

Chapter 2

Biodiversity, Adaptation and Biotechnological Importance of Bacteria Occurring in Cold Climates

Gundlapally Sathyanarayana Reddy, Madhab Kumar Chattopadhyay,
and Sisinthy Shivaji

1 Biodiversity of Psychrophilic Bacteria

The cold habitats span from the Arctic to the Antarctic and include the high-mountains such as Himalayas, the alpine glaciers, the deep ocean, snow, permafrost, sea ice, lakes, cold soils (especially sub-soils), cold deserts, and caves. All these permanently cold habitats have been successfully colonized by a class of microorganisms known as psychrophiles (grow from subzero to 30 °C) (Morita 1975; Helmke and Weyland 2004; Laucks et al. 2005). The ability of psychrophiles to survive and proliferate at low temperatures is intriguing and the exact mechanism is puzzling (see Sect. 2). The first part of this review summarizes the prokaryotic diversity from three major habitats, the Antarctica, Arctic and Himalayan regions which was reviewed recently by Chattopadhyay et al. (2014).

1.1 Diversity of Prokaryotes from Antarctica

Antarctica, the coldest, driest, windiest and iciest (with an average thickness of 1.9 km) of all known habitats is considered as one of the most extreme habitats of the world (Vincent 1988; Claridge and Campbell 1977; Campbell and Claridge 2000; Smith et al. 1992). Despite the harsh climatic conditions, diverse life forms (such as mites, ticks, seals, penguins, mosses, lichens, bacteria, yeasts, algae etc)([---

G. Sathyanarayana Reddy • M.K. Chattopadhyay
CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India](http://</p></div><div data-bbox=)

S. Shivaji (✉)
CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India

Jhaveri Microbiology Centre, L V Prasad Eye Institute, Hyderabad, India
e-mail: shivas@ccmb.res.in; shivas@lvepi.org

www.globalclassroom.org/antarct6.html) survive and multiply in this continent. The psychrophilic bacteria are the most dominant community in the continent and contribute to the Antarctic ecosystem especially with respect to nutrient recycling (Stokes and Reymond 1966; Herbert and Bell 1977; Tanner and Herbert 1981; Delille and Lagarde 1974; Tanner 1985; Voytek and Ward 1995; Chessa et al. 2000; Kelly et al. 1978; Cavanagh et al. 1996; Denner et al. 2001; Cavicchioli and Thomas 2000). Ekelof (1908a, b) was the first to demonstrate the occurrence of bacteria, yeasts and fungi in the soil and air of Antarctica and this observation was confirmed by Pirie (1904, 1912) and Tsiklinsky (1908). Five decades later these unique microorganisms from the continent of Antarctica were identified at the genus and species level (Boyd 1962; Boyd and Boyd (1962a, b); Friedman 1980; Margini and Castrelos 1963; Marshall and Ohye 1966; Meyer et al. 1962; Pfiser and Burkholder 1965; Tsyganov 1970). Subsequently, with the advent of culture independent identification of microorganisms based on 16S rRNA gene metagenomics a greater diversity of microbes was discovered from various habitats of Antarctica. The NCBI (<http://ncbi.nlm.nih.gov>) database has about 6000 16S rRNA gene sequences of bacteria from Antarctica. Of these about 500 sequences correspond to the viable isolates of bacteria from Antarctica (Shivaji and Reddy 2009; Chattopadhyay et al. 2014).

1.1.1 Bacterial Diversity of Antarctica as Studied by Culture Independent Methods

In an attempt to unravel the total bacterial diversity of the various habitats of Antarctica the 16S rRNA approach is used to identify the dominating and the not so dominant bacterial taxa from various habitats that include soil, cyanobacterial mats, water, sub-glacial out flow, sediments, crypto-endolithic sand stone communities, ice cores, geothermal vents, ornithogenic soils, penguins, sponges and intestinal microbiota of Antarctic fish (Shivaji and Reddy 2009; Chattopadhyay et al. 2014; Bottos et al. 2014). In the Antarctic soils bacterial diversity varied with respect to soil type (Bottos et al. 2014; Shivaji et al. 2004). For instance, Proteobacteria (47.0 %) is dominant in Antarctic Peninsula soils where as Actinobacteria and Bacteroidetes (42.0 % and 31 % respectively) are dominant in West Antarctic soils and Transantarctic Mountain soils (Bottos et al. 2014). In the Transantarctic Mountain soils *Deinococcus-Thermus* bacteria are the third most abundant community (18 %). Shivaji et al. (2011a) observed stratification of bacteria with respect to oxygen requirement in Antarctic soils and also identified quite a few clones belonging to *Caldiserica* group, a thermophilic candidate phylum from Antarctica. In addition, it is generally observed that up to 20.0 % of the bacteria in the Antarctic soils do not affiliate with any known taxa (Shivaji et al. 2004; Aislabie et al. 2006, 2009, 2013; Yergeau et al. 2007a, b; Niederberger et al. 2008; Lee et al. 2012; Tiao et al. 2012; Bajerski and Wagner 2013). These results would imply that the bacterial communities across Antarctic soils vary significantly with geography, climate, soil physicochemical parameters and local biological influences.

Bacterial diversity studies of Antarctic sediments both from fresh water sediments (Bratina island, Sjöling and Cowan 2003; Ardley island, Li et al. 2006a, b),

marine sediments (Vestfold Hills, Bowman et al. 2000; Ross ice shelf, Carr et al. 2013) and glacial sediments (Wright Glacier, Stibal et al. 2012) indicated that Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, Bacteroidetes, Actinobacteria, Acidobacteria Gemmatimonadetes, Firmicutes and Cyanobacteria, are common to soils and sediments. In addition taxa affiliated to Spirochaetaceae, Prochlorococcus, Deltaproteobacteria (specially the unique groups *Desulfosarcina*, *Syntrophus* and *Geobacter/Pelobacter/Desulphuromonas* group) (Bowman et al. 2000), order Chlamydiales (Parachlamydiaceae), *Planctomycetes* and members of *Spirochaetales* (Sjöling and Cowan 2003; Li et al. 2006a, b) are also present. Carr et al. (2013) also observed that the Betaproteobacteria contained predominantly (over 45 %) two genera *Thiobacillus* and *Teptidiphilus* and the occurrence of unusually high proportion of *Chloroflexi* group. All the above bacteria are uniformly distributed except the Gammaproteobacteria which is very high at a depth of 120–125 cm below sea surface. Bowman et al. (2000) detected more than 200 distinct phylotypes in anoxic marine sediment with close to 31.0 % belonging to a novel deep branch within the low GC Gram-positives.

Microbial diversity of water in Antarctica is limited as only 0.4 % of the total ice covered area of Antarctica is seasonally ice free (Wilkins et al. 2013). The aquatic habitat includes fresh to hypersaline water bodies, permanently ice covered to perennially ice free, and mixed to stratified lakes. Further the age of water within Antarctic lakes varies considerably from 1.5 million years in case of sub-glacial outflow from Blood Falls (Mikucki et al. 2009) to 300 years old in case of Lake Miers (Green et al. 1988) and as a result organisms inhabiting the lakes could be recent or ancient in origin (Gibson 2006; Cavicchioli 2007). Bacterial diversity in the water is generally reduced compared to soils and sediments (Laybourn-Parry 1997) and the majority of bacteria belong to the Proteobacteria (47.6 %, representing the Alphaproteobacteria, Betaproteobacteria and Deltaproteobacteria) with dominating genera being *Rhodobacter* and *Sphingomonas* (Huang et al. (2013). Besides, Bacteroidetes (15.1 %), Actinobacteria (14.8 %), Chloroflexi (10.2 %), Acidobacteria (6.7 %), Firmicutes (3.6 %), Gemmatimonadetes (1.3 %) and Verrucomicrobia (0.2 %) are the minor components and Deinococcus-Thermus, Nitrospira, Planctomycetes, and Fusobacteria are also present. The most common genera are *Sphingomonas*, *Caulobacter*, *Brevundimonas*, *Janthinobacterium*, *Duganella*, *Polaromonas*, *Variovorax*, *Rhodoferrax*, *Flavobacterium*, *Pedobacter*, *Prevotella*, *Hymenobacter*, and *Arcicella* (Wilkins et al. 2013). However, a shift in diversity is observed with depth wherein the dominant Bacteroidetes, Betaproteobacteria and Actinobacteria in the surface layers are replaced by Gammaproteobacteria and unclassified bacteria (10–20 %) in deeper zones of McMurdo ice shelf, Victoria land and in the Amundsen sea polynya (Archer et al. 2014; Kim et al. 2014). Two major clades representing *Polaribacter* (20–64 %) and uncultivated Oceanospirillaceae (7–34 %) are abundant in the surface water while the abundance of *Pelagibacter* increased with depth (7–42 %) (Kim et al. 2014).

Response of bacterial community to hydrocarbon contamination in sea water revealed that genera *Psychrobacter*, *Arcobacter*, *Formosa*, *Polaribacter*, *Ulvibacter* and *Tenacibaculum* are detected only in hydrocarbon contaminated water and the

abundance of *Sulfitobacter* group was high in sea water and decreased in contaminated seawater (Prabakaran et al. 2007). Distinct variation in diversity was obvious in marine and fresh water aquatic systems in Antarctica. The fresh water ecosystems are dominated by *Flavobacterium*, *Pseudomonas* and *Polaromonas* (up to about 56 % of total sequences) (Michaud et al. 2012) while *Sulfitobacter*, *Thalassospira*, members of *Roseobacter*, *Gelidibacter*, *Polaribacter*, *Psychroflexus*, and *Pseudoalteromonas* were common to marine waters (Prabakaran et al. 2007; Guibert et al. 2012; Lo Giudice et al. 2012).

Sea ice harbors a network of brine pores and channels (Junge et al. 2004; Søgaard et al. 2010) and supports a diverse (Brown and Bowman 2001; Brinkmeyer et al. 2003; Maas et al. 2012) community of bacteria represented by photosynthetic, chemolithotrophic and heterotrophic bacteria besides Archaea and several eukaryotes. Gammaproteobacteria, Alphaproteobacteria and Bacteroidetes are the predominant groups. Actinobacteria are very rarely present. Among the Gammaproteobacteria species of the genera *Colwellia* and *Glaciecola* are the most abundant and *Marinobacter* spp. were rare. The Alphaproteobacteria are represented by members of the *Roseobacter* lineage while Bacteroidetes group included *Polaribacter* genera (Bowman et al. 1997; Gosink et al. 1998; Staley and Gosink 1999; Brown and Bowman 2001; Junge et al. 2002; Brinkmeyer et al. 2003; Kuhn et al. 2014; Lanoil et al. 2009). Other genera in sea ice include *Shewanella*, *Planococcus*, *Alteromonas*, *Pseudoalteromonas*, *Psychrobacter*, *Halomonas*, *Pseudomonas*, *Hyphomonas*, *Sphingomonas*, *Arthrobacter*, *Planococcus* and *Halobacillus* (Bowman et al. 1997). Temporal community analyses over a period of 2 years indicated a shift in community wherein *Paenisporosarcina* was reduced by fivefold while *Bacillus* increased by fourfold. In addition, *Acinetobacter* and *Cohnella* (Firmicutes) replaced *Paenibacillus* and *Jeotgalibacillus* in a span of 2 years (Doyle et al. 2013). In conclusion Fig. 2.1 summarizes the contribution of each community to the total diversity of Antarctica.

1.1.2 Bacterial Diversity of Antarctica as Studied by Using Functional Genes

Characterization of functional genes of a physiological group of bacteria has been used to identify diverse groups of bacteria like the sulphate reducing bacteria (Karr et al. 2005), photosynthetic bacteria (Karr et al. 2003; Stibal et al. 2012; Kong et al. 2014), hydrocarbon degrading bacteria (Muangchinda et al. 2014; Marcos et al. 2009) chitinase and ketosynthase producing bacteria (Xiao et al. 2005) and the ammonium oxidizing bacteria (Magalhães et al. 2014). Such studies are normally attempted with the assumption that the primer set would identify the specific gene in all bacteria. But in the absence of a consensus sequence or known conserved sequence for a specific gene this approach could be biased and the diversity reported will be a function of the coverage of the primers used.

Antarctic hyper saline lakes in the Vestfold Hills have high concentration of dimethylsulfide (Yau et al. 2013). Therefore, it is not surprising that by targeting the

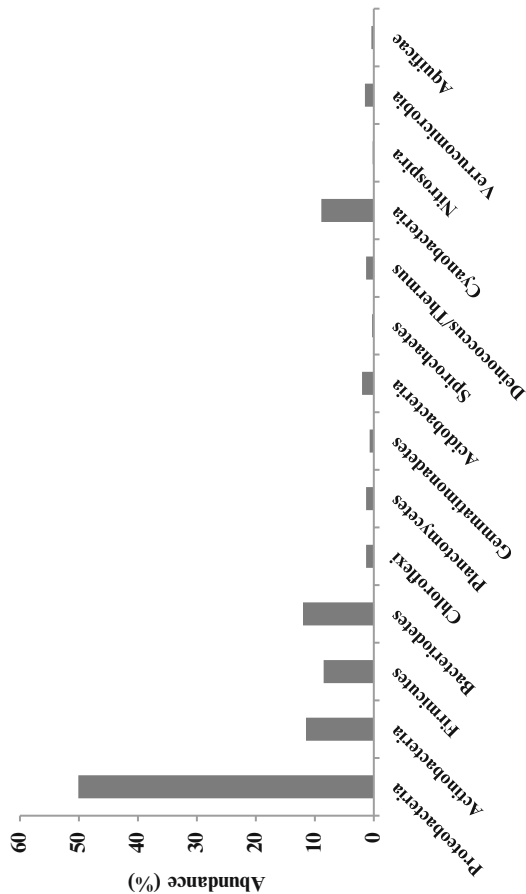


Fig. 2.1 Diversity and relative abundance (%) of bacteria from various samples from Antarctica based on culture independent methods. This figure was reconstructed from Shivaji and Reddy (2009)

gene *dsrA* (dissimilatory sulfite reductase), diverse group of sulfate-reducing bacteria were identified in Lake Fryxell, a permanently frozen freshwater lake, in Antarctica (Karr et al. 2005). It was also demonstrated that more than 70 % of sulfur transformation in subglacial lake sediments was contributed by two genera *Sideroxydans* and *Thiobacillus* (Purcell et al. 2014). Recently, Watanabe et al. (2013) based on *aprA* (adenosine-5'-phosphosulfate reductase alpha subunit) identified bacteria belonging to the genera *Thiocapsa*, *Sulfuricella*, *Desulfobacterium*, *Desulfofaba* and *Desulfotomaculum* from Antarctic fresh water lakes.

Scientific operations in Antarctica have led to the contamination of the pristine Antarctic environment with hydrocarbons in the form of fuel oils (Aislabie et al. 2004). Thus it was deemed relevant to identify bacteria with abilities to degrade polycyclic aromatic hydrocarbons (PAH). PAH degrading genes were detected from both Gram-positive and Gram-negative bacteria and were affiliated to the phyla Proteobacteria, Actinobacteria, Verrucomicrobia, Bacteroidetes, Firmicutes, Chloroflexi, Gemmatimonadetes, Cyanobacteria, Chlorobium, and Acidobacteria. *Sphingomonas*, one of the major PAH degraders in the environment, was observed in some locations. Thus indigenous bacteria have the potential to degrade PAHs and could thus facilitate bioremediation in Antarctica (Muangchinda et al. 2014). Based on the presence of the PAH degrading gene, bacteria belonging to the genera *Terrabacter*, *Mycobacterium*, *Diaphorobacter*, *Sphingomonas*, *Burkholderia*, *Rhodococcus*, *Mycobacterium*, *Nocardia*, *Terrabacter* and *Bacillus* were found to be predominant in Antarctic sediments (Muangchinda et al. 2014; Marcos et al. 2009) where as in soils *Pseudomonas* plays an important role (Ma et al. 2006). Diversity studies based on alkane monooxygenases genes (*alkB* and *alkM*), key enzymes in alkane degradation, from the Admiralty Bay and King George Island of Peninsula Antarctica indicated that the gene sequences were similar to the *alkB* gene reported in *Silicibacter pomeroyi*, *Gordonia* sp., *Prauserella rugosa*, *Nocardioides* sp., *Rhodococcus* sp., *Nocardia* sp., *Pseudomonas putida*, *Acidisphaera* sp., *Alcanivorax borkumensis*, and *alkM* described in *Acinetobacter* sp. (Kuhn et al. 2009). The penguins in Antarctica excrete huge amounts of chitin-containing droppings whose degradation is carried out by soil microbes. Studies based on chitinase genes (*chi67*, *chi69*, *chiA*, *chiB*, *chiF*) revealed the occurrence of *Janthinobacterium*, *Stenotrophomonas*, *Cytophaga* of Gram-negatives and *Streptomyces* and *Norcardiopsis* of Gram-positives as the abundant genera from a 1600 year old sediment obtained from Ardley Island, Antarctica (Xiao et al. 2005). It is well known that the microorganisms, particularly the members of Actinobacteria, are the reservoirs of natural compounds such as polyketides, alkaloids, peptides etc, and Antarctica prokaryotes are no exception. Owing to the significance of the community involved in polyketide synthesis, an attempt was made to investigate the diversity of bacteria based on ketosynthase (KS) gene. Phylogenetic analysis based on ketosynthase (KS) gene identified diverse bacterial groups, including Proteobacteria, Firmicutes, Planctomycetes, Cyanobacteria, Actinobacteria, some uncultured symbiotic bacteria and five independent clades. Most of the identified isolates showed below 80 % identity at the AA level to their closest match revealing great diversity and novelty of ketosynthase genes in Antarctic sediments (Zhao

et al. 2008). In addition, Antarctic lakes are known to support a photosynthetic bacterial community though most of the lakes are covered with thick sheet of ice. Based on gene *pufM* (coding for photosynthetic pigment-binding protein) 33 unique phylotypes related to *Rubrivivax*, *Acidiphilum*, *Rhodoferrax* and *Roseateles* were detected from Antarctic sediments (Karr et al. 2003; Stibal et al. 2012). While studying the diversity of *psbA* gene from Lake Bonney, unique phylotypes of genera *Nannochloropsis*, *Ochromonas* and *Isochrysis* were identified (Kong et al. 2014).

1.1.3 Bacterial Diversity of Antarctica as Studied by Cultivation Based Methods

The bacterial abundance from various habitats of Antarctica ranged from 0.2×10^2 to 0.6×10^{12} cells/g of ice (Carpenter et al. 2000; Priscu et al. 1999; Karl et al. 1999; Delille and Gleizon 2003), 0.2×10^2 to 10^7 cells/mL of water (Takii et al. 1986; Lo Giudice et al. 2012) and 8×10^6 to 2.4×10^7 cells/g of sediment (Lanoil et al. 2009; Stibal et al. 2012) and 10^5 to 10^{10} cells/g of soil (Aislabie et al. 2009). The culture dependent bacterial diversity was explored extensively from soil (Miwa 1975; Yi and Chun 2006; Ruckert 1985; Shivaji et al. 1988, 1989a, b; Wery et al. 2003; Bozal et al. 2007), water (Lo Giudice et al. 2012; Michaud et al. 2012; Söller et al. 2000; Labrenz et al. 2000; Cristóbal et al. 2011), cyanobacterial mats (Reddy et al. 2000, 2002a, b, 2003a, b, c, d, 2004; Van Trappen et al. 2002; Spring et al. 2003; Peeters et al. 2011), ice (Shivaji et al. 2004, 2013c; Antibus et al. 2012; Bowman et al. 1998) and sediments (Shivaji et al. 2011a; Yu et al. 2011) and have been reviewed by Shivaji and Reddy (2009) and Chattopadhyay et al. (2014) from Antarctica. Among the habitats, water, soil and mats are more diverse compared to ice and sediments (Fig. 2.1). In all the habitats communities representing Proteobacteria, Bacteroidetes, Actinobacteria and Firmicutes are wide spread while *Deinococcus-thermus* and *Spirochaetes* were detected only in soil (Hirsch et al. 2004; Antibus et al. 2012; Franzmann and Dobson 1992; Chattopadhyay et al. 2014). Among the Proteobacteria, Gammaproteobacteria were more commonly observed compared to Alphaproteobacteria, Betaproteobacteria and Deltaproteobacteria while members of Epsilonproteobacteria were absent. Alpha-, Beta- and Gamma-proteobacteria, Actinobacteria and Flavobacteria were also found to occur in Andean glacial ice, which is less impacted by anthropogenic interventions than the Arctic and Antarctic ice because of the difficulty in accessing it (Ball et al. 2014).

Relative percentage occurrence of cultivable bacteria from Antarctica indicated that the soils are dominated by Firmicutes (35 %), Actinobacteria (25 %) and Proteobacteria (18 %), water by Proteobacteria (42 %), Bacteroidetes (31 %) and Actinobacteria (23 %), algal mats by Proteobacteria (40 %), Firmicutes (28 %) and Bacteroidetes (24 %), ice by Proteobacteria (48 %), Bacteroidetes (21 %) and Firmicutes (19 %) and finally the sediment by Proteobacteria (50 %) and Actinobacteria (29 %) (Fig. 2.2). The above statistics clearly indicate that Proteobacteria is ubiquitously present abundantly in all the Antarctic habitats. The culturable bacteria isolated from Antarctica include 50 novel genera and 170 novel species. Only one novel family

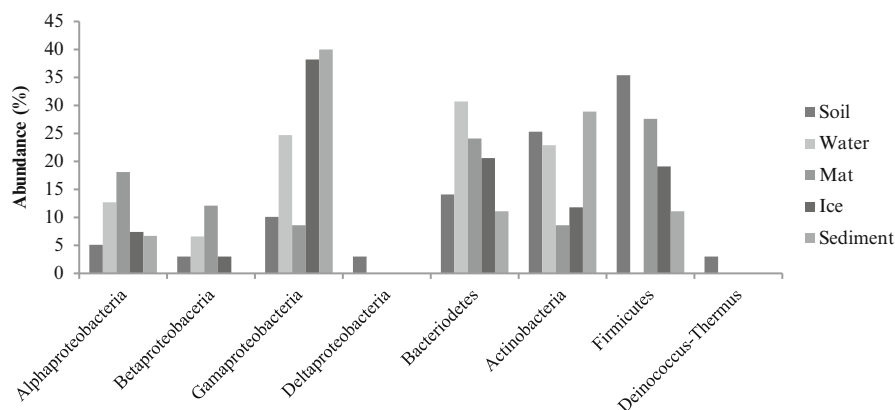


Fig. 2.2 Bacterial diversity and relative abundance (%) of culturable bacteria from soil, water, mat, ice and sediment samples from (communities contributing less than 3.0 % are omitted) Antarctica. Data compiled from references given in Sect. A-I-3

Granulosicoccaceae of Gammaproteobacteria has been described from Antarctica and it was isolated from seawater. It includes a single species *Granulosicoccus antarcticus* of the genus *Granulosicoccus* (Lee et al. 2007). In addition, some of the cultures attracted more interest, due to their thermophilic nature, such as *Alicyclobacillus pohliae*, *Aneurinibacillus terranovensensis*, *Anoxybacillus amylolyticus*, *Bacillus thermantarcticus* and *Brevibacillus levickii* which were isolated from geothermal soils of Mount Melbourne and Mount Rittmann (Lama et al. 1996; Allan et al. 2005; Poli et al. 2006; Imperio et al. 2008). Nevertheless, it may be mentioned that many of the phyla are also found in other cold habitats.

1.2 Diversity of Prokaryotes from Arctic

The Arctic is the Earth region that lies between 66.5°N and the North Pole and geographically spans the Arctic Ocean and covers land areas in parts of Canada, Finland, Greenland, Iceland, Norway, Russia, Sweden and the United States (Alaska). The Arctic is very cold and harsh for most of the year with scanty solar radiation. One of the unique characteristics of Arctic is the year round permafrost and thus the lack of lush vegetation. Arctic microbiology started much later compared to Antarctica and the first evidence of microorganisms was reported by Kriss (1945), Pady et al. (1948), Polunin and Kelly (1952), Kelly and Layne (1957) and Boyd and Boyd (1962a, b). However, the first culture independent study of Arctic tundra soil was carried out by Zhou et al. (1997). Currently the NCBI (<http://ncbi.nlm.nih.gov>) database contains about 3429 16S rRNA gene sequences of bacterial clones from Arctic. Of these only 79 sequences correspond to novel isolates from Arctic.

1.2.1 Bacterial Diversity of Arctic as Studied by Culture Independent Methods

The bacterial abundance and diversity of various ecological niches such as soil (van Dorst et al. 2014; Chu et al. 2010; Edwards et al. 2011; Zhou et al. 1997; Neufeld and Mohn 2005; Campbell et al. 2010; Schütte et al. 2010), ice (Junge et al. 2002; Brinkmeyer et al. 2003; Yu et al. 2006; Bottos et al. 2008; Collins et al. 2010), permafrost soil (Wilhelm et al. 2011; Steven et al. 2007; Hansen et al. 2007) and sediments (Zhang et al. 2014; Forschner et al. 2009; Li et al. 2006a, b, 2009; Lysnes et al. 2004; Perreault et al. 2007; Bienhold et al. 2012) from Arctic were explored by both culture dependent and independent methods (reviewed by Chattopadhyay et al. 2014). These studies indicate that soil microbial communities are very similar to that observed in Antarctica and Acidobacteria, Alphaproteobacteria, Actinobacteria, Betaproteobacteria and Bacteroidetes, account for more than 83 % of the diversity (Chu et al. 2010; Edwards et al. 2011; Zhou et al. 1997; Neufeld and Mohn 2005; Campbell et al. 2010; Schütte et al. 2010). In addition, Gammaproteobacteria, Verrucomicrobia, Gemmatimonadetes and Deltaproteobacteria were also reported. When the soil diversity was compared with that of the diversity in permafrost, as anticipated, a subset of the taxa were common. For instance in the permafrost soils Proteobacteria, Actinobacteria and Acidobacteria (Steven et al. 2007; Wilhelm et al. 2011) were dominant whereas Bacteroidetes, Gemmatimonas, Verrucomicrobia, and Planctomyces were less dominant. Studies have also indicated that the bacterial communities of these high latitude polar biocrusts did not show a consensus response to intermittent flow in water tracks over high Arctic permafrost (Steven et al. 2013). It was also observed that low pH supported the Proteobacteria at the expense of Acidobacteria and high pH supported Bacteroidetes (Ganzert et al. 2014). In case of sediments Proteobacteria was exuberantly present contributing 50.0–85.0 % of the diversity (Li et al. 2009; Bienhold et al. 2012; Lysnes et al. 2004; Steven et al. 2008a). Zhang et al. (2014) identified potential novel genera by both culture dependent and independent methods from Arctic marine sediments.

Sea-ice contained bacterial lineages that belonged to Proteobacteria, Bacteroidetes, Planctomycetes and Chloroflexi (Junge et al. 2002; Brinkmeyer et al. 2003; Bottos et al. 2008) and sea water harbored significant proportions of Proteobacteria (>50 %) and Bacteroidetes (25 %) and Actinobacteria and Verrucomicrobia were present below 25 % (Kirchman et al. 2010). So far, close to 284 genera (Schütte et al. 2010) belonging to Proteobacteria (131 genera), Actinobacteria (57 genera), Firmicutes (22 genera), Bacteroidetes (22), Chloroflexi (5 genera), Planctomyces (5 genera), Gemmatimonas (4 genera), Fibrobacter (2 genera), Acidobacteria (2 genera), Spirochaetes (1 genus), and other classes (34) have been detected from the various ecological niches of Arctic (Fig. 2.3). Relative percentage abundance in four extensively explored habitats soil, sediment, permafrost and ice indicated that the genera belonging to the class Proteobacteria are most dominating and members of the class Actinobacteria, Firmicutes and Bacteroidetes contribute 3–25 % (Collins et al. 2010).

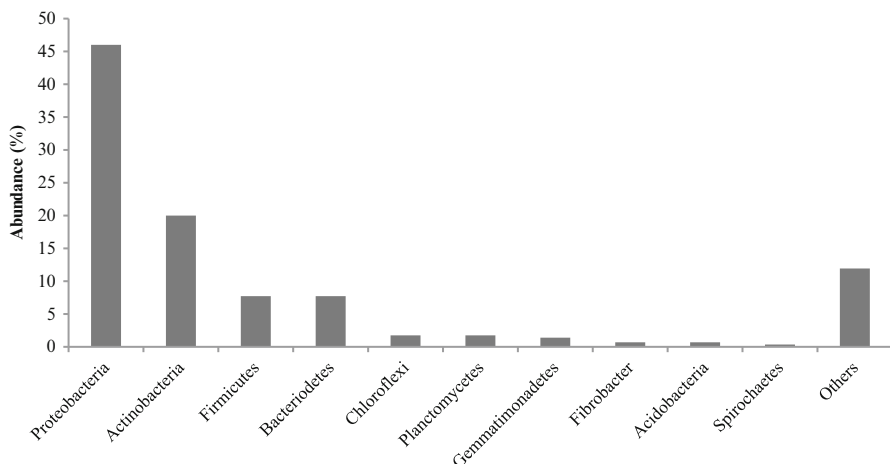


Fig. 2.3 Diversity and relative abundance (%) of bacteria from sea ice from Arctic based on a culture independent method. This figure was constructed from data obtained from Junge et al. (2002), Brinkmeyer et al. (2003) and Bottos et al. (2008)

1.2.2 Bacterial Diversity of Arctic as Studied by Functional Genes

Diversity of several physiological groups of bacteria such as nitrogen fixing communities (Deslippe and Egger 2006), ammonium oxidizers (Díez et al. 2012) and cyanobacterial diazotrophs (Díez et al. 2012) have been studied from various habitats of Arctic. Thus attempts have also been made to identify the diversity associated with nitrogen fixing communities based on the *nifH* gene. A good proportion (50–65 %) of the nitrogen fixing communities were affiliated to Alphaproteobacteria, Gammaproteobacteria, Deltaproteobacteria and Firmicutes and the genera were identified as *Rhodopseudomonas*, *Azospirillum*, *Azorhizobium*, *Rhizobium*, *Bradyrhizobium* of Alphaproteobacteria, *Herbaspirillum* and *Oryza* of Betaproteobacteria, *Pseudomonas*, *Azoarcus* of Gammaproteobacteria and *Paenibacillus* of Firmicutes. Using the same *nifH* gene the dominating cyanobacteria were identified as affiliated to Chroococcales, Nostocales, Oscillatoriales and *Phormidium* in brine and sea water (Díez et al. 2012). Further using *nitAB* gene sequences, *Nitrosospora* and *Nitrosomonas* were identified as the ammonium oxidizers present in the Arctic Ocean water (Bano and Hollibaugh 2000). In addition, thawing of permafrost due to climate change can result in mineralization of organic carbon into carbon dioxide and methane through microbial activity. Exploration of methanogenic community that contribute to the green house gases from Arctic would be interesting. It was also observed that *Methylobacter* (Type I methanotroph) and *Methylosinus* and *Methylocystis* (Type II methanotroph) were the methanotrophic members (Wartiainen et al. 2003; Liebner et al. 2009) from Arctic habitats and the community changed depending on the pH (Martineau et al. 2014). Arctic fresh water, marine water, ice shelf and coastal water receive solar radiation and thus support the photosynthetic bacterial community. Boeuf et al. (2013)

determined the Aerobic anoxygenic phototrophic (AAP) community in western Arctic Ocean using *pufM* gene and Alphaproteobacteria and Betaproteobacteria represented 49 % and 48 % respectively.

1.2.3 Bacterial Diversity of Arctic as Studied by Culture Dependent Methods

The bacterial abundance in major habitats from Arctic region was comparable to that observed in Antarctica and it ranged from 1.2 to 2.3×10^7 cells/g of sediment (Forschner et al. 2009), 5.2×10^4 – 1.7×10^9 cells/g of permafrost (Hansen et al. 2007), 0.9×10^3 – 2.4×10^6 cells/mL of ice (Møller et al. 2011; Brinkmeyer et al. 2003) and in case of water the abundance was 5×10^5 cells/mL (Møller et al. 2011). Cultivable bacterial diversity from major Arctic environments such as ice (Zhang et al. 2008; Auman et al. 2006, 2010; Gosink et al. 1998; Brinkmeyer et al. 2003; Groudieva et al. 2004; Bottos et al. 2008; Steven et al. 2008b), sediments (Prasad et al. 2014; Srinivas et al. 2009; Reddy et al. 2009b; Kim et al. 2009, 2012; Knittel et al. 2005; Knoblauch et al. 1999; Vandieken et al. 2006; Shivaji et al. 2012a; Begum et al. 2013), permafrost (Hansen et al. 2007; Steven et al. 2007, 2008a), mats (Dong et al. 2012), tundra soil (Jiang et al. 2012; Jiang et al. 2013; Männistö et al. 2012), water (Prasad et al. 2014; Yu et al. 2011; Van Trappen et al. 2004; Zhang et al. 2006; Kim et al. 2008; Jang et al. 2011; Al Khudary et al. 2008) and cryoconite holes (Singh et al. 2014) was explored and close to 675 strains belonging to 135 genera were identified and the bacterial diversity of the permafrost appeared to be more diverse compared to mats and water (Fig. 2.4). Relative percentage abundance indicated that Gammaproteobacteria, Bacteroidetes and Actinobacteria were abundant in ice and sediments and Bacteroidetes, Firmicutes and Actinobacteria were predominant in permafrost and soil (Fig. 2.2). The 675 bacteria isolated from Arctic included 12 novel genera (Ren et al. 2015; Storesund and Øvreås 2013; Qu et al. 2014; Prasad et al. 2013; Jiang et al. 2013; Steinsbu et al. 2011; Tamura et al. 2010; Steven et al. 2008b; Lee et al. 2007; Knoblauch et al. 1999; Gosink et al. 1998) and 70 novel species. The genera, *Parablastomonas* (Ren et al. 2015), *Psychroglaciecola* (Qu et al. 2014), *Arcticibacter* (Prasad et al. 2013), *Huanghella* (Jiang et al. 2013), *Dasania* (Lee et al. 2007) and *Augustibacter* (Tamura et al. 2010) have so far been reported only from the habitats in Arctic. Further, members of Deltaproteobacteria were detected in sediments (Knoblauch et al. 1999) and the class contains three novel genera *Desulfofrigus*, *Desulfofaba* and *Desulfotalea*, represented by nine novel species (Knoblauch et al. 1999). In addition, a novel species of the class *Verrucomicrobium* (*Luteolibacter luojiensis*) (Jiang et al. 2012), four novel species (*Granulicella arctica*, *Granulicella mallensis*, *Granulicella tundricola*, *Granulicella sapmiensis*) of the phylum *Acidobacteria* (Männistö et al. 2012) were described from Arctic. Most of the bacteria described from Arctic are psychrophilic except *Rhabdothermus arcticus* (37–65 °C), a novel thermophile isolated from a hydrothermal vent (Steinsbu et al. 2011). Comparison of the diversity between Antarctica and Arctic indicated similarity at the class level which was reduced at the genera level.

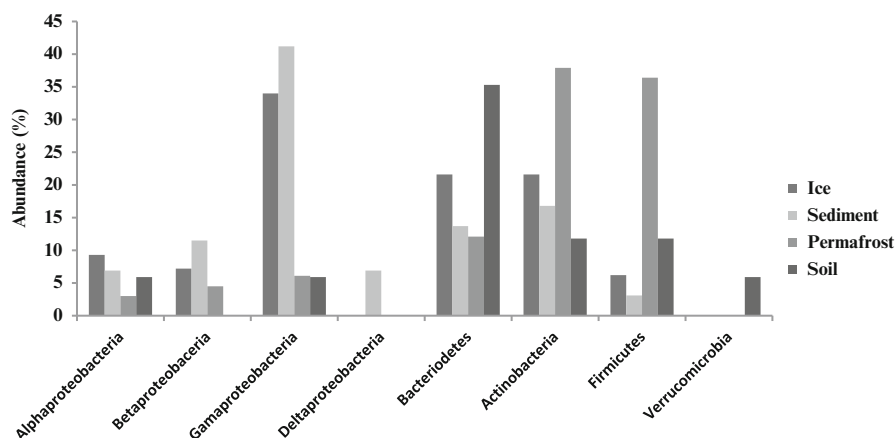


Fig. 2.4 Bacterial diversity and relative abundance (%) of culturable bacteria from ice, sediment, permafrost and soil samples from Arctic (communities contributing less than 3.0 % are omitted). Data compiled from references given in Sect. 1.2.3

1.3 Diversity of Prokaryotes from Himalayas

Seventy percent of the world's freshwater is frozen in glaciers, and the Himalayas have the largest concentration of glaciers outside the Polar Regions, covering about 33,000 km². The region has been referred to as the 'Water Tower of Asia', as it provides around 8.66106 m³ of water annually (Dyurgerov and Meier 1997). Further, the Himalayan environments are distinct from those in Polar Regions and are characterized by dramatic seasonal shifts in physical and biochemical properties in addition to the altitude gradient of climatic changes. In spite of the recent spurt of research activities in cold habitats, the bacterial diversity of the Himalayas has remained largely unexplored.

1.3.1 Bacterial Diversity of Himalayas as Studied by Culture Independent Methods

Culture dependent and culture independent based diversity of soils from three major glaciers of Himalayas, Pindari (Shivaji et al. 2011b), Kafni (Srinivas et al. 2011) and Roopkund (Pradhan et al. 2010), soil from western region of Himalayas (Gangwar et al. 2009) and snow and water (Liu et al. 2006, 2009, 2011) was reported recently. The total bacterial abundance was low in case of water (1.1 to 25×10^4 cells per mL) (Liu et al. 2011) and higher in case of sediments wherein it ranged from 0.9×10^7 to 30.7×10^8 cell per gram sediment (Shivaji et al. 2011a, b; Pradhan et al. 2010; Srinivas et al. 2011) and the Shannon diversity indices ranged from 2.7 to 3.4 in case of water to 0.9 to 4.89 for sediments (Srinivas et al. 2011). The three habitats, soil, water and sediments from three glaciers shared common taxa affiliated to Acidobacteria,

Actinobacteria, Bacteroidetes, Chloroflexi, Chlamydiae, Firmicutes, Nitrospirae, Proteobacteria, and Verrucomicrobia. However, sediments from the glaciers differed in their diversity in that sediments from Kafni glacier contained clones affiliated to Spirochaetae and Tenericutes (Srinivas et al. 2011; Shivaji et al. 2011a, b) where as samples from Pindari and Roopkund had sequences affiliated to Gemmatimonadetes and Planctomycetes. Gangwar et al. (2009) concluded the contribution of Proteobacteria as the highest in soil wherein it contributed 45–70 % to their niche followed by Actinobacteria (10–86 %) and Bacteroidetes (6.4–28 %) (Liu et al. 2006; Gangwar et al. 2009; Srinivas et al. 2011). The difference in community composition in the three habitats studied so far can be attributed to the nature of the soil. So far 135 diverse genera were identified from various environments of Himalayas and the number of genera followed the trend Actinobacteria (28.0 %), Betaproteobacteria (21.5 %), Alphaproteobacteria (9.6 %), Gammaproteobacteria (8.9 %), Deltaproteobacteria (11.1 %), Bacteroidetes (11.1 %), Firmicutes (3.7 %), Acidobacteria (1.4 %), Verrucomicrobia (3.0 %) and Epsilonproteobacteria (1.5 %) (Fig. 2.5).

1.3.2 Bacterial Diversity of Himalayas as Studied by Functional Genes

Compared to Antarctica and Arctic, very limited functional diversity studies have been carried out in the Himalayan region. The prokaryotic community in the Himalayas has been explored with respect to communities contributing to nitrogen fixation or production of green house gasses. Studies based on *nifH* gene indicated that majority of the diazotrophic community in rhizospheric soils of Himalayas included members of *Rhizobium* (53 %), *Dechloromonas* (7 %), *Bradyrhizobium* (7 %) and non-culturable bacteria (29 %) (Suyal et al. 2014). Diversity of methanogenic communities using *mcrA* gene and 16S rRNA gene sequence analysis indicated that the community was represented by the genera *Methanosarcina*, *Methanocella* and *Methanobacterium*

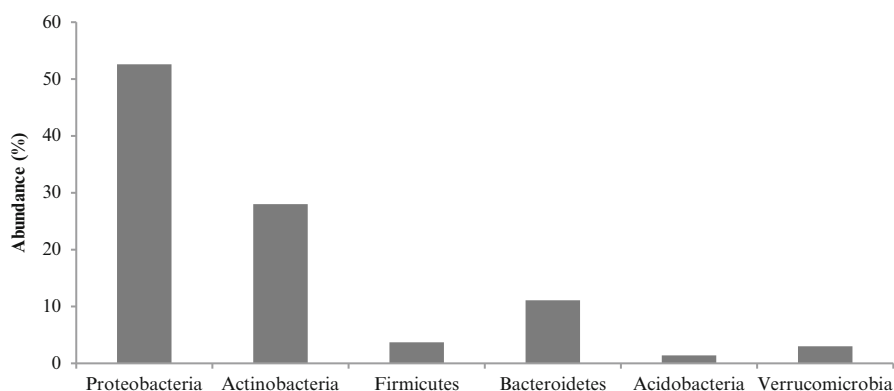


Fig. 2.5 Diversity and relative abundance (%) of bacteria from soil samples from Kafni Pindari and Roopkund glaciers of Himalayas based on culture independent methods. This figure was constructed from data compiled from references given in Sect. 1.3.1

(Aschenbach et al. 2013). More than 95 % of the methanotrophs as studied using *pmoA* gene belonged to the genera *Methylohalobius*, *Methylothermus*, *Methylococcus*, *Methylocaldum* and *Methylosoma* sp. (Zheng et al. 2012).

1.3.3 Bacterial Diversity of Himalayas as Studied by Culture Based Methods

Close to 466 strains have been isolated from Roopkund (Shivaji et al. 2008; Reddy et al. 2009a; Pradhan et al. 2010), Pindari (Shivaji et al. 2011a, b; Reddy et al. 2008, 2013a, b; Kishore et al. 2009; Pindi et al. 2009), Kafni (Kishore et al. 2009; Pindi et al. 2009; Srinivas et al. 2011), Hamta (Shivaji et al. 2005; Chaturvedi et al. 2005; Chaturvedi and Shivaji 2007) and Western Himalayan glaciers (Gangwar et al. 2009; Sahay et al. 2013; Yadav et al. 2015) and they represented the major taxa Proteobacteria, Bacteroidetes, Firmicutes and Actinobacteria. NCBI database revealed that so far only 21 novel species have been identified from the Himalayan mountain ranges. A novel genus, *Glaciihabitans* was described from Himalayan region (Li et al. 2013). Bioprospecting of these microbes indicated that a good proportion of the isolates from Pindari (Shivaji et al. 2011a, b) and Kafni (Srinivas et al. 2011) exhibited amylase, urease and or lipase activities at 4 and 20 °C. Gangwar et al. (2009) also demonstrated that cultures from high altitude cold habitats of Himalayan region exhibit lipase activity (Gangwar et al. 2009). In addition, culture based studies led to the identification of novel sulfate reducing and a phototrophic bacteria *Desulfovibrio psychrotolerans* (Jyothsna et al. 2008) and *Rhodobacter megaloophilus* (Arunasri et al. 2008) from Himalayas (Fig. 2.6).

1.4 Some Unique Features of Bacteria from Extremely Cold Environments

Interestingly, bacterial isolates from Antarctica, Arctic and Himalayas share many common features with respect to growth wherein the maximum growth temperature is below 30 °C and growth is possible even at 4 °C with very few exceptions such as *Alicyclobacillus pohliae* (42–60 °C), *Aneurinibacillus terranovensensis* (15–55 °C), *Anoxybacillus amylolyticus* (45–65 °C), *Bacillus thermantarcticus* (30–60 °C) and *Brevibacillus levickii* (20–55 °C) and *Rhabdothermus arcticus* (37–75 °C) (Lama et al. 1996; Allan et al. 2005; Poli et al. 2006; Imperio et al. 2008; Steinsbu et al. 2011). Earlier studies also revealed that the G+C content of 16S rRNA gene correlated well with the growth temperature in prokaryotes wherein the G-C content is concentrated in the stem regions of the molecule and offers structural stability and integrity to rRNA while its single stranded regions are enriched with purines (A and G). An elongation of helix 17 was observed in five out of eight true psychrophilic species of the genus *Cryobacterium* (unpublished) whose growth temperature was below 20 °C. Occurrence of 16S rDNA operons with psychrotolerant signatures, the transitions from C and G to T and A, higher uracil content and G:U mismatches from

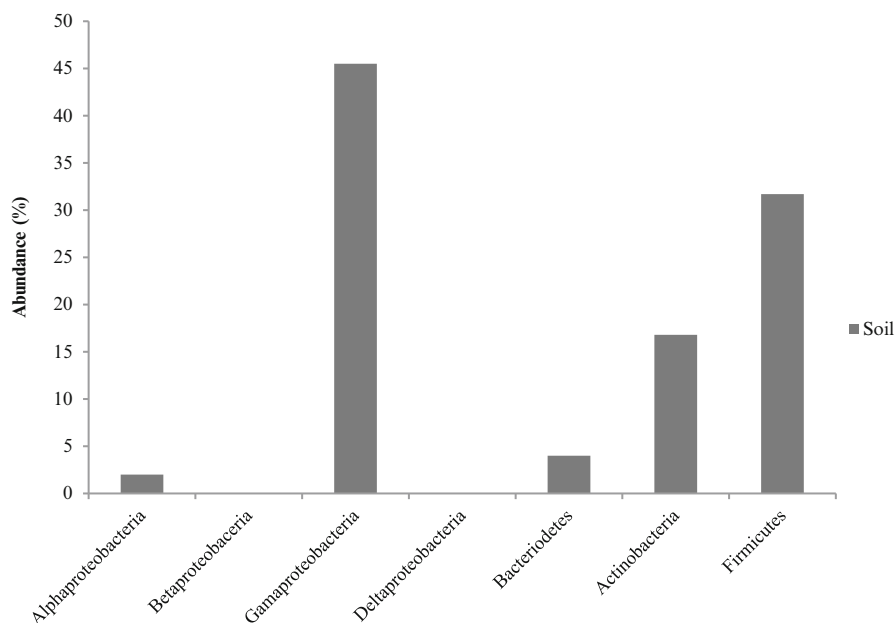


Fig. 2.6 Bacterial diversity and relative abundance (%) of culturable bacteria from soil samples collected from of Pindari, Hamta, Roopkund and Kafni glaciers of Himalayas. Data compiled from references given in Sect. 1.3.3

mesophilic to psychrotolerant, was reported in the strains of *Bacillus* (Prüss et al. 1999; Lauro et al. 2007). Further swollen sporangia were observed in psychrophilic strains of the genus *Bacillus* compared to their nearest mesophilic counterparts (Reddy et al. 2008; Abd El-Rahman et al. 2002; Larkin and Stokes 1967; Priest et al. 1988). *Bacillus cecembensis*, a psychrophilic species from Himalayas contained C_{16:1}ω7c alcohol in its membrane while it is absent in its nearest mesophilic neighbor (Reddy et al. 2008). In fact all the psychrophiles have a preponderance of unsaturated fatty acids compared to mesophilic counterparts. These bacteria also have cold active and heat labile enzymes (Ray et al. 1992; Reddy et al. 1994; Chattopadhyay et al. 1995) and have genes that are essential for their survival at low temperature (Singh et al. 2009; Singh and Shivaji 2010; Sundareswaran et al. 2010). Some other aspects of adaptation to low temperature are highlighted in the following section of this article.

2 Adaptation and Biotechnological Importance of Cold-Tolerant Bacteria

Bacterial isolates obtained from extreme cold habitats offer a challenging field of investigations. During the past few decades a vast body of information has been generated on various types of bacteria obtained from the Antarctic, Arctic and

Himalayan regions and also on the biochemical and genetic basis of their cold-tolerance (Chattopadhyay et al. 2014). A sizeable fraction of these cold-tolerant isolates are oligotrophic and eurythermal in nature. This section highlights some of the major clues obtained so far to the mechanism of cold-tolerance and biotechnological applications of cold-tolerant bacteria or their enzymes.

2.1 Mechanism of Cold-Tolerance: An Overview

Available evidences in the literature provide some idea as to the mechanism of bacterial cold-tolerance. Miniaturization and fragmentation of cells was a strategy used by an Arctic strain of *Psychrobacter* for increasing the chance of survival during lowering of environmental temperature (Ewert and Deming 2014). Further, as seen in fishes, insects, plants and fungi, some psychrophilic bacteria synthesize anti-freeze proteins to overcome the effect of sub-zero temperatures in the Antarctic environment. A report highlighting high level of thermal hysteresis and recrystallization inhibition activities in the cell-free extract of an Antarctic isolate added a new dimension to the present state of knowledge on bacterial anti-freeze proteins (Kawahara et al. 2007). The cold-adapted bacteria are known to produce some cold-tolerant and/or thermolabile enzymes (Feller and Gerday 2003; Singh et al. 2014), which help them sustain metabolic activities of the cell at non-permissible temperatures. It is also crucially important for them to sense the lowering of environmental temperature, which is accomplished by sensor molecules associated with the membrane (Ray et al. 1994). Temperature-dependent changes in the DNA topology is also postulated to play an important role in sensing the temperature of the outside environment (Shivaji and Prakash 2010). A two-component signal transduction mechanism has been demonstrated to be involved in sensing and responding to various stress conditions in the environment. Stress is normally detected by a membrane associated histidine kinase (HK) which acts as a sensor, gets phosphorylated under stress conditions and transduces the signal to a response regulator in the cytoplasm which upregulates genes essential for adaptation to the stress. Recently, the involvement of two HK-encoding genes viz, *ycy G* and *lis K* in the growth of the food-borne pathogen *Listeria monocytogenes* at low temperature is demonstrated (Pöntinen et al. 2015). Maintenance of the fluidity of cell membrane, which tends to get frigid at low temperature, is another challenge they are confronted with in the cold environment. Preferential synthesis of membrane-fluidizing fatty acids (unsaturated, short-chain and anteiso-fatty acids) coupled with involvement of some carotenoid pigments appear to help them in the homeoviscous adaptation of membrane fluidity (Chintalapati et al. 2004; Chattopadhyay and Jagannadham 2001). Most of the cold-adapted bacteria do not form endospores. So they are likely to continue metabolic activities at low temperature. It was believed earlier that at extreme low temperature, bacteria could continue only catabolic activities. Recent evidences of both catabolic and anabolic activities in bacteria at sub-zero temperatures have revealed flexibility of the metabolic machinery of cold-tolerant bacteria (Sengupta and

Chattopadhyay 2013). Transcription and translation were found to be continued at low temperature in the cell-free system of an Antarctic isolate while the same processes in the cell-free system of *Escherichia coli* did not continue at low temperature (Ray et al. 1998). Substantial increase in the intracellular concentration of ATP and ADP in *Psychrobacter cryohalolentis* K5, a eurythermal psychrophile, obtained from the Siberian permafrost, following lowering of the temperature indicated that it might be a strategy adopted by the organism to compensate for the lowering of the kinetic rate of metabolic reactions at low temperature (Amato and Christner 2009). Occurrence of the homologs of the gene *csp A*, which encodes the major cold shock protein in *E. coli*, was demonstrated in an Antarctic isolate (Ray et al. 1998). Hence cold shock proteins also might have a role in continuation of metabolism at low temperature. Growth of an Antarctic bacterium at low temperature was found to be enhanced in presence of some small molecular weight compounds (proline, betaine) in the culture (unpublished). So like some amphibians and insects, bacteria might get the help of some cellular cryoprotectants for adaptation to low temperature. Frequent arrest of the replication fork and fork-reversal during replication of DNA at low temperature was postulated as a reason behind inability of bacteria to grow in cold environments. The Rec BCD protein of an Antarctic lake isolate *Pseudomonas syringae* Lz 4 W, a psychrophile, appeared to degrade the reversed replication fork and facilitate re-initiation of replication (Sinha et al. 2013). The role of some other proteins (aspartate aminotransferase and t-RNA modification GTPase) in bacterial cold-tolerance was demonstrated using cold-sensitive mutants of an Antarctic bacterium as a tool (Singh et al. 2009; Sundareswaran et al. 2010). Degradation of RNA is a crucial step in the regulation of gene expression. The components of RNA-degradosome, a protein complex involved in RNA degradation, were found to be substantially different in an Antarctic bacterium compared to those in *E. coli* (Purusharth et al. 2007). Genomic and transcriptomic analysis of two cultures of a psychrophilic methanogen, *Methanobus psychrophilus* R15, one incubated at 18 °C and the other at 4 °C, indicated acceleration in the exosome-mediated RNA degradation at low temperature (Chen et al. 2012). In natural environments, stress conditions (extremities of temperature and pH, high salt, oxidative stress, ultraviolet radiation) seldom occur alone and most often they occur in various combinations. Consequently, cold-adapted bacteria might have to be adapted to more than one stressor in order to survive. Role of some proteins in adaptation of bacteria to low temperature and other environmental stress factors indicates stress response in bacteria might be interlinked (Chattopadhyay 2008). Increase in the intracellular production of free radicals (that contributes to the oxidative stress) was observed in an Antarctic bacterium when it was grown at low temperature (Chattopadhyay et al. 2011). The use of Entner-Duodoroff pathway (which contributes to the increase in the intracellular level of NADPH) by cold-adapted bacteria may help them in coping with increase in oxidative stress, associated with growth at low temperature (Moreno and Rojo 2014). Metabolism of polyhydroxyalkanoates, the carbon-storage polymers, also appears to relieve the cells of the elevated oxidative stress at low temperature (Ayub et al. 2009). A recent meta-analysis of the sequence of 66 plasmids obtained from various cold-tolerant and psychrophilic bacteria belonging

to various genera (e.g., *Allivibrio*, *Bacillus*, *Carnobacterium*, *Desulfotalea*, *Exiguobacterium*, *Flavobacterium*, *Pseudomonas*, *Psychrobacter*, *Runella*, *Spingopyxis*) revealed the presence of genes responsible for protection from low temperature and ultraviolet radiation and also resistance to heavy metals, metalloids and antibiotics (Dziewit and Bartosik 2014). Continuing investigations in this area are offering new clues to the mechanism of bacterial cryotolerance.

DNA sequencing has always provided insight into the regulation and functioning of genes and in the process has had a major impact on our understanding of processes involving human health and disease, agriculture and many other environmental processes involving living organisms. Thus any technology, which enhances the efficacy of deciphering genome sequences at an affordable cost and simultaneously provides whole genome sequence data within a short period of time, promises substantial addition to the present state of our knowledge on genes and their function. Next-generation sequencing (NGS) is such a technology which has facilitated whole-genome sequencing of multiple organisms from different and distinct habitats, helped generate genomic information and understand and appreciate unique features of organisms such as their adaptation to extreme environments. A recent study (Raiger Iustman et al. 2015) based on the genome sequence analysis of *Pseudomonas extremaustralis* provided new insights into environmental adaptability and adaptation to extreme conditions. In this psychrophilic bacterium from Antarctica, genes required for osmoregulation, cold adaptation, exopolysaccharide production and degradation of complex compounds were detected. Presence of genes acquired by horizontal transfer was also implied. Based on comparative genome analysis it was observed that genes coding for cold-shock proteins (Csps) and cold acclimation proteins (Caps) were present only in *Pseudomonas extremaustralis* which is a psychrophile. In contrast, in *P. Syringae* pv. *syringae* B278a and *P. aeruginosa* PAO1, which are mesophiles, the lowest number of Csps was present but no Cap was present. Thus, it was suggested that these proteins contribute to cold adaptation of *P. extremaustralis*. Draft genome sequence of a lake-isolate of *Hymenobacter*, tolerant to ultraviolet radiation and oxidative stress besides low temperature, was published some time back (Koo et al. 2014). Our group has recently reported the genome sequence of a number of psychrophiles from different cold habitats like Antarctica (Sreenivas et al. 2014; Reddy et al. 2013a, b, 2014; Kumar et al. 2013a, b), Arctic (Shivaji et al. 2013a, b; Kumar et al. 2013b), Himalayan glaciers (Reddy et al. 2014) and Stratosphere (Shivaji et al. 2012b).

A comparative genome analysis of Csps in the psychrophilic *Sphingobacterium antarcticum*, *Oceanisphaera arctica* and *Exiguobacterium indicum* indicated that CspA was present in all of them, Csp C, D, E and G were present in at least one of the three isolates whereas Csp B and I were absent (unpublished). The implications of this observation with respect to cold adaptation warrant further studies. Comparative genome analysis of psychrophiles besides providing information on the role of specific genes in cold adaptation would promise insight into the adaptive response of bacteria to other stressors (viz high salt, high and low pH).

2.2 *Biotechnological Potential*

Cold-active and /or thermolabile enzymes obtained from cold-tolerant organisms are of immense biotechnological importance. A thermolabile phosphatase, obtained from an Antarctic bacterium and patented (HK TM) some time back is active in neutral and alkaline pH. It is highly useful in performing sequential steps in a single tube viz, restriction enzyme digestion, dephosphorylation, enzyme inactivation, and ligation or end-labelling. Thus it simplifies the experimental procedure and minimizes the amount of nucleic acid required. Cold-adapted bacteria capable of degrading hydrocarbons are useful in waste water treatment (Margesin and Schinner 2001). Some strains isolated from the cryoconite holes in the Arctic glaciers were found to produce cellulase having higher activity at low temperature (Singh et al. 2014). Cold-active proteases isolated from cold-tolerant organisms are very suitable for food processing and in leather industries since they remain active at the temperature of tap-water and therefore eliminate the necessity of heat-activation. They are also useful in laundries for removal of stains. A cold-active lipase, obtained by cloning a lipolytic gene from an Arctic bacterium (*Rhodococcus* sp. AW25M09) in *E. coli*, has been found to retain activity at high pH, organic solvents (acetonitrile, diethyl ether) and salt (1 M NaCl). Thus it appears to be an interesting candidate for industrial applications (De Santi et al. 2014). A number of cold-adapted strains of Pseudomonads are known to produce lipases, which have high activity at moderate or low temperature. Such strains could be useful in lipase-mediated biodiesel production (Moreno and Rojo 2014). In view of the widespread resistance of pathogenic microorganisms to the presently used antibiotics, attention is focussed on alternative source of antibiotics. Bacteria occurring in Polar Regions are one of the potential candidates for this purpose. Notwithstanding substantial evidence of antibiotic resistance in polar bacteria (Liu et al. 2013; Maida et al. 2014; Fondi et al. 2014) this aspect remains relatively unexplored.

Human activities in cold climate are leading to the accumulation of a lot of garbage, which poses a serious threat to the environment. Petroleum products are widely used for heating, which is unavoidable during camping in such extreme harsh climate. Consumption of the petroleum products generates pollutants. Moreover, spillage of petroleum products from the aircrafts and reservoirs leads to serious environmental pollution. In spite of precautionary measures, accidental spillage is likely to occur because of increase in human intervention in these pristine environments. Airlifting of the contaminated soil for removal of the pollutants to some other place being prohibitively costly, in situ bioremediation using indigenous bacteria appears to be the most preferred option. Bioremediation involves transformation of organic pollutants by microorganisms (or microbial enzymes) into less hazardous products which are integrated into the biogeochemical cycle. Biodegradation in high temperature environments is associated with some advantages (e.g., enhanced solubility, bioavailability), not available to the bacteria in the cold environments. However, isolation of autochthonous bacteria having capacities to degrade hydrocarbons from Arctic and Antarctic soil has been reported from time

to time. They are found not only in oil contaminated soil but also in soil that has no history of oil contamination. An Antarctic strain of *Pseudomonas* was found to grow optimally in presence of ammonium sulphate, nitrate, nitrite and 3.5 % diesel at pH 7.0 within 10 to 20 °C (Shukor et al. 2009). In general, the degraders adapt rapidly to the contaminants and increase in number quickly following an episode of contamination. Hydrocarbon compounds associated with oil are widely diverse in nature (i.e., iso-, cyclo, and linear alkanes, monoaromatic compounds and polycyclic aromatic hydrocarbons). So microorganisms with specific biochemical mechanisms to metabolize different types of hydrocarbons are required for biodegradation of the pollutants (Timmis et al. 2010). In one study, organisms having previous exposure to oil-contamination were observed to degrade the contaminants at a faster rate indicating the importance of adaptation. So pre-exposure appears to be essential for quick degradation. Successful application of real-time PCR during the past decade has revealed the presence of a number of genes responsible for hydrocarbon biodegradation (e.g. monooxygenases, dioxygenases) in different oil-contaminated sites (Powell et al. 2006). However, despite their capacity to degrade a wide range of hydrocarbons, all the microbial communities occurring in cold climate, cannot degrade all sorts of petroleum-derived pollutants. Moreover, some of the pollutants (e.g. highly substituted and high molecular weight compounds) are recalcitrant in nature and resist microbial degradation. They are immune to microbial degradation. For example, asphalt (or bitumen) is a highly viscous liquid or semi-solid form of petroleum. Asphalt pavements (mineral aggregate bound with asphalt) were detected years after a spillage in Chile and another spillage in Canada. Following the Deep water Horizon blow out in August 2010, a substantial amount of hydrocarbons were found to be left though another large portion was degraded by microbial metabolism and removed by human intervention (Kimes et al. 2014). The rate of degradation is slow at low temperature. Significant improvement in the rate of oil-degradation could be achieved in one case by spraying surfactant-foam containing oil-degrading microbe. The surfactant facilitates dissolution of oil from the soil. Its insulating effect maintains a warmer environment in the soil (Jeong et al. 2015). Besides petroleum products, other types of environmental contaminants (e.g., heavy metals) also occur in Antarctic soil because of anthropogenic activities (Claridge et al. 1995; Lohan et al. 2001; Chaparro et al. 2007). A bacterial isolate obtained from the South Shetlands Islands, Antarctica, tentatively identified as a *Pseudomonas* sp. was found to convert sodium molybdate or Mo^{6+} to molybdenum blue. The optimum temperature range for the reaction was 15–20 °C. Thus, the strain was suitable for bioremediation in both cold and temperate regions (Ahmad et al. 2013). Polychlorinated biphenyls (PCBs) widely used for industrial and commercial purposes also occur in the polar regions because of aerial transportation, inputs by the rivers (in the Arctic regions) and improper disposal of PCB-containing articles (e.g., electrical equipment) at the research site. Microorganisms having the capacity to degrade PCBs have been isolated from both the Arctic and Antarctic regions from time to time (Master and Mohn 1998; De Domenico et al. 2004).

Besides low temperature, deficiency of nutrients in the soil is another limiting factor for growth of bacteria used for bioremediation. Hence, sometimes it may be

needed to stimulate the activities of the soil bacteria by addition of nutrients (Ruberto et al. 2009). Sometimes it appears realistic to use bioremediation in combination with some physical process of cleaning (use of boomers and skim). It has been possible to improve the cold-tolerance of the mesophilic organism *E. coli* by cloning the genes encoding two chaperonin proteins obtained from an Antarctic organism (Ferrer et al. 2003) and also by cloning a gene encoding an antifreeze protein occurring in a cold-tolerant plant (Deng et al. 2014). The use of such genetically engineered microorganisms with high capacity to degrade pollutants appears to be an attractive option. But introduction of foreign microorganism in the environment is prohibited in Antarctica.

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Conflict of Interest Authors declare that they have no conflict of interest.

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