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#### **RESEARCH ARTICLE**

# The Diversity of *Pseudomonas* species from the Accumulation Zone of Kanchengayao Glacier, North Sikkim, India

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## **Abstract**

Glaciers are the cryospheric niches which support concealed microbial life. They inhabit broadspectrum culturable and non-culturable bacterial diversity. There is virtually very little information on the psychrophilic/psychrotolerant bacterial diversity found in the glaciers in India. Indian Himalayas are regarded as the world heritage of flora and fauna. As it houses many largest glaciers in its lap, a new venture into glaciers has been started. Microbiological investigation of the glaciers in North-East India will help us to have an insight into the hidden treasure of microflora. We are providing the first report on the Psuedomonas sp. diversity from Kanchengayao glacier, North Sikkim, India. It is one of the most dominant genera isolated from glacier ice samples. This genus is one of the most medically and ecologically important groups of Gamma-proteobacteria present in environment. In the present study, the diversity of Pseudomonas species isolated from ice core sample was carried out based on the phenotypic and genotypic analysis. It was found that the glacier was abundant in Pseudomonas azotoformans; Pseudomonas poae; Stenotrophomonas maltophilia; Pseudomonas fluorescens; Pseudomonas reactants; Pseudomonas hibiscicola and Pseudomonas synxantha. Interestingly, the antibiotic susceptibility test showed that all the isolates were resistant to Ampicillin (10mcg) but all were sensitive to Streptomycin (10mcg), 19 isolates were resistant to Vancomycin (30mcg) and six were resistant against Tetracycline (30mcg) whereas majority of the isolates showed intermediate response. The antibiotic resistance found in this unexplored area is an important study and first of its kind reported from this glacier.

Keywords: Pseudomonas, Kanchengayao glacier, Sikkim, 16S rRNA, antibiotic resistance.

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#### INTRODUCTION

In 1887 Forster had discovered bacteria which can replicate at 0°C. After a few years, Schmidt-Nielsen for the first time coined the term 'psychrophilic' to define the bacteria living under extremely cold conditions<sup>1,2</sup>. As only minimum growth temperature was believed in this early definition some confuse arose due to the lack of comprehensible definition between cold-loving and cold-tolerant adaptation types<sup>3</sup>. After the isolation of true psychrophiles in 1960s, cold adapted bacteria were placed into the steno-thermic and eurythermic category and finally Morita coined them into psychrophilic and psychrotrophic / psychrotolerant microorganisms<sup>2</sup>. True psychrophilic bacteria shows growth at or below 0°C, optimally grows around 15°C to 20°C, whereas psychrotolerant can grows and tolerate temperature above 20°C2.

Temperature governs the abiotic and biotic factors which in turn directly dictate the protein machinery and adaptive features of the cryospheric microflora<sup>4-6</sup>. Cold-dwelling microbes have evolved many such traits that adapt their growth at low temperatures<sup>7-8</sup>. Both the psychrophilic and psychrotolerant microorganisms influence the ecology of cryosphere portions of the earth<sup>9</sup>. They play major roles in the biodegradation and recycling of organic matter as well as inorganic nutrients<sup>9</sup>.

The potential for biotechnological applications of psychrophilic and psychro-tolerant bacteria are receiving escalating attention nowadays. Psychrophiles are potential source of novel enzymes for industrial applications and some pigments produced by these microbes are also used as food additive<sup>10</sup>. One of the important habitats of psychrophiles are glaciers<sup>11</sup>. However, the majority of the glaciers studies demonstrate only broad-spectrum bacterial diversity on the surface of the galciers, and virtually very little information exists on which particular psychrophilic or psychrotolerant bacterial species diversity actually reside in those glaciers in the depth zone.

Pseudomonas is one of the most dominant genera reported from many glaciers<sup>12-14</sup>. Along with glaciers, they are present in other cold environments and very often in intimate association with plants and animals. It is one of

the most versatile and ecologically important groups of gamma-proteobacteria present in many environments and it plays a very significant role in nitrogen and carbon cycles<sup>15</sup>. Therefore their species diversity studies in glacier ecosystems are crucial in relation to climate change because if there is a sudden deficit of these species diversity in a glacier, then we can co-relate the effects of climate change in glaciers<sup>9</sup>.

In this paper, the diversity of psychrotolerant *Pseudomonas* species isolated from Kanchengayao glacier ice, North Sikkim, India was studied based on the phenotypic and genotypic analysis. This is the first ever report of *Pseudomonas* species diversity from Kanchengayao glacier of Himalayan valley located at North Sikkim, India.

# MATERIALS AND METHODS

## Sampling Site

GPS MAP 78S, which is an automated Global Positioning device GPS was used for mapping and to determining the coordinates and land elevation of glacier study sites<sup>16</sup>.

# Sample collection and preparation

The ice core samples from the Accumulation zone of Kanchengayao glacier was aseptically collected in a sterile thermal cryo sampling box. These sterile sampling containers were sealed tightly and were immediately brought to the laboratory<sup>16-19</sup>. For microbiological analysis, the ice core samples were cut aseptically with a sterilized sawtooth knife and around 5 mm annulus of glacial ice core was discarded<sup>20</sup>. The remaining inner core was first rinsed with cold ethanol (95%) and later on washed with cold sterile water. The ice samples were allowed to melt in the sterile beaker placed at 4°C cold incubator<sup>21</sup>. As described by Zhang all the handling procedures carried out aseptically below 20°C using positive pressure laminar flow hood<sup>22</sup>.

# Physicochemical analysis of glacial ice core samples

The glacial ice core samples were melted at 4°C cold incubator. Physical parameters such as temperature, conductivity, pH, dissolved oxygen (DO) and turbidity were measured with the help of Multi Water Quality Checker U-50 Series Instrument (Horiba, Japan). Chemical constituents like magnesium, calcium, nitrite, nitrate, sulfate,

fluoride, alkalinity, ortho-phosphate, total dissolved solids, silica, iron, and sodium was analyzed by Multi- Parameter Water Testing Kit, WTO15 (Himedia, India). Piper diagram was plotted to draw the analysis<sup>23</sup>.

#### Isolation of bacteria

Bacterial isolation were carried on Pseudomonas Isolation Agar (Peptic digest of animal tissue 20g/L; MgCl<sub>2</sub> 1.4g/L; K<sub>2</sub>SO<sub>4</sub> 10g/L; Triclosan 0.025g/L; Glycerol 20mL; distilled water 1L). Briefly, 200µL of thawed inner ice core samples were spread plated and incubated at 15°C for 3 weeks. Also, bacterial enrichment was carried out by incubating 100µL water sample in 50 mL Pseudomonas isolation broth in 250mL conical flask and then incubated at 15°C for 14 days in incubator cum shaker at 120rpm. After enrichment, bacterial isolation was carried on Pseudomonas isolation agar as mentioned above. Morphologically different colonies were selected and sub-cultured by streak plate method<sup>16-19</sup>. A total of 22 pure bacterial isolates were isolated from Kanchengayao glacier samples and stored at -80°C in 40% glycerol.

# **Characterization of bacterial isolates**

The morphological, physiological and biochemical characteristics of the selected isolates were evaluated<sup>16</sup>. The morphological characters such as colony morphology, Gram-staining, spore staining were performed. The growth of isolates were checked in LB broth at different temperature i.e., 5°C, 10°C, 15 °C, 20°C, 30°C and 40°C in an incubator. Similarly, NaCl dependent growth profile was determined by incubating bacterial isolates in LB media containing different concentrations of NaCl (0%, 1% 2%, 4%, 6%, 8% and 10%) at 15°C incubator. For 0% NaCl concentration in LB media following media composition was used (Casein enzymic hydrolysate: 10g/L; Yeast Extract: 5g/L; d.w. 1L) and pH dependent growth profile were also checked at different range pH (4, 6, 8 and 10) at 15°C in an incubator<sup>16-19</sup>.

For protease enzymatic activities SM Agar (Skim Milk powder 28g/L; Tryptone 5g/L; Yeast Extract 2.5g/L; Dextrose 1g/L; Agar 25g/L; distilled water 1L) was used for the demonstration of coagulation and proteolysis<sup>24</sup>. The proteolytic bacteria hydrolyzed casein to form soluble nitrogenous compounds indicated as clear zone surrounding the colonies. Amylase enzyme

activities were detected by flooding the surface of 48 hours old pure culture on Starch Agar media (Meat extract 3g /L; Peptic digest of animal tissue 5g /L; Starch 2g/L; Agar 25g/L; distilled water 1L) with Iodine solution (Iodine crystals 0.34g; KI 0.66g; distilled water 100mL)<sup>25</sup>. Amylase positive organisms showed clear halo zone around the colony. Size of the clear halo zone is directly proportional to the starch hydrolyzing activity of the strain under study. Gelatinase hydrolysis was detected on Gelatin Agar (Gelatin 30g/L; Casein enzymic hydrolysate 10g/L; NaCl 10g/L; Agar 25g/L; distilled water 1L). Gelatin positive organisms showed clear halo zone of inhibition around the colony. Size of the clear zone is directly proportional to the gelatin hydrolyzing activity of the strain under study.

# Antibiotic resistance profiling of the bacterial isolates

All the bacterial isolates were tested for their response to various antibiotics by disc diffusion method<sup>26</sup>. The isolates were tested using antibiotic discs for their response to four antibiotics: Ampicillin (10mcg), Vancomycin (30mcg), Tetracycline (30mcg) and Streptomycin (10mcg). All the antibiotic tests were performed in Muller Hinton Agar (MHA) at 15°C incubator. The results were recorded as diameter of the inhibition zone formed which was interpreted from the Zone Size Interpretative Chart.

# PCR amplification, sequencing, and analysis of 16S rDNA

The 16S rRNA gene was amplified using universal bacterial primers 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-CGGTTACCTTGTTACGACTT-3')13. For amplification of PCR product, following cycle conditions were used: 94°C for 5 min; 35 cycles of 1min at 95°C, 1min at 55°C, and 2 min at 72°C; and a final extension step of 10 min at 72°C. QIAquick PCR purification kit (Qiagen, Germany) was utilized for purifying the PCR products and subsequently PCR products were sequenced by ABI Applied Biosystems (3500 Genetic Analyzer) using each universal primer i.e., 27F and 1492R. The 16S rRNA gene sequences were aligned with reference gene sequences of related taxa using Clustal W software<sup>27</sup>. A phylogenetic tree was constructed by MEGA 7 software<sup>28</sup> using the neighbor-joining method<sup>29</sup>.

# RESULTS

## Physicochemical analysis

The physicochemical analysis of Kanchengayao glacier ice core samples, suggested that all the elements were present in very low concentration (Table 1). The physiochemical parameters were plotted as piper diagram for classification on the basis of chemical composition<sup>23</sup>. Piper diagram divides water into four basic types conferring to their location near the four corners of the diamond. Water samples which are rich in  $(Ca^{2+} + Mg^{2+})$  and  $(Cl^{-} + SO_4^{-2-})$  are considered as permanent hardness and placed at the top of diamond, whereas water samples which are rich in  $(Ca^{2+} + Mg^{2+})$  and  $HCO^{3-}$  are considered as temporary hardness and placed near

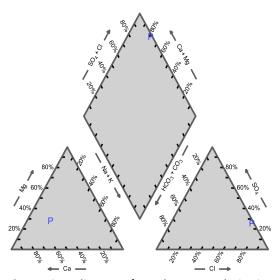
Table 1. Physicochemical Analysis of glacier sample

Name of the Chemical test	Millipore Water (Control)	Glacier sample	
рН	6.9	7.2	
Total Dissolved Solid	BDL	16	
(TDS) (mg/L)			
Fluoride Test (ppm)	BDL	0.5	
Sulfate Test (ppm)	BDL	10	
Nitrate Test (ppm)	BDL	10	
Chloride Test (ppm)	BDL	20	
Total Hardness Test	BDL	100	
(ppm)			
Orthophosphate Test	BDL	0.0	
(ppm)			
Arsenic Test (ppm)	BDL	0.05	
Alkalinity Test (ppm)	BDL	200	
Nitrite Test (ppm)	BDL	15	
Iron Test (ppm)	BDL	0.3	
Silica Test (ppm)	BDL	0.0	
Free Chlorine Test	BDL	0.0	
(ppm)			
Turbidity (NTU)	BDL	≥ 10	
Dissolve Oxygen (DO)	BDL	0.36	
(ppm)			
Fluoride (ppm)	BDL	0.5	
Conductivity (µS/cm)	BDL	0.12	
Magnesium (ppm)	BDL	05	
Sodium (ppm)	BDL	07	
Calcium (ppm)	BDL	14	

The data was measured by AQUA CHECK kit (HiMedia, Mumbai, India and Multi Water Quality Checker U-50 Series Instrument (Horiba, Japan)) where BDL refers to "Below Detection Level"; ppm= parts per million.

the left corner of diamond. Water samples mainly composed of alkali carbonates (Na<sup>+</sup> + K<sup>+</sup>) and (HCO<sup>3</sup> <sup>-</sup> + CO<sub>3</sub> <sup>2-</sup>) are plotted at the lower corner whereas near the right-hand side of the diamond may be reflected as saline (Na<sup>+</sup> + K<sup>+</sup>) and (Cl<sup>-</sup> + SO<sub>4</sub> <sup>2</sup>). The piper diagram suggested that the Kanchengayao glacier ice was Ca-Cl type (Fig. 1).





**Fig. 1.** Piper diagram of Kanchengayao glacier ice physicochemical analysis

# Isolation and biochemical characterization of psychrotolerant *Pseudomonas* sp.

Incubation in *Pseudomonas* Isolation Agar at 15°C for 3 weeks at 15°C helped us to isolate psychrotolerant Pseudomonas sp. from glacier ice core samples. Twenty two pure bacterial isolates, isolated from enrichment method and streak plate method, were preserved in 40% glycerol at -80°C. Based on morphological characteristics, these bacterial isolates were selected for further analysis, i.e., Gram-staining, spore staining, colony morphology, growth temperature, NaCl and pH tolerance (Table 2). The bacterial isolates were all rod-shaped, non-spore formers and mostly produced white cream color colonies as shown in (Table 2). The Gram-staining results showed that all the isolates were Gram-negative. Among 22 bacterial isolates, during the initial screening for enzymatic activity of the isolates, it was observed that four isolates (KGG15, KGG22, KGG60, KGG62) were positive for amylase production, four isolates

Table 2. Morphological characterization of the bacterial isolates

Growth on agar plates					Morphology on the basis of staining		
Isolates	Colony color	Margin	Elevation	Form	Simple Staining	Gram Staining	Spore Staining
KGG2	Yellow	Erose	Flat	Irregular	Rod	-ve	-ve
KGG6	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG13	White	Entire	Flat	Circular	Rod	-ve	-ve
KGG14	White	Entire	Flat	Circular	Rod	-ve	-ve
KGG15	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG16	White	Erose	Flat	Circular	Rod	-ve	-ve
KGG17	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG20	Yellow	Entire	Flat	Irregular	Rod	-ve	-ve
KGG22	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG25	White	Entire	Flat	Circular	Rod	-ve	-ve
KGG28	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG29	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG35	Brown	Erose	Flat	Circular	Rod	-ve	-ve
KGG38	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG44	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG50	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG45	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG51	White	Entire	Flat	Circular	Rod	-ve	-ve
KGG53	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG59	White	Undulate	Flat	Circular	Rod	-ve	-ve
KGG61	White	Entire	Convex	Circular	Rod	-ve	-ve
KGG62	White	Undulate	Flat	Circular	Rod	-ve	-ve

where (-ve) indicates in the case of Gram staining that the isolates were Gram Negative bacteria and in case of spore staining the isolates showed negative response i.e. they did not form any spores.

(KGG17, KGG25, KGG28, KGG59) were positive for protease production and all the isolates were catalase positive as shown in Fig. 2. Carbohydrate fermentation test showed that majority of the isolates were able to ferment simple sugars like dextrose, whereas few isolates were able to ferment sugars like dulcitol, lactose, mannose, arabinose, raffinose, and ribose, however, most

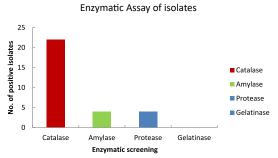


Fig. 2. Enzymatic activity test of Kanchengayao glacier isolates

of the bacterial isolates were unable to ferment fructose, sucrose, and xylose as shown in Table 3.

# **Antibiotic resistance**

Recent studies have detected antibiotic resistant bacteria and their resistance genes in the natural environment which are geo-graphically isolated from such area<sup>30-32</sup>. Interestingly from Kanchengayao glacier ice core samples we also found three class of antibiotic resistant bacteria against penicillin (Ampicillin 100%), glycopeptides (Vancomycin 86.36%) and Tetracycline 27% respectively (Table 4). This paves for an interesting study for future as these glaciers are never exposed to antibiotics and also are usually free of any anthropogenic activities.

## Tolerance to different; Temperature, NaCl and pH

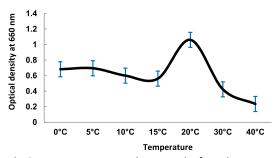
The temperature dependent growth profile of the isolates showed that the majority of the isolates had optimum growth at 20°C but all could tolerate temperature >25°C≤ 40°C (Fig.

Table 3. Carbohydrate Fermentation Test of the bacterial isolates

Carbohydrate										
Isolates	(D-) Arabinose	(D+) Dextrose	(D+) Dulcitol	(D-) Fructose	(D+) Lactose	(D-) Mannose	(D+) Raffinose	(D-) Ribose	(D+) Sucrose	D+) Xylose
KGG2	+	+	-	-	+	+	-	-	-	-
KGG6	-	+	-	-	-	-	-	-	-	-
KGG13	-	-	-	-	-	-	-	-	-	-
KGG14	-	-	-	-	-	-	-	-	-	-
KGG15	-	+	-	-	-	-	-	-	-	-
KGG16	-	+	-	-	-	-	-	-	-	-
KGG17	-	+	-	-	-	-	-	-	-	-
KGG20	+	+	-	-	+	+	-	-	-	-
KGG22	-	+	-	-	-	+	-	-	-	-
KGG25	-	-	-	-	-	+	-	-	-	-
KGG28	-	+	-	-	-	-	-	-	-	-
KGG29	-	+	-	-	-	-	-	-	-	-
KGG35	-	-	-	-	-	-	-	-	-	-
KGG38	-	+	-	-	-	-	-	-	-	-
KGG44	-	+	-	-	-	-	-	+	-	-
KGG50	-	+	-	-	-	-	-	-	-	-
KGG45	-	+	-	-	-	-	-	-	-	-
KGG51	-	-	+	-	-	-	+	+	-	-
KGG53	-	-	+	-	-	-	+	+	-	-
KGG59	-	+	+	-	-	-	-	-	-	-
KGG61	-	-	-	-	-	-	-	-	-	-
KGG62	-	+	+	-	-	-	-	-	-	-

The isolates were tested against various carbohydrates and the (+) sign indicates that the isolates were able to ferment that particular carbohydrate and (-) sign indicates that the isolates were unable to ferment that particular carbohydrate.

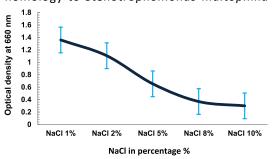
3). It suggested that these isolates are psychrotolerant, rather than psychrophilic in nature. The salinity tolerance was also tested and it was found that majority of the isolates grew well at minimum concentrations of NaCl at 15°C (Fig. 4). pH dependent growth profile suggested that nine isolates showed good growth at pH5 and pH6, followed by three isolates at pH8 and two isolates at pH2 (Fig. 5). From our study we found that 11 bacterial isolates were acidophilic in nature, while others preferred neutral pH or slightly alkaline pH.



**Fig. 3.** Temperature Dependent growth of Kanchengayao glacier isolates

# Phylogenetic analysis of 16S rDNA sequencing of isolates

Based on the similarity criterion of at least 99% of the 16S rRNA gene sequence, it was found that all 22 bacterial isolates belonged to genus *Pseudomonas* and was from seven diversified *Pseudomonas* species. 13 isolates showed 99% homology to *Pseudomonas* azotoformans, two isolates had 99% homology to *Pseudomonas* poae, three isolates had 99% homology to *Stenotrophomonas* maltophilia



**Fig. 4.** NaCl Dependent growth of Kanchengayao glacier isolates

Table 4. Antibiotic Assay of the bacterial isolates

Antibiotic disc with their Concentration

	Zone of inhibition (in mm)					
Isolates	Van30	TE30	Amp10	S10		
KGG2	R	R	R	S		
KGG6	R	R	R	S		
KGG13	R	R	R	S		
KGG14	R	S	R	S		
KGG15	R	1	R	S		
KGG16	R	1	R	S		
KGG17	R	1	R	S		
KGG20	S	R	R	S		
KGG22	R	1	R	S		
KGG25	S	R	R	S		
KGG28	R	I	R	S		
KGG29	R	I	R	S		
KGG35	S	R	R	S		
KGG38	R	1	R	S		
KGG44	R	1	R	S		
KGG50	R	I	R	S		

KGG45

KGG51

KGG53

KGG59

KGG61

KGG62

R

R

R

R

R

R

The isolates were tested against various antibiotics and the (R) sign indicates that the isolates were resistant, (I) sign indicates that the isolates intermediate and (S) sign indicates that the isolates sensitive.

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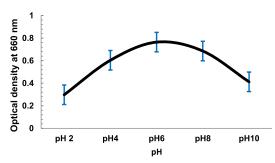
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**Fig. 5.** pH Dependent growth of Kanchengayao glacier isolates

and others were *Pseudomonas fluorescens*, *Pseudomonas reactants*, *Pseudomonas hibiscicola* and *Pseudomonas synxantha*. The accession number and identity of all the isolates are given in Table 5. The phylogenetic tree was made using MEGA7 using the Neighbor-Joining method Fig. 6.

#### DISCUSSION

Diverse form of microorganisms, including algae and fungi, has been reported on the surface of many glaciers around the world. These microorganisms make up the primary colonizer of the snow and ice, which also include coldtolerant animals such as insects and copepods. In North East Himalayas, Kanchen-gayao glacier is located at North Sikkim, India and it is a debrisfree (clear glacier) transverse valley glacier (Fig 7). This glacier originated from the southern slope of Mount Kanchengayao, treading north-south face having latitude 27°59'57.872'N and longitude 88°37'8.785'E at an altitude of 1393m. The melt water of this glacier feeds into river Thangu which is a tributary of river Lachen. Kanchengayao glacier is surrounded by a cold desert and in its lower valley small Rhododendron trees are present along with some other vegetation. Possibly, nutrient and bacteria from nearby or distantly located places gets transferred to accumulation zone of glacier through air currents<sup>33</sup>. Also, the soil bacteria might affect the distribution of Pseudomonas species on the surface of the glacier accumulation zone.

Our result showed that the most dominant Pseudomonas species on Kanchen-gayao glacier were Pseudomonas azotoformans followed by Pseudomonas poae, Stenotrophomonas maltophilia, Pseudomonas fluorescens, Pseudomonas reactants, Pseudomonas hibiscicola and Pseudomonas synxantha. Diversity of Pseudomonas sp. in glaciers has been reported in various parts of the world  $^{\rm 12-14}.$  These gram negative bacteria are abundant in environmental niches and are clinically important also. The most abundant Pseudomonas sp. in our glacier ice core samples was Pseudomonas azotoformans. This gram negative bacterium has been reported as an effective biocontrol agent against plant pathogens<sup>34-36</sup> and it also was reported as a good biotechnological candidate which has biomineralization property to fix the concrete cracks by producing calcite<sup>37</sup>. So, it will be interesting to study this psychrotolerant bacterium isolated from glacier in future. Pseudomonas poae is also reported to have biocontrol activity<sup>38,39</sup>. Pseudomonas fluorescens is an aerobic plant growth promoting rhizobacterium (PGPR) and has biocontrol activity<sup>40, 41</sup>. Some bacteria have the ability to synthesize nanoparticles metabolically and this has amazed the scientific

Table 5. Identification of the bacterial isolates through GenBank 16S rRNA gene sequence accession numbers

Isolates	Closest Relative Species	% of Identify	Gene Bank Accession No.	
KGG35	Pseudomonas fluorescens	99.42	KY129832	
KGG59	Pseudomonas reactants	99.3	KY129833	
KGG13	Pseudomonas hibiscicola	99.4	KY129834	
KGG2	Stenotrophomonas maltophilia	99	KY129838	
KGG14	Pseudomonas synxantha	99	MH079449	
KGG15	Pseudomonas azotoformans	99	MH079450	
KGG51	Pseudomonas poae	99.4	MH079451	
KGG62	Pseudomonas azotoformans	99	MH079452	
KGG6	Pseudomonas azotoformans	99	MH157226	
KGG20	Stenotrophomonas maltophilia	99	MH157227	
KGG25	Stenotrophomonas maltophilia	99	MH157228	
KGG28	Pseudomonas azotoformans	99	MH157229	
KGG38	Pseudomonas azotoformans	99	MH157230	
KGG44	Pseudomonas azotoformans	99	MH157231	
KGG45	Pseudomonas azotoformans	99	MH157232	
KGG53	Pseudomonas poae	99.33	MH157233	
KGG50	Pseudomonas azotoformans	99	MH157234	
KGG61	Pseudomonas azotoformans	99	MH157235	
KGG16	Pseudomonas azotoformans	99	MH157236	
KGG17	Pseudomonas azotoformans	99	MH157237	
KGG22	Pseudomonas azotoformans	99	MH157238	
KGG29	Pseudomonas azotoformans	99	MH157239	

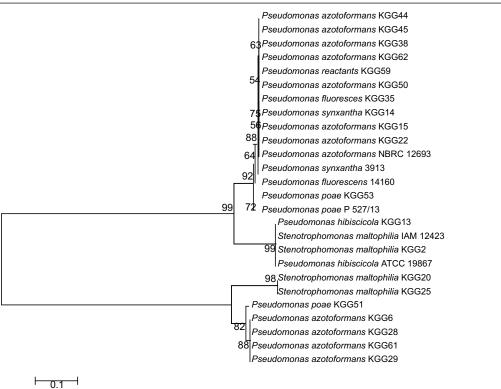


Fig. 6. Phylogenetic tree of Kanchengayao glacier isolates



Fig. 7. Kanchengayao glacier

community and industries at large for harnessing this unique capability to produce nanoparticles in cost effective method<sup>42,43</sup>. One of our isolates *Pseudomonas hibiscicola* have been reported in many literatures as a potential candidate showing this property<sup>44,45</sup>. So, it will be another interesting study in future. *Stenotrophomonas maltophilia* is an environmental bacterium found in various ecological niches like river, plant rhizospheres, soil etc. It is an emerging multi-drug-resistant global opportunistic pathogen and it was also present in our glacier sample.

Glacier study shall reveal in future many such diversified microorganisms and their biotechnological applications render them as suitable candidates for future industrial strains. Sikkim glacier houses plethora of microbes and it's an important one in terms of monitoring climatic changes in the Himalayas.

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# **CONFLICT OF INTEREST**

The author declares that there are no conflict of interest.

#### **REFERENCES**

- Priscu J C, Christner B C, in Microbial Diversity and Bioprospecting (ed. Bull, A.) 130–145 (ASM Press, 2004)
- Miteva V, Miteva V, Psychrophiles: from biodiversity to biotechnology. Springer, New York, 2008; pp78–99
- Boetius A, Anesio A M, Deming J W, Mikucki J A, Rapp JZ, Microbial ecology of the cryosphere: sea ice and glacial habitats, *Nature Rev. Microbiol*, 2015; 13: 677–690. https://doi.org/10.1038/nrmicro3522
- Inouye M, Phadtare S, Cold shock response and adaptation at a near-freezing temperature in microorganisms, Sci. STKE, 2004; 9: 237-2247.
- D'Amico S, Collins T, Marx JC et al, Psychrophilic microorganisms: challenges for life, EMBO Rep., 2006; 7: 385-389
- Siddiqui K S, Cavicchioli R, Cold-adapted enzymes, Annu Rev. Biochem, 2006; 8: 403-433.
- Lorv J S H, Rose D R, Glick B R, Bacterial ice crystal controlling proteins, Scientifica, 2014; 3: 1–20. https:// doi.org/10.1155/2014/976895.
- Feller G, & Drychrophilic enzymes: hot topics in cold adaptation, *Nat. Rev. Microbiol.*, 2003;
  200–208.
- Anesio A M, Hodson A J, Fritz A, Psenner R, Sattler B, High microbial activity on glaciers: importance to the global carbon cycle, *Glob. Chang. Biol.*, 2009; 15: 955–960
- Raman K V, Singh L, Dhaked R, Botechnological application of psychrophiles and their habitat to low temperature, J. Sci. Indian Res., 2000; 59: 87–101.
- Jansson J K; Tas N, The microbial ecology of permafrost, Nat. Rev. Microbiol., 2014; 12: 414–425.
- Taj M K, Ji X, Lin L, Zhang Q, Wei Y, Taj I, et al, Diversity and phylogenetic analysis of *Pseudomonas* strains isolated from Mingyong glacier China, *Journal of Biodiversity and Environmental Sciences*, 2016; 9(4): 232-236.
- Rafiq M, Hayat M, Anesio AM, Jamil SUU, Hassan N, Shah AA, et al. Recovery of metallo-tolerant and antibiotic resistant psychrophilic bacteria from Siachen glacier, Pakistan. *PLoS ONE*, 2017; 12(7): e0178180. https://doi.org/10.1371/journal.pone.0178180
- Mannista MK, Haggblom M, Characterization of psychrotolerant heterotrophic bacteria from Finnish Lapland, Syst Appl Microbiol., 2006, 29(3): 229–243.
- Spiers A J, Buckling A, Rainey P B, The causes of Pseudomonas diversity, Microbiology, 2000; 146: 2345-2350.
- Sherpa M T, Najar I N, Das S, Thakur N, Bacterial diversity in an Alpine debris-free and debris-cover accumulation zone glacier ice, North Sikkim, India, Indian J Microbiol., 2018; 58(4): 470-478.
- Liu Y, Yao T, Jiao N, Kang S H, Culturable bacteria in glacial meltwater at 6350 m on the East Rongbuk Glacier, Mount Everest, Extremophiles, 2009; 13: 89–99. https://doi.org/10.1007/s00792-008-0200-8
- Hong S, Zhang H, Yang W, Bacteria recovered from a high-altitude, tropical glacier in Venezuelan Andes, World J. Microbiol. Biotechnol., 2010, 3: 931–941. https://doi.org/10.1007/s11274-013-1511-1

- Shen L, Yao T, Xu B, Wang H, Jiao N, Kang S, Variation of culturable bacteria along depth in the East Rongbuk ice core, Mt. Everest, Geosci. Front., 2012; 3: 327–334. https://doi.org/10.1016/j.gsf.2011.12.013
- Xiang S, Yao T, An L, Xu B, 16S rRNA sequences and differences in bacteria isolated from the Muztag Ata Glacier at increasing depths, *Appl Environ Microbiol.*, 2005; 71: 4619–4627. https://doi.org/10.1007/ BF02931042
- Xiang S R, Yao T D, An L Z, Xu BQ, Li Z, Wu G J, Bacterial diversity in Malan ice core from the Tibetan Plateau, Folia Microbiology, 2004; 49: 269–275. https://doi. org/10.1007/BF02931042
- Zhang X, Diversity of 16S rDNA and environmental factor influencing microorganisms in Malan ice core, Chin. Sci. Bull., 2003; 48: 1146–1152. https://doi. org/10.1360/02wd0409
- Piper AM, A graphical procedure in the geochemical interpretation of water analyses Transactions, American Geophysical Union, 1994; 25: 914-928.
- Zhou M Y, Chen X L, Zhao H L, Dang H Y, Luan X W, et al, Diversity of both the cultivable protease-producing bacteria and their extracellular proteases in the sediments of the South China Sea, Microb. Ecol., 2009; 58: 582–590. https://doi.org/10.1360/19301066
- Lu M, Fang Y, Li H, Liu W S, Isolation of a novel cold adapted amylase-producing bacterium and study of its enzyme production conditions, *Ann. Microbiol.*, 2010; 60: 557–563. https://doi.org/10.1007/s13213-010-0090-8
- Aneja R K, Experiments in Microbiology, Plant Pathology and Biotechnology, New age International (P) Ltd, New Delhi, India, 2003.
- Metsalu T, Vilo J, Clustvis: a web tool for visualizing clustering of multivariate data using Principal Component Analysis and heatmap, Nucleic Acids Res., 2015; 43: 566–570
- Tamura K, Dudley J, Nei M, Kumar S, Molecular evolutionary genetics analysis (MEGA) software version 4.0, Mol. Biol. Evol., 2007; 24: 1580–1596. https://doi.org/10.1093/molbev/msm092
- Saitou N, The neighbor-joining method: a new method for reconstructing phylogenetic trees, Molecular Biology and Evolution, 1987; 4: 406-425.
- Clemente J C, Pehrsson E C, J. Blaser M, Sandhu K, Gao Z, Wang B, Magris M, Hidalgo G, Contrera M, The microbiome of uncontacted Amerindians. *Microb. Ecol.*, 2015; 4: 1–12.
- Goethem1 M W, Van Pierneef R, Bezuidt O K I, Peer Y, Van De Cowan D A, et al. A reservoir of 'historical' antibiotic resistance genes in remote pristine Antarctic soils. *Microbiome.*, 2018; 6: 1–12.
- Pawlowski AC, Wang W, Koteva K, Barton H A, McArthur A G, Wright G D, A diverse intrinsic antibiotic resistome from a cave bacterium. Nat. Commun., 2016; 7: 1–10.
- Yung P T, Shafaat H S, Connon S A, Ponce A, Quantification of viable endospores from a Greenland ice core, FEMS Microb. Ecol., 2007; 59: 300–336. https://doi.org/10.1111/j.1574-6941. 2006.00218
- Fang Y, Wu L, Chen G, Feng G, Complete genome sequence of Pseudomonas azotoformans S4, a potential

- biocontrol bacterium, *Journal of Biotechnology*, 2016; **227**: 25- 26 doi: 10.1016/j.jbiotec.2016.04.020
- 35. Sang M K, Kim E N, Han G D, Kwac k M S, Jeun Y C, et al, Priming-mediated systemic resistance in cucumber induced by *Pseudomonas azotoformans* GC-B19 and *Paenibacillus elgii* MM-B22 against Colletotrichumorbiculare, *Phyto-pathology*, 2014; 104: 834-842.
- Anzai Y, Kim H, Park J Y, Wakabayashi H, Oyaizu H, Phylogenetic affiliation of the pseudomonads based on 16S rRNA sequence, *International Journal of* Systematic and Evolutionary Microbiology, 2000; 50(4): 1563–1589.
- Nonakaran S H, Pazhouhandeh M, Kevyani A, Abdollahipour FZ, Shirzad A, Isolation and identification of *Pseudomonas azotoformans* for induced calcite precipitation, *World Journal of Microbiology and Biotechnology*, 2015; 31: 1993-2001. doi 10.1007/ s11274-015-1948-5.
- Zachow C, Jahanshah G, de Bruijn I, Song C, Ianni F, Pataj Z et al, The novel lipopeptide Poaeamide of the endophyte *Pseudomonas poae* RE\*1-1-14 is involved in pathogen suppression and root colonization, *Molecular Plant-Microbe Intera-ctions*, 2015; 28(7): 800-810. doi 10.1094/MPMI-12-14-0406-R
- Behrendt U, Ulrich A, Schumann P, Fluorescent pseudomonads associated with the phyllosphere of grasses; Pseudomonas trivialis sp. nov., Pseudomonas poae sp. nov. and Pseudomonas congelans sp. nov., International Journal of Systematic and Evolutionary Microbiology, 2003; 53: 1461–1469. doi 10.1099/ijs.0.02567-0.
- David B V, Chandrasehar G, Selvam P N, Pseudomonas fluorescens: A Plant-Growth-Promoting Rhizobacterium (PGPR) with potential role in biocontrol of pests of crops, In: Crop improvement through microbial Biotechnology, New and future developments in microbial biotechnology and bioengineering, 2018: 221-243. doi 10.1016/B978-0-444-63987-5.00010-4
- 41. Ganeshan G, Kumar A M, *Pseudomonas fluorescens*, a potential bacterial antagonist to control plant diseases, *Journal of Plant Interactions*, 2007; **1**(3): 123-134. doi: 10.1080/17429140600907043.
- Horikoshi S, Serpone N, Introduction to nanoparticles.
  In: Microwaves in Nanoparticle Synthesis, Wiley-VCH Verlag GmbH and Co. KGaA, 2013.
- Babu M M G, Sridhar J, Gunasekaran P, Global transcriptome analysis of *Bacillus cereus* ATCC 14579 in response to silver nitrate stress, *Journal of* Nanobiotechnology, 2011; 9(1): 1-12.
- 44. Punjabi K, Mehta S, Yedurkar S, Jain R, Mukherjee S, et al, Extracellular synthesis of silver nanoparticle by Pseudomonas hibiscicola – Mechanistic approach, Advances in Nano Research, 2018; 6(1): 81-92 doi: https://doi.org/10.12989/anr.2018.6.1.081
- Punjabi K, Yedurkar S, Doshi S, Deshapnde S, Vaidya S, Biosynthesis of silver nanoparticles by *Pseudomonas* spp. isolated from effluent of an electroplating industry, *IET Nanobiotechnology*, 2017; 11(5): 584-590.