

Bacterial diversity and bio-potentials of culturable bacteria associated with different age sediments of Svalbard, Arctic

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Permafrost is a unique habitat in polar environment and has ecological and biotechnological importance. The present study is focused on characterization of bacterial communities from permafrost pit profiles of Svalbard, Arctic. The culturable count of the isolates ranged from 1.50×10^3 to 2.22×10^5 CFUs/g while the total bacterial numbers ranged from 1.14×10^5 and 5.52×10^5 cells/g soil. Representative bacterial isolates were identified through 16S rRNA gene sequencing and results indicate that *Arthrobacter* and *Pseudomonas* were the most dominant genera with *A. sulfonivorans*, *A. bergeri*, *P. mandelii* and *P. jessenii* as the dominant species. Rest of the species belonged to genera *Acinetobacter*, *Bacillus*, *Enterobacter*, *Nesterenkonia*, *Psychrobacter*, *Rhizobium*, *Rhodococcus*, *Sphingobacterium*, *Sphingopyxis*, *Stenotrophomonas* and *Virgibacillus*. Radiocarbon dates of the Permafrost pit profile sediments were analysed. The bacteria preserved in the different sediments studied aged 12250 to 44800 years old. To the best of our knowledge this is the first record of culturable bacterial communities and their chronological characterization from permafrost pit profile from Svalbard, Arctic. Physiological, biochemical, antibiotic susceptibility and enzyme screening tests were carried out. Cold-adapted enzyme production ability of the bacterial isolates provides a clue to their potential prospect in biotechnological research.

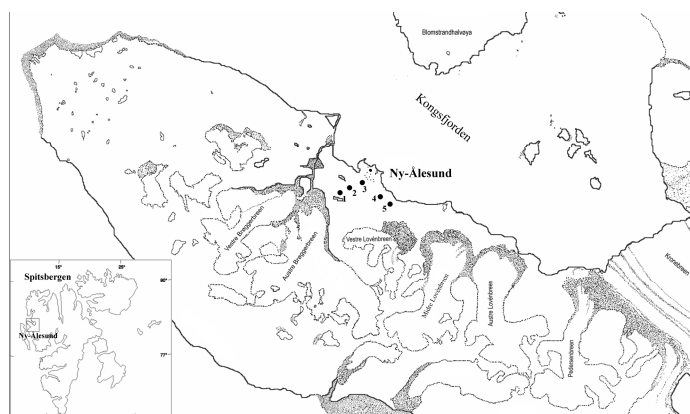


Figure 1 Map of Spitsbergen, Kongsfjord, Arctic showing sampling sites (•1 to •5).

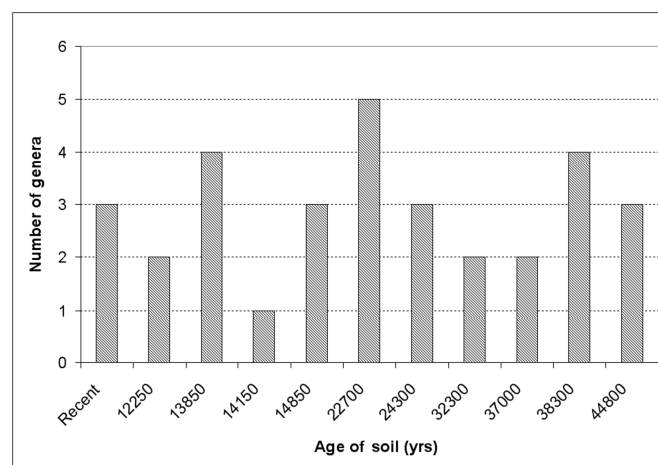


Figure 2 Number of genera reported at each permafrost soil age.

Table 1. Showing the enzyme production by the isolated strains, AMS dates of sediments, NCBI sequences deposition numbers and identification of strains through 16S rRNA gene sequences similarity (%).

Strain no.	NCBI Sequence deposition no.	Identification (16S rRNA gene sequences similarity (%))	Age	Amylase	Cellulase	Lipase	Protease	Urease
PF1T3	KC311567	<i>Arthrobacter sulfonivorans</i> (FM955860) 99.0%	Recent	-	-	-	-	++
PF1T1	KC311565	<i>Arthrobacter bergeri</i> (AJ609630) by 98.1%	Recent	+	-	-	+	+
PF3T1	KC311585	<i>Arthrobacter</i> sp. (JF313086) by 99.1%	Recent	-	+	+	-	++
PF1T4	KC311568	<i>Arthrobacter</i> sp. (JF313088) by 99.4%	Recent	-	+	-	-	++
PF4T1	KC311591	<i>Arthrobacter</i> sp. (GU733460) by 98.2%	Recent	-	-	+	+	++
PF4T2	KC311592	<i>Arthrobacter</i> sp. (GU733460) by 98.6%	Recent	-	-	-	+	+
PF5B1	KC311599	<i>Acinetobacter johnsonii</i> (KC422707) by 99.8%	Recent	-	-	-	+	++
PF3T4	KC311615	<i>Pseudomonas</i> sp. (AY035996) by 98.8%	Recent	-	-	-	-	+
PF3T5	KC311616	<i>Pseudomonas</i> sp. (GU391451) by 98.2%	Recent	-	-	-	-	+
PF3T2	KC311613	<i>Pseudomonas</i> sp. (HM224459) by 98.4%	Recent	-	-	-	-	++
PF5T1	KC311623	<i>Pseudomonas</i> sp. (AF105385) by 97.7%	Recent	-	-	-	-	+
PF3T6	KC311627	<i>Sphingobacterium</i> sp. (HM352330) by 97.7%	Recent	-	-	+	+	++
PF5B2	KC311625	<i>Psychrobacter</i> sp. (FN377742) by 99.3%	12250	-	-	+	-	+
PF1B1	KC311564	<i>Acinetobacter johnsonii</i> (KC422707) by 99.8%	13850	-	-	+	-	+
PF1B3	KC311602	<i>Pseudomonas</i> sp. (JF313066) by 99.8%	13850	-	-	-	-	++
PF1B6	KC311630	<i>Virgibacillus pantothenicus</i> (AB681789) by 99.7%	13850	-	-	-	-	++
PF4M4	KC311596	<i>Arthrobacter</i> sp. (JQ396586) by 97.8%	14850	-	+	-	+	++
PF5M1	KC311598	<i>Arthrobacter</i> sp. (JF313088) by 98.6%	14150	-	+	-	-	+
PF4M3	KC311595	<i>Arthrobacter</i> sp. (JF313071) by 99.3%	14850	-	-	-	-	++
PF1M2	KC311617	<i>Stenotrophomonas</i> sp. (JQ977692) by 99.8%	22700	-	+	+	+	++
PF4B2	KC311629	<i>Arthrobacter</i> sp. (JQ396594) by 99.3%	24300	-	-	+	+	++
PF3M2	KC311617	<i>Pseudomonas mandelii</i> (KF484687) by 99.8%	32300	-	-	+	+	++
PF3B4	KC311590	<i>Arthrobacter</i> sp. (HF548458) by 99.6%	37000	-	-	-	+	-
PF3B2	KC311588	<i>Arthrobacter</i> sp. (JF313088) by 99.6%	37000	-	-	-	-	++
PF3B5	KC311621	<i>Pseudomonas</i> sp. (AY263478) by 99.6%	37000	+	-	-	+	+
PF2M1	KC311576	<i>Arthrobacter</i> sp. (AM491456) by 99.9%	38300	-	+	+	-	++
PF2M3	KC311578	<i>Arthrobacter</i> sp. (JF313079) by 99.9%.	38300	-	-	-	-	+
PF2M8	KC311608	<i>Pseudomonas jessenii</i> (AM933510) by 99.8%	38300	-	-	+	+	++
PF2M12	KC311612	<i>Pseudomonas mandelii</i> (NR_024902) 98.7%	38300	-	-	-	+	+
PF2M7	KC311607	<i>Pseudomonas</i> sp. (KC236872) by 98.6%	38300	-	-	+	+	++
PF2M9	KC311609	<i>Pseudomonas</i> sp. (JF312955) by 99.8%	38300	-	-	+	+	++
PF2B4	KC311600	<i>Bacillus</i> sp. (DQ084543) by 99.8%	44800	+	-	+	+	++