The 23rd World
Congress of Soil Science

The 23rd World Congress of Soil Science

Proceedings

June 7–12, 2026 Nanjing·China

June 7-12, 2026
Nanjing, China
https://www.23wcss.org.cn/

Tillage Intensity as a Driver of Soil Bacterial Composition and Functional Potential

Mohammad Yaghoubi Kanghahi[1,2], Francesco Maria Calabrese[2], Carmine Crecchio[2], Rosangela Addesso[1], Adriano Sofo[1*]

[1] Department of Agricultural, Forestry, Food and Environmental Sciences (DAFE), University of Basilicata, Potenza, Italy
[2] Department of Soil, Plant and Food Sciences, University of Bari "Aldo Moro", Bari, Italy
*adriano.sofo@unibas.it

ABSTRACT

Soil microbial communities play a critical role in nutrient cycling and agroecosystem resilience, yet their responses to long-term tillage practices in semiarid environments remain poorly understood. This study evaluated the effects of 20 years of conventional tillage (CT), minimum tillage (MT), and no-tillage (NT) on soil bacterial communities, integrating physicochemical analyses with high-resolution 16S rRNA amplicon sequencing to characterize shifts in microbial diversity and taxonomic composition. Soil samples were collected from a long-term tillage experiment established in Policoro, Southern Italy, where durum wheat (*Triticum durum*) and faba bean (*Vicia faba*) have been grown under a biennial rotation for over 20 years. Composite soil samples (0–30 cm depth) were taken from replicated plots.

Although major chemical properties, such as pH, organic matter, total nitrogen, and carbonates showed no significant differences among treatments, MT and NT soils improved the availability of key micronutrients relative to CT. Copy numbers of the functional microbial genes involved in denitrification (*nirK*, *nirS*), iron reduction (*gltA*), and sulfate reduction (*dsrAB*) were significantly higher under NT and MT than CT, indicating stimulated anaerobic microbial processes in reduced-tillage systems.

Sequencing revealed a pronounced compositional restructuring of bacterial communities across treatments. NT and MT soils were enriched in copiotrophic phyla such as Actinobacteria and Firmicutes, consistent with improved nutrient retention and reduced physical disturbance. Conversely, CT soils were dominated by oligotrophic phyla adapted to nutrient-poor and disturbed environments. Venn analysis highlighted distinct microbial signatures for each management system, with MT harboring the greatest number of unique genera, followed by NT and CT, demonstrating that long-term tillage intensity strongly filters community membership. Beta-diversity analyses (PCoA, PCA, PERMANOVA) demonstrated clear community separation among tillage regimes, confirming robust shifts in bacterial assemblages, although alpha diversity (Faith's PD) showed no significant differences among treatments.

Overall, long-term NT and MT practices reshape soil bacterial communities toward functionally enriched, nutrient-responsive taxa and promote key microbial processes, underscoring the ecological advantages of conservation tillage for sustainable soil management in semiarid agroecosystems.

Acknowledgments

This research was conducted within the project "The Effects of Tillage Practice on Soil Carbon Sequestration Mechanisms (TilSoilC)", supported by EJP Soil, which provided financial assistance for experimental activities, laboratory analyses, and sequencing efforts.