Identification of fungal taxa with pathogenic potential in soil samples from Perunika Glacier's newly formed forefields - Livingston Island, Antarctica

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Abstract

Antarctica peninsula periphery islands undergo one of the most dramatic ecological changes due to ongoing global warming. The front fields of the Antarctic glaciers are extreme environments and pioneering sites for ecological succession. Rising temperatures lead to deglaciation in the Antarctic habitats, and the new terrain is subjected to the process of soil formation and microbial colonization. In the present study, we investigated the formation of pathogenic fungal soil microbiomes as an effect of forefield deglaciation. Soil samples were taken from two different forefields, one formed several years ago and the other freshly uncovered. Both habitats were in the vicinity of the Perunika Glacier situated in the northeastern direction of Hurd Peninsula, Livingston Island, the second largest island from the South Shetland Archipelago, about 100 km north of the Antarctic Peninsula. Total DNA was extracted and targeted ITS amplicon sequencing was applied. The ITS marker sequences were then taxonomically identified. The abundance of the fungal taxa was calculated. Alpha and Beta diversity analyses to obtain fungal richness in samples were performed. Our results showed that soil habitat formation, initiated by deglaciation, was such that:

1. In the newly deglaciated forefield, there was almost no fungal DNA, which prevented further analysis;
2. At older drier fields metagenome content was much higher;
3. Further analysis showed that the most abundant genera were Pseudogymnoascus, Simplicillium, Hanseniaspora, Mycothermus, and Malassezia.

It is known that Pseudogymnoascus and Malassezia species have pathogenic keratinolytic activity. In conclusion, the phylum Ascomycota, which dominated the core microbiome showed much higher ecological diversity and abundance, i.e. potential for colonization of the glacier forefields. In contrast, the phylum Basidiomycota appeared to be less fit for these conditions.

Keywords

soil fungal pathogens, metagenomics, deglaciation, Antarctica

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