

Polar solar panels: Arctic and Antarctic microbiomes display similar taxonomic profiles

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Summary

Solar panels located on high (Arctic and Antarctic) latitudes combine the harshness of the climate with that of the solar exposure. We report here that these polar solar panels are inhabited by similar microbial communities in taxonomic terms, dominated by *Hymenobacter* spp., *Sphingomonas* spp. and Ascomycota. Our results suggest that solar panels, even on high latitudes, can shape a microbial ecosystem adapted to irradiation and desiccation.

Introduction

The microbial ecology of some artificial structures, including solar panels, has been poorly explored up to date (Shirakawa *et al.*, 2015; Dorado-Morales *et al.*, 2016). These reports suggest that photovoltaic surfaces display a diverse microbial community, highly tolerant to thermal fluctuations, ultraviolet (UV) irradiation and desiccation (Dorado-Morales *et al.*, 2016). In this work, we aimed to study, through Next Generation Sequencing (NGS) and microbial culturing techniques, the microbiome of photovoltaic solar panels from two cold locations, lying close or inside the polar circles: Tromsø, Norway (69°40'N 18°56'E) and two Antarctic islands (62°0'S 58°0'W) (Fig. 1A).

Tromsø is the largest urban area in northern Norway. It is located on the coast, above the Arctic Circle, and experiences a subarctic climate. Average temperatures in winter range between 0.9 and –3.6°C and in summer between 5.3 and 12.4°C. The South Shetlands constitute a group of islands of the Maritime Antarctica. Monthly average temperature is between –3.1 and –10.9°C from March to October, when the sea around the islands is closed by ice, and slightly warmer from November to February, with temperatures ranging between –1.7 and 0.5°C.

Results and discussion

A total of 14 individual solar panels were sampled in January and May 2017 in Antarctica (9 panels, 3 from Deception Island and 6 from Livingston Island) and Tromsø (5 panels), respectively (Fig. 1A). Aliquots were spread on LB and R2A media and incubated at 4°C for three weeks to select psychrotrophic and psychrophilic microorganisms (Fig. 1B). A collection of 44 isolates was characterized by genetic identification, growth ability and UV-light and desiccation resistance (Fig. 1C). A detailed explanation of all the experimental procedures used in this study can be found on the research group website that can be accessed using the following link: <http://www.uv.es/synbio/solpan>. The isolates from Antarctic panels able to grow at 4°C were identified as either *Rhodotorula mucilaginosa* (pink pigmentation) or *Alcaligenes faecalis*/*Curtobacterium* sp. (yellow pigmentation). Samples from Tromsø yielded a larger diversity of microorganisms including *Cryobacterium arcticum*, *Sphingomonas* sp., *Curtobacterium* sp., *Microbacterium* sp. and *Dioszegia fristingensis*, all of them able to grow at 15°C. Interestingly, despite the low temperatures of their original habitats, 37 isolates were able to grow at 30°C and 11 also grew at 37°C. One of these was identified as *R. mucilaginosa*, a cold-adapted (with activity at up to –5°C), carotenoid-producing, cosmopolitan, mesophilic yeast that has previously been isolated from a wide range of remote environments, including Antarctic ice cores or 11 000 m deep sea vents (Gadanhó and Sampaio, 2005; Amato *et al.*, 2009; Moliné *et al.*, 2012; Nunes *et al.*, 2013; Connell *et al.*, 2014; Yu *et al.*, 2015).

Regarding UV resistance, many of the isolates (a total of 30) were able to survive 30 s of irradiation with

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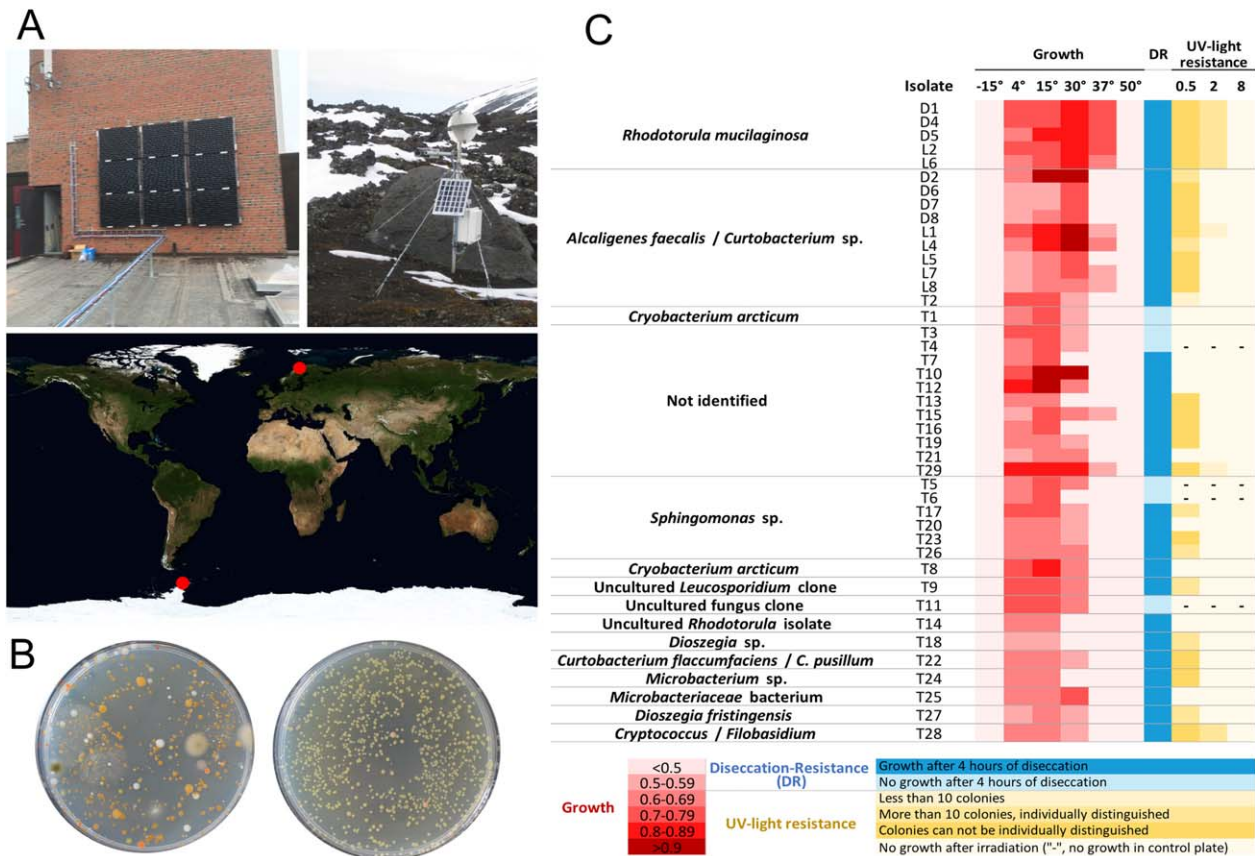


Fig. 1. (A) Solar panels sampled from Tromsø, Norway (top, left) and South Shetlands, Antarctica (top, right), indicated by red dots in the map below; (B) microbial colonies obtained culturing aliquots of surface biomass on R2A at 4 °C for 21 days (left, Tromsø; right, Antarctica); (C) heatmap displaying taxonomic identification, location ('D' Deception, Antarctica; 'L' Livingston, Antarctica; or 'T' Tromsø, Norway; followed by an identification number), growth (colony diameter in cm) at temperatures from -15 to 50 °C (data in red), resistance to desiccation (data in blue) and resistance to UV light (after 0.5, 2 and 8 min of irradiation; data in yellow) of the isolated colonies.

a monochromatic 254 nm light, whereas only seven isolates were able to survive two minutes of irradiation and none resisted eight minutes of irradiation. The most frequent isolate able to resist two minutes of UV irradiation was *R. mucilaginosa*, in which carotenoid accumulation may play an essential role in photoprotection against UV-light (Moliné *et al.*, 2010). Finally, desiccation-resistance assays revealed that 38 out of the 44 isolates were able to resist four hours of desiccation. *R. mucilaginosa* was present among these 38 isolates, an expected result when considering previous studies that describe this species as highly resistant to desiccation (Connell *et al.*, 2008). The large heterogeneity in UV-resistance is in contrast with the high irradiance in the sampled site, suggesting that a tridimensional biofilm-like structure may play an important role, not only in survival under desiccation conditions, but also in UV-protection in the natural biocenosis (Gorbushina, 2007; Villa *et al.*, 2015). Our results support the hypothesis of the existence of a specific solar panel microbial community adapted to the harsh

conditions that characterize these artificial environments: UV-radiation and desiccation.

The taxonomic profiles obtained through NGS of three panels from each location were analysed (Breitwieser and Salzberg, 2016; Kim *et al.*, 2016; Martí, 2017) and found to exhibit a rather low variation within locations, although both sites proved to differ in some taxa (Fig. 2A and B). All the obtained Recentrifuge-Krona plots can be accessed on the research group's website through the following link: <http://www.uv.es/synbio/solpan>. First, tree sequences were dominant in Tromsø and not in the Antarctica; similarly, sequences from *Equisetum* were found exclusively in the solar panels from Norway. This can be explained by the proximity and abundance of vegetation and the lack of it in Tromsø and Antarctica respectively, since Tromsø is in a forest area, whereas the South Shetlands are at least 800 km away from the nearest forest land (South America). Second, many more fungal sequences, including many yeasts, and, especially, the lichen-associated *Trebouxia* algae were more frequent in the Antarctica

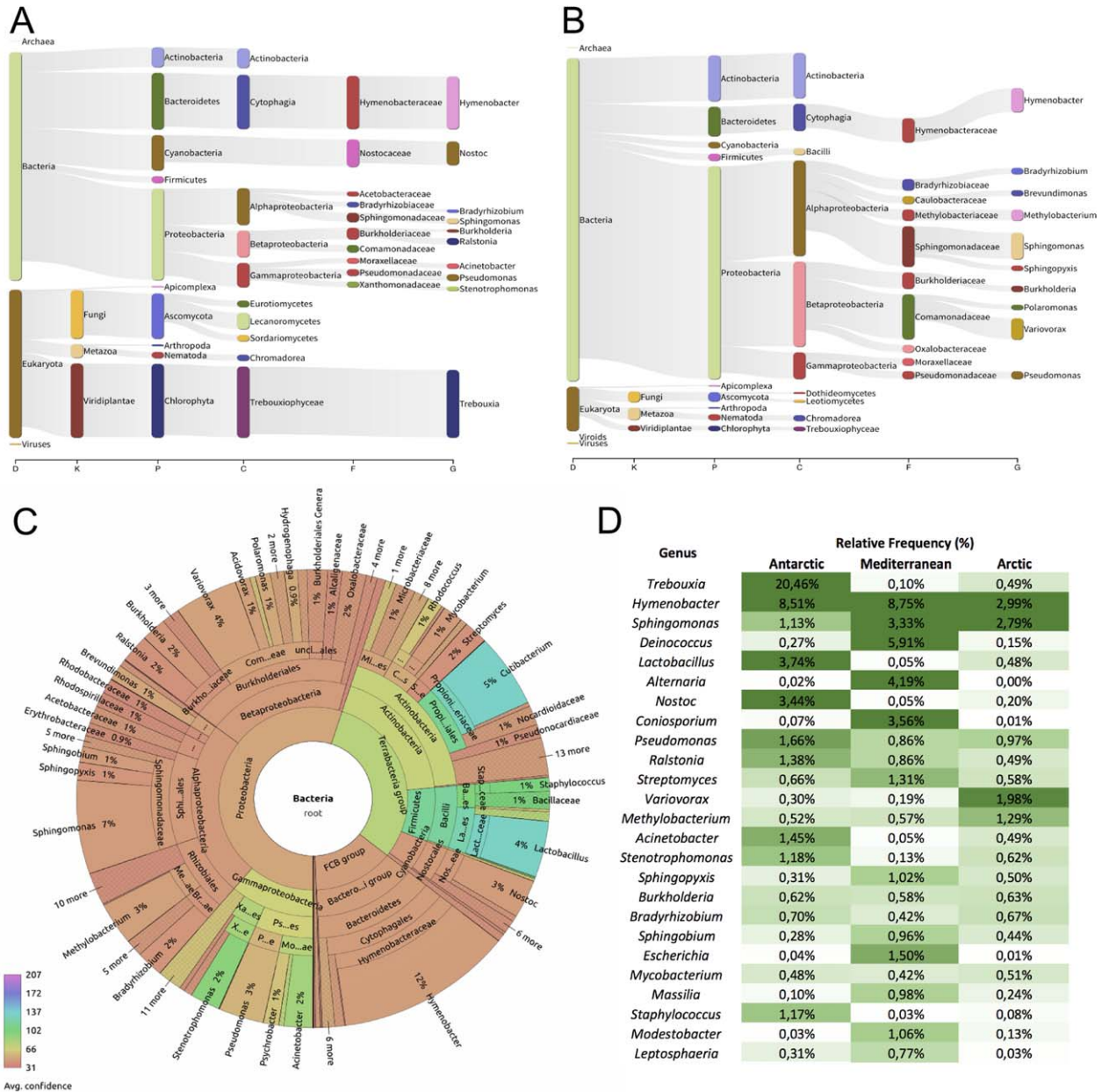


Fig. 2. Sankey diagram with the 10 most abundant taxa in different taxonomical levels (Domain D, Kingdom K, Phylum P, Class C, Family F, Genus G) in the solar panels of Livingston, Antarctica (A) and Tromsø, Norway (B); (C) Reentrifuge-Krona plot snapshot of the shared bacterial taxa at the genus level among all the polar panels (from Livingston and Tromsø), where the percentage shows the relative abundance at the genus level averaged for all the polar samples; (D) heatmap showing the 25 most abundant genera versus geographical location ordered by overall relative frequency; the average for all the solar panels sampled per location is given; the colour scale is quasilogarithmic to improve visualization of taxa with similar order of magnitude among locations. Taxa under the clade Streptophyta have been removed throughout the figure to improve resolution at the microbial level.

samples. Antarctica is not only characterized by its low temperatures but also by displaying very low values of environmental humidity, conditions which *Trebouxia* can easily overcome thanks to its cryo- and desiccation-resistant properties (Hájek *et al.*, 2012; Carniel *et al.*, 2016). Finally, other taxa that differed in frequency between the two locations were *Variovorax*, more

frequent in Norway, and *Lactobacillus* and *Acinetobacter*, more frequent in the solar panels from Antarctica.

Despite these differences, the global taxonomic profile of the two locations had relevant and abundant similarities (Fig. 2C and D). Interestingly, many of the shared genera have also been found while reanalysing the sequences of the first NGS report of the solar panel

microbiome (Dorado-Morales *et al.*, 2016), carried out in a Mediterranean city (Fig. 2D). On the contrary, some other genera are more frequently found in Mediterranean solar panels than in the polar ones, such as *Alternaria*, *Coniosporium*, *Escherichia*, *Massilia* and *Modestobacter*.

Our results not only reveal the existence of a diverse community of microorganisms in solar panels from polar environments, which is in concordance with previous reports about the diversity of microbial life in polar regions, but it also highlights the importance of adaptation in extreme environments (Friedmann, 1982; 1993; Boetius *et al.*, 2015). From the identification of a clear core of shared microbial taxa, it would be tempting to conclude that our results support the well-known microbial ecology *mantra* by Baas Becking 'everything is everywhere, but, the environment selects'. However, it has to be stressed that the location of the studied solar panels (either close or beyond the Antarctic and Arctic circles respectively) does not assure a common environment: both polar environments have different wind regimes and key differences in terms of climate or distance to other biomes (which is clearly reflected by the high frequency of tree sequences in the Tromsø samples, which were missing in Antarctica, for example). Yet, the striking co-presence of bacterial genera (Fig. 2D) such as *Sphingomonas*, *Pseudomonas*, *Ralstonia*, *Streptomyces*, *Methylobacterium* and, especially, *Hymenobacter* (the most abundant genus in solar panels from both poles as well as in those previously characterized in a Mediterranean city), indicates that solar panels are not mere stockers of wind-borne microorganisms. On the opposite, our results demonstrate that solar panels in extreme latitudes bear a similar, native microbiome, characterized by marker taxa shared with panels from other latitudes, fitting nicely with previous work performed on geothermal communities of Antarctica that aimed at assessing the role of aeolian transport and environmental selection in the establishment of microbial communities (Herbold *et al.*, 2014). This fact suggests that the strong selection pressures – desiccation and irradiation, very likely – of the solar panels themselves – rather than their location – are what shape the microbiome developing on them.

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