



Tropentag, September 10-12, 2025, hybrid conference

“Reconcile land system changes
with planetary health”

Nitrogen forms and cropping systems influence soil prokaryotic diversity in organic and conventional farming trial

SUSAN MURIUKI¹, ANN KAMBURA², JULIUS MUGWERU¹

¹*University of Embu, Biological Sciences, Kenya*

²*Taita University, Earth Agricultural and Extension, Kenya*

Abstract

Soil prokaryotes are vital to agroecosystem functions, influencing soil health, crop productivity, disease suppression, and climate resilience. We conducted an exploratory study to investigate how crop type, crop growth stage, and nitrogen forms influenced soil prokaryotic diversity within a 15-year organic and conventional farming systems trial at Chuka and Thika, Kenya. The trial included high- and low-input organic and conventional plots, representing commercial and subsistence farming systems, respectively. Soil samples were collected during cereal and potato cropping seasons at vegetative, reproductive, and maturity crop stages. Biological replicates from each farming system and stage were pooled for 16S rRNA amplicon sequencing using the Illumina MiSeq platform. Sequence data were processed using the phyloseq package (v1.36.0) in RStudio to assess prokaryotic community structure and diversity. Soil chemical properties including pH, nitrogen forms, and phosphorus were analysed on individual replicates to support interpretation of microbial patterns. Soil nutrients varied across sites, seasons, crop stages, and input levels. Organic high-input systems consistently exhibited significantly higher pH across all stages and seasons. In contrast, conventional high-input systems had higher available phosphorus and ammonium-N during vegetative and reproductive periods. Low-input systems showed more variable trends: organic low-input systems were associated with higher pH and nitrate-N, while conventional low-input systems showed elevated ammonium-N and phosphorus at distinct stages. Site-specific correlations were observed: Chuka showed strong positive associations among pH, total N, nitrate-N, and ammonium-N, whereas Thika exhibited a negative correlation between pH and nitrate-N. Ammonium-N and pH emerged as key abiotic drivers of prokaryotic diversity across systems and crop stages. Organic systems demonstrated more consistent and higher prokaryotic alpha diversity, while conventional systems exhibited greater variability. Diversity was generally stable during vegetative and reproductive stages but shifted at maturity. More prokaryotic phyla were detected during the potato season than cereal season. Actinobacteria, Acidobacteria, and Proteobacteria were dominant across all farming systems, while Nitrospirae was consistently enriched in organic systems. These exploratory findings highlight how long-term farming practices, crop development stages, and nitrogen forms interact to shape soil microbial communities in agroecosystems.

Keywords: Cropping systems, farming systems, nitrogen forms, prokaryotic diversity

Contact Address: Edward Karanja, International Centre of Insect Physiology and Ecology (icipe), Plant Health, Nairobi, Kenya, e-mail: ekaranja@icipe.org