Uncultured fungi in air and snow of Livingston Island, South Shetland Islands, Antarctica

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Introduction

Due the isolation from the rest of the world by the circumpolar current and atmospheric circumpolar vortex, lack of trophic complexity, vulnerability of endemic biodiversity to climate changes and anthropologic influence, Antarctica represents a unique opportunity to micro-aerobiology studies and how they are transported to Antarctica as well as circulate in the region. However, detailed information about this influence how microorganisms arrive and circulate in Antarctica is still poorly known.

Biological dispersal by aerial agent can represent an important factor in shaping patterns of biodiversity and some pioneer organisms could arrive constantly in a certain environment from the atmosphere by air currents and precipitation. Viable organisms found in the atmosphere may be represented by dormant and in a cryptobiotic state and metabolically inactive due the harsh dry, low nutrient and high irradiance growth conditions. Among these aerial biological propagules, those of microorganisms seem to represent the more diverse group, which include virus, bacteria, microalgae and fungi. However, there are few mycological aerobiology studies in Antarctica and still missing information of how these cosmopolitan fungi arrive and disperse in the different environments of Antarctica. For the reasons described above, in the present study we assessed uncultured fungal diversity present in freshly deposited snow and air samples obtained from Livingston Island, Antarctica (**Fig. 1**), using the DNA metabarcoding through high throughput sequencing.

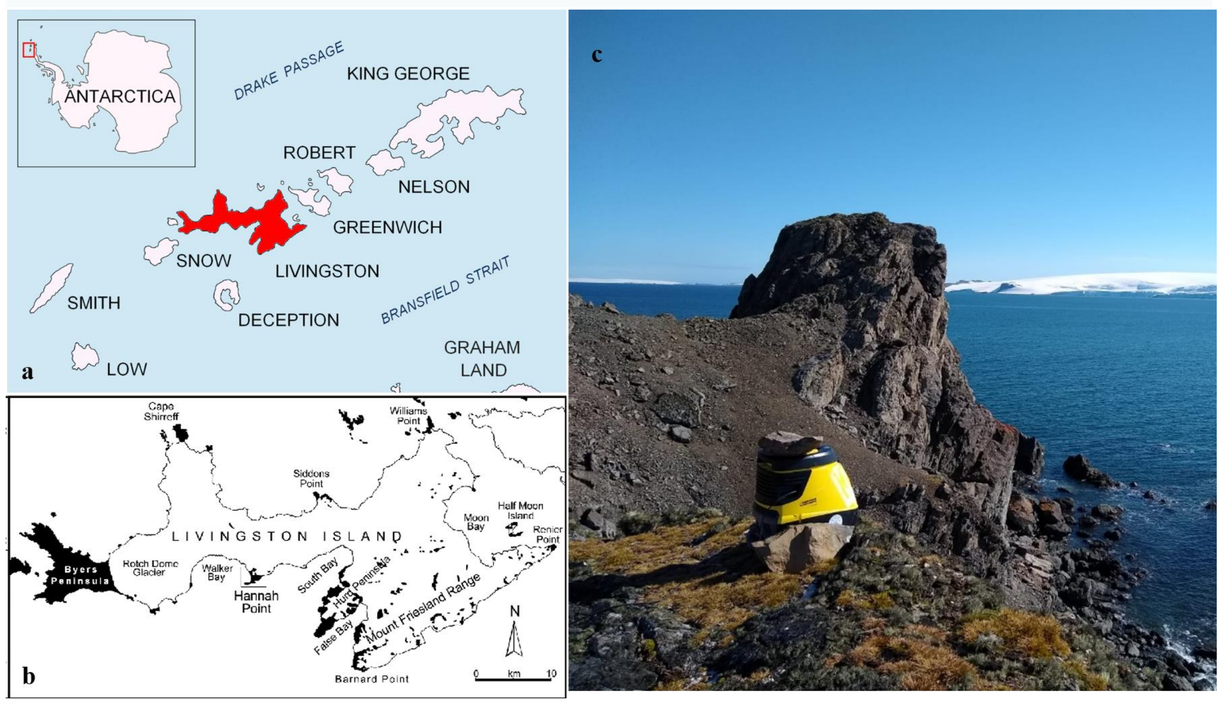

Fig. 1. Location of soil sample collections. (**a**) Antarctic Peninsula, (**b**) Livingston Island and (**c**) the Punta Polaca at Hurd Peninsula, where the air and snow were sampled [-62,6711923653644 (Lat) -60,3786921607402 (Lon)].

Methods

Aliquots of 500 mg of each soil samples

DNA extraction with Powersoil kit (Qiagen)

Amplicon-metagenomic with Miseq (Illumina), primers ITS3/ITS4

Trimmed sequences (300bp size, without primers and chimeras)

Sequences compared against the UNITE database (≥97% identity)

Sequences clustered into amplicon sequence variants (ASVs)

Results and Discussion

We detected 139 fungal amplicon sequence variants (ASVs), 63 in 740 m^3 of air and 76 in 3760 mL of snow. The ASVs were represented and dominate by the phyla *Ascomycota*, *Basidiomycota*, *Mortierellomycota*, and *Mucoromycota*, respectively. In the air, *Pseudogymnoascus roseus*, *Cladosporium* sp., *Mortierella* sp., *Mortierella fimbricystis*, *Pseudogymnoascus* sp., *Mortierella gamsii*, *Pseudogymnoascus appendiculatus,* and *Helotiales* sp. were most dominant at fungi detected (>1,000 reads), respectively. In snow we detect more ASVs as dominant fungi and identified as Fungi sp., *Meyerozyma* sp., *Penicillium* sp., *Lecidea cancriformis*, *Malassezia restricta*, *Hanseniaspora* sp., *Austroplaca darbishirei*, *Rhodotorula diobovata*, *Malassezia globosa*, *Agaricomycetes* sp., *Thelebolus globosus*, *Malassezia* sp., *Pseudogymnoascus* sp., and *Penicillium polonicum*. In addition, 117 ASVs (55 in air and 62 in snow) were detected in low DNA amount and may represent the rare portion of the fungal assemblages. Several ASVs were identified in higher hierarchical levels (phylum, class, order, or family) and might represent new fungi and/or new records for Antarctica. Forty-one ASVs were exclusive of air and 53 of snow (**Fig. 2**). Only 22 ASVs were common with both substrate (**Fig. 2a**). When the dominant ASVs from both substrate were compared (**Fig. 2b**), no one occurred between the two substrates.

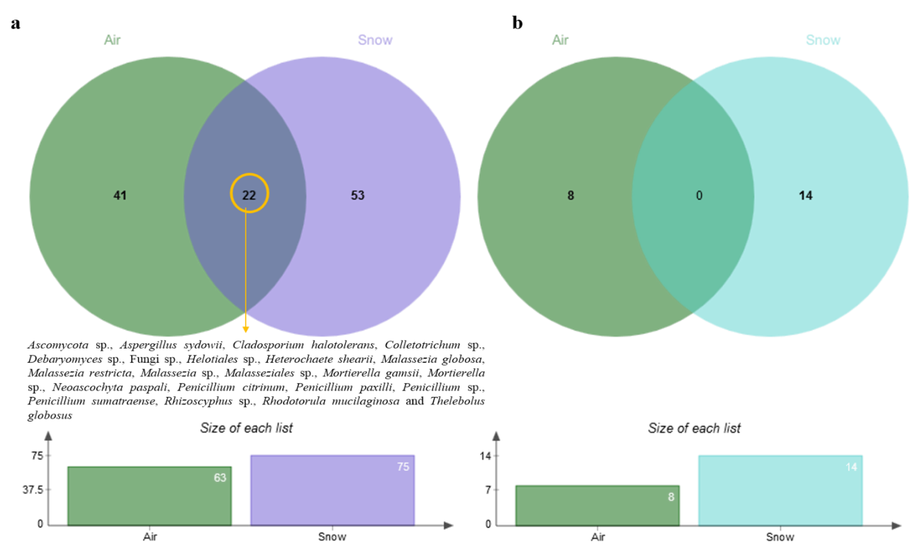

Fig. 2 (a) Venn diagram showing the total and **(b)** dominant (those with >1,000 reads) fungal taxa distribution between those detected in air and snow of Livingston Island, Antarctica.

Conclusion

HTS study revealed the presence of a rich fungal community in air and snow of Livingst Island when compared with studies using traditional isolation methods. The assemblages were dominated by cold-adapted and cosmopolitan fungal taxa, including members *Pseudogymnoascus*, *Malassezia* and *Rhodotorula* genera, which have been reported as opportunistic fungi. In addition, our results reinforce that hypothesis and the presence in these fungi airspora supports the possibility of dispersal around Antarctica in the air column. However, further aeromycobiology studies are required to understand the dynamics of fungal dispersal within and beyond Antarctica.

Acknowledgements