Long-term mineral fertilizer application influences soil bacterial community structure, diversity and functioning

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Introduction

Mineral fertilizer application could influence soil bacterial communities and their functioning, and thus has indirect effects on plant nutrition. However, its potential long-term influence on soil bacteria requires further study.

Question

How does the long-term (over 45 years) application of mineral fertilizer influence:

(i) Bacterial community structure?
(ii) Bacterial community diversity?
(iii) Bacterial community functioning?

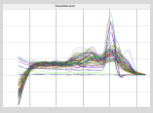
Methods

- Experiment established in 1972
- Yearly application of mineral fertilizer
- Varying P, K & N (n = 6)

No nutrient addition (Cont)
80 kg ha^{-1} yr^{-1} P_2O_5 + 240 kg ha^{-1} yr^{-1} K_2O (PK)
PK + 75 kg ha^{-1} yr^{-1} N (NPK, **typical N**)
PK + 150 kg ha^{-1} yr^{-1} N (NNPK, **2 x typical N**)

Sampling (20 cm)
- Peak biomass
- 46 years after establishment

Metabarcoding
- Soil DNA extraction
- Bacterial 16S rRNA
- ASV* construction



quantitative PCR
- Soil N mineralization
- Soil P mineralization

*amplicon sequence variant

Bacterial community Structure

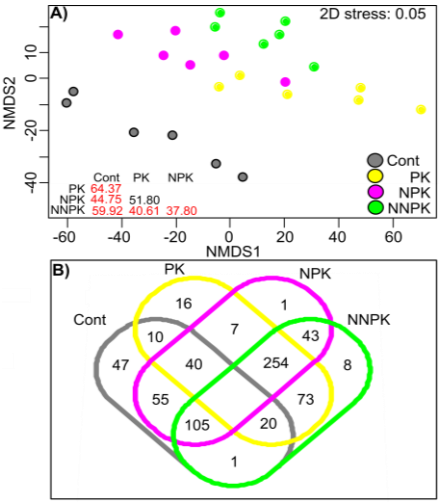


Figure 1A: Non-metric multidimensional scaling graph (NMDS) showing the effect of treatment on soil bacterial community structure. Insert is the community centroid distance between treatments, Significance: red = $P \leq 0.05$. **B**) Unique and shared indicator ASVs between treatments. Indicators defined as: IndVal = 0.80 and $P \leq 0.05$.

Bacterial community diversity

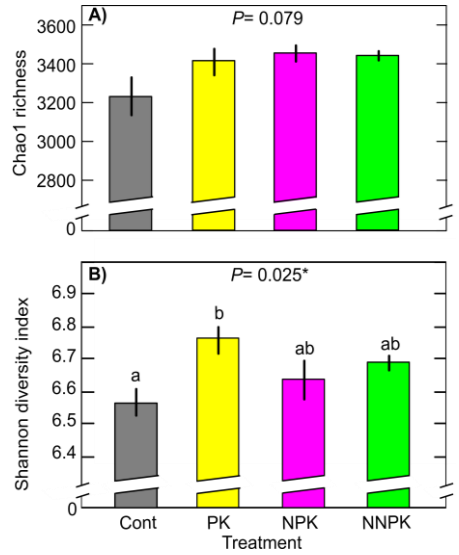


Figure 2: Chao1 richness (**A**) and Shannon diversity index (**B**) of the soil bacterial community. Error bars = Standard error. Different letters indicate statistically significant difference at $P \leq 0.05$

Bacterial community functioning

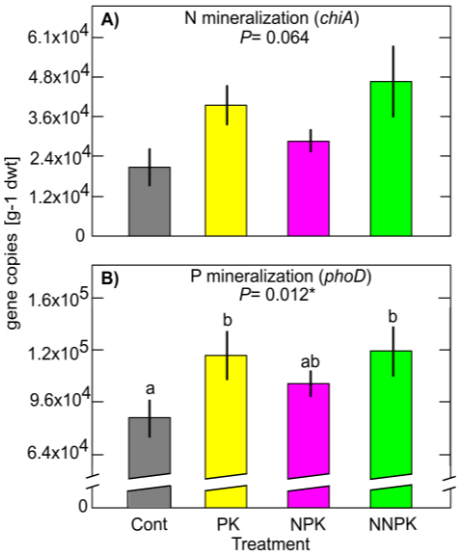


Figure 3: Gene copy numbers of bacterial genes involved in soil N (**A**, *chiA*) and P mineralization (**B**, *PhoD*). Error bars = Standard error. Different letters indicate statistically significant difference at $P \leq 0.05$

Results

- Significant differences between Cont and all three fertilized treatments in soil bacterial community structure (**Fig 1A**, all $P \leq 0.05$), and nearly all fertilized treatments. Each treatment also had unique indicator ASVs (**Fig 1B**).
  → Long-term mineral fertilizer application strongly influence soil bacterial community structure.
- Significant effect of fertilization on bacterial diversity (increase in PK, P=0.02, **Fig 2B**). Similar trend with richness.
  → Long-term mineral fertilizer application can *increase* soil bacterial diversity, maybe due to a change in soil pH.
- *phoD* was significantly inceased in PK (P=0.02) and NNPK (P=0.01) over Cont (**Fig 3B**), same trend seen in *chiA*.
  → Long-term mineral fertilizer application can *increase* the potential activity of bacteria for soil nutrient turnover. This maybe due to soil priming effects.

Take-home

Long-term mineral fertilizer application strongly influenced soil bacterial community structure, with significant differences even being seen between different fertilized treatments. Soil bacterial diversity and potential activity for soil nutrient turnover also significantly increased.

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