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Agroforestry: tree roots impact on soil microorganisms



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Background & aims

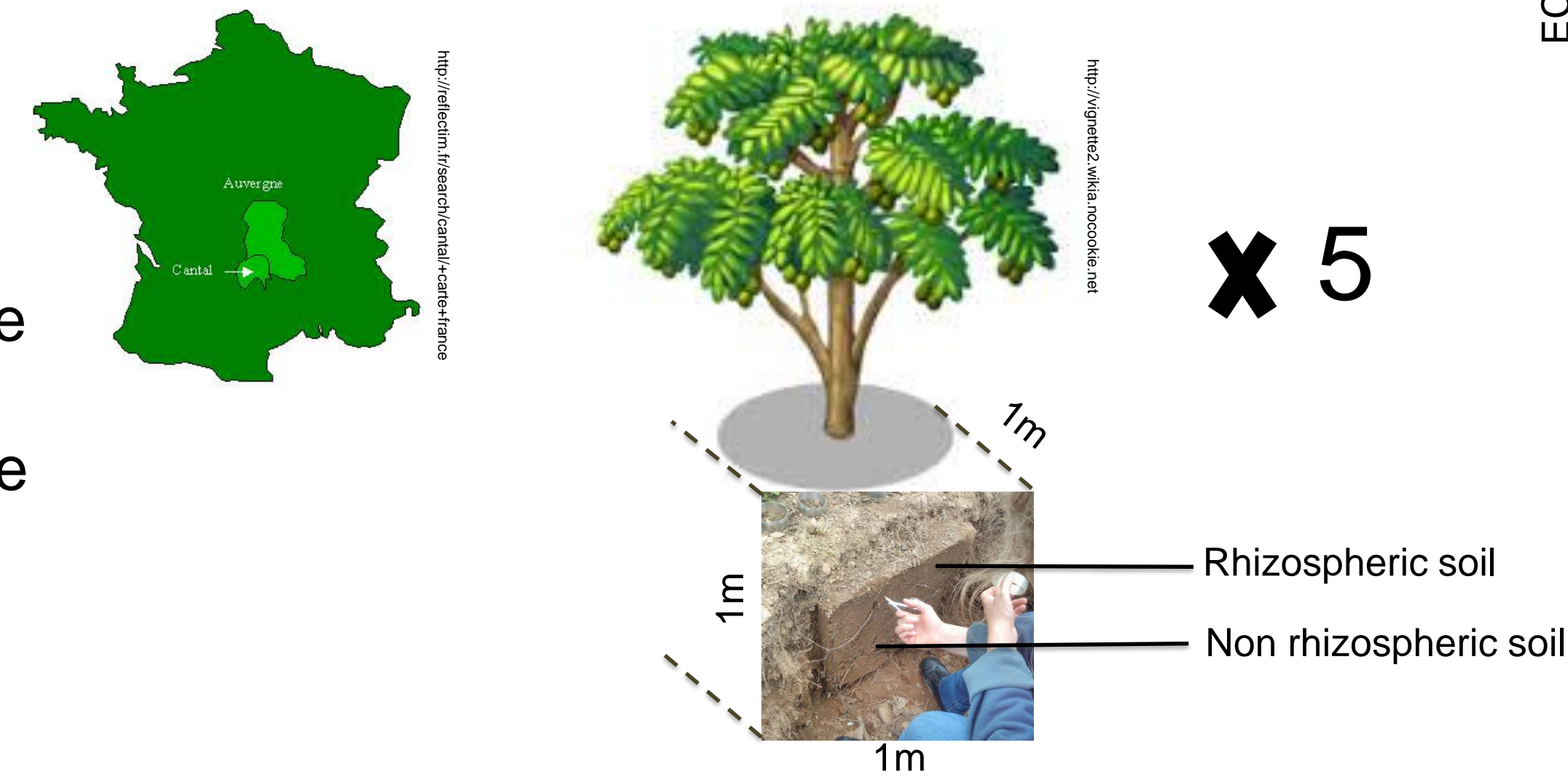
Agroforestry mixes annual culture or permanent pasture with permanent trees which is widely known to improve soil biodiversity, especially macro and micro fauna¹, as compared to monoculture². However, the specific role of fine tree roots on microbial community is still poorly known in field conditions³. Microorganism community (biomass, activity and Bacteria/Fungi ratio) is supposed to evolve with roots dynamic and morphological characteristics (“hot spots”, “hot moments”⁴). We focussed here on the presence effect of fine tree roots on the microbial communities in an agroforest field, in France. We hypothesized that the microbial communities are influenced by the roots characteristics, but also by the soil past events (apex history, months with roots...).

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Methods & Analysis

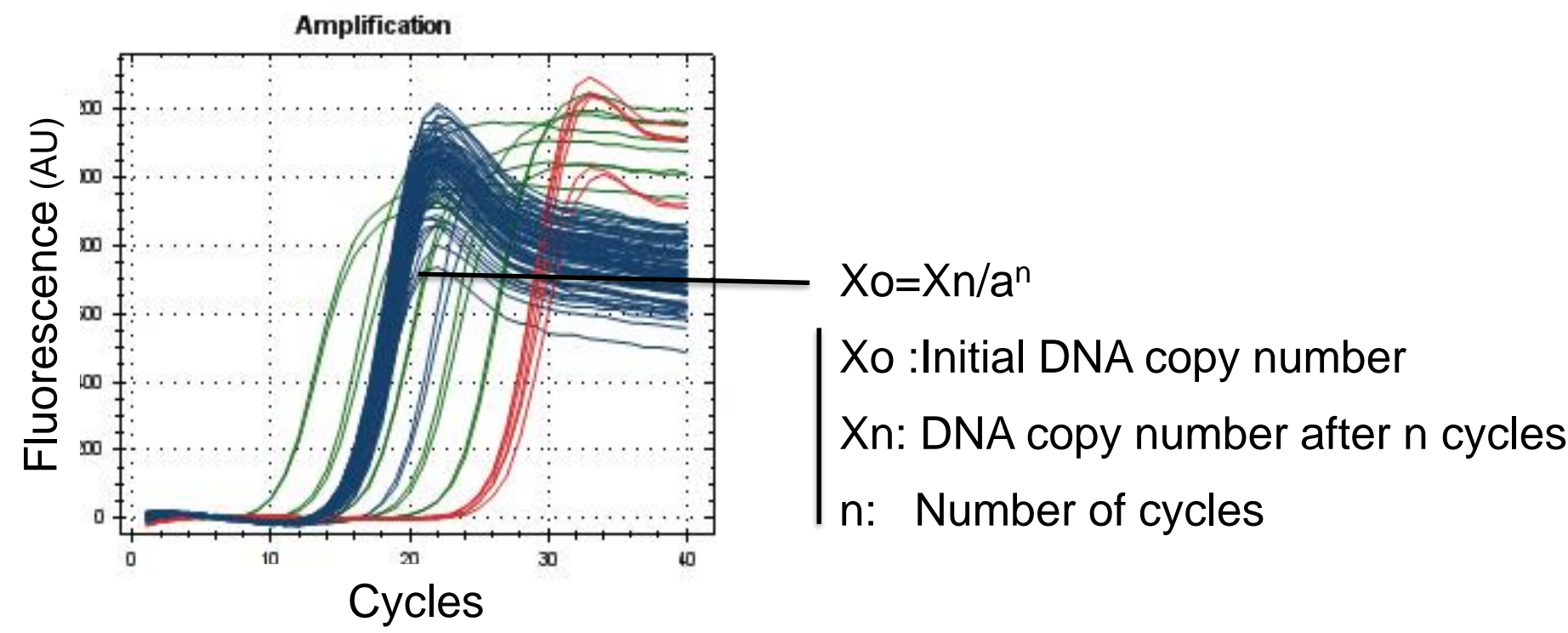
Field site & Sampling

- ☀ Continental climate
- 🌳 12 y/o Hybrid walnuts intercropped with permanent pasture
- 📏 10 samples soil per tree (X5) in rhizospheric and non rhizospheric soil
- 📍 530m
- 📍 Cantal region, France
- 🌱 Silty soil/ 5°-10° slope

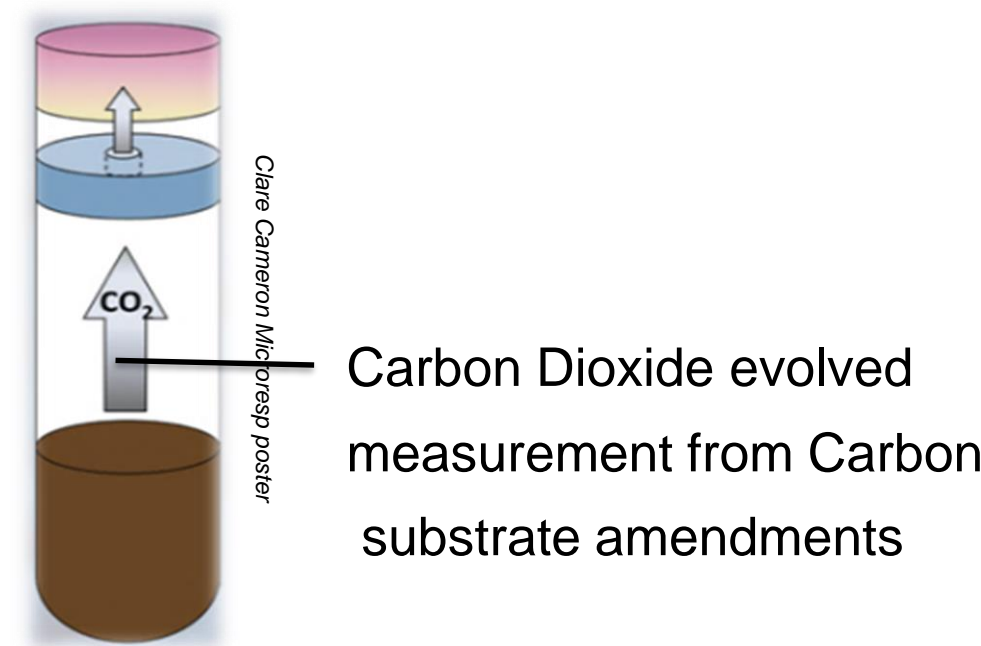


Analysis

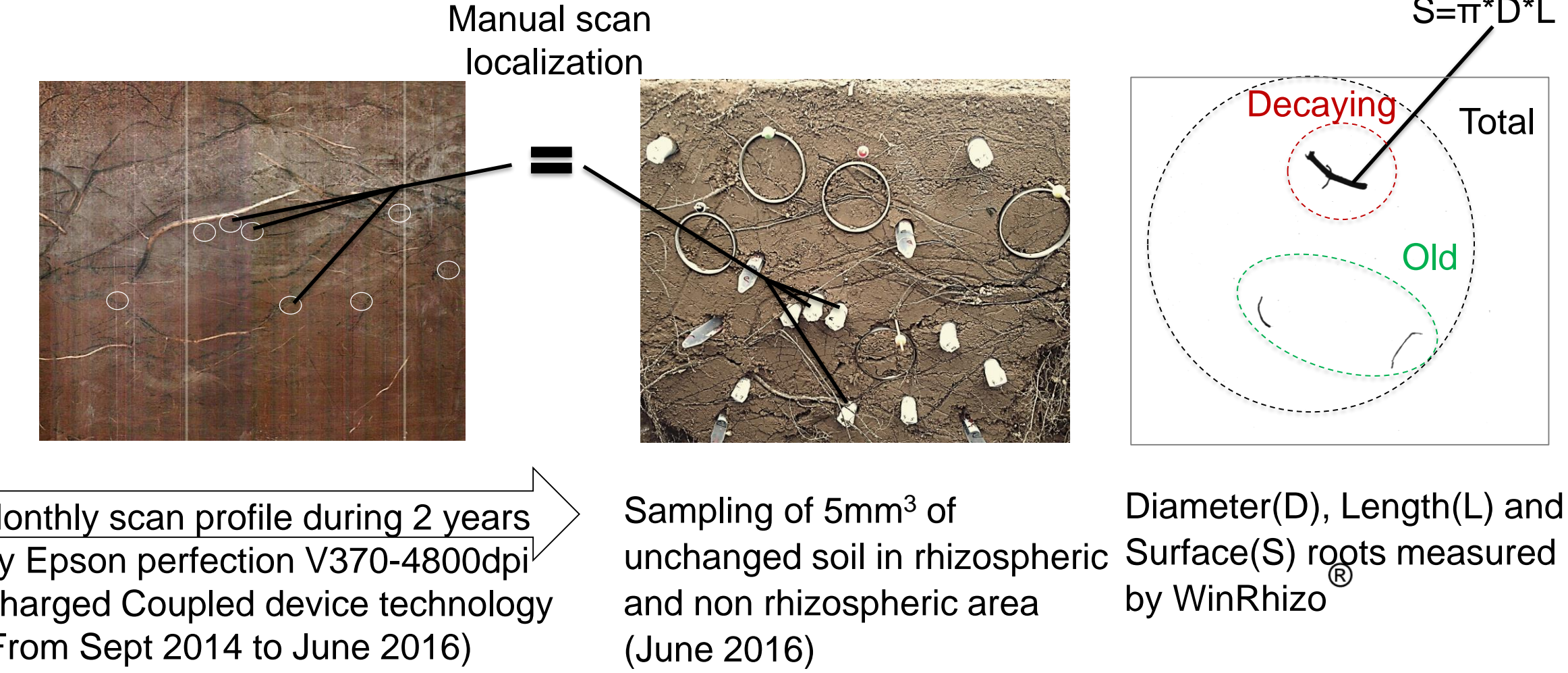
Relative quantification of bacteria (16S DNA) and fungi (18S DNA) by Real time PCR⁵



Microorganism substrate induced respiration SIR quantified by Microresp^{®6}



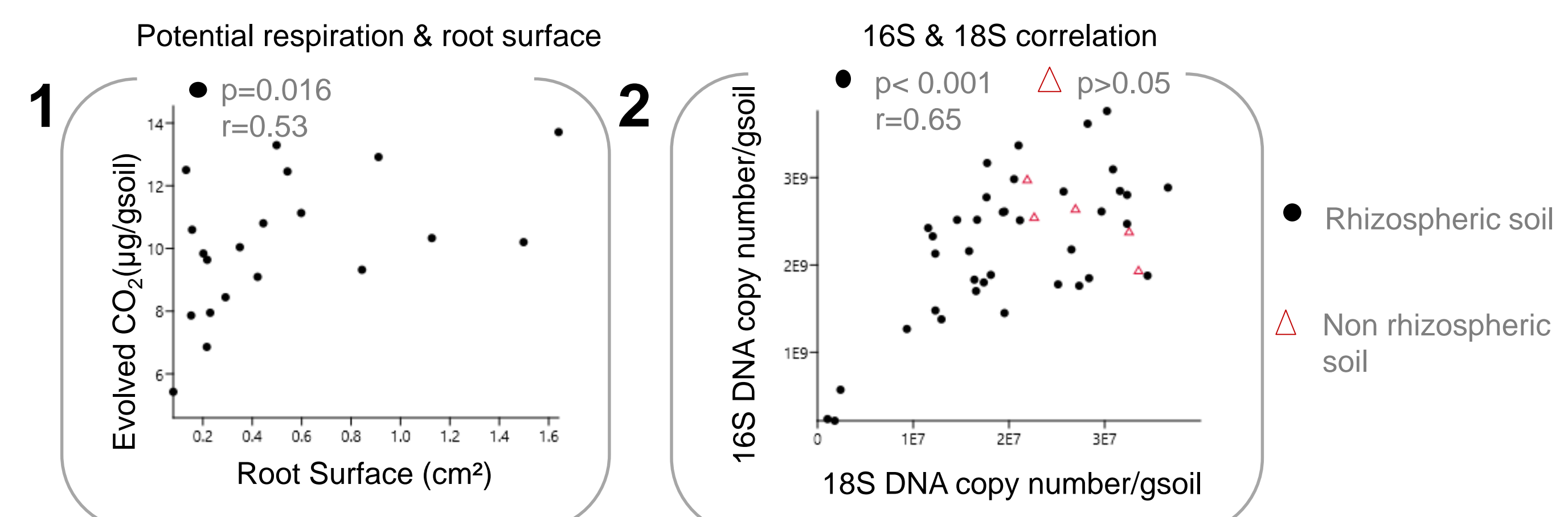
Tree roots temporal dynamics and morphological characteristics determined by image analyses (scans & WinRhizo[®])



Results & Discussions

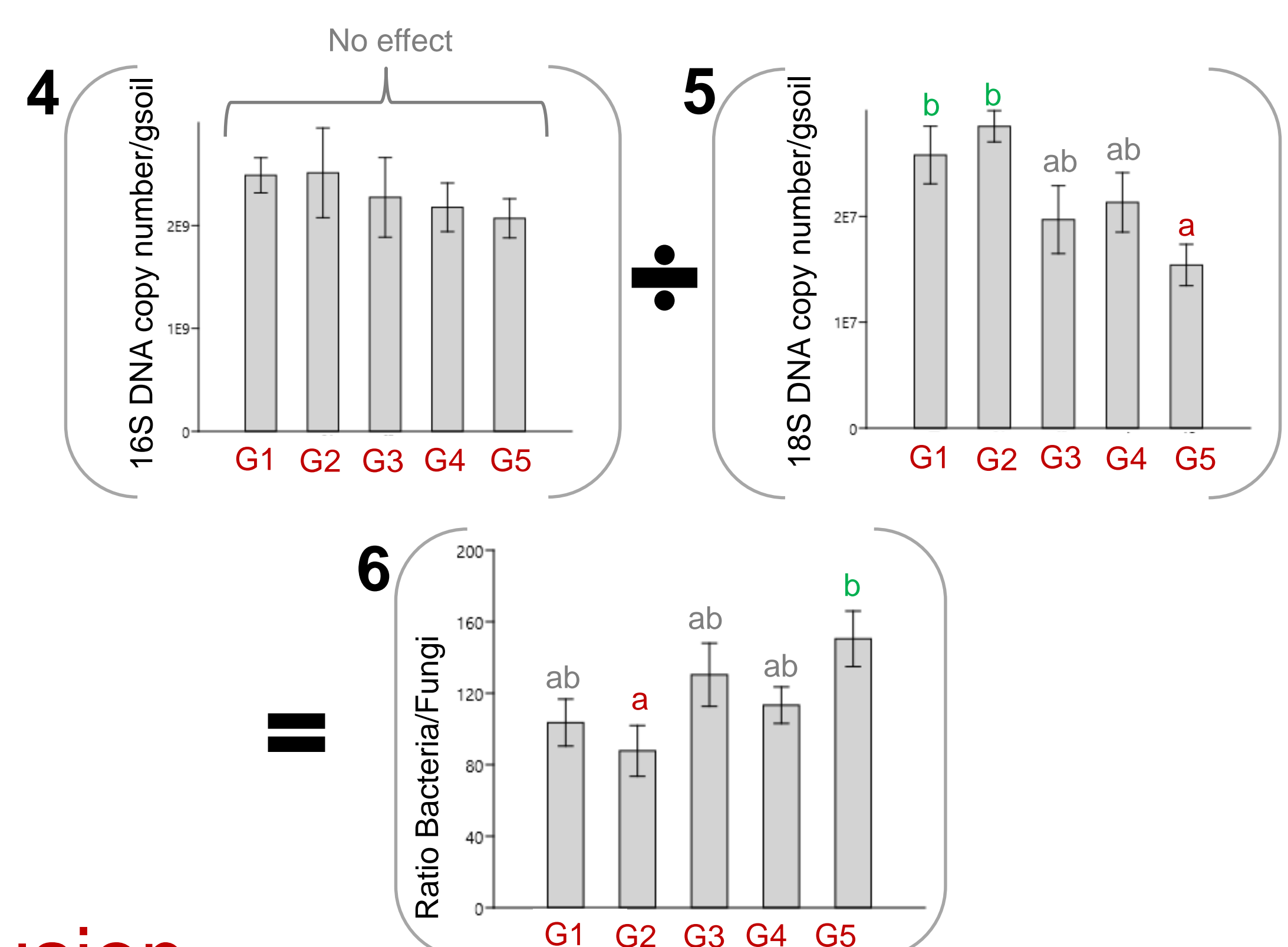
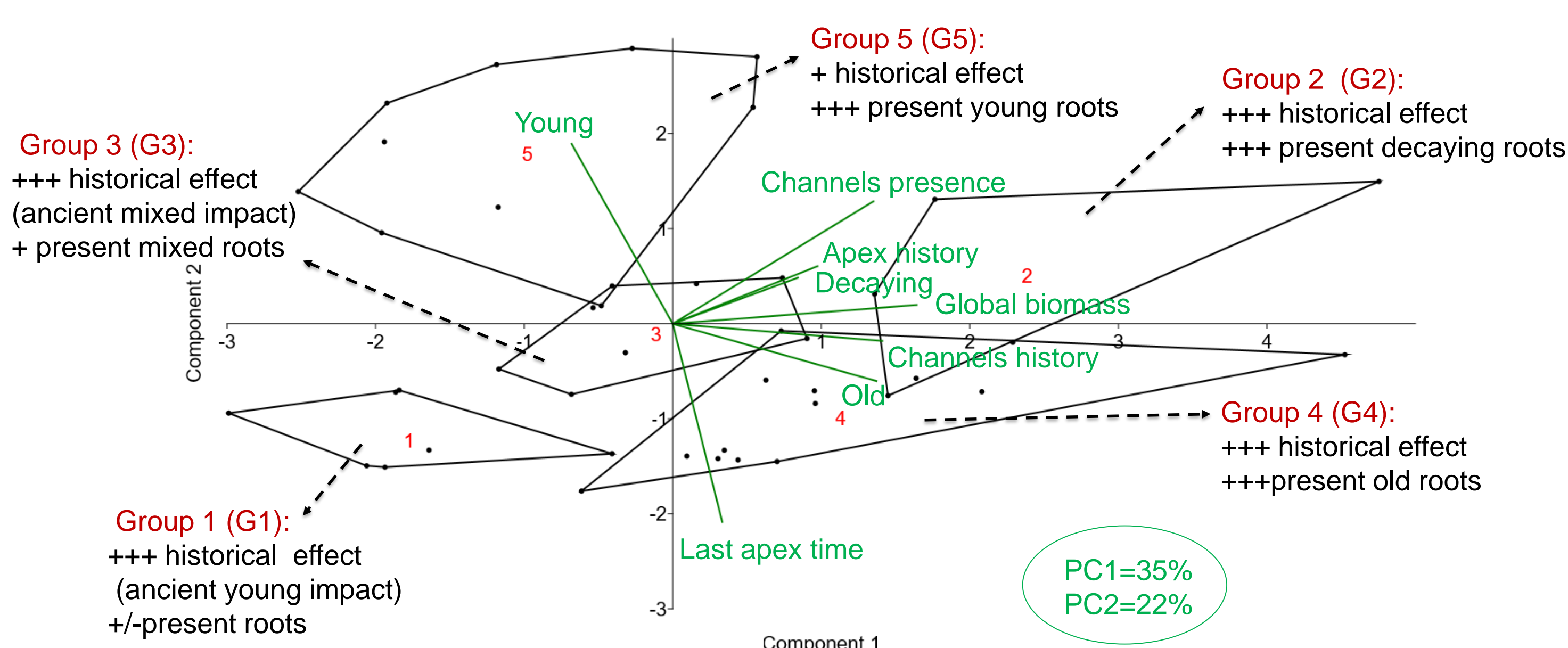
What about root biomass and microorganisms?

- 1 Tree roots surface increased significantly microorganisms potential respiration.
- 2 Tree roots presence induced bacteria (16S DNA) and fungi (18S DNA) positive correlation or “synergism” as compared to its in non rhizospheric soil.



And fine tree roots history impact?

3 Identification of groups of samples by cluster analysis followed by SIMPER analysis and visualisation by Principal Component Analysis



- 3 We highlighted 5 different groups according to historical and morphological roots variables.
- 4 16S (bacteria) DNA copy number is not significantly different between the 5 Groups.
- 5 18S (fungi) DNA copy number is significantly lower for Group 5 (young roots) than for Group 1 (ancient young roots effect) and Group 2 (decaying roots).
- 6 Ratio 16S/18S is significantly higher for Group 5 (young roots) than for Group 2 (decaying roots), which is related to its significantly different fungi relative quantity (18S).

Conclusion

Fine tree roots in agroforestry system impact microorganisms in soil by increasing their potential respiration and inducing a positive correlation between them. Permanent trees also significantly impact fungi relative quantity and bacteria/fungi ratio according to its roots morphology, roots age and especially roots past events.

Perspective

Further investigations are needed to understand the mechanisms of aggregate stability enrolling bacteria and fungi ratio near tree roots compare to herbaceous roots in agroforestry systems.

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³Heijden, Marcel G. A. van der, and Cameron Wagg. 2012. 'Soil Microbial Diversity and Agro-Ecosystem Functioning'. Plant and Soil 363 (1-2): 1-5.
⁴Kuznyakov, Yakov, and Evgenia Blagodatskaya. 2015. 'Microbial Hotspots and Hot Moments in Soil: Concept & Review'. Soil Biology and Biochemistry 83 (April): 184-99.
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⁶Campbell, C. D., S. J. Chapman and al.. 2003. A Rapid Microtiter Plate Method To Measure Carbon Dioxide Evolved from Carbon Substrate Amendments so as To Determine the Physiological Profiles of Soil Microbial Communities by Using Whole Soil. *Applied and Environmental Microbiology* 69 (6): 3593-99.