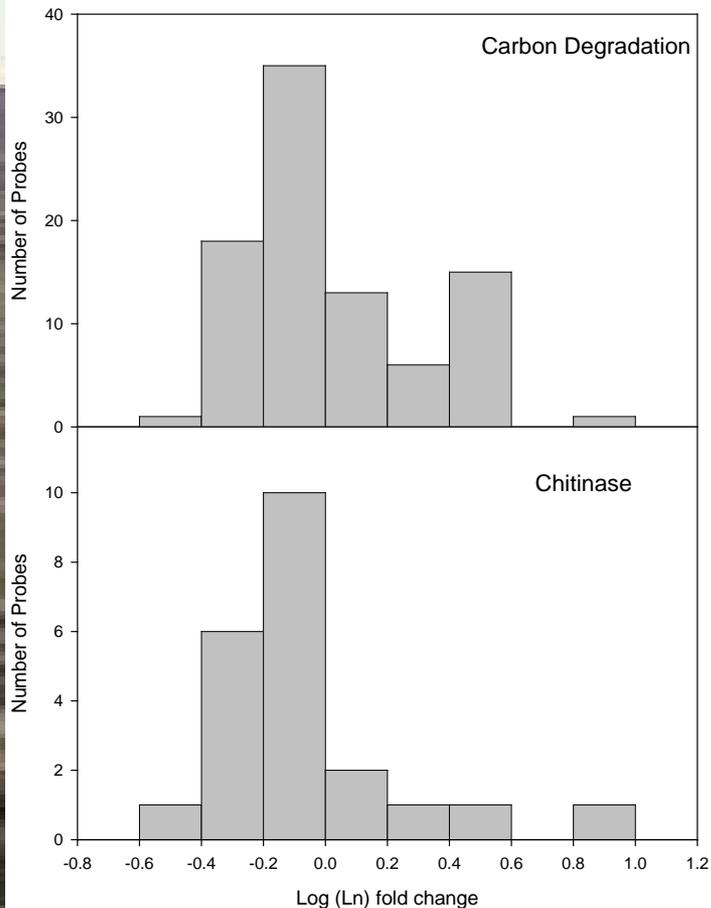


Afforestation Alters the Composition of Functional Genes in Soil and Biogeochemical Processes

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- Afforested systems are oft proposed as offsets for atmospheric carbon accumulation, however their belowground carbon cycle changes have not been fully investigated.
- Functional genes associated with carbon & nitrogen transformations, microbial community dynamics and soil level processes associated with changes in afforestation were investigated in *Eucalyptus* plantations.
- Changes in soil carbon and nitrogen cycle transformations were found to be correlated with the abundance of corresponding microbial functional gene markers
- In the long term, these biogeochemical shifts might have important implications for both the productivity of successive rotations of plantations and the rate at which carbon and nitrogen are incorporated into soil.

Berthrong, S. T., Schadt, C. W., Piñeiro, G., and R. B. Jackson. 2009. Afforestation alters soil functional gene composition and biogeochemical processes in South American grasslands. *Appl. Environ. Microbiol.* **75**:6240–6248

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Abstract: Soil microbes are highly diverse and control most soil biogeochemical reactions. We examined how microbial functional genes and biogeochemical pools responded to the altered chemical inputs accompanying land use change. We examined paired native grasslands and adjacent Eucalyptus plantations (previously grassland) in Uruguay, a region that lacked forests before European settlement. Along with measurements of soil carbon, nitrogen, and bacterial diversity, we analyzed functional genes using a microarray, which simultaneously quantified several thousand genes involved in soil carbon and nitrogen cycling. Plantations and grassland differed significantly in functional gene profiles, bacterial diversity, and biogeochemical processes. Most grassland profiles were similar, but plantation profiles generally differed from those of grasslands due to differences in functional gene abundance across diverse taxa. Eucalypts decreased ammonification and N fixation functional genes by 11% and 7.9% ($P < 0.01$), which correlated with decreased microbial biomass N and more NH_4^+ in plantation soils. Chitinase abundance decreased 7.8% in plantations compared to levels in grassland ($P = 0.017$), and C polymer-degrading genes decreased by 1.5% overall ($P < 0.05$), which likely contributed to 54% ($P < 0.05$) more C in extractable soil pools and 27% less microbial C ($P < 0.01$) in plantation soils. In general, afforestation altered the abundance of many microbial functional genes, corresponding with changes in soil biogeochemistry, in part through altered abundance of overall functional gene types rather than simply through changes in specific taxa.

Citation: Berthrong, S. T., Schadt, C. W., Piñeiro, G., and R. B. Jackson. 2009. Afforestation alters soil functional gene composition and biogeochemical processes in South American grasslands. *Appl. Environ. Microbiol.* **75**:6240–6248

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