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Microbial response to fertilization intensity and cropping systems: Insights from a 42-year-old long-term experiment

The study system

(Krause et al., 2024, Sci Rep)

The DOK field experiment investigates long-term effects of organic and conventional cropping systems since 1978. The experiment includes two organic (BIODYN, BIOORG), one conventional system with mixed fertilization (CONFYM), a solely mineral-fertilized system (CONMIN) and an unfertilized control (NOFERT). BIODYN, BIOORG and CONFYM are maintained at two fertilization levels (0.7 and 1.4 livestock units/ha). The trial follows a 7-year crop rotation and is arranged in a randomized split-block design with four replicates.

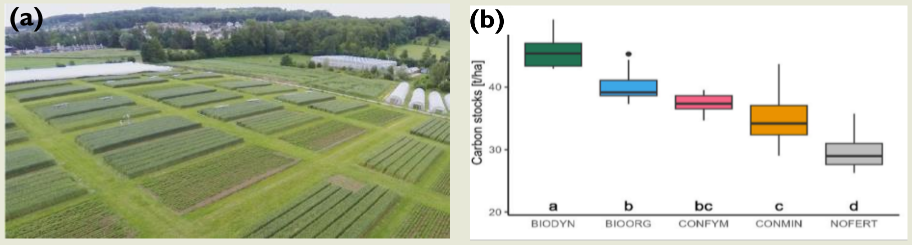

Figure 1: Aerial view of the DOK (a) and cropping system-specific carbon stocks in fully fertilized, mineral-only, and unfertilized systems (b).

Soil microbial communities are sensitive to differences in fertilization intensity in organic and conventional farming systems

(Lori et al., 2023, SBB)

Motivation and Methodology

While farmyard manure can significantly improve soil health, it can also lead to the accumulation of heavy metals or antibiotic-resistant organisms in the soil. Furthermore, animal husbandry is a major contributor to greenhouse gas emissions. We present how soil microbial communities react to long-term animal manure-based fertilization at 0.7 and 1.4 livestock units/ha using amplicon sequencing and lifestyle classification based on ribosomal RNA copy numbers.

Outcomes and Implications

Microbial α-diversity was largely unaffected by fertilization intensity; however, community structure changed consistently (Figure 2A and B), with bacterial communities more strongly influenced by fertilization intensity and fungal communities more strongly affected by the cropping system. Also, high-input systems showed an increased bacterial copiotroph-to-oligotroph ratio (Figure 2C). Low-input systems selected more oligotrophic microbes adapted at utilizing diverse carbon sources, a potential advantage for future agroecosystems.

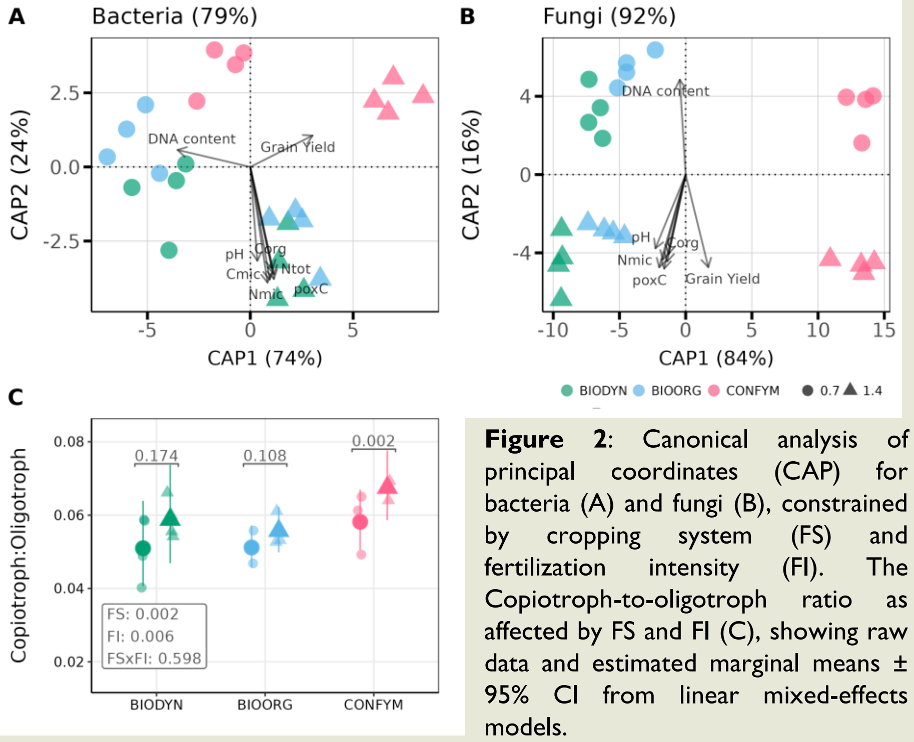

Figure 2: Canonical analysis of principal coordinates (CAP) for bacteria (A) and fungi (B), constrained by cropping system (FS) and fertilization intensity (FI). The Copiotroph-to-oligotroph ratio as affected by FS and FI (C), showing raw data and estimated marginal means ± 95% CI from linear mixed-effects models.

Organic cropping systems alter metabolic potential and carbon, nitrogen and phosphorus cycling capacity of soil microbial communities

(Krause et al., 2025, SBB)

Motivation and Methodology

To assess the impact of cropping systems on soil metabolic potential and nutrient cycling capacities, shotgun metagenomics was used, and 11.4 billion reads were annotated using nutrient cycling gene databases (CAZy, NCycDB, and PCycDB) and general databases (SEED and EC).

Outcomes and Implications

Manure application was the main driver of soil metabolic changes consistent across all annotations. Overall, organic practices enriched genes for organic P acquisition, nitrate transformation, organic matter degradation, and carbohydrate cleavage (Figure 3). Conventional systems favored genes for inorganic nutrient uptake and transcription (Figure 3).

We show that cropping systems influence the functional potential of soils, affecting fundamental mechanisms of nutrient cycling. Consequently, cropping systems can be utilized to steer the regulating potential of agricultural soils and to lower the environmental impact of food systems.

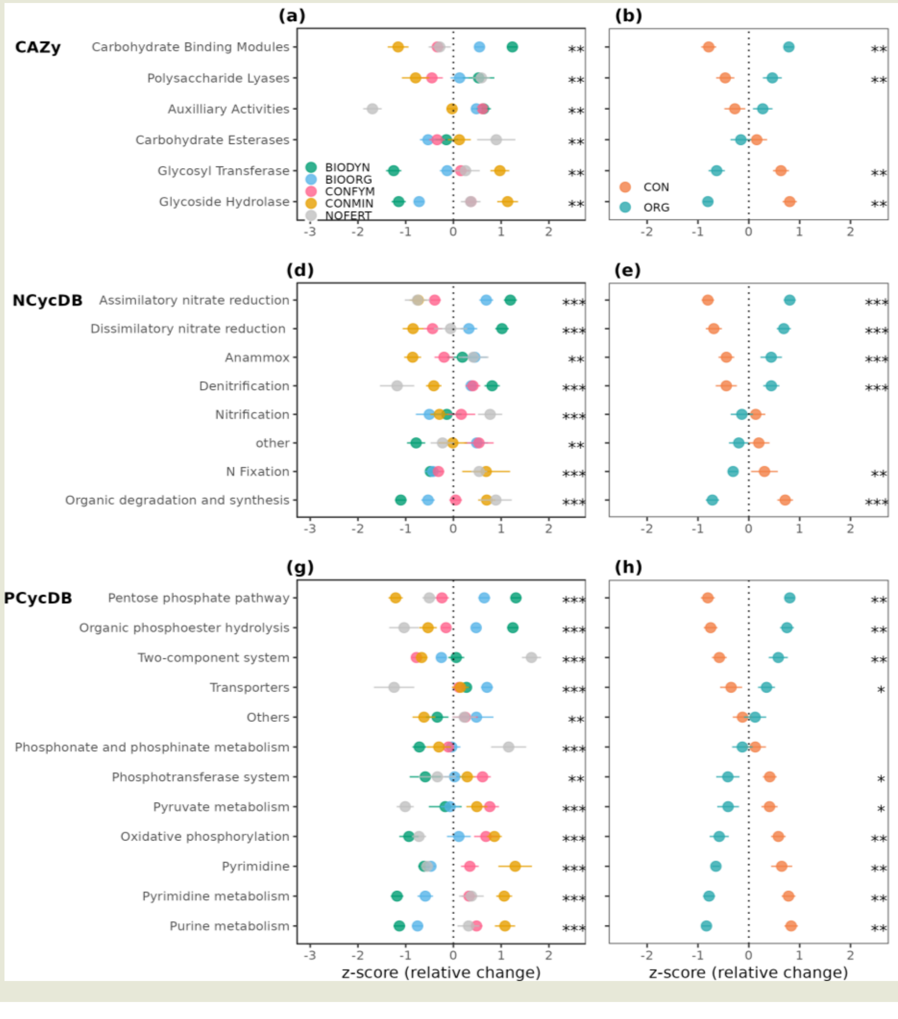

Figure 3: Relative change in gene class abundance at the highest classification level based on ztransformed TPM data. The mean and standard error is plotted along with the significance of effects assessed by PERMANOVA.

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