

Opposing phylogenetic diversity gradients of plant and soil bacterial communities

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Supplementary Material 1

Principal Component Analysis of Soil Properties

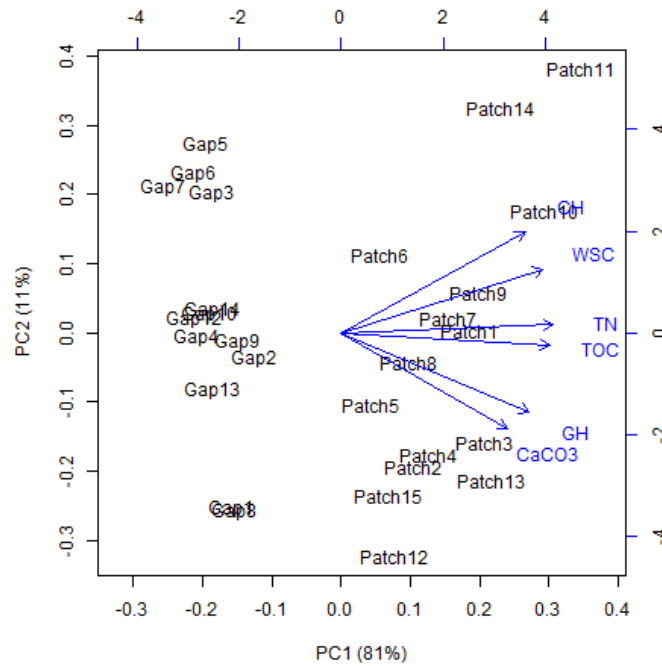


Fig. S1. Biplot of the first and second principal components (PC) obtained from PC analysis of the soil parameters in plant patches and gaps. Arrows indicate loading factors of soil parameters on PCs (CaCO₃: carbonates, CH: water-soluble carbohydrates, GH: gravimetric humidity, TN: total nitrogen, TOC: total organic C, WSC: water-soluble C). For each PC, the explained variance is given in parentheses.

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Supplementary Material 2

Results obtained with standardized MNTD (Mean Nearest Taxon Distance)

Results obtained with standardized (std) MPD and MNTD were similar, since both indices were significantly correlated for plant ($r = 0.72$, $P < 0.001$) and soil bacterial communities ($r = 0.64$, $P < 0.001$).

As with std MPD, plant richness and std MNTD were directly correlated ($r = 0.42$, $P \leq 0.05$), while soil bacterial richness and std MNTD had an inverse relationship ($r = -0.74$, $P < 0.001$).

Structural equation modelling (SEM) also yielded similar results for both indices, with plant std MNTD showing a direct positive effect on soil fertility, and this variable reducing soil bacterial std MNTD (Fig. S2). This SEM explained 15 % of the variation in soil fertility, and 43 % of that in bacterial phylogenetic diversity. The model showed a good fit to our data, as suggested by the non-significant χ^2 test ($N = 28$, $\chi^2 = 0.78$, $df = 1$, $P > 0.3$). Several indices - goodness-of-fit index (GFI), root mean square error of approximation (RMSEA), comparative fit index (CFI) and standardized root mean square residual (SRMR) - also suggested a good fit of this SEM to our data (GFI = 0.98, RMSEA = 0.0, CFI = 1.0, SRMR = 0.049).

Finally, high levels of plant phylogenetic diversity (std MNTD) correlated with high relative abundances of Proteobacteria ($r = 0.37$, $P \leq 0.05$), which associated with reduced bacterial phylogenetic diversity (std MNTD; $r = -0.47$, $P \leq 0.01$).

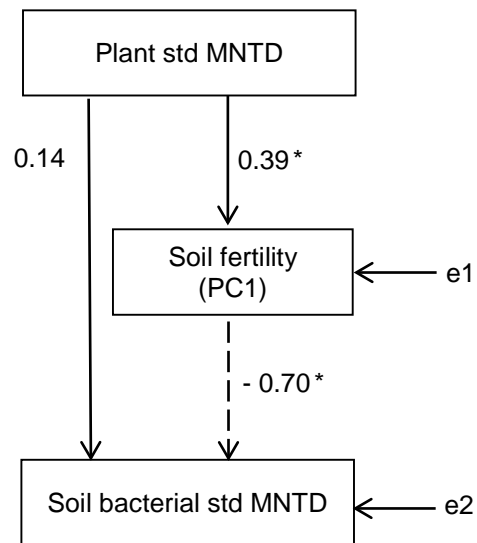


Fig. S2. Structural equation modelling shows that plant phylogenetic diversity (standardized MNTD) has a positive effect on soil fertility, which reduces soil bacterial phylogenetic diversity (standardized MNTD). Soil fertility represents the first principal component (PC1) of a PC analysis considering total organic C, total N, water-soluble C, water-soluble carbohydrates, gravimetric humidity and carbonates. Solid and dashed arrows respectively indicate positive and negative standardized coefficients (* $P < 0.05$). e indicates error term.