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Marine protist diversity in European coastal waters and sediments as revealed by high-throughput sequencing

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Summary

Although protists are critical components of marine ecosystems, they are still poorly characterized. Here we analysed the taxonomic diversity of planktonic and benthic protist communities collected in six distant European coastal sites. Environmental deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) from three size fractions (pico-, nano- and micro/mesoplankton), as well as from dissolved DNA and surface sediments were used as templates for tag pyrosequencing of the V4 region of the 18S ribosomal DNA. Beta-diversity analyses split the protist community structure into three main clusters: picoplankton-nanoplankton-dissolved DNA, micro/ mesoplankton and sediments. Within each cluster, protist communities from the same site and time clustered together, while communities from the same site but different seasons were unrelated. Both DNA and RNA-based surveys provided similar relative abundances for most class-level taxonomic groups. Yet, particular groups were overrepresented in one of the two templates, such as marine alveolates (MALV)-I and MALV-II that were much more abundant in DNA surveys. Overall, the groups displaying the highest relative contribution were Dinophyceae, Diatomea, Ciliophora and Acantharia. Also, well represented were Mamiellophyceae, Cryptomonadales, marine alveolates and marine stramenopiles in the picoplankton, and Monadofilosa and basal Fungi in sediments. Our extensive and systematic sequencing of geographically separated sites provides the most comprehensive molecular description of coastal marine protist diversity to date.