



## Distribution of eukaryotic picoplankton assemblages across hydrographic fronts in the Southern Ocean, studied by denaturing gradient gel electrophoresis

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Limnol. Oceanogr., 49(4), 2004, 1022-1034 | DOI: 10.4319/lo.2004.49.4.1022

**ABSTRACT:** We used a molecular fingerprinting technique to analyze the distribution and composition of eukaryotic picoplankton along latitudinal transects in the Southern Ocean. First, primers specific for eukaryotic 18S rDNA were used in a polymerase chain reaction (PCR) with environmental DNA. The amplification products were subjected to denaturing gradient gel electrophoresis (DGGE). Transect DOVETAIL (44° W) went from the ice edge (at 60° S) across the Weddell-Scotia confluence and north to 58° S; it was sampled in January 1998 (summer). Transect DHARMA (between 53° W and 58° W) went from the ice edge in the Weddell Sea (63° S) across the Drake Passage to the South American continental platform (55° S); it was sampled in December 1998 (late spring). DGGE band patterns were used to build dendrograms combining samples from each cruise. Samples were grouped in several distinct clusters that were generally consistent with the hydrography of the area. In DOVETAIL, the upper water column was stratified and the DGGE band patterns varied with depth. In DHARMA the upper mixed layer showed the same composition of the eukaryotic picoplankton at all depths. The most dominant DGGE bands were excised and sequenced. Some were closely related to well-known components of the plankton such as prasinophytes, prymnesiophytes, dinoflagellates, and diatoms. A significant number of sequences were related to previously unknown phylogenetic groups, including novel stramenopiles and alveolates or to poorly known groups such as cercozoans. This fingerprinting technique is useful for a rapid evaluation of the spatial distribution of picoeukaryotic assemblages in the oceans.

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