



Evaluating the Impact of Tillage on Soil Biological Communities: Fungi, Bacteria and Actinomycetes

ASHRUTI KESHARWANI¹, GIRISH GOYAL², DEVENDRA KUMAR³, RAGINI KUMARI^{4*},
AMIT KUMAR PANDEY⁵, ANITROSA INNAZENT⁶, TOKO NAAN⁷, NIHAL OJHA⁸ and
VIKAS KUMAR⁹

¹Rajmata Vijayaraje Scindhia Krishi Vishwavidyalay, Gwalior (M.P.), India.

²Directorate of Research, ANDUAT, Kumarganj Ayodhya, India.

³Department of Agricultural Chemistry & Soil Science, R. B. S. College Bichpuri,
Agra (Dr. B. R. A. University, Agra), India.

^{4*}Department of Soil Science & Agricultural Chemistry, Bihar Agricultural University,
Sabour/Bhagalpur- 813210, India.

⁵Department of Soil Science and Agricultural Chemistry, Bihar Agricultural University,
Sabour, Bhagalpur, Bihar, India.

⁶Kerala Agricultural University, India.

⁷Division of Sericulture, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu, India.

⁸Department of Agronomy, Jodhpur Agriculture University, India.

⁹Faculty of Agricultural sciences, SKD University, Hanumangarh, Rajasthan-335801, India

*Corresponding author E-mail: drkbaus@yahoo.in

<http://dx.doi.org/10.13005/ojc/410533>

(Received: April 04, 2025; Accepted: October 17, 2025)

ABSTRACT

Soil microbial communities play a foundational role in maintaining soil fertility, regulating nutrient cycling, enhancing plant productivity, and promoting ecosystem resilience. Among them, fungi, bacteria, and actinomycetes are key biological indicators of soil health, each contributing uniquely to organic matter decomposition, nutrient mobilization, and pathogen suppression. Tillage practices, particularly the intensity and frequency of soil disturbance, have a profound influence on the abundance, diversity, and functionality of these microbial groups. This review synthesizes current findings on how conventional tillage and conservation tillage including no-tillage and reduced tillage-affect soil microbial communities, with an emphasis on fungi, bacteria, and actinomycetes. Evidence from global meta-analyses reveals that conservation tillage significantly enhances microbial biomass, especially in the biologically active topsoil layers (0–20 cm), with fungal and bacterial biomass increasing by 31% and 11%, respectively. NT systems foster fungal dominance, increase the fungal-to-bacterial ratio, and support the survival of sensitive groups like *Arbuscular mycorrhizal* fungi, while also promoting copiotrophic bacteria such as *Proteobacteria*. Actinomycetes, though resilient to moderate disturbance, thrive best under NT and residue-retained conditions. The



review also highlights the influence of environmental modulators-such as soil texture, moisture, pH, and organic carbon-on microbial responses to tillage. Despite substantial progress, knowledge gaps remain, particularly regarding actinomycetes' functional roles under different tillage regimes. Future research should prioritize long-term, multi-location studies and the use of advanced molecular tools to unravel microbial pathways and resilience mechanisms. Conservation tillage emerges as a biologically favorable strategy to support microbial health and soil sustainability.

Keywords: Soil microbial, Fungi, Bacteria and Actinomycetes, *Arbuscular mycorrhizal* fungi, *Proteobacteria*.

INTRODUCTION

The health of agricultural soils is intrinsically tied to the activity and composition of the biological communities they harbor. Among these, fungi, bacteria, and actinomycetes constitute the core of soil microbial life, serving as critical agents in ecosystem processes, including nutrient cycling, organic matter decomposition, soil aggregation, and the suppression of pathogens. The nature and intensity of soil tillage-ranging from conventional deep ploughing to conservation-oriented minimal disturbance practices-exert significant influence on the abundance, diversity, and function of these microbial communities. As global efforts intensify toward sustainable agricultural intensification, understanding how tillage practices shape microbial dynamics has become central to the development of resilient, low-input, and biologically enriched farming systems (Gupta *et al.*, 2022)⁷. Historically, conventional tillage was adopted to prepare seedbeds, incorporate residues, and manage weeds. However, such practices often involve extensive soil disturbance that disrupts soil aggregates, depletes organic matter, and destroys microbial habitats-especially for organisms like fungi and actinomycetes that rely on stable niches (Kabir, 2005)^{11,12}. The repetitive breakdown of the soil structure from CT leads to enhanced oxidation of organic carbon, thereby reducing microbial biomass and shifting the balance toward bacterial dominance in the microbial community. In contrast, conservation tillage (CTi)-including reduced tillage (RT) and no-tillage (NT)-preserves the soil structure, increases surface organic matter, and stabilizes moisture and temperature regimes, all of which create more hospitable environments for microbial proliferation (Doran, 2002)⁵.

Multiple studies, including global meta-analyses, have consistently shown that conservation tillage significantly increases total soil microbial biomass, particularly fungal and bacterial

communities (Chen *et al.*, 2020)³. In a meta-analysis spanning over 60 field studies, conservation tillage was found to increase total microbial biomass by 37%, fungal biomass by 31%, and bacterial biomass by 11% compared to conventional practices. These benefits were most pronounced in the upper 20 cm of the soil, where the majority of microbial activity occurs due to higher concentrations of organic residues and root exudates. Furthermore, the fungal-to-bacterial ratio (F:B), often used as an ecological indicator of soil health and stability, tended to be higher under conservation practices, indicating a shift toward more self-regulating microbial systems (Van Groenigen *et al.*, 2010)^{21,22}. Fungi, especially arbuscular mycorrhizal (AM) fungi, are profoundly affected by tillage. These organisms form extensive hyphal networks that facilitate nutrient and water uptake, enhance soil structure through the production of glomalin, and provide protection against soilborne pathogens. The disruption of these networks through mechanical tillage not only impairs fungal colonization but also decreases the infectivity and survival of fungal propagules such as spores and hyphae. Beare (1997)¹ emphasized that tillage diminishes AM fungi by severing hyphae and diluting spore densities in deeper soil layers. In contrast, no-till systems preserve root channels and allow for the continuity of fungal hyphae, leading to enhanced colonization and functionality, particularly under crop rotation and cover cropping systems.

Bacterial communities, although generally more resilient to disturbance, also respond distinctly to changes in tillage. Soil bacteria are pivotal in mineralizing nutrients, fixing nitrogen, solubilizing phosphorus, and producing growth-promoting compounds. The shift in carbon availability and oxygen status induced by tillage influences bacterial community structure. For instance, copiotrophic bacteria (such as *Proteobacteria* and *Bacteroidetes*) flourish in nutrient-rich, recently tilled soils, while oligotrophic groups (e.g., Actinobacteria and Acidobacteria) are more prominent in undisturbed

or organically rich environments (Bielinska *et al.*, 2012)². Moreover, the presence of plant residues under NT enhances rhizosphere complexity, enriching bacterial populations with biocontrol and nitrogen-cycling capabilities (Kiprotich *et al.*, 2025)⁷. The filamentous *Gram-positive* bacteria, Actinomycetes, occupy an ecological place between fungi and true bacteria. They play essential roles in decomposing recalcitrant organic matter such as cellulose and lignin and are prolific producers of antibiotics that suppress pathogens. Tillage can negatively impact actinomycetes by physically destroying their hyphal structures and reducing the availability of organic matter. However, they are relatively more tolerant than fungi due to their ability to form spores. Conservation tillage has been reported to favor actinomycetes by enhancing surface organic inputs and providing undisturbed microhabitats (Luo *et al.*, 2010)¹⁵.

Environmental conditions such as soil texture, moisture, temperature, and nutrient status modulate the response of microbial communities to tillage. Conservation tillage tends to improve water infiltration, reduce erosion, and moderate soil temperatures—all of which enhance microbial activity. Importantly, microbial carbon-use efficiency (CUE), a measure of how effectively microbes convert carbon into biomass rather than respiring it as CO₂, tends to be higher under no-till systems, suggesting better carbon sequestration potential (Manzoni *et al.*, 2012)⁹. This positions conservation tillage as not only a strategy for enhancing biological activity but also a tool for mitigating climate change through improved carbon dynamics. Recent advances in metagenomics, phospholipid fatty acid (PLFA) profiling, and high-throughput sequencing have provided new insights into the functional and taxonomic shifts in microbial communities under different tillage systems. These technologies allow for the detection of subtle changes in microbial composition and help uncover the complex interactions among microbial groups. For example, the application of PLFA-based methods has shown increased fungal and bacterial lipid biomarkers under NT conditions, further validating field observations of enhanced microbial biomass (Morugán-Coronado *et al.*, 2022)¹⁸.

Despite these promising findings, adoption of conservation tillage remains limited in many developing regions, hindered by socio-economic barriers, equipment availability, and lack of

awareness. However, integrating microbial ecology into tillage decision-making offers a promising avenue for sustainable agriculture. Practices that promote microbial diversity—such as reduced tillage, organic amendments, cover cropping, and crop rotation—can lead to more productive and resilient agroecosystems (Nkongolo *et al.*, 2020)¹⁹. This review seeks to comprehensively evaluate the current understanding of how tillage practices influence the composition and activity of key soil microbial communities—fungi, bacteria, and actinomycetes—across different agroecosystems. By synthesizing insights from global meta-analyses, field studies, and mechanistic investigations, we aim to clarify the microbial consequences of tillage intensity and inform sustainable land management strategies. Our focus on the functional roles and ecological responses of these microbial groups will help bridge the gap between soil biology and agricultural practice, contributing to the broader goals of soil health, climate resilience, and food security.

Effect of Tillage on Soil Microbial Biomass

Soil microbial biomass, representing the living component of soil organic matter excluding roots and larger soil fauna, is a key driver of nutrient cycling, organic matter decomposition, and ecosystem stability. Tillage practices, being one of the most influential components of land management, greatly impact this microbial pool by altering the physical structure, organic matter availability, and microhabitats within the soil. Among various approaches, conservation tillage—particularly reduced tillage and no-tillage—has consistently demonstrated its ability to enhance microbial biomass, especially when compared to conventional tillage, which involves intensive plowing and residue removal. The biological consequences of this shift are substantial, influencing not just microbial numbers but also the diversity, functionality, and ecological resilience of soil systems (Johnsen *et al.*, 2001)¹⁰. Meta-analyses have offered strong empirical support for the superiority of conservation tillage in promoting microbial biomass. In a comprehensive synthesis of global field studies, Chen *et al.*, (2020)³ reported that soils managed under conservation tillage exhibited, on average, a 37% increase in total microbial biomass relative to CT systems. This enhancement was more prominent in fungal communities, which saw a 31% rise, whereas bacterial biomass also increased by 11%. These differences underscore

the greater sensitivity of fungi to soil disturbance and their stronger response to residue retention and undisturbed microenvironments. The structural complexity and hyphal nature of fungi make them particularly vulnerable to tillage, so reducing soil disruption has an outsized benefit for fungal survival and proliferation.

A significant portion of this biological activity is concentrated in the upper soil profile—specifically, the top 0-20 cm—where root exudates, decaying residues, and favorable aeration create optimal conditions for microbial life. Conservation tillage practices maintain these favorable conditions by preventing the mechanical breakdown of soil aggregates, preserving pore continuity, and reducing temperature and moisture fluctuations. Unlike conventional plowing, which homogenizes the soil and disperses organic matter throughout the profile, NT and RT systems allow for organic residues to accumulate near the surface, creating a nutrient-rich habitat for microbes. This stratification benefits microbial biomass by providing a concentrated resource zone, especially for organisms adapted to surface-dwelling lifestyles (Beare, 1997)¹. Moreover, the retention of crop residues in conservation tillage systems acts as a continuous source of organic substrates, fueling microbial metabolism and growth. This residue layer also shields the soil from erosive forces and helps in moisture conservation, factors that are directly linked to microbial abundance. The stable microclimate beneath the residue layer fosters higher microbial activity, enzymatic functions, and microbial interactions, contributing to an active and self-sustaining soil food web. These biological improvements are not only beneficial for soil health but also translate into enhanced nutrient availability, improved soil structure, and better crop productivity in the long term.

Impact on Bacterial Communities

Soil bacterial communities are highly adaptive and play a central role in regulating ecosystem functions such as organic matter decomposition, nutrient cycling, and disease suppression. Though often more resilient than fungi to environmental disruptions, bacterial populations are not immune to the impacts of agricultural management—especially tillage. Soil disturbance from conventional tillage (CT) alters the physical structure, moisture dynamics, and organic matter distribution

in the soil, leading to significant shifts in bacterial community composition. These shifts influence not only the abundance of different bacterial taxa but also their functional capabilities, ultimately impacting soil fertility and plant productivity (Holland, 2004; Mangalassery *et al.*, 2015)¹⁴. Conventional tillage systems, which involve repeated plowing and turning of the soil, break down soil aggregates and accelerate the oxidation of organic carbon. This sudden release of nutrients initially stimulates bacterial activity, but over time, it depletes the pool of stable organic matter essential for sustaining microbial diversity. In such disturbed environments, stress-tolerant bacterial groups, particularly members of the phylum Actinobacteria, tend to dominate. Actinobacteria are known for their resilience under nutrient-poor and physically disturbed conditions, owing to their ability to form spores and utilize complex organic compounds. While their persistence is advantageous in harsh environments, their dominance may signal a shift toward a less diverse, stress-adapted microbial ecosystem (Dai *et al.*, 2018)¹⁵. In contrast, conservation tillage (CTi), particularly no-tillage and reduced tillage systems, promotes a more favorable environment for bacterial diversity and functional richness. These systems maintain soil structure, reduce physical disruption, and allow crop residues to remain on the surface, creating a nutrient-rich microhabitat. The retained organic matter provides a steady supply of carbon substrates, supporting the proliferation of copiotrophic bacteria—organisms that prefer high-nutrient conditions. Among these, Proteobacteria and Bacteroidetes are particularly responsive to the improved habitat conditions under NT systems. These phyla include many beneficial taxa involved in nitrogen fixation, organic matter mineralization, and production of plant growth-promoting compounds (Dai *et al.*, 2018)¹⁶.

One of the most important benefits of NT systems is the enhancement of bacterial diversity. The presence of undecomposed residues and stable moisture regimes under conservation tillage supports a wider variety of microbial niches, allowing different bacterial taxa to coexist. This increased diversity is not just ecological decoration—it underpins the stability and resilience of the microbial community. Diverse bacterial assemblages are more capable of withstanding environmental stressors, performing redundant functions, and facilitating nutrient transformations more efficiently and

sustainably (Wang *et al.*, 2017)¹⁷. Furthermore, the vertical stratification of bacterial populations is more pronounced under NT systems. Without the mixing effects of tillage, nutrient-rich residues accumulate in the upper soil layers, supporting high microbial activity and localized community development. This stratification contributes to spatial heterogeneity, which further enhances microbial interactions and ecological specialization. As such, conservation tillage not only maintains bacterial abundance but also fosters a complex, well-structured microbial ecosystem critical for long-term soil health.

Impact on Soil Fungal Communities

Fungi are vital architects of soil ecosystems, playing essential roles in nutrient cycling, soil aggregation, and plant health. Among soil microbial communities, fungi—particularly filamentous types such as arbuscular mycorrhizal fungi (AMF)—are especially vulnerable to mechanical disturbances caused by tillage. Their extensive hyphal networks, which traverse soil particles to form symbiotic associations with plant roots, are critical for accessing nutrients like phosphorus, maintaining soil structure, and fostering biological communication between soil and plant systems. However, these fragile networks are readily disrupted by the physical inversion of soil during conventional tillage (Jansa *et al.*, 2002). Tillage operations break the continuity of fungal hyphae, dilute spore populations deeper into the soil profile, and reduce the fungi's ability to recolonize plant roots, ultimately impairing fungal biomass and diversity. *Arbuscular mycorrhizal* fungi are particularly sensitive to these disturbances because their life cycle relies heavily on intact hyphal connections for reproduction and root colonization. Kabir and Koide (2002)^{11,12} emphasized that tillage reduces the viability of AMF spores and diminishes the infectivity of fungal propagules, especially when tillage is performed post-harvest in the absence of living host plants. This leads to a breakdown in the mutualistic relationship between fungi and plants, compromising nutrient uptake efficiency and increasing the plant's reliance on synthetic fertilizers. Additionally, the redistribution of spores into deeper, less favorable soil layers limits their access to emerging roots, further reducing colonization rates. In contrast, no-tillage systems maintain a more continuous habitat for AMF by minimizing soil disturbance and preserving root channels from previous crops, which serve as avenues for fungal colonization in subsequent growing seasons (Kabir, 2005)¹⁸.

No-tillage practices have been consistently associated with a shift toward fungal dominance in soil microbial communities. This is often reflected in an increased fungal-to-bacterial biomass ratio (F:B), a widely accepted indicator of ecosystem maturity and biological stability (Lienhard *et al.*, 2013)¹⁹. High F:B ratios in NT systems suggest a self-regulating soil environment with enhanced organic matter retention, improved nutrient recycling, and better resistance to disturbance. Fungal dominance under NT also promotes the formation of glomalin-related soil proteins, which are instrumental in aggregate formation and carbon sequestration. This structural benefit enhances soil porosity, water retention, and erosion resistance—attributes essential for sustainable agricultural productivity. Furthermore, fungi in NT systems benefit from the accumulation of undecomposed crop residues on the soil surface, which serve as carbon-rich substrates supporting saprotrophic fungal communities. These residues not only enhance microbial diversity but also create microclimatic buffers against temperature and moisture fluctuations, both of which can influence fungal metabolism and growth. The layered residue cover also facilitates the formation of micro-niches where specific fungal guilds can thrive without competitive suppression from fast-growing bacteria.

Response of Actinomycetes to Tillage

Actinomycetes, a distinctive group of filamentous, *Gram-positive* bacteria, occupy a unique niche in soil microbial ecology. Morphologically and functionally bridging the gap between fungi and bacteria, these microbes are renowned for their ability to decompose complex, recalcitrant organic matter such as lignin, cellulose, and chitin-substances that are resistant to rapid microbial breakdown. Moreover, actinomycetes are prolific producers of secondary metabolites, including antibiotics and enzymes, which play a crucial role in disease suppression and competitive interactions within the soil microbiome (Gupta *et al.*, 2022)⁷. As such, the abundance and activity of actinomycetes directly influence nutrient cycling, plant health, and overall soil biological quality. Like other microbial communities, actinomycetes respond distinctly to soil management practices, particularly tillage, which alters their habitat, substrate availability, and microclimatic conditions.

Conventional tillage, through aggressive soil inversion and physical disruption, significantly modifies the soil environment. While actinomycetes possess certain traits-such as spore formation and slow but persistent colonization capacity-that enable them to tolerate moderate disturbance, intensive tillage can reduce their abundance and enzymatic activity. Soil mixing dilutes organic matter inputs across the profile, disturbs actinomycetal networks, and accelerates the oxidation of surface residues, thereby depriving these organisms of their preferred carbon sources. Furthermore, frequent soil disruption negatively affects soil aggregation and microhabitat stability, both of which are crucial for the long-term establishment of actinomycetes in the rhizosphere (Wang *et al.*, 2017)²¹. In contrast, conservation tillage practices such as no-tillage and reduced tillage foster conditions that are highly favorable for actinomycetes. By minimizing mechanical disturbance and maintaining crop residues on the soil surface, NT systems preserve organic matter-rich microhabitats and create a protective layer that buffers temperature and moisture fluctuations. These environments are ideal for the growth and enzymatic activity of actinomycetes, which rely on steady access to lignocellulosic substrates for metabolism. Studies have reported increased populations of actinomycetes under NT systems, particularly in the top 5–15 cm of soil where organic inputs are concentrated (Morugán-Coronado *et al.*, 2022)¹⁸. This layer also benefits from enhanced moisture retention and reduced erosion, creating a stable ecological niche for actinomycetal proliferation.

The residue-covered surface in conservation tillage systems further supports actinomycetes by acting as a continual source of decomposable organic carbon. Unlike fast-growing bacteria that prefer easily mineralizable substrates, actinomycetes thrive on more resistant compounds, which become available during the slow decomposition of plant residues. Their filamentous structure allows them to colonize these substrates efficiently, often extending across residue-soil interfaces to facilitate nutrient cycling. Additionally, the antibiotics and antifungal compounds produced by actinomycetes play a role in modulating microbial community composition, often suppressing pathogenic organisms and contributing to soil suppressiveness against diseases (Gupta *et al.*, 2022)⁷. Importantly, while actinomycetes can sporulate to survive adverse conditions-such

as desiccation or temporary nutrient scarcity-their metabolic activity is highest under stable, undisturbed conditions. Conservation tillage not only supports their survival but actively encourages their ecological functions by promoting biological continuity, organic matter stratification, and a less oxidative soil environment. These benefits are particularly crucial in systems aiming for sustainable soil health, carbon sequestration, and reduced chemical input dependency.

Environmental Modulators of Microbial Response to Tillage

Soil microbial communities exist within a complex matrix of environmental variables that directly influence their structure, function, and resilience. Factors such as soil texture, moisture, temperature, pH, and organic carbon content act as environmental modulators, shaping how microbes respond to different tillage practices. While tillage remains a dominant driver of microbial abundance and community composition, the interactive effects of these environmental parameters determine the depth and longevity of microbial shifts in agricultural systems. Among these, soil moisture and organic carbon availability emerge as particularly influential under varying tillage regimes, especially in conservation tillage systems (Guo *et al.*, 2016)⁶.

Soil texture governs the soil's capacity to retain water and nutrients, thereby shaping microbial habitat quality. Fine-textured soils like clay retain more water and support microbial proliferation under stable moisture regimes, while sandy soils, with larger pores and lower water-holding capacity, may show limited microbial responses to tillage changes. However, conservation tillage can partially compensate for texture limitations by promoting surface residue cover, which reduces evaporation and enhances infiltration, particularly in sandy or degraded soils (Van Kessel *et al.*, 2013)²². By preserving surface organic inputs, conservation tillage improves water availability in the upper soil layers, where microbial activity is most intense, especially during dry spells or fluctuating weather conditions. Temperature is another key modulator, influencing enzymatic rates and microbial metabolism. Tillage practices impact soil temperature dynamics by altering surface albedo and insulation. Conventional tillage, which removes residue cover and exposes bare soil, can lead to rapid heating and cooling cycles, stressing microbial communities.

In contrast, conservation tillage insulates the soil, buffering extreme temperatures and creating a more favorable thermal environment for microbial processes (Doran *et al.*, 2002)⁵. This stabilization of temperature and moisture synergistically enhances microbial carbon-use efficiency (CUE)-the ratio of microbial biomass production to substrate carbon consumption. Higher CUE under conservation tillage implies a more efficient transformation of carbon inputs into microbial biomass, reducing CO₂ losses through respiration and thereby contributing to carbon sequestration in the soil profile (Manzoni *et al.*, 2012).

Soil pH also affects microbial diversity and activity by influencing nutrient solubility and the availability of essential elements. While tillage may not drastically alter pH in the short term, repeated exposure of subsoil layers and enhanced mineralization under CT can lead to localized

acidification. Conservation tillage, with its minimal disturbance and organic inputs, tends to stabilize or slightly increase pH, supporting a broader microbial spectrum and improving nutrient exchange dynamics (Chen *et al.*, 2020)³. Conservation tillage significantly enhances microbial biomass in the biologically active topsoil but shows reduced or non-significant effects in deeper layers. The response is more pronounced for fungi than bacteria, indicating greater sensitivity of fungal hyphae to soil disturbance (Table 1). Interestingly, despite the critical role of environmental conditions, recent global meta-analyses indicate that tillage practices and organic amendments exert a stronger influence on microbial abundance than inherent soil properties or climatic variables (Morugán-Coronado *et al.*, 2022)¹⁸. This finding underscores the importance of management decisions in shaping soil biological communities, even across varied soil types and climate zones.

Table 1: Comparative Changes in Soil Microbial Biomass under Different Tillage Systems

Soil Depth (cm)	Tillage Type	Fungal Biomass Change (%)	Bacterial Biomass Change (%)	Total Microbial Biomass Change (%)
0–20	Conservation Tillage (NT/RT)	+33%	+13%	+37%
>20	Conservation Tillage (NT/RT)	–12%	–8%	Not Significant
0–20	Conventional Tillage	Baseline	Baseline	Baseline

Functional Implications of Enhanced Microbial Activity under Conservation Tillage

The biological engine of soil-its microbial community-drives many of the key processes underpinning agroecosystem sustainability. When conservation tillage is adopted, not only does microbial biomass increase, but the functionality of these communities is profoundly improved, with direct implications for nutrient cycling, soil structure, and plant health. By preserving soil integrity and maintaining surface residues, conservation tillage fosters a microenvironment that stimulates microbial metabolism, enhances enzymatic activity, and elevates the ecological roles played by fungi, bacteria, and actinomycetes in supporting productive, resilient soil systems (Gupta *et al.*, 2022)⁷.

One of the most significant functional outcomes of increased microbial activity under conservation tillage is the improved cycling of essential nutrients, particularly nitrogen and phosphorus. Microorganisms, especially free-living and symbiotic bacteria such as *Rhizobium* and *Azotobacter*, are key agents in nitrogen fixation and mineralization processes. Conservation

tillage enhances the stability and diversity of these bacterial populations, thereby supporting a steady transformation of organic nitrogen into forms accessible to plants. Similarly, *Arbuscular mycorrhizal* fungi, which thrive in undisturbed soils, play a pivotal role in phosphorus solubilization and uptake by plants through their extensive hyphal networks (Kabir, 2005)^{11,12}. These networks extend the root system's reach into phosphorus-limited zones of the soil, thereby improving nutrient acquisition and reducing the need for external fertilizers. Beyond nutrient mobilization, microbial communities under conservation tillage also exhibit enhanced functional traits such as enzyme production. Key enzymes involved in carbon, nitrogen, and phosphorus cycling-like dehydrogenase, phosphatase, and urease-are consistently found in higher concentrations in reduced-tillage systems. These enzymes accelerate the breakdown of organic matter, increasing the efficiency of nutrient release and uptake (Vo íšková and Baldrian, 2013)¹⁷. The consistent supply of organic substrates from surface residues further stimulates microbial respiration and biomass turnover, creating a self-sustaining system of nutrient regeneration that benefits plant growth throughout the season.

Another critical function of a robust microbial community is its capacity to suppress soilborne pathogens. Under conservation tillage, the microbial diversity and abundance act as a natural barrier against disease outbreaks. This biocontrol potential arises from the production of antimicrobial compounds, competitive exclusion of pathogens, and activation of plant immune responses. For example, certain strains of *Bacillus* and *Streptomyces*, which are often more abundant in NT soils, release antibiotics and lytic enzymes that inhibit the growth of phytopathogens, thereby reducing the incidence of diseases such as root rot and damping-off (Bielinska *et al.*, 2012)². Equally important is the role of fungi, particularly AMF, in improving physical soil properties. The increased fungal biomass under conservation tillage contributes significantly to the formation of soil aggregates through the production of glomalin, a glycoprotein excreted by AMF that binds soil particles into stable clumps. These aggregates enhance water infiltration, aeration, and resistance to erosion, while also protecting organic matter from rapid decomposition. The improvement in soil structure not only supports root penetration and plant anchorage but also boosts the soil's capacity to buffer environmental stress, making cropping systems more resilient to drought, compaction, and nutrient leaching (Kabir and Koide, 2002)^{11,12}.

Agronomic and Ecological Significance of Microbial Shifts under Conservation Tillage

The agronomic and ecological value of soil microbial communities cannot be overstated—they are the unseen workforce that sustains plant productivity, regulates nutrient dynamics, and drives soil regeneration. As tillage practices evolve, so too does the composition and function of microbial communities, with profound implications for both crop performance and ecosystem sustainability. Shifting from conventional to conservation tillage, particularly long-term no-tillage systems, alters the soil environment in ways that favor microbial biodiversity, functional efficiency, and ecological resilience. These biological shifts are not merely academic observations but carry tangible benefits in the field, influencing yield stability, input-use efficiency, and the overall health of agroecosystems (Zhang *et al.*, 2012)²⁴.

One of the most immediate agronomic benefits of microbial enrichment under NT systems

is improved nutrient use efficiency. Microbial communities optimized under reduced disturbance become more proficient at mobilizing key nutrients such as nitrogen and phosphorus. For example, bacteria like *Azospirillum* and *Rhizobium* enhance biological nitrogen fixation, while fungi such as *Arbuscular mycorrhizal* fungi significantly improve phosphorus uptake. These interactions reduce dependency on synthetic fertilizers, lower production costs, and minimize nutrient runoff into surrounding environments (Chen *et al.*, 2020)³. The microbial mediation of nutrient supply also improves synchronization with plant demand, which translates into better root development, higher biomass accumulation, and ultimately, enhanced crop yields. Beyond immediate productivity gains, the long-term ecological benefits of NT systems are particularly noteworthy. Continuous application of NT promotes the establishment of a stable, diverse microbial community that strengthens the soil food web and buffers against external stresses. These systems support a balance between fungi and bacteria, enhancing nutrient cycling efficiency and fostering natural pest and disease suppression. Moreover, stable microbial networks contribute to the formation and preservation of soil structure through aggregate stabilization and organic matter retention. This translates into soils that are better able to retain water, resist erosion, and withstand periods of drought or heavy rainfall—traits that are increasingly valuable under the pressures of climate variability (Tamburini *et al.*, 2020)²⁰.

The integration of NT with crop residue retention and organic inputs such as compost or green manure further amplifies microbial and agronomic benefits. Retained residues act as continuous carbon sources that nourish microbial populations and improve surface soil moisture, while organic amendments enrich microbial diversity and stimulate enzymatic activity. Together, these practices create a biologically enriched soil ecosystem capable of supporting not just one growing season but a sustainable cropping system for decades. Additionally, by fostering conditions that favor beneficial microbes over pathogens, such practices reduce the need for chemical pesticides and promote more environmentally friendly farming. Fungal communities thrive under NT due to reduced disruption and residue cover. Bacterial diversity and functional richness are

positively associated with moisture and carbon availability in NT systems. Actinomycetes, though resilient, perform optimally when residues are retained on the soil surface (Table 2). Importantly, the ecological significance of these microbial shifts extends beyond the farm. Enhanced microbial activity contributes to carbon sequestration, greenhouse gas mitigation, and improved biodiversity at the landscape level. In this way,

conservation tillage is not only a tool for improving soil health but also a strategy for achieving broader environmental goals. By understanding and leveraging microbial responses to NT systems, farmers and land managers can build agroecosystems that are productive, sustainable, and resilient—an essential requirement for feeding future generations while preserving the planet (Luo *et al.*, 2010; Van Kessel *et al.*, 2013)^{15,22}.

Table 2: Functional Shifts in Microbial Groups under Tillage Practices

Microbial Group	Conventional Tillage (CT)	Conservation Tillage (NT/RT)
Fungi	Severed hyphal networks; low AMF colonization	Enhanced hyphal development, AMF abundance, increased F:B ratio
Bacteria	Dominated by stress-tolerant taxa (e.g., <i>Actinobacteria</i>)	Enriched with copiotrophic groups (e.g., <i>Proteobacteria</i> , <i>Bacteroidetes</i>)
Actinomycetes	Survive via spores, but less active due to residue loss	Higher abundance and metabolic activity under residue-rich NT soils
Functional Traits	Reduced enzyme activity, lower biocontrol potential	Elevated enzymatic function, greater nutrient cycling, enhanced biocontrol potential

Research Gaps and Future Directions

Despite significant advancements in our understanding of how tillage influences soil microbial communities, considerable gaps remain—especially concerning specific groups like actinomycetes, whose ecological roles are often overshadowed by the focus on fungi and bacteria. Actinomycetes, though functionally critical for the breakdown of complex organic compounds and the natural suppression of soilborne pathogens, remain poorly characterized in the context of soil management. Their adaptive strategies, functional contributions, and resilience mechanisms under different tillage regimes—particularly in long-term conservation tillage systems—are still not well understood. This lack of clarity limits our ability to fully harness their potential in sustainable farming systems (Gupta *et al.*, 2022)⁷. One major limitation in current research is the scarcity of long-term, multi-location field studies that evaluate microbial responses across diverse agro-climatic zones. Most available data come from short-duration studies with site-specific conditions, which cannot capture the temporal dynamics or ecological stability of microbial communities under different tillage practices. Soil microbial populations are highly influenced by seasonal changes, crop type, residue input, and climate variability. Therefore, to draw robust conclusions about the sustainability and scalability of conservation tillage practices, we must invest in regionally diverse, long-term

experiments that integrate both biological and agronomic metrics. These trials should aim to monitor not only microbial biomass and diversity but also functional attributes such as enzymatic activities, nutrient cycling efficiency, and disease suppression capacity over multiple cropping cycles (Morugán-Coronado *et al.*, 2022)¹⁸.

The application of advanced molecular and biochemical tools holds great promise in addressing these research gaps. Traditional culture-based techniques, while informative, capture only a fraction of the microbial diversity in soil. Newer methodologies such as metagenomics, phospholipid fatty acid (PLFA) analysis, and quantitative polymerase chain reaction (qPCR) offer more comprehensive and accurate profiling of microbial communities. Metagenomics allows researchers to sequence entire microbial genomes directly from soil samples, revealing not only "who is there" but also "what they are doing" by identifying genes involved in nutrient metabolism, stress response, and antimicrobial production. Similarly, PLFA provides quantitative data on microbial biomass and community composition by analyzing lipid biomarkers specific to different microbial groups, while qPCR enables precise quantification of target genes related to microbial functionality (Chen *et al.*, 2020)³.

Future research should also explore the functional redundancy and resilience of microbial

communities under conservation tillage. It remains unclear how these communities respond to episodic disturbances such as drought, pest outbreaks, or fertilizer shocks. Do NT-associated microbes recover faster or maintain functional stability better than those in conventionally tilled soils? Answering such questions could guide the development of microbial indicators for soil health assessment and help predict agroecosystem performance under future climate scenarios.

CONCLUSION

Soil microbial communities are central to sustaining agroecosystem productivity and ecological balance, and their structure and functioning are strongly influenced by tillage practices. This review underscores the profound impact of soil disturbance intensity on key microbial groups—fungi, bacteria, and actinomycetes—and how conservation tillage systems offer a more supportive environment for microbial proliferation and functionality. Conventional tillage disrupts soil structure, dilutes organic residues, and breaks microbial networks, leading to lower microbial biomass and a shift toward stress-tolerant bacterial taxa such as Actinobacteria. In contrast, conservation tillage enhances surface organic matter, stabilizes soil temperature and moisture, and creates favorable conditions for microbial diversity and activity. Notably, no-tillage systems significantly

increase fungal biomass, promote *Arbuscular mycorrhizal* fungi (AMF) colonization, and contribute to improved soil aggregation through glomalin production. Bacterial communities under NT exhibit greater diversity and a shift toward copiotrophic taxa like Proteobacteria and Bacteroidetes, which are essential for nutrient cycling and plant-microbe interactions. Actinomycetes, while relatively robust, show higher abundance and metabolic activity under minimal disturbance and organic-rich conditions, emphasizing the importance of surface residue retention. The agronomic and ecological implications of these microbial shifts are far-reaching. Enhanced microbial function under conservation tillage supports nutrient efficiency, disease suppression, improved soil structure, and greater resilience against environmental stresses. However, current research remains limited in scale and scope, especially regarding actinomycetes' specific roles and adaptive traits.

ACKNOWLEDGMENT

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Conflict of interest

The author declare that we have no conflict of interest.

REFERENCES

1. Beare, M.; Hu, S.; Coleman, D., & Hendrix, P. Influences of mycelial fungi on soil aggregation and organic matter storage in conventional and no-tillage soils., *Applied Soil Ecology.*, **1997**, 5, 211–219.[https://doi.org/10.1016/S0929-1393\(96\)00142-4](https://doi.org/10.1016/S0929-1393(96)00142-4)
2. Bielinska, E., & Mocek-Płóćiniak, A., Impact of the tillage system on the soil enzymatic activity., *Archives of Enviro., Protection.*, **2012**, 31, 75–82.
3. Chen, H., Global meta-analyses show that conservation tillage practices promote soil fungal and bacterial biomass., *Agriculture, Ecosystems & Enviro.*, **2020**, 293, 106841. <https://doi.org/10.1016/j.agee.2020.106841>
4. Dai, Z.; Su, W.; Chen, H.; Barberán, A.; Zhao, H.; Yu, M.; Yu, L.; Brookes, P. C., Schadt, C. W., & Chang, S. X. **2018**. Long-term nitrogen fertilization decreases bacterial diversity and favors the growth of Actinobacteria and Proteobacteria in agroecosystems across the globe. *Global Change Biology.* <https://doi.org/10.1111/gcb.14343>
5. Doran, J.W., Soil health and global sustainability: Translating science into practice., *Agricul., Ecosystems Enviro.*, **2002**, 88, 119–127.[https://doi.org/10.1016/S0167-8809\(01\)00246-8](https://doi.org/10.1016/S0167-8809(01)00246-8)
6. Guo, L. J.; Lin, S.; Liu, T. Q.; Cao, C. G., & Li, C. F., Effects of conservation tillage on topsoil microbial metabolic characteristics and organic carbon within aggregates under a rice (*Oryza sativa L.*)–wheat (*Triticum aestivum L.*) cropping system in central China., *PLoS ONE.*, **2016**, 11, e0146145. <https://doi.org/10.1371/journal.pone.0146145>
7. Gupta, A., Linking soil microbial diversity to modern agriculture practices: A Review. *International Journal of Environmental Research and Public Health.*, **2022**, 19, 3141. <https://doi.org/10.3390/ijerph19063141>

8. Holland, J.M., The environmental consequences of adopting conservation tillage in Europe: Reviewing the evidence., *Agriculture, Ecosystems & Environment.*, **2004**, *103*, 1–25. <https://doi.org/10.1016/j.agee.2003.12.018>
9. Jansa, J.; Mozafar, A.; Anken, T.; Ruh, R.; Sanders, I. R., & Frossard, E. Diversity and structure of AMF communities as affected by tillage in a temperate soil., *Mycorrhiza.*, **2002**, *12*, 225–234. <https://doi.org/10.1007/s00572-002-0163-z>
10. Johnsen, K.; Jacobsen, C. S.; Torsvik, V.; & Sørensen, J., Pesticide effects on bacterial diversity in agricultural soils-A Review. *Biology and Fertility of Soils.*, **2001**, *33*, 443–453. <https://doi.org/10.1007/s003740100334>
11. Kabir, Z., Tillage or no-tillage: Impact on mycorrhizae., *Canadian Journal of Plant Science.*, **2005**, *85*, 23–29. <https://doi.org/10.4141/P03-160>
12. Kabir, Z., & Koide, R. T., Mixed cover crops, mycorrhizal fungi, soil properties and sweet corn yield., *Plant and Soil.*, **2002**, *238*, 205–215. <https://doi.org/10.1023/A:1014281812326>
13. Kelvin Kiprotich.; Muema, E.; Wekesa, C.; Ndombi, T.; Muoma, J.; Omayio, D.; Ochieno, D.; Motsi, H.; Mncedi, S., & Tarus, J., *Discover Soil.*, **2025**, *2*(10).
14. Lienhard, P.; Terrat, S.; Prévost-Bouré, N. C.; Nowak, V.; Régnier, T.; Sayphoummie, S., Panyasiri, K., Tivet, F., Mathieu, O., Levêque, J., Pyrosequencing evidences the impact of cropping on soil bacterial and fungal diversity in Laos tropical grassland., *Agronomy for Sustainable Development.*, **2014**, *34*, 525–533. <https://doi.org/10.1007/s13593-013-0182-3>.
15. Luo, Z.; Wang, E., & Sun, O. J. Can no-tillage stimulate carbon sequestration in agricultural soils? A meta-analysis of paired experiments. *Agriculture., Ecosystems & Environment.*, **2010**, *139*, 224–231. <https://doi.org/10.1016/j.agee.2010.08.006>
16. Mangalassery, S.; Mooney, S. J.; Sparkes, D. L.; Fraser, W. T., & Sjøgersten, S., Impacts of zero tillage on soil enzyme activities, microbial characteristics and organic matter functional chemistry in temperate soils., *European Journal of Soil Biology.*, **2015**, *68*, 9–17. <https://doi.org/10.1016/j.ejsobi.2015.02.005>
17. Manzoni, S.; Taylor, P.; Richter, A.; Porporato, A., & Ågren, G. I., Environmental and stoichiometric controls on microbial carbon-use efficiency in soils., *New Phytologist.*, **2012**, *196*, 79–91. <https://doi.org/10.1111/j.1469-8137.2012.04225.x>
18. Morugán-Coronado, A., The impact of crop diversification, tillage and fertilization type on soil microbial abundance., *Agriculture, Ecosystems & Environment.*, **2022**, *329*, 107867. <https://doi.org/10.1016/j.agee.2022.107867>
19. Nkongolo, K. K., & Narendrula-Kotha, R. Advances in monitoring soil microbial community dynamic and function., *Journal of Applied Genetics.*, **2020**, *61*, 249–263. <https://doi.org/10.1007/s13353-020-00548-6>
20. Tamburini, G.; Bommarco, R.; Wanger, T. C.; Kremen, C.; van der Heijden.; M. G. A.; Liebman, M., & Hallin, S., Agricultural diversification promotes multiple ecosystem services without compromising yield., *Science Advances.*, **2020**, *6*, eaaz7433. <https://doi.org/10.1126/sciadv.aaz7433>
21. van Groenigen, K.; Bloem, J.; Bååth, E.; Boeckx, P.; Rousk, J.; Bodé, S.; Forristal, D.; & Jones, M. B., Abundance, production and stabilization of microbial biomass under conventional and reduced tillage., *Soil Biology and Biochemistry.*, **2010**, *42*, 48–55. <https://doi.org/10.1016/j.soilbio.2009.09.023>
22. Van Kessel, C.; Venterea, R.; Six, J., Adviento Borbe.; M. A., Linquist, B., & van Groenigen, K. J., Climate, duration, and N placement determine N O emissions in reduced tillage systems: A Meta Analysis. *Global Change Biology.*, **2013**, *19*, 33–44. <https://doi.org/10.1111/j.1365-2486.2012.02779.x>
23. Wang, Y.; Li, C.; Tu, C.; Hoyt, G. D.; De Forest, J. L., & Hu, S., Long-term no-tillage and organic input management enhanced the diversity and stability of soil microbial community., *Science of the Total Environment.*, **2017**, *609*, 341–347. <https://doi.org/10.1016/j.scitotenv.2017.07.054>
24. Zhang, B.; He, H.; Ding, X.; Zhang, X.; Zhang, X.; Yang, X., & Filley, T. R. Soil microbial community dynamics over a maize (*Zea mays L.*) growing season under conventional- and no-tillage practices in a rainfed agroecosystem., *Soil & Tillage Research.*, **2012**, *124*, 153–160. <https://doi.org/10.1016/j.still.2012.06.001>