



Soil microbial community composition in natural *Picea abies* mountain forest with different time since the last disturbance



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Background:

In a primary Norway spruce (*Picea abies* (L.) Karst.) forest in Calimani National Park (Romania), we hypothesized soil rejuvenation driven by forest disturbance regime. The soil developmental stage seems to be related to the time elapsed since the last stand-replacing disturbance (Tab. 1). Together with soil morphology and chemistry survey, analysis of soil microbial communities was conducted to examine the hypothesis.

Questions:

Is there a sign of post-disturbance succession of the soil microbial community composition? Which pedochemical characteristics drive this process?

Results:

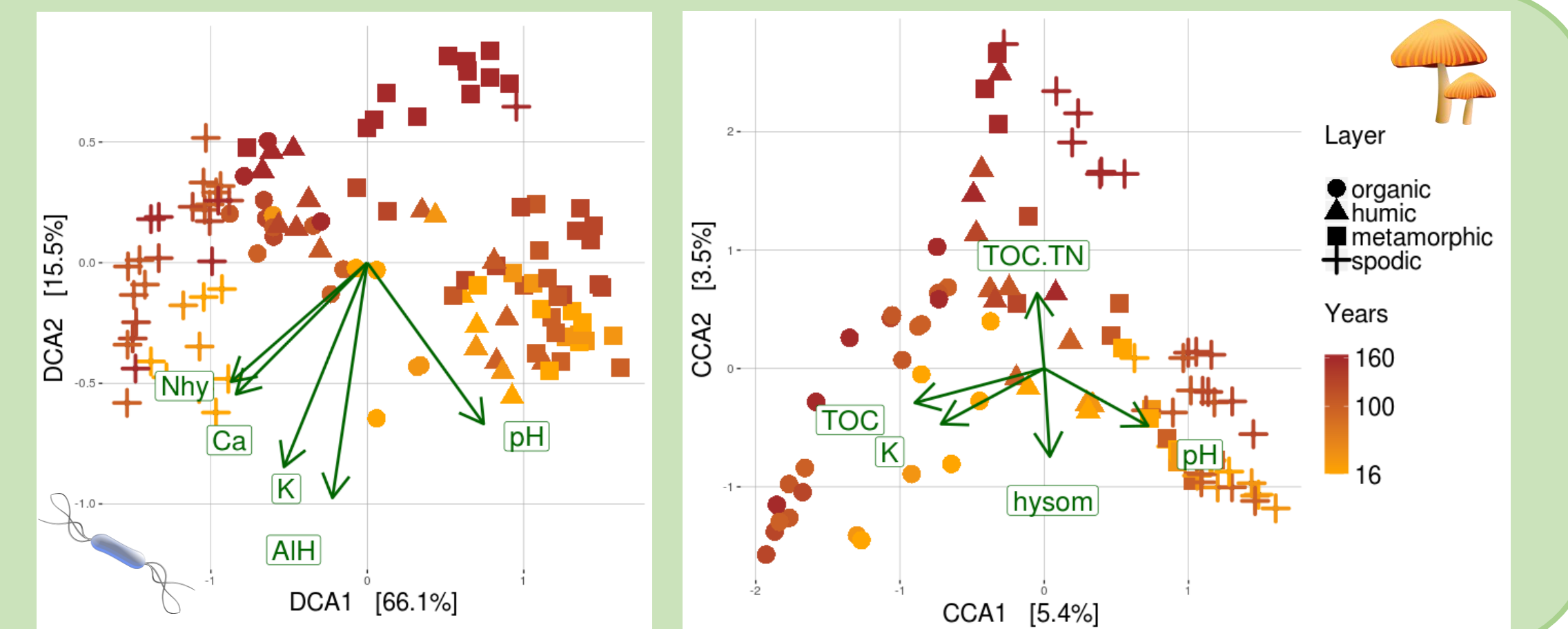
All soil samples

- Significant shift along time gradient for both prokaryotes and fungi (Tab. 2)
- Systematic shift down the profile for fungi, not prokaryotes (note the point shape)

Note: prokaryote's ordination diagram shows unconstrained DCA with passive projection of the best explaining variables as detected by constrained ordination due to a significant arch effect when constrained ordination visualised.

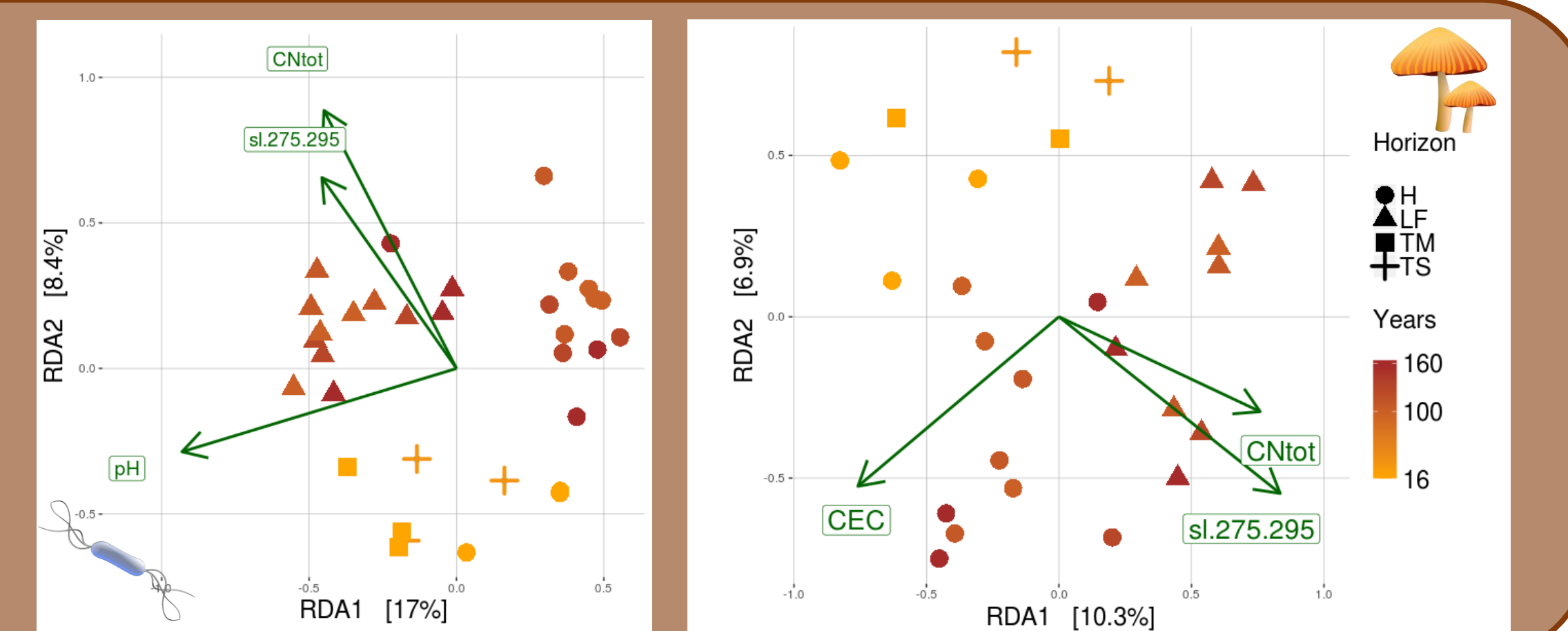
Methods:

- A series of six sites forming a chronosequence of time elapsed since the last severe disturbance from 16 to 160 years selected (Tab. 1)
- Soil sampled (May 2015) and divided to layers: upper organic (L, F and H horizons), upper mineral (A horizons), metamorphic (E horizon or its analogy in less developed soils) and illuvial (B horizons)
- Soil chemistry analysis: nutrient concentrations (C, N, P, base cations); pH; cation exchange capacity (CEC); organic matter (OM) quality (UV absorbance); Al, Si and Fe forms
- Soil microbial community analysis: Illumina sequencing of 16S rRNA gene (prokaryotes) and ITS region (fungi)
- Ordination analysis: time effect on microbial community composition; best explaining soil properties (where more, only 5 best shown)
- Soil properties correlation with time, only correlations with $p < 0.001$ mentioned



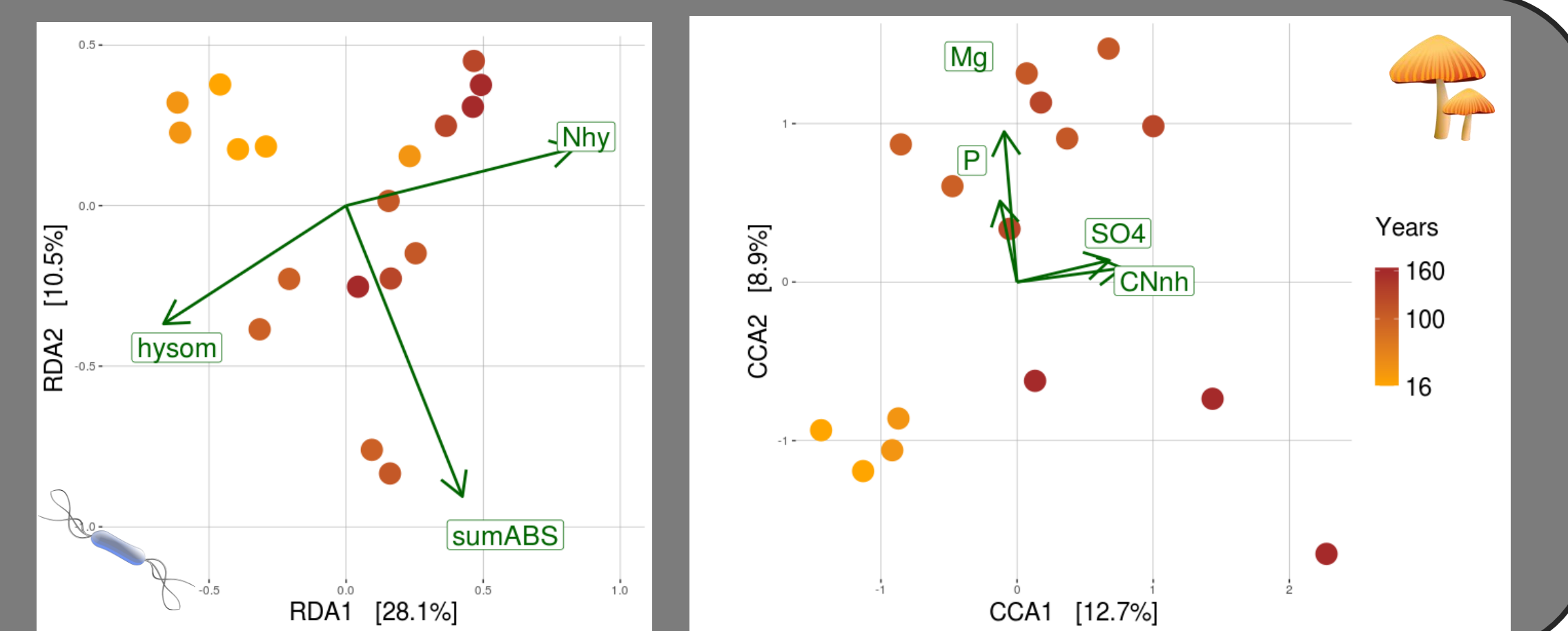
Upper organic layer

- Significant shift along time gradient for both prokaryotes and fungi (Tab. 2)
- Litter character significant factor (note the point shape): Ts and Tm (16 and 36 y, grass understorey), H and LF layer in fully grown (100+ y) stands
 - OM quality responsible: total pool C:N (*CNtot*), spectral slope of UV absorbance 275:295 (*sl.275.295*) and *pH* or cation exchange capacity (*CEC*)
- In time \uparrow dissolved OM C:N ($R^2=0.71$) and \downarrow OM molecular weight (spectral slopes of UV absorbance 275:295, 300:700, 350:400; all $R^2 > 0.7$),



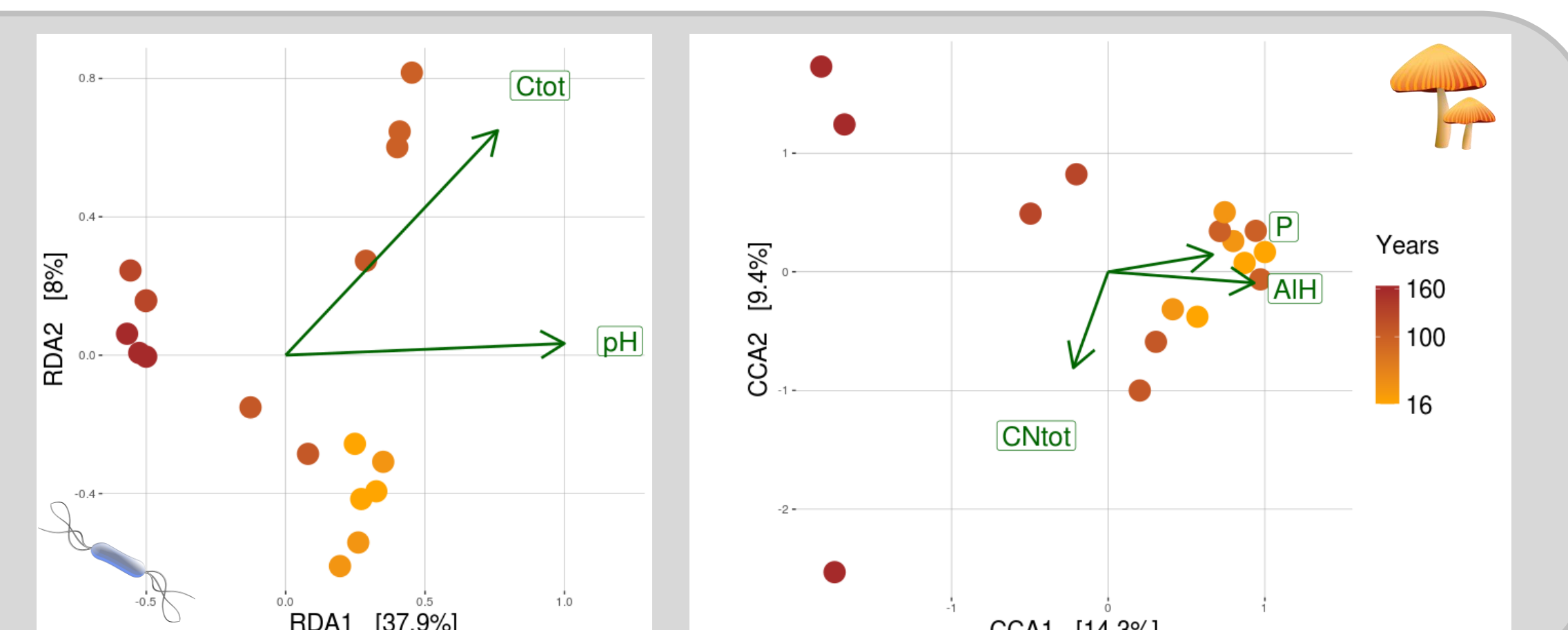
Upper mineral layer

- Significant shift along time gradient for both prokaryotes and fungi (Tab. 2)
- Prokaryotes: OM quality – proportion of hydrolysable OM (*hysom*) and N in „hysom“, sum of absorbance (*sumABS*)
- Fungi: time gradient connected with C:N in non-hydrolysable OM fraction (*CNnh*); 100 – 130 y stands \uparrow extractable phosphorus (*P*) and magnesium (*Mg*) content
- \downarrow pH in time ($R^2=0.84$) and \uparrow Na content ($R^2=0.95$)



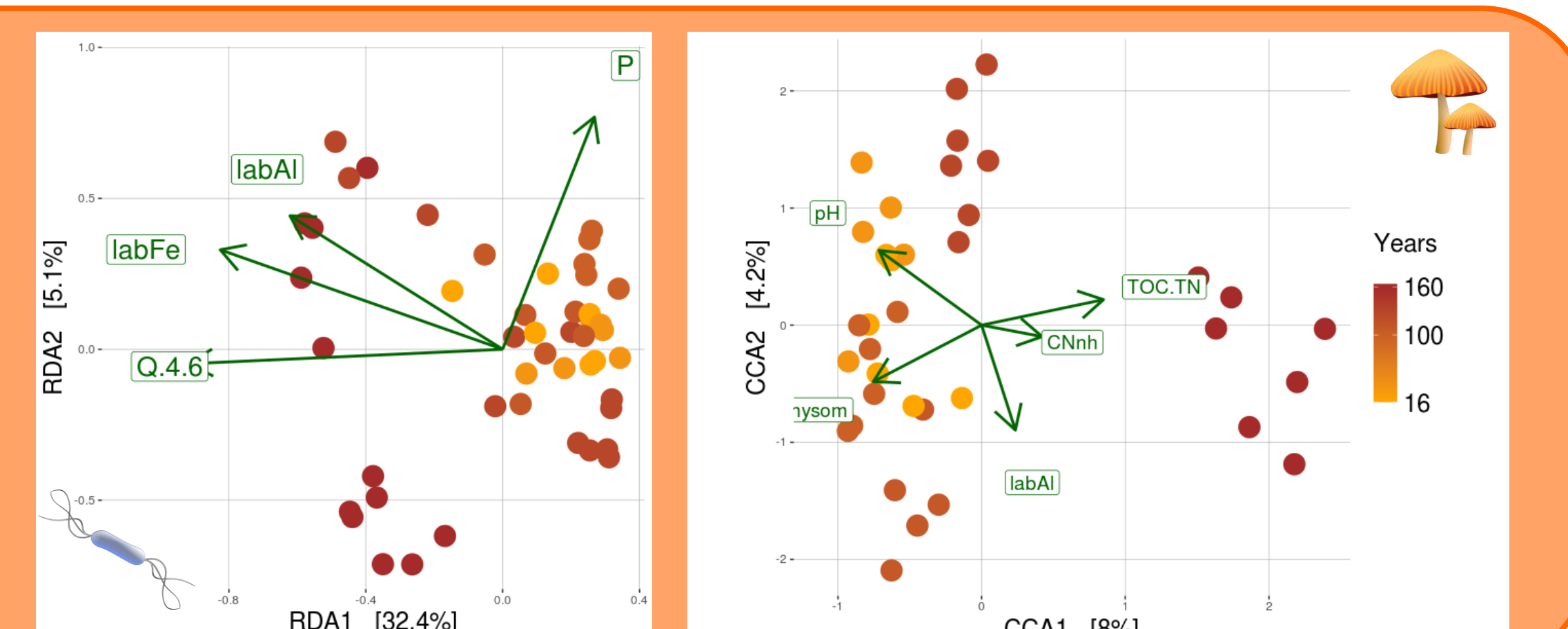
Metamorphic layer

- Significant shift along time gradient for prokaryotes only (Tab. 2)
- Prokaryotes: time gradient related to *pH*; 100 y stand \uparrow total C pool (*Ctot*; local conditions)
- Fungi: time gradient best explained by exchangeable acidity (*AlH*) and extractable phosphorus (*P*)
- \downarrow CEC ($R^2=0.75$) in time



Illuvial layer

- Significant shift along time gradient for both prokaryotes and fungi (Tab. 2)
- Prokaryotic community responds to OM quality (*Q4/6*), labile forms of iron (*labFe*) and aluminium (*labAl*) and extractable P (*P*)
- Fungal community: time gradient best connected to dissolved OM C:N (*TOC.TN*) increase and *pH* increase
- \uparrow dissolved OM C:N ($R^2=0.74$), \downarrow K ($R^2 = 0.71$) with time



Conclusions:

- In the studied forest soils, the microbial community composition is driven by various soil characteristic in different soil horizons. Moreover, drivers of the diversity are mostly not shared between prokaryotes and fungi.
- However, irrespective of inconsistency in the most influencing factors, microbial communities develop with recovery as indicated by significant effect of time.

Tab. 1 Recovery time and soil unit of selected sites. EP – entic podzol, AP – albic podzol

Years	16	36	100	110	130	160
Soil unit	EP	EP	strong EP	EP to AP	AP	strong AP

Tab. 2 ANOVA test for models explaining the effect of recovery time on the community composition of prokaryotes and fungi in different soil layers.

Layer	Prokaryotes		Fungi	
	F	p	F	p
All samples	1.82	0.004	1.87	0.001
Upper organic	2.52	0.008	1.81	0.008
Upper mineral	2.29	0.011	1.36	0.016
Metamorphic	1.93	0.011	1.14	0.247
Spodic	1.97	0.032	1.33	0.008