduced in the muddy sediments.