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Soil bacterial community structure, metabolic adaptations, and their functional interactions to abiotic factors in Antarctica

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Abstract: Antarctica features one of the most ancient, largest glacier reserves and the most pristine environment left on the earth. However, in the last few decades disturbances due to industrialization and release of greenhouse gases have led to serious consequences such as melting of polar ice sheets, changing atmospheric chemistry and ozone depletion. Here, we use high-throughput sequencing to understand the impact of subtle changes in environmental parameters on bacterial communities. We observed dominance of *Cyanobacteria* (41.93%) followed by *Bacteroidetes* (14.8%), *Acidobacteria* (13.35%), *Proteobacteria* (9.67%), *Actinobacteria* (7.79%), *Firmicutes* (3.46%) among all the samples collected every alternate day for 20 days. Additionally, metagenomic imputations revealed a higher abundance of gene families associated with DNA repair and carotenoid biosynthesis enabling bacterial communities to resist and function under the high UV radiations. We further observed bacterial communities are dependent on the single carbon metabolism as a strategy for nutrient uptake in such nutrient deprived conditions.

Keywords: Antarctica, UV radiations, adaption strategies, extreme environments, DNA repair.

Introduction

Antarctic continent represents one of the most extreme ecosystems experiencing arrays of abiotic stress such as, low temperatures and sunlight, high solar radiations and low nutrient availability, making it unsustainable for most organisms (Molina-Montenegro *et al.* 2019). Additionally, over the last few decades, anthropogenically emitted chlorofluorocarbons (CFCs) have led to severe ozone destruction in the stratosphere over Antarctic continent, leading to increased UltraViolet (UV) radiation at the surface (Manney *et al.* 2011; Carpenter *et al*. 2014). UV radiation has been known to cause detrimental impacts either by affecting the DNA or inhibiting the photosynthetic apparatus or inducing oxidative stress by the production of reactive oxygen species (Schmidt *et al*. 2010; Pichrtová *et al*. 2013; Reis-Mansur *et al*. 2019). The latter may have adverse effects on the resilient biota like seaweed, microorganisms, *etc*. (Caldwell *et al.* 2007). Previous studies on higher plants and microorganisms have noted a striking impact of UV radiation, leading to the alteration in cellular ultra-structures, inhibition of germination and impairing the yield of photosynthesis (Hughes *et al*. 2003; Steinhoff *et al*. 2008). However, this perpetual impact of high UV irradiation has led to development of various defense mechanisms (Warnecke *et al.* 2005; Fernández Zenoff *et al.* 2006; Pérez *et al*. 2017). Alternatively, it has been hypothesized that such perpetual increase in UV radiation, certain organisms might lose the ability to adapt to the changing environment resulting in extinction and further burden of ecosystem imbalance (Blumthaler *et al.* 2007). Hence, the polar ecosystem including glaciers and marine coasts represent a model system to test the fate of ecosystems under the impact of climate change (Lütz *et al.* 2016; Sharma *et al.* 2018; Kajale *et al.* 2021).

Additionally, there are reports of subtle and gradual rises in the surface temperature evidencing impact of global climate change, which further affects the light dependent, temperature sensitive organisms (Wynn-Williams 1996; Yergeau *et al.* 2012). A recent report regarding the analysis of bacterial communities from Antarctic soil suggests influence of limited nutrient availability having more pronounced effect than temperature variations (Newsham *et al*. 2019). Community succession under the composite impact of climate change on bacterial communities still remains in its infancy. Tracking the shift in these communities would serve as an indicator to define the magnitude of perturbation caused, if any (Wynn-Williams 1996). Similarly, it becomes vital to monitor other abiotic factors (*i.e*, precipitation, temperature, ultraviolet radiation, *etc*.) known for their impact on the microbial community composition. In spite of evident potential of extremophiles, including those isolated from Antarctica, bacterial community composition under such poly-extremophilic conditions has scarcely been studied (Peter and Sommaruga 2016; Almela *et al.* 2021; George *et al.* 2021).

There are several efforts to reveal the role of uncultivable bacterial communities residing in Antarctica sediments or in mutualism with higher organisms by using multiple approaches targeting 16S rRNA genes (Cid *et al*. 2016). Over the last decade, deep sequencing approach has not only helped in investigating microbial community structures but also in acquiring in-depth knowledge of their functions from various ecological niches viz. hot springs, coalmines, deep sea and polar sediments (Rastogi *et al*. 2012; Sharma *et al*. 2014, 2017, 2019; Molina-Montenegro *et al*. 2019; Newsham *et al*. 2019). In the light of these observations, the objective of the present study is to elucidate the bacterial community composition under the poly-extremophilic conditions of Antarctic continent. We further examine the functional adaptations with respect to the survival and nutrient adaptations endorsed by bacterial communities, with the help of imputed metagenomics.

Material methods

Sample collection. — The surface sediment samples were collected (in triplicates) during the Antarctic spring and early summer from Larsemann Hills (69°24'54.9"S, 76°12'48.8"E) near the *Bharati* Station of India located in the southeastern region of Prydz Bay, Antarctica. A total of ten samples were collected on alternate days spanning across 20 days to generate robust sequencing data to assess the microbial community composition under poly-extremophilic conditions. These series of samples were termed as ST01–ST10 corresponding to its time of collection (*e.g.*, ST01 represents sample collected on Day 1 and the ST10 represents the sample collected on Day 20). The sediments samples were collected in sterile falcon tubes and stored at –20ºC until further processing.

Additionally, an onsite assessment of environmental parameters was also carried out throughout the sampling period. Monitoring of the abiotic factors such as temperature, overhead ozone (DU), total radiation, UV-A radiation, UV-B radiation was done continuously for the sampling period. Moreover, the overhead ozone was measured using a hand-held multi-band sunphotometer (MICROTOPS II) and was validated using satellite retrievals (Ozone Monitoring Instrument); see Table 1.

Community DNA extraction and amplicon sequencing. — The samples were transported to the laboratory by maintaining the cold chain. The total community DNA was extracted from the sediment samples by using PowerSoil kit (Qiagen, The Netherlands) according to the manufacturer's protocol, further checked for the qualitative and quantitative assessment of the DNA (Jani *et al*. 2018a) and stored at –20ºC until further processing. The template for the amplicon sequencing was prepared by amplification of V4 region of the 16S rRNA gene using primer pairs 515F/806R and followed for the library preparation using Illumina 16S metagenomic protocol (Caporaso *et al*. 2011).

Table 1

Assessment of physical parameters under temporal variation of UV radiation.

Sample ID	Date	Overhead ozone (DU)	Temperature (ºC)	Total radiation (MJ m^{-2})	UVA Radiation (MJ m^{-2})	UVB radiation (MJ m^{-2})	Wind Speed (m s^{-1})
ST01	8-Jan-19	271.26	0.44	0.14	0.011	78.16	17.88
ST02	10-Jan-19	272.44	3.09	0.18	0.014	78.08	12.43
ST03	12-Jan-19	276.86	1.57	0.18	0.013	78.09	13.33
ST04	14-Jan-19	277.53	0.98	0.19	0.013	78.07	8.58
ST05	16-Jan-19	307.67	1.6	0.19	0.013	77.64	16.79
ST06	18-Jan-19	306.21	0.46	0.19	0.013	78.14	10.17
ST07	20-Jan-19	295.83	0.05	0.11	0.009	78.17	10.06
ST08	22-Jan-19	299.81	0.85	0.17	0.011	78.13	10.71
ST09	24-Jan-19	305.79	-2.53	0.12	0.009	78.15	7.8
ST10	26-Jan-19	304.04	-0.78	0.06	0.006	78.07	7.98

The equimolar libraries were pulled and sequenced on Illumina Miseq platform using 2 x 250bp, V2 chemistry. The raw reads can be obtained under the SRA BioProject Id PRJNA587651.

NGS analysis. — The obtained raw reads were subjected to downstream analysis using DADA2 pipeline (Callahan *et al*. 2016). The latter involves quality trimming by computing error model, followed by removal of substitution and chimeric reads. Here, we used cutoff of 240 bp and 160 bp for filtering the paired R1 and R2 reads, respectively, with maximum expected error rate of 2, 2. These filtered, high quality reads were assigned to amplicon sequence variants (ASVs) using similarity cutoff of 100%. The taxonomic classification of ASVs was performed by using RDP naive Bayesian classifier using SILVA reference database (Wang *et al*. 2007; Quast *et al*. 2013). Further analysis was performed using R environment, which predisposes conversion of abundance table to the phyloseq object (Oksanen *et al*. 2013).

Estimation of bacterial load. — The total bacterial load was evaluated by quantification of the 16S rRNA gene as a proxy-using real time PCR (RT-PCR) (Jani *et al*. 2018b). It involves template preparation (in triplicates) and amplification using Power SYBR Green PCR Master Mix and subsequent amplification on ABI 7300 thermo-cycler. Subsequently, the 16S rRNA gene copy number was determined by comparing observed values against the standard curve. The standard curve was plotted by using 10-fold serial dilution of known concentration of PCR product of the bacterial isolate, with efficiency and correlation coefficient cutoff of >90%, (r^2) > 0.99, respectively.

Functional predictions. — Metabolic potentials of the bacterial communities to thrive and sustain under the extreme conditions of high UV radiation and cold stress were evaluated by using the Phylogenetic Investigation of Communities by Reconstruction of Unobserved States 2 (PICRUSt2) package (Douglas *et al*. 2020). It represents an improved version of PICRUSt1 with expanded reference dataset and novel prediction methods using MinPath to derive more reliable metagenomic inferences (Langille *et al*. 2013).

Statistical analysis. — Statistical analysis of the data generated during this study was performed using R (R Development Core Team, 2013). The R packages vegan, PhyloSeq, ggplot2, corrplot were used to carry out the correlation analysis between the bacterial communities and the changing environmental factors. Further, the functional attributes of the bacterial communities were correlated with the bacterial diversity to derive the influence of subtle changes in the bacterial diversity on the metabolic turnover. The data visualization was performed using shiny package in R.

Results

Estimates of abiotic factors. — We observed notable difference in the abiotic factors such as temperature, total radiation, and overhead ozone, during the course of sampling period as described in Table 1. The variation in temperature was recorded in the range of –2.5 to 3ºC during the entire studied period. We note that the overhead ozone varied in the range of 271.26 to 307.66 DU during the course of this study. Similarly, the overall radiation also ranged between 0.064 to 0.191 MJ m^{-2}. The UVA radiation, as a determinant of total radiation was found to range between 0.0057 and 0.0137 MJ m^{-2} whereas, the most harmful subset of it *i.e.* UVB radiation was in the range of 77.64 to 78.17 MJ m^{-2}.

Composition of bacterial communities. — Amplicon sequencing using Illumina MiSeq platform yielded an average of 176941.7 ± 481229 (mean ± SD) reads per sample. Taxonomic assignment of the high-quality reads against the SILVA database using DADA2 pipeline resulted in 6010 ASVs. We computed non-parametric alpha diversity indices viz. Chao1, Shannon, and observed ASVs to reveal the bacterial diversity under the constantly fluctuating environmental conditions of Antarctica. We noted variability among the alpha diversity indices across the study duration (Table 2). However, computation of Shannon index, a representative of both diversity richness and evenness depicted gradual variability in the bacterial diversity across the study period, which was marked by ≤0.07-fold deviation in the bacterial diversity (Shannon index). It was supported by the observed variations in the RT-PCR based determination of bacterial load across all the time points (Fig. 1). Moreover, we noted the lowest values of Chao1 (1151), observed ASVs (1151) and Shannon (6.76) for the ST02, the

Table 2

Estimates of alpha diversity parameters.

Sample ID	Chao1	Observed ASVs	Shannon
ST01	1863	1863	7.28
ST02	1151	1151	6.76
ST03	1550	1550	7.13
ST04	1431	1431	6.89
ST05	1629	1629	7.06
ST06	1746	1746	7.19
ST07	1448	1448	6.97
ST08	1240	1240	6.90
ST09	1584	1584	7.08
ST10	1431	1431	7.03

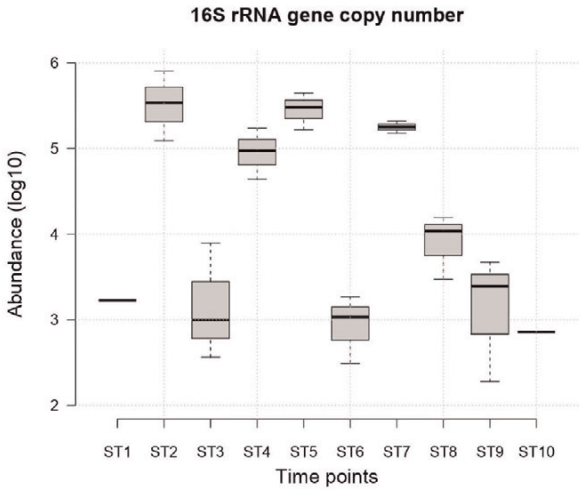

Fig. 1. Real time PCR based estimates of bacterial biomass. Absolute copy number of 16S rRNA gene (represented as $\log_{10}$) observed across the temporal gradient under the UVB radiation.

sediment having highest noted temperature of 3.08ºC among all the time points. Further, the assessment of relationship between the increasing temperature and Shannon indices based on the Spearman's correlation indicated negative correlation between Shannon *vs*. temperature (r = –.34). Alternatively, ST01 represents the sediment having highest species richness (Chao1, 1863). Sample ST07 exhibits highest recorded UVB radiation (78.17 MJ m^{-2}) which, accounts for 1.27x 10^{-3} folds higher radiation than the observed average (78.07 ± 0.15 MJ m^{-2}) across the study duration. Interestingly, correlating UVB radiation with

the bacterial diversity for sample ST07 suggested 0.04-fold lowered species richness over the recorded mean of 1507.3 ± 215.91 (mean ± SD). Moreover, intensity of UVA radiation on ST02 was found to be 18.6x 10^{-2} fold higher than the noted average (0.011 ± 0.002 MJ m^{-2}), which further may contribute for 0.30-fold deterioration in the species richness (Chao1, 1151). Further, we computed Spearman's correlation to derive the relationship among bacterial diversity and UV radiation which suggested negative correlation between Shannon *vs.* UVA Radiation (r = –0.13) and UVB radiation (r = 0.05).

Bacterial community structure under the advent of the high temperature and increased UV radiation demonstrates augmentation of phyla as: Cyanobacteria (41.93%), Bacteroidetes (14.8%), Acidobacteria (13.35%), Proteobacteria (9.67%), Actinobacteria (7.79%), Firmicutes (3.46%), *Chloroflexi* (2.46%), Armatimonadetes (1.28%), Verrucomicrobia (1.17%) and Deinococcus-Thermus (0.94%), contributing for 96.9% of total bacterial communities (Fig. 2). Interestingly, phylum Cyanobacteria (41.93 ± 3.36) predominates in all the sediments samples. Followed by other photo-autotrophs and early heterotrophs viz. phylum Bacteroidetes (14.8 ± 4.89%), Acidobacteria (13.35 ± 4.78%), Proteobacteria (9.67 ± 2.51%), Actinobacteria (7.79 ± 3.7%) (Warnecke *et al.* 2005). Assessment based on Spearman's correlation to evaluate the influence of rise in temperature on the bacterial phyla revealed relatively lower impact on the phylum Cyanobacteria. Similarly, phylum Acidobacteria, Armatimonadetes and Verrucomicrobia were found to suffer minimal impact. Conversely, Actinobacteria and *Chloroflexi* experience the significant alterations due to rising temperatures (r = –0.76, $p \leq 0.01$; r = –0.64, $p \leq 0.05$, respectively). Interestingly, we observed positive correlation between temperature and bacterial phyla Proteobacteria and Firmicutes. The observation can be supported by increased abundance of phylum Firmicutes and Proteobacteria in samples ST02 and ST03, which are marked by relatively highest noted temperature of 3.09ºC and 1.57ºC, respectively (Fig. 2). Moreover, the impact of UV on the bacterial phyla depicted

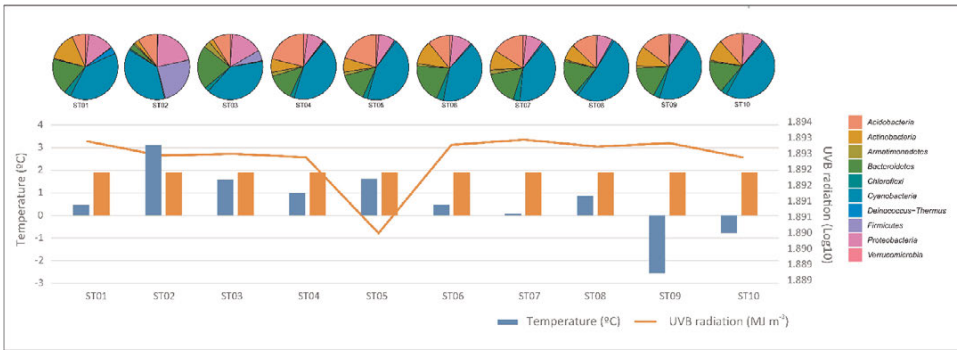

Fig. 2. Distribution of most abundant bacterial phyla against the subtle changes in environmental parameters. The blue and orange column represents the changes in the temperature and UV-B radiation (represented as $\log_{10}$) during the course of study period. Orange line defines the trend of changes in the UV-B radiation.

partial negative impact on phylum Cyanobacteria whereas Acidobacteria experiences the lower impact of UV radiation. Moreover, UVA imparts negative impact on other phyla like. Actinobacteria (VA $r = -0.72$, $p \leq 0.01$) and *Chloroflexi* which constitutes members practicing photo-autotrophy. Additionally, phylum Deinococcus-Thermus was also found to sustain the impact of significant UVA radiation ($r = -0.75$, $p \leq 0.01$).

Similarly, we noted variation in the sediment bacterial communities exhibiting the differential abundance of ASVs (relative abundance >1%) which corresponds to 12 bacterial families such as Chroococcidiopsaceae (21.93%), Blastocatellaceae (12.42%), Nostocaceae (9.2%), Chitinophagaceae (5.48%), Phormidiaceae (5.25%), Hymenobacteraceae (3.76%), Phormidesmiaceae (3.48%), Burkholderiaceae (3.1%), Spirosomaceae (3.02%), Sphingomonadaceae (2.91%), Clostridiaceae (2.51%) and Nocardioidaceae (1.76%). Spearman rank correlation in case of bacterial family suggested negative impact of temperature on the Nocardioidaceae and Phormidesmiaceae ($r = -0.98$, $p \leq 0.05$; $r = -0.73$, $p \leq 0.01$, respectively). Chitinophagaceae and Hymenobacteraceae also suffer loss of abundance with rising temperature. Whereas bacterial families *e.i.*, Clostridiaceae, Nostocaceae and Burkholderiaceae were found to flourish with respect to the changes in the surface temperature. Impact of UV radiation on the bacterial family revealed negative impact on the Phormidesmiaceae (*vs.* UVA, $r = -0.83$, $p \leq 0.01$) and Nocardioidaceae (*vs.* UVA, $r = -0.86$, $p \leq 0.01$). Whereas Clostridiaceae was found to adapt to the UV radiation and cast positive correlation (*vs.* UVA, $r = 0.65$, $p \leq 0.05$). At lower taxonomy rank, we note differential abundance of ASVs (relative abundance >1%) representing bacterial genera like *Aliterella* (21.35%), *Blastocatella* (11.52%), *Nostoc* (7.77%), *Tychonema* (5.06%), *Phormidesmis* (3.73%), *Hymenobacter* (3.38%), *Sphingomonas* (2.68%), *Spirosoma* (2.52%), Clostridium (2.39%), Segetibacter (2.31%), Polaromonas (1.57%) and Flavisolibacter (1.37%). Assessment of Spearman rank correlation inferred positive correlation between bacterial genera Nostoc and rising temperature and, UV radiation (*vs.* UVA, $r = 0.63$, $p \leq 0.05$). Likewise, for *Polaromonas* (*vs.* UVA, $r = 0.72$, $p \leq 0.05$). In contrast *Phormidesmis* was found to be negatively correlated under impact of both temperature ($r = -0.73$, $p \leq 0.05$) and UV radiation (*vs.* UVA, $r = -0.83$, $p \leq 0.01$). Bacterial genera *Hymenobacter* and *Segetibacter* also found to experience the negative impact of rising temperature.

Functional predictions. — The extreme environmental conditions in Antarctica may confer a high stress condition for the microorganism, but such perpetual pressures have often been found to cast an emergence of novel mechanism for survival and adaptation. Thus, we employed an approach of metagenomic imputations using PICRUSt2 to dissect the adaptative mechanism of these bacterial communities sustaining varied abiotic stress. We found functional variability among the time points under study, which corresponds to the functional attributes of thriving bacterial communities under changing environment. Additionally, niche adaptation and nutrient acquisition represent the

primary and key elements for bacterial communities (Fig. 3a–b). Gene families associated with carbohydrate metabolism, lipid metabolism, amino acid metabolism, metabolism of terpenoids and polyketides, metabolism of cofactors and vitamins, nucleotide metabolism, biosynthesis of other secondary metabolites, energy metabolism, metabolism of amino acids and glycan biosynthesis and metabolism were collectively found directly proportional to the order of Shannon index. Such comparisons of the functional attributes to that of the diversity measures provide an insight into the plausible functional redundancy, enabling ecosystem functioning even under instances of altered community composition. The observation was also supported by Peter and Sommaruga (2016), evaluating the bacterial functional redundancy upon glacier retreat. Further, with an intend to decipher the mechanism for niche adaptation under the poly-extremophilic conditions (especially rising temperature and high UV radiation) and nutrient acquisition in nutrient deprived environments like Antarctica, we targeted the gene families involved in DNA repair and one carbon mechanism. We noted dominance of genes belonging to the base excision repair, DNA repair and recombination proteins and mismatch repair (Fig. 3b).

Additionally, the strategies for nutrient acquisition represented either photoautotrophy or heterotrophy by involving in methane metabolism. The former could be supported by the observed specific augmentation of Cyanobacteria, the pioneer communities adapting under the perpetual abiotic pressures. Prevalence and persistence of genes governing anomalies of methane metabolism suffice the probable pivotal involvement of these bacterial communities to avail heterotrophic mode of nutrient acquisition by utilizing the one carbon metabolism with the major contribution in driving the geochemical pathways (Fig. 4). Similarly, we noted the abundant acquisition of elements of energy metabolism such as sulfur metabolism, oxidative phosphorylation, nitrogen metabolism and photosynthesis would enable effective survival of the bacterial communities under harsh conditions of Antarctica (Fig. 3a).

An attempt to establish the relationship between the functional potential of bacterial communities and rising temperature using Spearman rank correlation suggested negative correlation with gene families involved in the methane metabolism, photosynthesis ($r = –0.27$, $p \leq 0.05$), oxidative phosphorylation, sulfur metabolism except nitrogen metabolism and mismatch repair. Whilst we also noted fluctuations in the levels of these genes families with respect to the sampling time point (Fig. 3a, 3b). Moreover, the abundance and distribution of these gene families was correlated with the UV radiation, however, it does not follow the order of time of sample collection. Further we noted unhindered prevalence of genes involved in carotenoid biosynthesis, which is found to be a vital strategy opted by bacterial communities to survive in low temperatures and high UV radiation (Dieser *et al*. 2010). Similarly, we noted minimal alteration in the abundance of base excision repair, DNA repair and recombination proteins and mismatch repair.

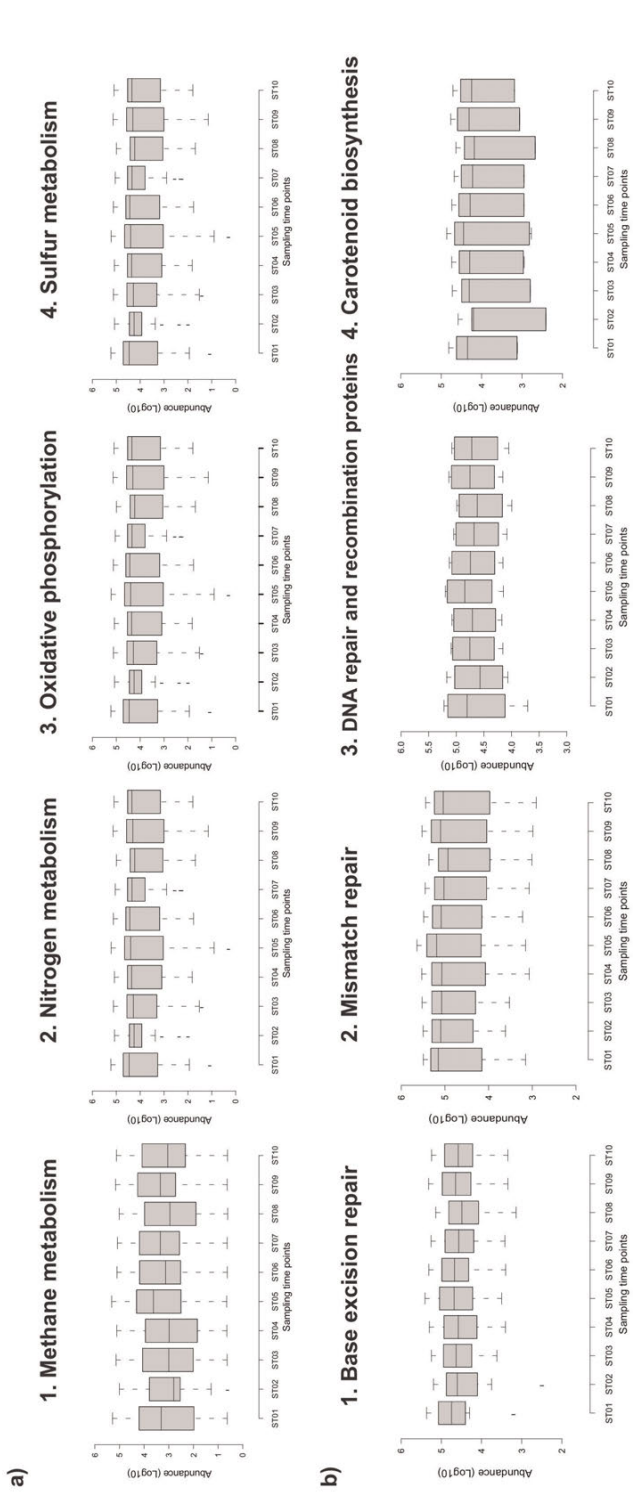

Fig. 3. Functional imputations. Box plots depicting the distribution of genes involved in: **a**, nutrient acquisition and biogeochemical processing 1. methane metabolism, 2. nitrogen metabolism, 3. oxidative phosphorylation and 4. sulfur metabolism; **b**, adaption surgeries (1. base excision repair, 2. Mismatch repair, 3. DNA repair and recombination proteins and 4. carotenoid biosynthesis) under the temporal impact of UV radiation.

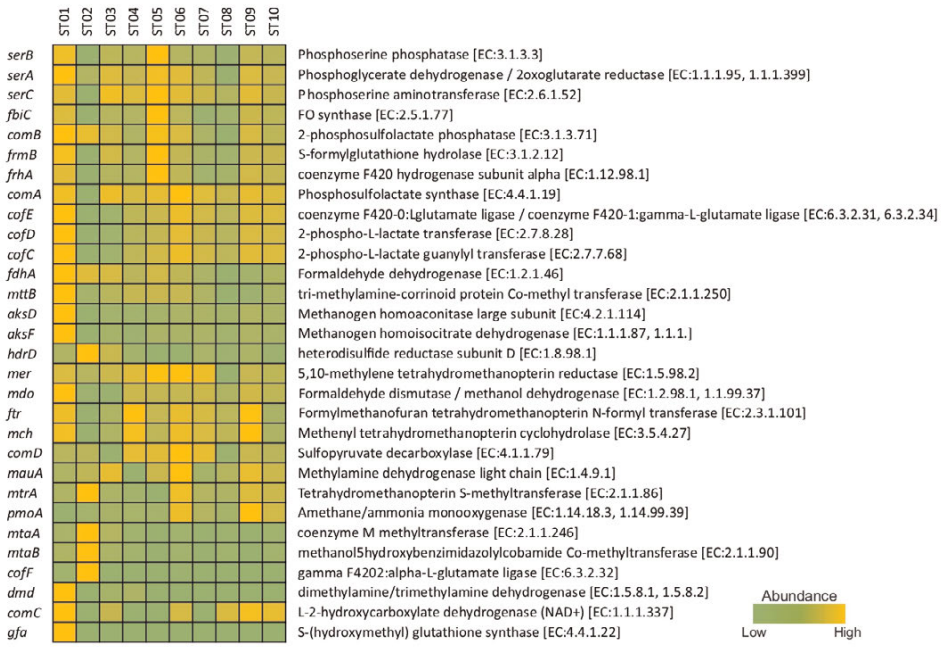

Fig. 4. Heat map to demonstrate strategies for one carbon metabolism and differential abundance of associated genes along the temporal gradient of UV radiation.

Discussion

The present study showed the changes in bacterial community composition with subtle changes in environmental conditions. Further the reveals abundance of the genes responsible for the survival of bacterial communities under the rising temperature, low nutrient, and high UV radiations.

Interestingly, we noted predominance of bacterial phyla like Proteobacteria, Actinobacteria and Bacteroidetes in soils of Antarctica and, abundance of Firmicutes and lower to rare persistence of Acidobacteria, respectively, which corroborates the observations of Teixeira *et al*. (2010) and Molina-Montenegro *et al*. (2019). We observed positive correlation between the rising temperature and abundance of phylum Firmicutes suggests the establishment of phylum Firmicutes with rise in temperature. Our findings were in agreement with the previously reported observations regarding the variable and spatial abundance of phylum Firmicutes in soil bacterial communities of Antarctic region (Malard *et al*. 2019; Ramos *et al*. 2019). Additionally, Deinococcus-Thermus was found to survive the constrains of UV radiation due to its ability to tolerate the poly-extremophilic conditions with the biosynthesis of carotenoids (Tian and Hua 2010). These observations could be suggestive of significant impact of UV on the bacterial communities affecting its composition with unusually reduced abundance of major bacterial phyla (Hughes *et al*. 2003; Yergeau *et al*. 2012;

Pérez *et al*. 2017). Although we observed changes in the bacterial community composition however it doesn't follow an obligatory order of specific environmental stressor. Instead, it depicts the composite impact of altering abiotic factors, which is in coherence with the earlier data demonstrating gene families responsible for replication, recombination, and repair being the most abundant functional trait (Molina-Montenegro *et al*. 2019). Further extending the analysis of the high throughput data to understand the potential of bacterial communities thriving in extreme environmental conditions using PICURSt2. The data revealed the presence of various key gene families, especially those involved in the carotenoid biosynthesis and DNA mismatch repair enabling bacterial communities to surpass the lethal impact of UV radiation. The observed enumeration of the genes belonging to the categories viz. base excision repair, DNA repair and recombination proteins and mismatch repair was in coherence with the Fernández Zenoff *et al.* (2006) and Pérez *et al.* (2017). Such morphological and cellular changes represent effective adaption strategies to survive the poly-extremophilic conditions (Chen *et al*. 2017; Louca *et al*. 2018; Molina-Montenegro *et al*. 2019). Production of accessory pigments (viz. phycocyanin and phycoerythrin) in addition to the red-fluorescing chlorophyll pigments has been found to aid the species of Cyanobacteria and some micro algae (*Nannochloropsis* sp., *Tetraselmis* sp., *Chaetoceros mualleri* and *Pavlova lutheri)* to tolerant extreme abiotic stress (Rodriguez *et al*. 1989; Wynn-Williams 1996). Moreover, the microorganisms can survive the strain of UV radiation either by biosynthesis of phlorotannins, phenolic secondary metabolite enabling absorption of UV-B radiations or proportionate accumulation of sporophytes with respect to the intensity of irradiation (Arrage *et al*. 1993; Lüder *et al*. 2004; Warnecke *et al*. 2005; Wiencke *et al.* 2007).

Similarly, further characterization of bacterial communities to carryout nutrient acquisition depicted presence of gene families driving the single carbon metabolism and energy metabolism. The genes involved in the energy metabolism (viz. sulfur metabolism, oxidative phosphorylation, nitrogen metabolism and photosynthesis) aid effective sequestering of the nutrients by participating in the geochemical cycling (Newsham *et al*. 2019). The abundance and correlation of the gene families involved in the methane metabolism follow a similar observation to the gene families associated with the energy metabolism. As we noted the diverse and differential distribution of these gene families, which were prone to alter with respect to the changing abiotic conditions. Eventually, it enables the adaptation of bacterial communities by opting heterotrophic mode of nutrition.

In conclusion, the high throughput DNA analysis of Antarctic sediments under the temporal variation of environmental parameters shows persistence of diverse bacterial communities with specific augmentation of Cyanobacteria and establishment of Firmicutes with slight changes in the temperature. The study also emphasizes the gene families attributing the unique adaptation, biogeochemical processing, and nutrient acquisition strategies by microbes under the polyex-

tremophilic conditions. Observations on the alteration of bacterial communities suggest the need to conserve these microorganisms and their long-term storage to explore their potential for the production of secondary metabolites.

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