## Organic and conventional agriculture promote distinct soil microbiomes with contrasting metabolic potentials

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**Aim:** Soil microorganisms deliver numerous ecosystem functions essential for crop production. Changes in agricultural practices can alter soil microbial diversity and the underlying metabolic potential encoded in their collective genomes. This offers opportunities to harness microbial resources for developing sustainable cropping systems. Here, we explored how different organic and conventional farming systems shape diversity and functional potential of the soil microbiome.

**Method:** Soils were collected from the DOK long-term field trial comparing five different farming systems since 1978. The soil microbiome was characterized by DNA metabarcoding and shotgun metagenome sequencing. Extensive auxiliary data on soil properties, greenhouse gas emissions, and crop performance from decades of research allow for a comprehensive system comparison.

**Results:** Organic fertilization as an integral part of organic farming increased diversity and altered the taxonomic and functional structure of the soil microbiome compared to stockless systems. The plant protection regime was of subordinate importance. Organic fertilization promoted microbial guilds involved in degradation of complex organic compounds, whereas minerally fertilized systems were characterized by oligotrophic communities adapted to carbon-limited environments. Functional gene composition showed a gradual change based on the type of fertilizer inputs from organic to conventional and unfertilized systems. While conventional stockless farming systems were dominated by genes indicative of accelerated elemental cycles and molecule transport, the genetic capacity of organically managed soils were dominated by genes required for degradation of complex lignocellulolytic compounds and internal nutrient cycling.

**Conclusions:** These results add to the emerging evidence that long-term organic and conventional management can promote soil microbiomes with unique genetic capacities that might ultimately alter key biogeochemical processes in agriculturally managed soils.