



Composition and temporal variability of picoeukaryote communities at a coastal site of the English Channel from 18S rDNA sequences

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ABSTRACT: We analyzed picoeukaryote assemblages at a French coastal site of the English Channel by sequencing cloned eukaryotic 18S rRNA genes in eight genetic libraries constructed from environmental samples (seven coastal, one estuarine) collected at different periods of the year. Eight hundred clones were examined by amplified restriction fragment length polymorphism (RFLP) using the restriction enzyme *Hae*III. The coverage value calculated from the relative distribution of RFLP types was low, indicating that the library diversity was not entirely recovered. A variable region of the rRNA gene was partially sequenced (550 bases) and analyzed for 397 clones. Thirty-two clones were affiliated with metazoans. Of the remaining clones, 132 were affiliated to algal classes (especially Prasinophyceae, Cryptophyceae, Dinophyceae, and Prymnesiophyceae) and 107 to known heterotrophic groups (Cercozoa, choanoflagellates, stramenopiles, and ciliates). One hundred three sequences fell into uncultivated groups of stramenopiles (43 clones) and alveolates (60 clones). We also found two potentially novel eukaryotic lineages, represented by 9 and 14 clones, respectively, not belonging to any known eukaryotic group. The overall composition of the picoeukaryote community remained fairly stable at the class/division level except during the early summer diatom bloom, when groups such as the Cryptophyceae and the ciliates completely disappeared. However, at a finer taxonomic level (corresponding to 98% sequence identity), the majority of the operational taxonomic units (OTU) were only observed once.

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