

# SPATIAL AND TEMPORAL SCALES FOR THE MONITORING OF BACTERIAL COMMUNITY STRUCTURE IN COASTAL ECOSYSTEMS.

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## Summary

One of the challenges in microbial ecology is to determine at what temporal and spatial scales the structure of natural communities should be monitored. Samples of different volumes and taken at different spatial (vertical and horizontal) and temporal (from hours to seasons) scales were analyzed to investigate at which scale one should monitor community structure at a coastal station. Investigations were performed in the Bay of Banyuls (Mediterranean, France). No changes in the community structure was detectable within a radius of 200 meters around the station whereas changes were found at both weekly and monthly scales.

*Keywords : marine bacterial communities, diversity, sampling strategy*

The last decade of microbial ecology has resulted in a veritable explosion of studies that use new molecular biological techniques to analyse the structure of microbial communities. These studies have improved our perception of microbial diversity and community composition in marine ecosystems (1). However, the temporal and spatial scales at which bacterial populations vary remained poorly documented. A comparison of recent studies of bacterial community dynamics in pelagic marine waters showed minimal differences in community compositions at stations a few miles apart near Anvers Island, Antarctica (2) or 1500 km apart in the Arabian Sea (3), in opposition to clear differences observed along the Catalan Coast, Spain (4). Short-term studies showed major changes in bacterial communities consequent to qualitative changes in the pool of organic matter (5, 6). These evidences for space- and time-dependent bacterial community changes emphasized the importance of sampling strategies when studying the dynamic of natural communities.

Although a large set of methodologies have been developed to investigate the structure of bacterial communities, the selection of the most appropriate method depends on the questions to be answered and on the amount of samples to be processed within a reasonable period of time. Fingerprinting approaches offer the best compromise for the monitoring and comparison of microbial assemblages and for the assessment of temporal and spatial changes that would not have been feasible using time-intensive 16S rDNA sequence analysis. Denaturing gradient gel electrophoresis (DGGE) has become a very popular fingerprinting technique in marine microbial ecology, especially because bands with particular melting behaviour can be excised from the gel and subsequently sequenced to reveal the phylogenetic affiliation of the community members (7). However, its laborious technical optimisation including calibration of the linear gradient of DNA denaturants that makes gel-to-gel comparison difficult have made this technique impractical for the fine comparison of more than samples loaded on one gel (8). The recently developed capillary electrophoresis-single strand conformation polymorphism (CE-SSCP) fingerprinting technique permitted high reproducibility for reliable comparison of patterns from a theoretically infinite number of samples. Because a size standard with a different fluorescent

label is added to each sample, CE-SSCP and further computing correction encompassed the problem of gel-to-gel comparison (9).

In this study, CE-SSCP technique was used to determine spatial and temporal scale changes in the structure of bacterial communities in a coastal ecosystem. Samples of different volumes and taken at different spatial (vertical and horizontal) and temporal (from hours to seasons) scales were analyzed to investigate at which scale one should monitor community structure at a coastal station. Investigations were performed in the Bay of Banyuls (Mediterranean, France).

No changes in the community structure was detectable within a radius of 200 meters around the SOLA station but changes occurred at larger scales. Changes were found at both weekly and monthly scales. Cluster analysis based on a one-year monitoring at the SOLA station showed changes in the seasonal distribution of bacterioplankton community structure, without any return to the initial community structure after one year (Fig. 1).

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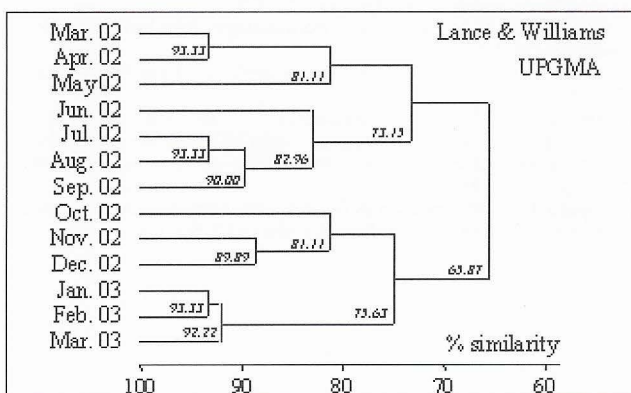


Fig. 1. Cluster analysis dendrogram based on comparison of 16S PCR-CE-SSCP patterns from one year sampling at the SOLA station (Mediterranean, France). The tree was constructed by applying unweighted pair group average linkage rules on a Lance and Williams index of similarity matrix calculated from the CE-SSCP profiles.