Effect of warming-induced shrub encroachment on soil fungal communities in Western Greenland

Canini Fabiana[1,2], Geml József[2,3], Onofri Silvano[1], D'Alò Federica[1], Ripa Caterina[1], Zucconi Laura[1]

[1]Department of Ecological and Biological Sciences, University of Tuscia, Viterbo, Italy; [2]Biodiversity Dynamics Research Group, Naturalis Biodiversity Center, Leiden, The Netherlands; [3]MTA-EKE Lendület Environmental Microbiome Research Group, Eszterházy Károly University, Eger, Hungary.

INTRODUCTION

In cold and nutrient-poor arctic terrestrial environments, fungi dominate soil microbial biomass and play key roles as plant symbionts (mycorrhizae, endophytes, lichens), pathogens and decomposers (Newsham et al., 2009). However, very few studies addressed the interactions between vegetation and soil fungi in arctic environments. Moreover, arctic regions are experiencing some of the highest rates of increase in temperature and precipitation, resulting in an overall greening, with a well-documented expansion in shrub cover and corresponding decrease in bryophytes and lichens (Vowles and Björk, 2019). A better understanding of the interactions between vegetation and soil fungi is fundamental for improving our predictions regarding possible responses of these ecosystems to climatic changes.

OBJECTIVES

We analyzed three different microhabitats, with increasing coverage complexity in Western Greenland. Our aims were (i) to understand how fungal diversity, community composition and functional guilds distribution relate to a different type of vegetation coverage and edaphic conditions and (ii) to gain some insights into the dynamics of vegetation and soil fungi in this landscape.

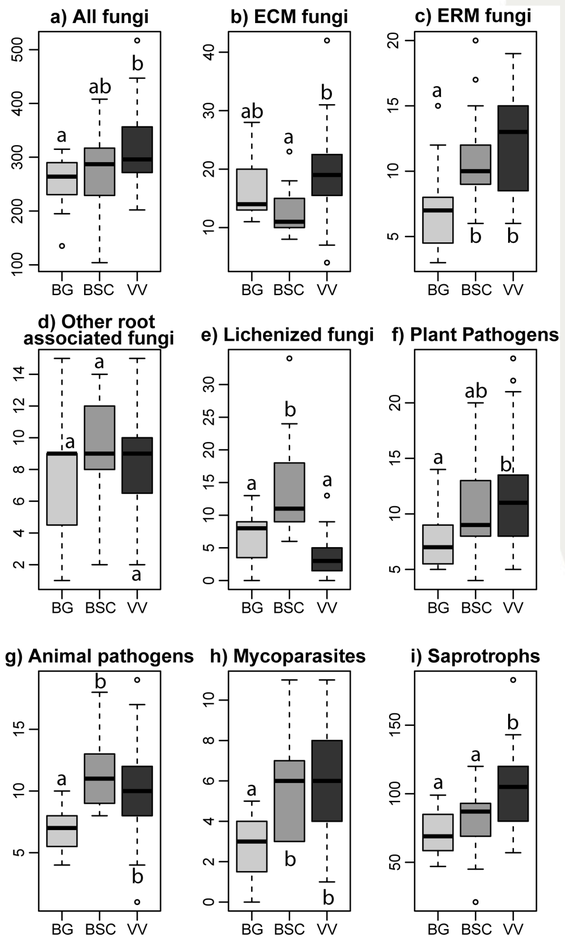

Fig. 1: Richness of the total fungal communities and of the eight fungal functional guilds (ECM: ectomycorrhizal fungi; ERM: ericoid mycorrhizal fungi) in each habitat (BG: Bare Ground; BSC: Biological Soil Crust; VV: Vascular Vegetation). Letters indicate significant differences in one-way ANOVA with post-hoc TukeyHSD test (significant for $p<0.05$) (Canini et al., 2019).

METHODOLOGY

Samples were collected in Summer 2017 in Kobbefjord (64°08' N, 51°23' W). 9 soil plots covered by vascular vegetation (VV) (*Betula*, *Salix*, *Vaccinium*, *Empetrum*), 6 of biological soil crusts (BSCs) with mosses and lichens, and 5 corresponding to bare grounds (BG) were selected. Soil fungal communities were analyzed by DNA metabarcoding of ITS1 rDNA sequences. Soil C, N, P and water content and pH were measured, to be correlated to the total richness, the richness and abundance of the functional guilds identified, and the community composition.

RESULTS

Richness of fungal community increased with increasing vegetation cover (fig. 1), except for lichenized fungi. These trends were generally positively correlated with the relative water and P content of the soil and negatively with soil pH (fig. 2). The carbon (C) and nitrogen (N) content and C/N ratio had a marginal effect on richness (data not shown).

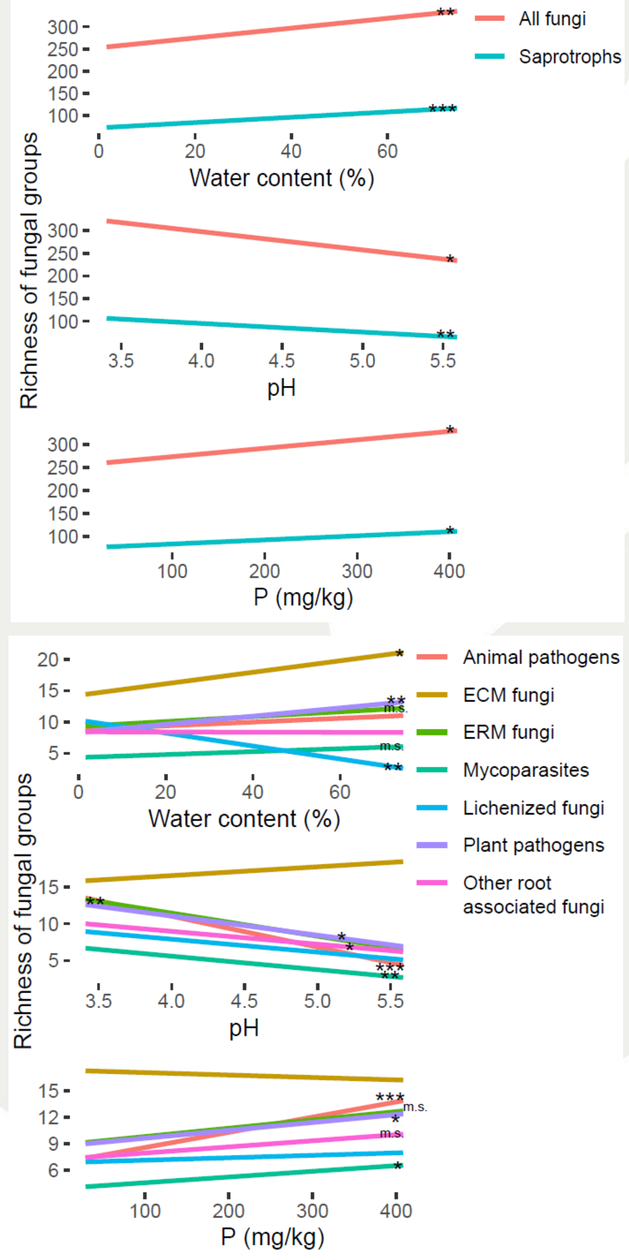

Fig. 2: Linear regressions of richness (y-axis) of the total fungal community and of functional guilds (ECM: ectomycorrhizal fungi; ERM: ericoid mycorrhizal fungi) in response to the edaphic parameters (x-axis). Significance is reported as *** $p<0.001$, ** $p<0.01$, * $p<0.05$, m. s. (marginally significant) $p<0.1$ (Canini et al., 2019).

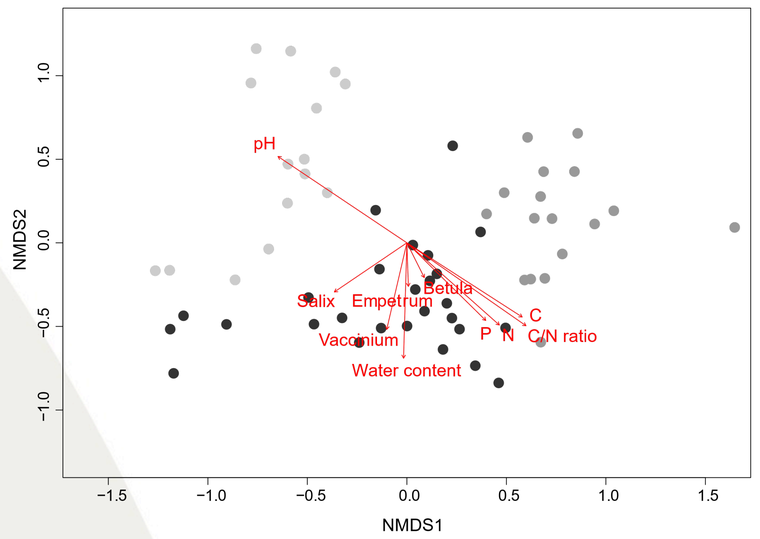

Fig. 3: NMDS ordination of fungal communities in the microhabitats studied, based on Bray–Curtis distance on Hellinger-transformed OTU matrix. Light grey: bare ground; dark grey: biological soil crusts; black: vascular vegetation (Canini et al., 2019).

Table 1: Proportion of variation in fungal community composition explained by edaphic variables and habitat type in a combined model, accounting for correlations among them. Variables were added sequentially, in decreasing order of their explained variance, based on individual PerMANOVA analyses (Canini et al., 2019).

Variable	Variance (%)	p
Habitat	18.145	0.0001
pH	3.697	0.0004
C/N ratio	2.886	0.0017
C	1.355	0.3958
N	3.708	0.0001
Water content	2.119	0.0302
P	1.779	0.1001
Residuals	66.311	

RESULTS

Community composition was structured according to the type of habitat (fig. 3; MRPP: $A=0.082$, $p=0.001$), which explained the highest proportion of variance in the combined model, followed by N, pH, C/N, and water content (Table 1).

CONCLUSION

Richness and community composition are mainly driven by the type of vegetation cover and the interconnected edaphic parameters, with the pH being the strongest one for the total community and the functional groups identified.

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