

Original Article

Bacterial Diversity of Ny-Ålesund, Arctic Archipelago Svalbard

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Abstract

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The bacterial diversity of the water sample, collected from Ny-Ålesund, Arctic Archipelago Svalbard was analyzed by a phenotypic as well as a genotypic approach. Pure colonies of the culturable bacteria were established and grown at a range of temperatures: 4°C, 15°C, 22°C and 37°C. Optimum growth was found at 15°C, and around 28 colonies were obtained. The library was dominated by 16S rDNAs of Gram-negative bacteria (γ -Proteobacteria). Twenty two isolates exhibited sequences were similar to that of known bacterial isolates (>97% sequence similarity), represented by the species of the genera *Psychrobacter*, *Pseudomonas*, and *Acinetobacter*. Six isolates exhibited sequences showed less affiliation with known taxa (<97% sequence similarity), and may represent novel taxa.

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Introduction

An enormous amount of effort is being made worldwide by microbial ecologists to identify microorganisms from environmental samples. In recent years, growing attention in research has been devoted to cold-adapted microorganisms. They successfully colonize cold habitats, which compose more than 80% of the earth's biosphere, and play a major role in the processes of nutrient turnover at low temperatures (Kottmeier & Sullivan, 1990; Rivkin *et al.*, 1989). Polar regions are of interest since they provide diverse terrestrial and marine habitats for psychrophilic microorganisms. Several authors have isolated a number of psychrophiles from Arctic sea that showed considerable phylogenetic diversity. Physiological types include proteolytic, cellulolytic, amyloytic, lipolytic, acetogenic and

sulfate-reducing bacteria (Tatiana *et al.*, 2004)

Among sea-ice prokaryotes, members of eight phylogenetic groups, subclasses α , β and γ of Proteobacteria, the Cytophaga-Flavibacterium-Bacterioides (CFB) phylum group, the high- and low-G+C Gram positives, and the orders Verrucomicrobiales and Chlamydiales have been detected by using the 16S rDNA approach (Brown & Bowman, 2001; Petri & Imhoff, 2001).

Plankton communities of polar oceans appeared to be more diverse than sea-ice bacterial communities. Archaea, δ and ϵ Proteobacteria, and green non-sulfur bacteria were detected in seawater in addition to the phylogenetic groups known from sea ice (DeLong *et al.*, 1994; Massana *et al.*, 1998).