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TITLE: Composition and population dynamics of planktonic bacteria and bacterivorous flagellates in seawater chemostat cultures

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ABSTRACT:

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Composition and population dynamics of planktonic bacteria and bacterivorous flagellates in seawater chemostat cultures Ramon Massana¹, Klaus Jürgens^{2,3,*} ¹Institut de Ciències del Mar, CSIC, Passeig Marítim de la Barceloneta 37-49, 08003 Barcelona, Catalonia, Spain ²Max Planck Institute for Limnology, Department of Physiological Ecology, PO Box 165, 24302 Plön, Germany ³Present address: Baltic Sea Research Institute, Seestrasse 15, 18119 Rostock, Germany *Corresponding author. Email: klaus.juergens@io-warnemuende.de
ABSTRACT: We studied the effects of protist predation on the composition and morphological structure of a marine bacterioplankton assemblage. A mixed bacterial assemblage (0.6 µm filtered North Sea inoculum) was cultivated with unamended seawater as medium in four 1-stage chemostats. After the establishment of a bacterial community, 2 of the chemostats received a 2 µm filtered seawater inoculum which enabled the development of heterotrophic nanoflagellates (HNF). The dynamics of bacterial and protist community composition in the chemostat cultures was followed by terminal-restriction fragment length polymorphism (T-RFLP) and denaturing gradient gel electrophoresis (DGGE). These fingerprinting techniques revealed that continuous cultivation with unsupplemented seawater altered the bacterial community composition compared to the inoculum. Fluorescent in situ hybridisation (FISH) analysis showed that the bacterial assemblages in the chemostats were dominated by γ -Proteobacteria, particularly of the genus *Alteromonas*. Despite this shift, the overall richness of bacteria in the chemostats remained relatively high with up to 30 different operational taxonomic units (OTUs). HNF exerted efficient grazing control on the bacterial communities during 3 wk of cultivation and reduced bacterial biomass to approximately 10% of that in the predator-free chemostats. Only a modest development of grazing-resistant bacteria occurred, which contrasts with previously published chemostat experiments with freshwater microbial communities. T-RFLP and DGGE analyses also revealed that protist grazing did not result in significant changes in bacterial community composition. However, both fingerprinting techniques showed a relatively high richness (up to 15 different OTUs) and an ongoing succession within the protist assemblage, which might be one explanation for only low feed-back effects and low appearance of grazing-resistance in the predation-controlled bacterial community. KEY WORDS: Protist predation · Bacterial community composition · Heterotrophic nanoflagellates · Population dynamics · Chemostat cultures · T-RFLP · DGGE · FISH Full article in pdf format PreviousNextExport citation RSS - Facebook - Tweet - linkedIn Cited by Published in AME Vol. 32, No. 1. Online publication date: May 12, 2003 Print ISSN: 0948-3055; Online ISSN: 1616-1564 Copyright © 2003 Inter-Research.

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