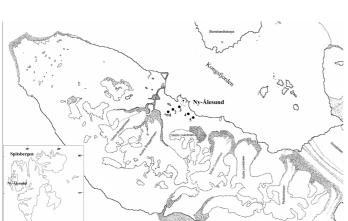
## Bacterial diversity and bio-potentials of culturable bacteria associated with different age sediments of Svalbard, Arctic

Purnima Singh<sup>1\*</sup> • Shiv Mohan Singh<sup>2</sup> • Alok Srivastava<sup>3</sup> • Utpal Roy<sup>1</sup>

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 x 10<sup>3</sup> to 2.22 x 10<sup>5</sup> CFUs/g while the total bacterial numbers ranged from 1.14 x 10<sup>5</sup> and 5.52 x 10<sup>5</sup> 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.



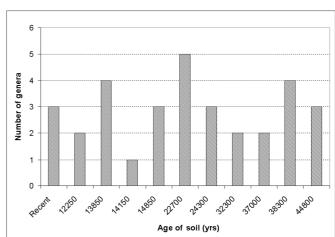


Figure 1 Map of Spitsbergen, Kongsfjord, Arctic showing sampling sites (•1 to •5).

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

.

<sup>&</sup>lt;sup>1</sup>Birla Institute of Technology and Science (BITS), Pilani-K.K. Birla Goa Campus, Zuarinagar, Goa 403726, India

<sup>&</sup>lt;sup>2</sup>National Centre for Antarctic and Ocean Research, Ministry of Earth Sciences, Vasco-da-Gama, Goa 403804, India

<sup>&</sup>lt;sup>3</sup>National Bureau of Agriculturally Important Microorganisms (NBAIM), Uttar Pradesh-275101, India

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	Arthrobacter sulfonivorans (FM955860) 99.0%	Recent	-	-	-	-	++
PF1T1	KC311565	Arthrobacter bergeri (AJ609630) by 98.1%	Recent	+	-	-	+	+
PF3T1	KC311585	Arthrobacter sp. (JF313086) by 99.1%	Recent	-	+	+	-	++
PF1T4	KC311568	Arthrobacter sp. (JF313088) by 99.4%	Recent	-	+	-	-	++
PF4T1	KC311591	Arthrobacter sp. (GU733460) by 98.2%	Recent	-	-	+	+	++
PF4T2	KC311592	Arthrobacter sp. (GU733460) by 98.6%	Recent	-	-	-	+	+
PF5B1	KC311599	Acinetobacter johnsonii (KC422707) by 99.8%	Recent	-	-	-	+	++
PF3T4	KC311615	Pseudomonas sp. (AY035996) by 98.8%	Recent	-	-	-	-	+
PF3T5	KC311616	Pseudomonas sp. (GU391451) by 98.2%	Recent	-	-	-	-	+
PF3T2	KC311613	Pseudomonas sp. (HM224459) by 98.4%	Recent	-	-	-	-	++
PF5T1	KC311623	Pseudomonas sp. (AF105385) by 97.7%	Recent	-	-	-	-	+
PF3T6	KC311627	Sphingobacterium sp. (HM352330) by 97.7%	Recent	-	-	+	+	++
PF5B2	KC311625	Psychrobacter sp. (FN377742) by 99.3%	12250	-	-	+	-	+
PF1B1	KC311564	Acinetobacter johnsonii (KC422707) by 99.8%	13850	-	-	+	-	+
PF1B3	KC311602	Pseudomonas sp. (JF313066) by 99.8%	13850	-	-	-	-	++
PF1B6	KC311630	Virgibacillus pantothenticus (AB681789) by 99.7%	13850	-	-	-	-	++
PF4M4	KC311596	Arthrobacter sp. (JQ396586) by 97.8%	14850	-	+	-	+	++
PF5M1	KC311598	Arthrobacter sp. (JF313088) by 98.6%	14150	-	+	-	-	+
PF4M3	KC311595	Arthrobacter sp. (JF313071) by 99.3%	14850	-	-	-	-	++
PF1M2	KC311617	Stenotrophomonas sp. (JQ977692) by 99.8%	22700	-	+	+	+	++
PF4B2	KC311629	Arthrobacter sp. (JQ396594) by 99.3%	24300	-	-	+	+	++
PF3M2	KC311617	Pseudomonas mandelii (KF484687) by 99.8%	32300	-	-	+	+	++
PF3B4	KC311590	Arthrobacter sp. (HF548458) by 99.6%	37000	-	-	-	+	-
PF3B2	KC311588	Arthrobacter sp. (JF313088) by 99.6%	37000	-	-	-	-	++
PF3B5	KC311621	Pseudomonas sp. (AY263478) by 99.6%	37000	+	-	-	+	+
PF2M1	KC311576	Arthrobacter sp. (AM491456) by 99.9%	38300	-	+	+	-	++
PF2M3	KC311578	Arthrobacter sp. (JF313079) by 99.9%.	38300	-	-	-	-	+
PF2M8	KC311608	Pseudomonas jessenii (AM933510) by 99.8%	38300	-	-	+	+	++
PF2M12	KC311612	Pseudomonas mandelii (NR_024902) 98.7%	38300	-	-	-	+	+
PF2M7	KC311607	Pseudomonas sp. (KC236872) by 98.6%	38300	-	-	+	+	++
PF2M9	KC311609	Pseudomonas sp. (JF312955) by 99.8%	38300	-	-	+	+	++
PF2B4	KC311600	Bacillus sp. (DQ084543) by 99.8%	44800	+	-	+	+	++