



## Abundance and diversity of prymnesiophytes in the picoplankton community from the equatorial Pacific Ocean inferred from 18S rDNA sequences

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**ABSTRACT:** Picoplankton, i.e., cells smaller than 2-3  $\mu\text{m}$ , dominate in most open oceanic regions, such as in the Pacific Ocean. In these areas, the dominant carotenoid of photosynthetic eukaryotes is 199-hexanoyloxyfucoxanthin (19HF), considered to be a diagnostic marker for prymnesiophytes. This suggests that this class could be a major component of eukaryotic picoplankton, despite the fact that virtually no prymnesiophyte has been described to date from this size class. To address this question, we assessed prymnesiophyte diversity and abundance in natural picoplankton communities, using a molecular approach. Total genomic DNA was isolated from 3- $\mu\text{m}$ -filtered samples collected in the Pacific Ocean. Small subunit (18S) ribosomal RNA genes (rDNA) were amplified by the polymerase chain reaction (PCR) using universal eukaryotic primers. The relative abundance of 18S rDNA from prymnesiophytes was quantified using group-specific and eukaryotic 18S rDNA probes. The percentage of the prymnesiophyte versus total 18S rDNA was much lower than the percentage of prymnesiophytes calculated on the basis of pigment analyses for the same samples. 18S rDNA libraries from five samples were screened using a prymnesiophyte-specific oligonucleotide probe, and 14 nearly complete 18S rDNA sequences were retrieved. Phylogenetic analysis of these sequences established the presence of several prymnesiophyte lineages with no equivalent among cultivated species.

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