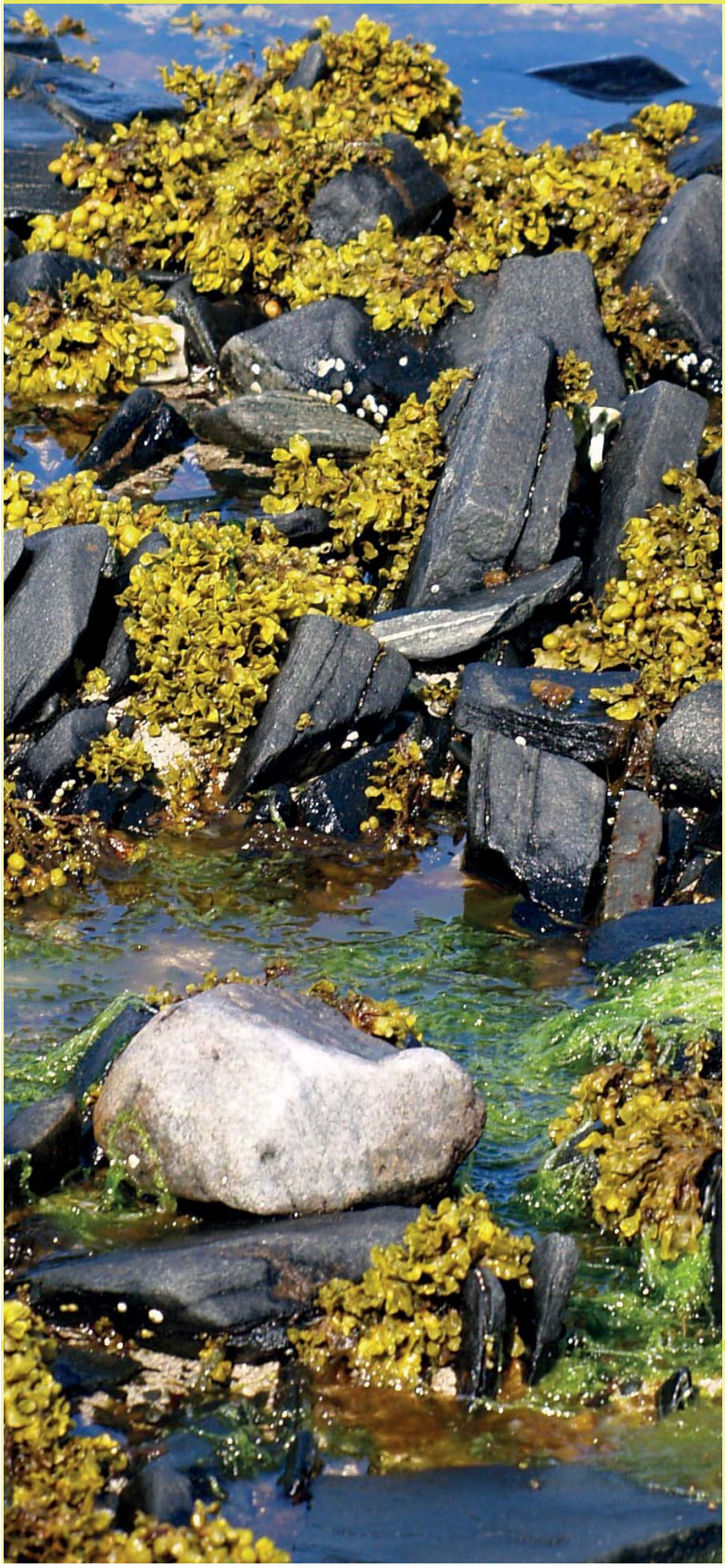
The 12th Symposium on Aquatic Microbial Ecology



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Morphological- versus molecular-based diversity surveys of planktonic microbial eukaryotes: the case of tintinnid ciliates

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During the last decade, the use of culture-independent molecular approaches to describe the communities of microbial eukaryotes present in natural environments has led to the discovery of a huge diversity of these organisms. However, these analyses have rarely taken into account the temporal pattern of variation of diversity and most often lacked of a comparison of morphological- and molecular-based estimates. In this context, we have studied the temporal pattern of genetic diversity of tintinnids (Ciliophora) over a two-year survey in a Mediterranean Sea location (Villefranche-sur-Mer, France). The species-rich order Tintinnida contains freshwater and marine ciliates easily distinguishable based on morphological characters, in particular their conspicuous organic or inorganic tests. This allowed us to couple morphological observations with a double molecular approach (using *single cells and environmental DNA) to analyse the SSU*-rRNA *and the ITS coding regions.* Using a fingerprinting technique (DGGE), we detected a strong relationship between the structure of the tintinnid communities and the sampling depth. Despite an extensive work of single-cell isolation, identification, and subsequent *SSU*-rRNA *and ITS* sequencing, the analysis of tintinnid communities by direct PCR amplification and sequencing of rRNA genes from plankton samples revealed a number of phylotypes without any closely related known species. Conversely, several sequences from single-cell analyses were never found in the environmental sequence libraries. Using this well-characterized protist group, we discuss the limitations of morphological- and molecular-based studies to assess the diversity and temporal dynamics of microbial eukaryotic communities.