

Paper report

Oceanic 18S rDNA sequences from picoplankton reveal unsuspected eukaryotic diversity.

SY Moon-van der Staay, R De Wachter, D Vault. *Nature* 2001, **409**: 607-610.

Techniques commonly applied to the discovery of unknown prokaryotes have now been used to identify new eukaryotic lineages within picoplankton

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Significance and context

Over the past decade, environmental microbiologists have used molecular techniques to discover a wide diversity of previously unknown prokaryotes, including major lineages of both archaea and eubacteria. The methodology of these studies is now routine; PCR primers for highly conserved regions of the small-subunit ribosomal RNA gene are used to amplify a portion of the rDNA sequence from DNA extracted directly from environmental samples; the products are then cloned and sequenced. Phylogenetic analysis of such sequences has revealed a startling bacterial diversity in every environment so far investigated, from deep Antarctic Ocean water to thermal springs and from paddy-field sediment to desert soils. Some of the most exciting results have come from studies of plankton communities.

These methods have been very little used on eukaryotic microorganisms, however. Despite a growing sense of our ignorance of the extent of biodiversity, the feeling seems to have been that the largest branches of the tree of eukaryotic life are largely described. Recent culture-based studies have, however, identified two new groups of marine planktonic eukaryotes, raising expectations that tiny plankton may harbor more surprises. Moon-van der Staay and colleagues report one of the first large-scale molecular studies of marine picoplankton (microorganisms of < 3 µm diameter), revealing for the first time the true diversity of eukaryotes in this environment.

Key results

Moon-van der Staay *et al.* used primers to regions of the 18S rRNA gene conserved across most, but not all, eukaryotes, to clone 103 and sequence 35 almost full-length 18S sequences derived from picoplankton of the equatorial Pacific. Only two of the sequences showed 99% identity to known organisms, but phylogenetic analysis revealed that most of the sequences are either from new members of known eukaryotic lineages or are related to known organisms. The results confirm the importance of autotrophic groups such as haptophytes and prasinophytes in this environment. Among the more arresting discoveries is a new lineage that appears to be very common among the picoplankton: 6 out of 35 sequenced clones belong to a lineage related to both the dinoflagellates and the parasitic Perkinsozoa. This clade could be related to the currently unsequenced heterotroph *Oxyrrhis*. Also well represented are acantharians, stramenopiles and dinoflagellates. In most cases, it is unclear whether the divergent environmental clones belong to auto- or heterotrophic clades within these groups, although the majority of dinoflagellate sequences seem, rather surprisingly, to form a lineage with a parasitic organism, *Amoebophrya*.

Links

The full text of Moon-van der Staay *et al.*'s article together with a similar article on Antarctic picoplankton by a different group in the same issue are available to [Nature] [<http://www.nature.com>] subscribers.

Reporter's comments

Any study that claims to have discovered important new lineages of living organisms is exciting, and this is no exception. Although the new lineages identified in this study may not be as significant as the Korarchaeota, a major division of life, they will undoubtedly attract much interest, and molecular microbiologists will already be planning experiments to learn more about the morphology and ecology of these organisms using the full battery of molecular techniques now available.

It is perhaps not surprising that picoplankton diversity seems to be poorly understood from culture-based work - the small size and low morphological disparity of these organisms gives morphological systematists little information by which to classify them. This study confirms that molecular environmental studies can uncover new organisms among the smallest eukaryotes, to almost the same extent as they have among prokaryotes. It will be intriguing to see how these techniques perform in studying the small organisms that exist in every environment. Zoologists may assume that they have described the vast majority of higher taxa, but the last new animal phylum distinguished, the Cycliophora, was discovered only in 1995, and another unusual organism, *Limnognathia maerski*, was described only in 2000. It would be intriguing to see what molecular techniques would reveal lurking among the meiofauna, where *Limnognathia* and

the Loricifera, another recently described phylum, were found. I am sure that other biologists can think of other environments where new members of their favourite taxonomic group could be uncovered by similar experiments.

An important conclusion of this work is that heterotrophic, and specifically parasitic, lineages seem to be well represented among the sequenced clones and so, presumably, are important in the plankton environment. This shows the potential of molecular techniques for learning about the ecology of microbes. Molecular methods have produced an explosion in our understanding of bacterial community structure and function, and it is no exaggeration to claim that this has led to a renaissance in microbial ecology and evolution. Molecular studies have moved microbiology back into the mainstream of biology, and it would be surprising if their introduction into a wider sphere of environmental biology did not bring surprising new insights across the whole range of biological diversity.

Table of links

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