



HAL
open science

Agroforestry: tree roots impact on soil microorganisms

Juliette Bodez, Yogan Monnier, Isabelle Bertrand, Amandine Erktan, Awaz Mohamed, Jean-Luc Maeght, Alexia Stokes

► **To cite this version:**

Juliette Bodez, Yogan Monnier, Isabelle Bertrand, Amandine Erktan, Awaz Mohamed, et al.. Agroforestry: tree roots impact on soil microorganisms. EcoSummit 2016 Ecological Sustainability: Engineering Change, Aug 2016, Montpellier, France. hal-01837367

HAL Id: hal-01837367

<https://hal.science/hal-01837367>

Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Agroforestry: tree roots impact on soil microorganisms



j.bodez@esitpa.fr

Background & aims

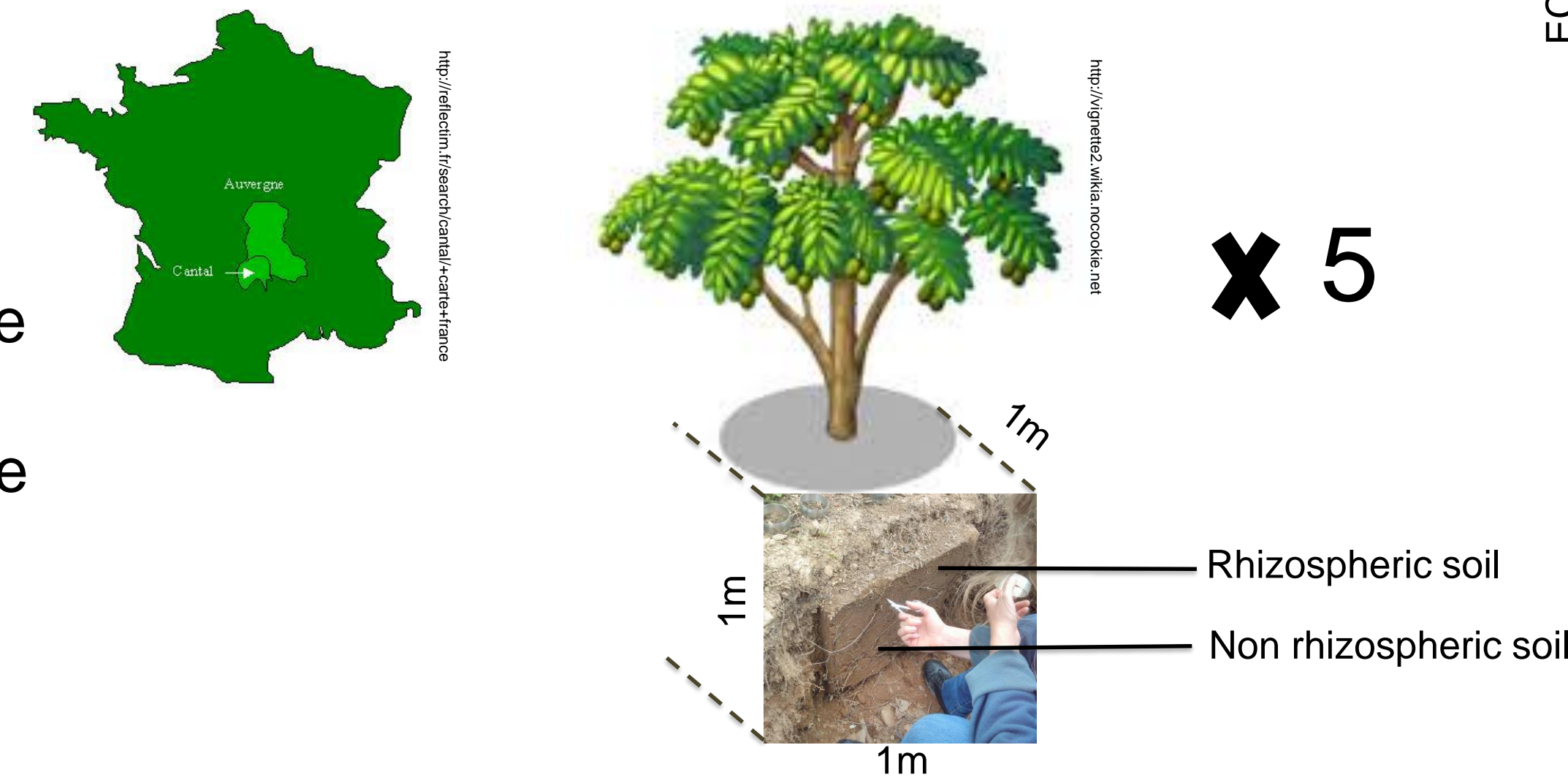
Agroforestry mixes annual culture or permanent pasture with permanent trees which is widely known to improve soil biodiversity, especially macro and micro fauna¹, as compared to monoculture². However, the specific role of fine tree roots on microbial community is still poorly known in field conditions³. 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...).

Methods & Analysis

Field site & Sampling

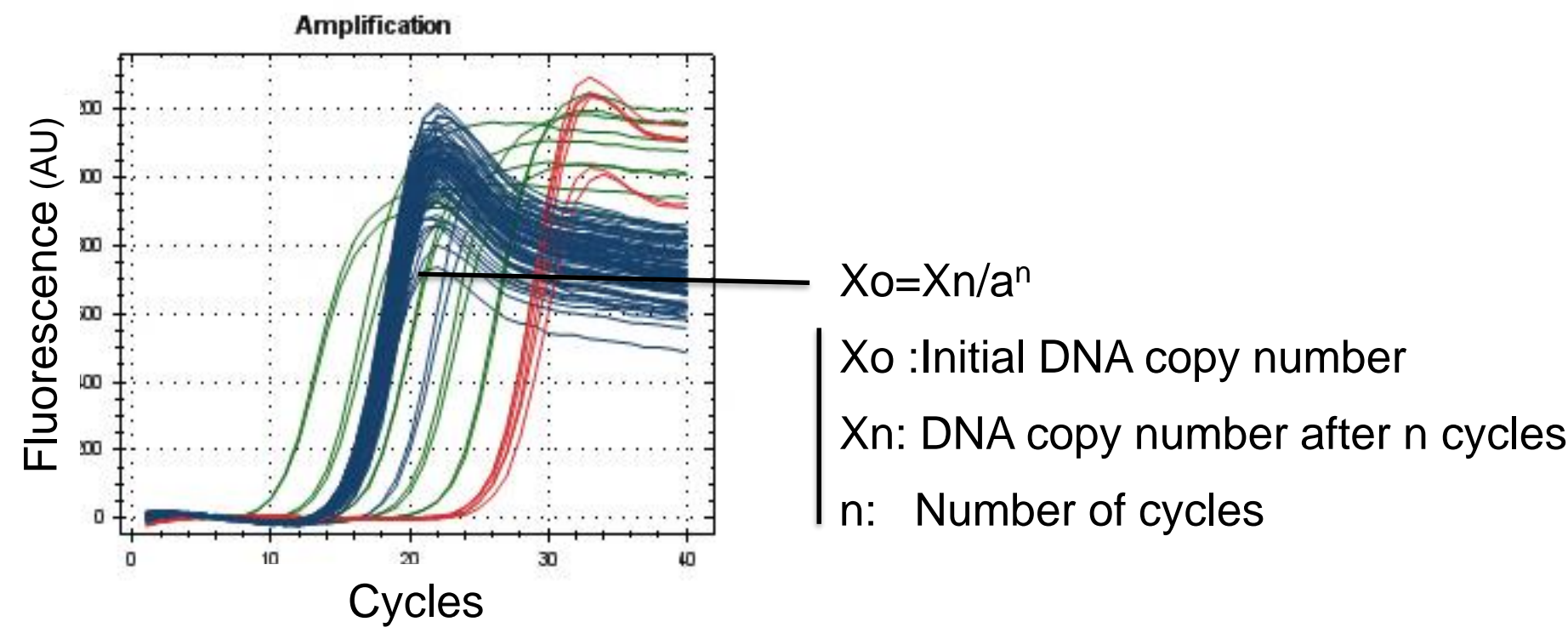
- ☀ Continental climate
- 🌳 12 y/o Hybrid walnuts intercropped with permanent pasture
- 📏 10 samples soil per tree (X5) in rhizospheric and non rhizospheric soil
- 📍 530m
- 📍 Cantal region, France
- 🌱 Silty soil/ 5°-10° slope

Bodez, J.¹ Monnier, Y.¹ Bertrand, I.² Erktan, A.¹ Mohamed, A.¹ Maeght, J.-L.³ Stokes, A.¹
¹INRA UMR AMAP, Montpellier, France
²Cirad UMR Eco&Sols, Montpellier, France
³UMR 242 IEES-Paris c/o SFRI Vietnam

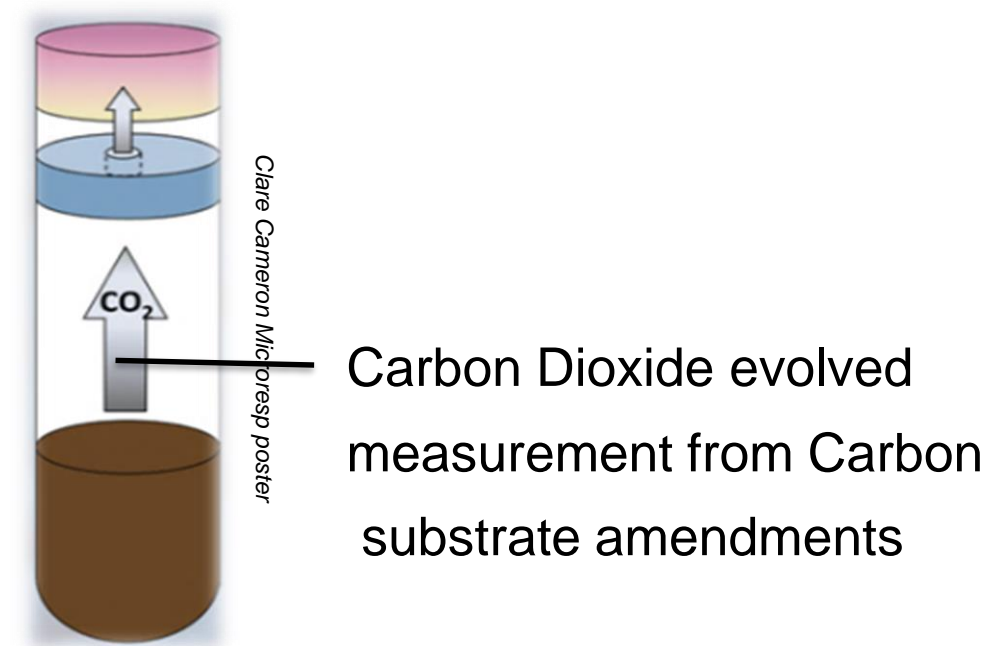


Analysis

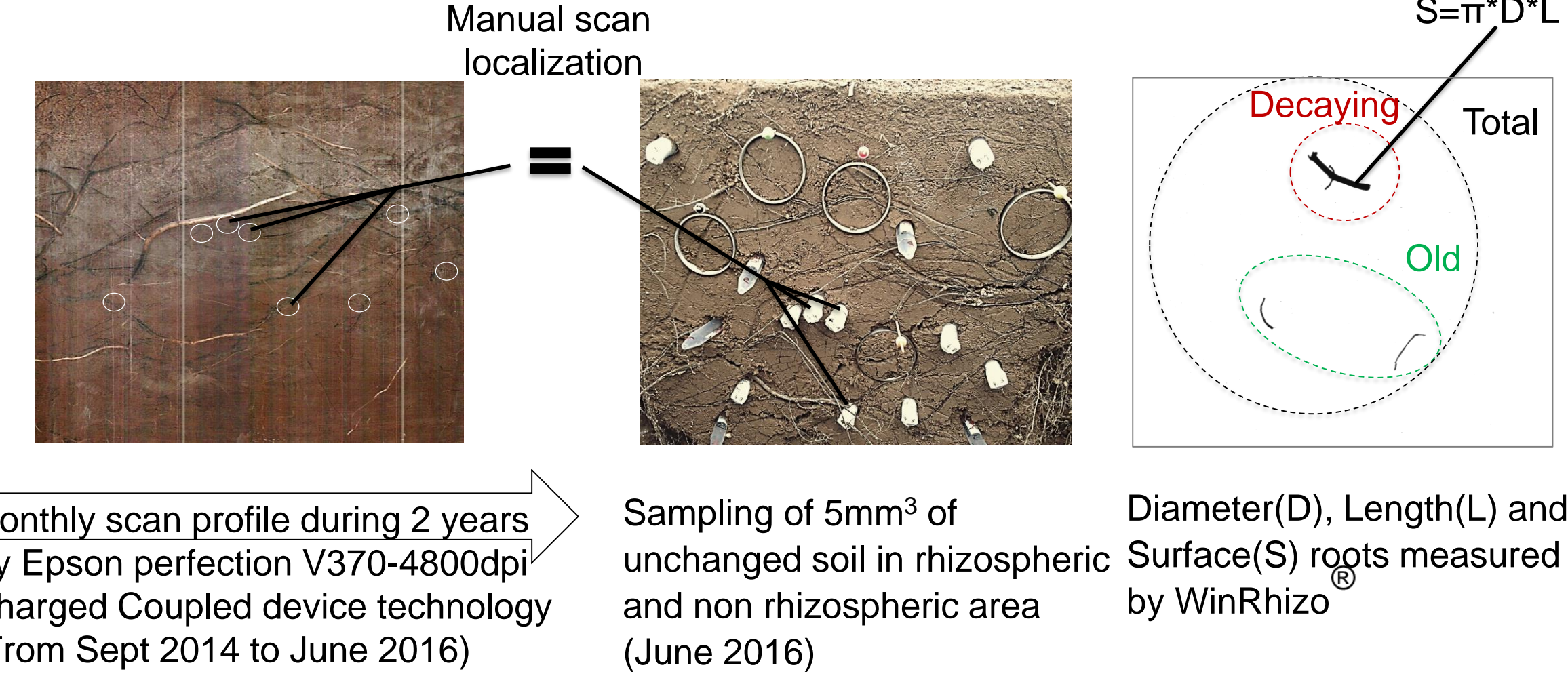
Relative quantification of bacteria (16S DNA) and fungi (18S DNA) by Real time PCR⁵



Microorganism substrate induced respiration SIR quantified by Microresp⁶



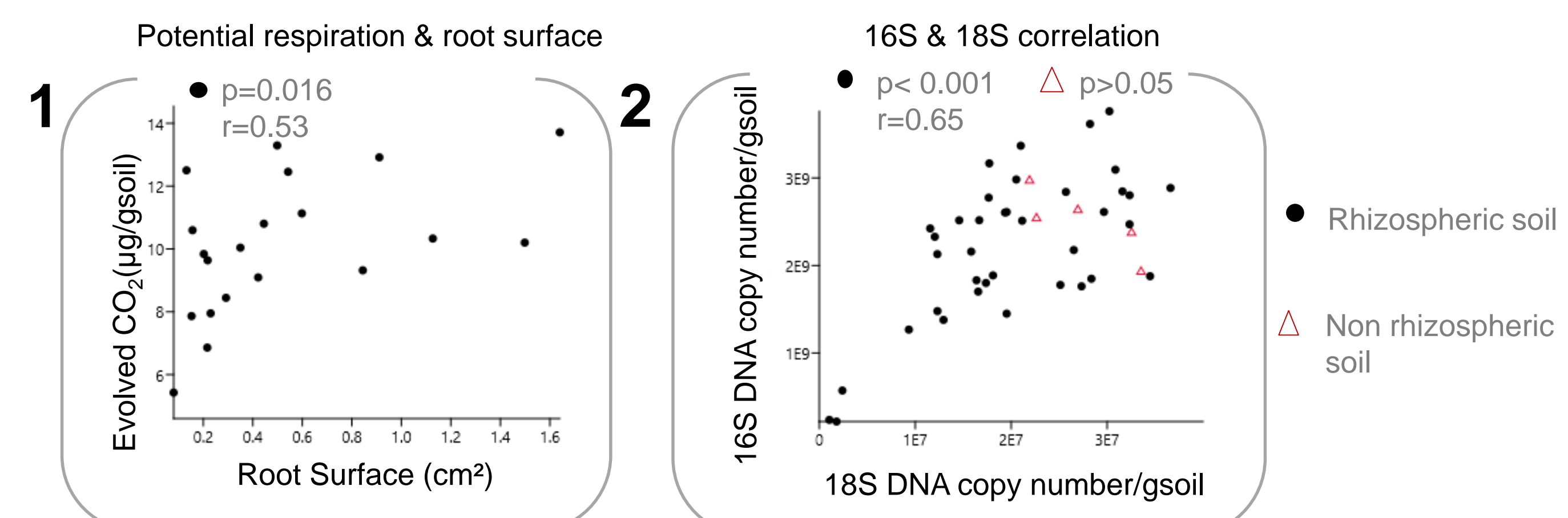
Tree roots temporal dynamics and morphological characteristics determined by image analyses (scans & WinRhizo[®])



Results & Discussions

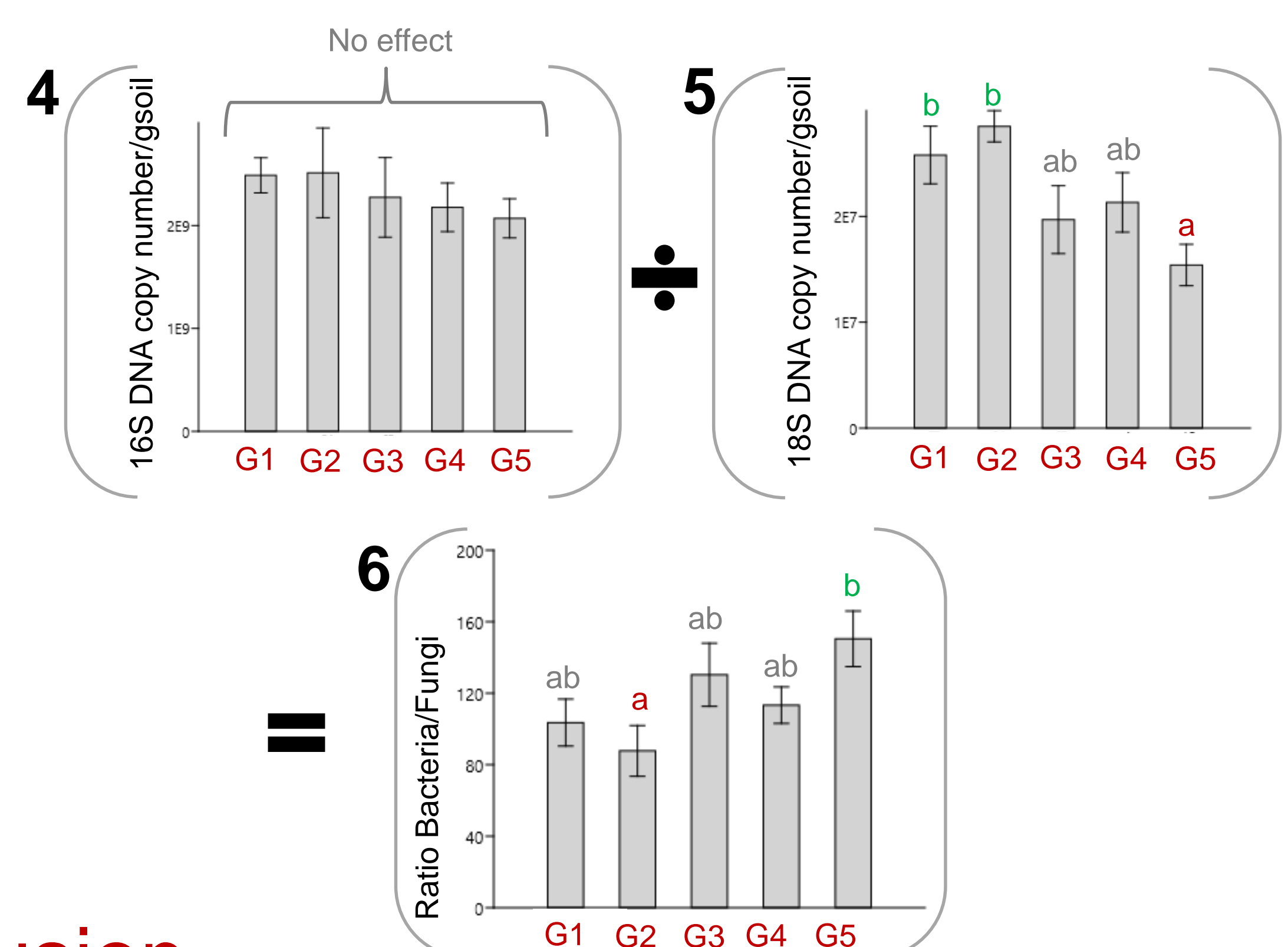
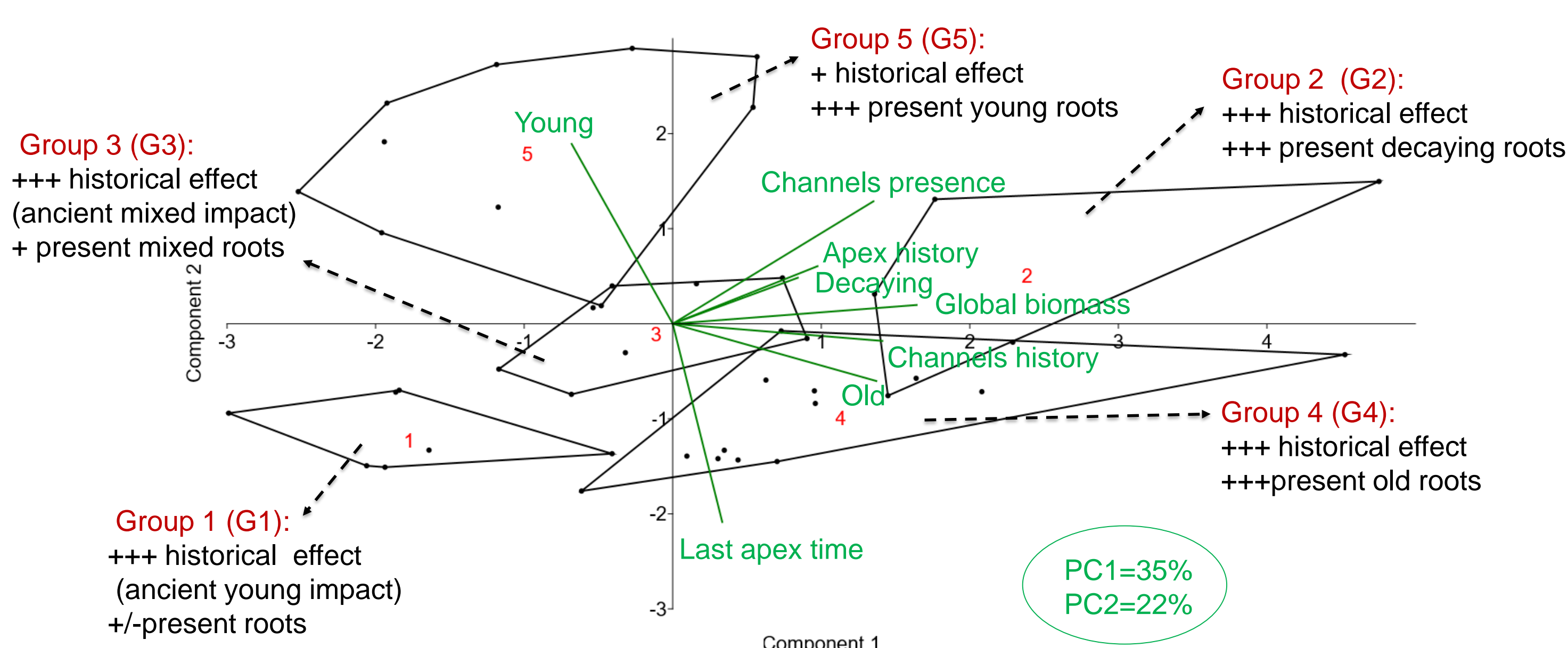
What about root biomass and microorganisms?

- 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.

¹Bender, S. Franz, Cameron Wagg, and Marcel G. A. van der Heijden. 2016. 'An Underground Revolution: Biodiversity and Soil Ecological Engineering for Agricultural Sustainability'. Trends in Ecology & Evolution.
²Plassart, Pierre, Marthe Akpa Vincelas, Christophe Gangneux, Anne Mercier, Sylvie Barry, and Karine Laval. 2008. 'Molecular and Functional Responses of Soil Microbial Communities under Grassland Restoration'. Agriculture, Ecosystems & Environment 127 (3-4): 286-93.
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.
⁵Wong, M.L., and J.F. MEDRANO. 2005. Real-time PCR for mRNA quantitation. *Biotechniques* 39: 75.
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.