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The archaebacterial communities in Antarctic bathypelagic sediments

David C. Gillan[a,*], Bruno Danis[b]

[a]*Marine Biology Laboratory, CP160/15, Université Libre de Bruxelles, 50 av. Roosevelt, 1050 Brussels, Belgium*
[b]*Royal Belgian Institute of Natural Sciences, 29 Rue Vautier, 1000 Brussels, Belgium*

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Abstract

16S ribosomal DNA clone library analysis was performed to assess archaeal diversity within three surficial sediment samples obtained from the bathypelagic zone (depth: 2165–3406 m) of the Weddell Sea, Antarctica. The nearly complete 16S rDNA gene (1440 bp) was obtained for 146 clones and 46 phylotypes were defined. The majority of the sequences (>99%) formed three clusters within the Marine Group I Crenarchaeota. The most important cluster, with 78.8% of the clones, included Candidatus *Nitrosopumilus maritimus*, a mesophilic archaeon able to oxidize ammonia. The most important subgroup in that cluster was the APA4-0cm subgroup (with 62.3% of the clones). This subgroup might represent important Crenarchaeota in the functioning of the bathypelagic sedimentary ecosystems of the Weddell Sea because it dominated the clone libraries in all sampling stations, and was found in sediments separated by very large geographic distances. Only one clone grouped within the Euryarchaeota. This euryarchaeal clone could not be affiliated with any of the previously defined clusters and might represent a novel euryarchaeal lineage.

Keywords: Archaebacteria; Crenarchaeota; Sediments; Antarctic; 16S rDNA; Marine Group I

1. Introduction

Phylogenetic analyses based on ribosomal DNA have shown that the archaeal domain of life is mainly composed of two kingdoms, the Euryarchaeota and the Crenarchaeota (Woese et al., 1990). Other deeply branching archaeal clades such as the Korarchaeota and the Nanoarchaeota also have been found (Huber et al., 2002; Auchtung et al., 2006). Within the last several years, the two main lineages have been recovered from many realms such as coastal seawater (e.g., DeLong, 1992), deep-sea plankton (e.g., Karner et al., 2001), marine sediments (e.g., Vetriani et al., 1999), freshwater lakes (e.g., Jurgens et al., 2000), terrestrial soils (e.g., Leininger et al., 2006) and macrobiota (e.g., van der Maarel et al., 1998), and it is becoming evident that Euryarchaeota and Crenarchaeota are important members of marine and terrestrial ecosystems (Herndl et al., 2005; Könneke et al., 2005; Leininger et al., 2006). Despite the high abundance and richness of archaea in the deep-sea plankton (Karner et al., 2001; Bano et al., 2004) and in the Southern Ocean (Massana et al., 1998; Murray et al., 1999;

*Corresponding author. Tel.: +32 2 6502970; fax: +32 2 6502796.
E-mail address: dgillan@ulb.ac.be (D.C. Gillan).

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Church et al., 2003; Bano et al., 2004), little work has been carried out on the diversity of the archaeal communities in deep-sea Antarctic sediments. Only two studies addressing mesopelagic sediments (150–1000 m) have been published so far and were carried out in the Eastern sector of the Southern Ocean (Bowman and McCuaig, 2003; Bowman et al., 2003). The other reports dealing with archaeal diversity in Antarctic sediments have been restricted to shallow coastal environments (Bowman et al., 2000; Powell et al., 2003; Purdy et al., 2003).

In the study of Bowman and McCuaig (2003), conducted in the continental shelf area (depth, 761 m), the Marine Group I Crenarchaeota predominated in the sediment 16S ribosomal DNA libraries, particularly in the surface sediments (0–2 cm), where the group represented 88.4% (76 sequences) of the archaeal 16S rDNA clones. The rest of the archaeal clones in the surface sediments grouped within the crenarchaeal APA3-11 group (5.8%; five sequences) and the Euryarchaeota (5.8%; five sequences) (Bowman and McCuaig, 2003). In the latter group, only one clone in the surface sediments grouped with the previously described Marine Benthic Group D, the other clones being affiliated with the pBRC84, the ACE-6 or the PENDANT-33 groups (Bowman and McCuaig, 2003). In the second study, focused on the mesopelagic zone, sediments were sampled at a depth of 709–940 m (Bowman et al., 2003) and the relative abundance of archaebacteria was assessed by using the group-specific ARC915 oligonucleotide probe, which targets the 16S rRNA molecule. The results indicated that archaeal 16S rRNA represented only 1–6% of the total 16S rRNA pool in the surface sediments. Similar quantities of archaeal 16S rRNA have been observed at other depths in other sediments such as Arctic sediments (Ravenschlag et al., 2001) and Atlantic sediments (Vetriani et al., 1999).

The aim of the present work was to investigate the archaeal diversity in three bathypelagic (1000–3500 m) stations of the Weddell Sea (Antarctica) using a 16S rDNA cloning and sequencing strategy (Gillan et al., 2005). To the best of our knowledge, sediments from the bathypelagic zone have never been investigated in the Southern Ocean using this approach.

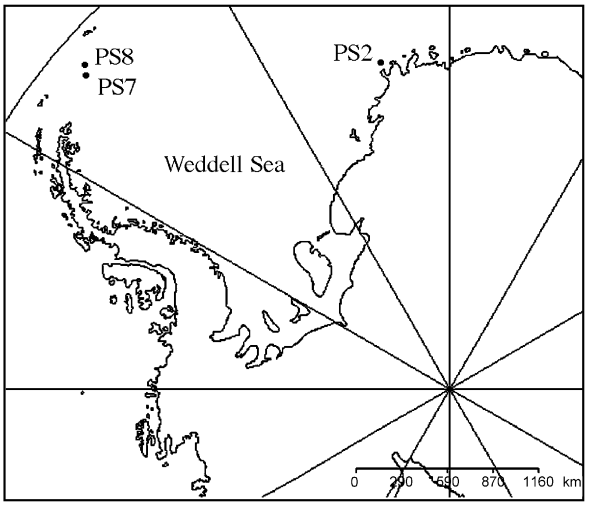

Fig. 1. Position of the sampling stations.

2. Methods

2.1. Sampling

Archaeal communities were analyzed in sediments in three bathypelagic stations (2200–3400 m) sampled during the ANTXXII-3 cruise of R.V. *Polarstern* (ANDEEP3) (Fig. 1). Characteristics of the sampling stations are described in Table 1. Sediments were sampled using a box-corer. The sediments were immediately and aseptically sampled using 3 ml polyethylene (PET) cryovials (top 2 cm of the sediments). The cryovials were immediately frozen in liquid nitrogen and the samples were then stored at −20 °C. Six replicate samples of the same core were collected at each site.

Table 1
Characteristics of stations sampled during ANDEEP3 for Archeal communities analysis

Station names	Official names	Date (2005)	Latitude (S)	Longitude (W)	Depth (m)	Seafloor
PS2	PS67-78	21.02.05	71°9.49′	13°59.92′	2164	Mud, rocks
PS7	PS67-121	14.03.05	63°41.74′	50°42.99′	2621	Mud
PS8	PS67-142	18.03.05	62°11.61′	49°29.45′	3406	Mud