

Review article

Herbicide Effects on Bacterial Communities and Soil Functions in Rice Agroecosystems: A Critical Narrative Review

Famubo Joseph ^{a,b}, Sule Manga ^a, Adamu Aliero ^a, Adamu Muhammad ^c,
Musa Isah ^{a,*} & Peter Olugbemi ^c

^a Department of Microbiology, Faculty of Life Sciences, Kebbi State University of Science and Technology, Aliero, Kebbi State, Nigeria

^b Health System Consulting Limited, Birnin Kebbi, Kebbi State, Nigeria

^c Department of Crop Science, Faculty of Agriculture, Kebbi State University of Science and Technology, Aliero.

Abstract

Rice fields are complex agroecosystems in which soil bacterial communities play essential roles in nutrient cycling, organic matter decomposition, soil fertility, and plant health. Herbicides are widely used in rice production to control weeds and enhance crop productivity; however, their effects extend beyond target plants and influence non-target soil microorganisms. This narrative review synthesises current knowledge on how herbicides influence bacterial populations in rice ecosystems. Evidence indicates that herbicide application often causes short-term reductions in bacterial abundance, microbial biomass, and soil enzymatic activities, particularly during the first few weeks after application. Nevertheless, many bacterial communities exhibit partial or complete recovery as herbicide residues degrade over time. Herbicides can alter bacterial community composition by suppressing sensitive functional groups, including nitrifying and nitrogen-fixing bacteria, while promoting herbicide-degrading taxa such as certain *Bacillus* and *Actinobacteria* species. These shifts may affect critical ecosystem processes, especially nitrogen cycling, nutrient availability, and soil multifunctionality. Long-term or excessive herbicide exposure can reduce microbial diversity, simplify ecological networks, and weaken soil resilience, potentially compromising sustainable rice production. The review also highlights how rice establishment systems, herbicide dosage, and environmental conditions influence bacterial responses. Emerging alternatives, including bioorganic fertilizers, microbial inoculants, integrated weed management, and microbiome-based remediation approaches, show promise for minimizing adverse effects on soil bacteria while maintaining effective weed control.

Keywords: Herbicides, Rice Fields, Soil Bacteria, Microbial Diversity, Sustainable Weed Management

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* Corresponding author:

Dr. Musa Isah is a lecturer in the Department of Microbiology at Kebbi State University of Science and Technology, Aliero, Kebbi State, Nigeria. His research focuses on antimicrobial resistance, with particular interest in the mechanisms, epidemiology, and control strategies of resistant pathogens.
Email: isah.mg97@ksusta.edu.ng

INTRODUCTION

Rice fields are dynamic agroecosystems where soil bacteria play indispensable roles in nutrient cycling, organic matter decomposition, and plant health. The intensification of rice cultivation to meet global food demands has led to widespread, often indiscriminate, herbicide use for weed management. While these chemicals effectively control unwanted vegetation and support crop yields, their impact extends beyond target weeds, influencing the structure and function of non-target soil microbial communities, particularly bacteria (Michael et al., 2024; Sibalekile et al., 2025).

Herbicides such as glyphosate, 2,4-dichlorophenoxyacetic acid (2,4-D), butachlor, and others are commonly applied in rice paddies across Africa, Asia and other rice-producing regions (Magnoli et al., 2020; Yadav et al., 2025). Glyphosate, for instance, is the most widely used non-selective herbicide globally due to its efficacy and compatibility with genetically modified (GM) crops. However, its extensive application has raised concerns about environmental persistence and toxicity effects on soil microorganisms (van Bruggen et al., 2018). Glyphosate residues can persist in soils through strong sorption mechanisms but may also be released back into the environment via desorption processes. These residues and their metabolites have been shown to alter microbial diversity and functionality within the rhizosphere, the narrow region of soil influenced by root exudate, potentially affecting plant growth-promoting bacteria as well as pathogenic species (Martinez et al., 2018; Jeyaseelan et al., 2023).

The influence of herbicides on bacterial populations is complex and context-dependent. Some studies report that certain herbicides exhibit antimicrobial properties, inhibiting the growth of beneficial bacteria such as *Bradyrhizobium* and *Azotobacter*, key players in nitrogen fixation, while others suggest that herbicide application can increase microbial richness by promoting the proliferation of potential nitrogen-fixing taxa (Meena et al., 2020). For example, glyphosate exposure has been associated with both suppression and enrichment of specific bacterial groups depending on factors such as soil type, application rate, crop variety, and environmental conditions (Martinez et al., 2018). Similarly, 2,4-D has been shown to reduce populations of *Rhizobium* genus bacteria and suppress enzymatic activities essential for nutrient cycling (Baćmaga et al., 2024).

Beyond direct toxicity, herbicides can disrupt symbiotic relationships between plants and microbes. They may interfere with root nodulation processes in legumes or alter phytochemical signaling required for effective biological nitrogen fixation (Meena et al., 2020). Such disruptions can reduce nutrient availability for crops or increase susceptibility to diseases due to shifts in rhizosphere microbial ecology (Martinez et al., 2018). Moreover, high-dose applications may select for resistant microbial strains and promote horizontal gene transfer events that facilitate the spread of antibiotic resistance genes within soil bacterial communities, a phenomenon with implications for both agricultural sustainability and public health (Bearson et al., 2024; Shafiq et al., 2024).

The broader ecological consequences of herbicide use include changes in soil enzymatic activities (such as dehydrogenase activity), altered rates of organic matter decomposition, disruption of nutrient cycles (notably nitrogen), and potential impacts on crop productivity over time (Michael et al., 2024). While some studies indicate these effects may be transient under certain conditions, especially when recommended field rates are followed, others highlight persistent alterations in community composition that could compromise long-term soil fertility (Daisley et al., 2022; Karpouzas et al., 2022).

Due to these complexities, there is a growing emphasis on adopting integrated weed management strategies that minimize reliance on chemical herbicides. Approaches such as crop rotation, cover cropping, conservation tillage, use of biofertilizers and plant growth-promoting rhizobacteria (PGPR), and bioremediation using microbial consortia are being explored to mitigate negative impacts while sustaining rice yields (Chaudhary et al., 2023; De Andrade et al., 2023). Advances in molecular techniques, including next-generation sequencing (NGS) platforms, are enhancing the ability to monitor changes in microbial diversity at finer taxonomic levels and inform more sustainable agricultural practices (Vischetti et al., 2020). While herbicides remain vital tools for modern rice production systems, their influence on bacterial populations is multifaceted, ranging from inhibition of key functional groups to selective enrichment depending on numerous biotic and abiotic factors. Understanding these interactions is crucial for developing management practices that safeguard both crop productivity and the ecological integrity of rice field soils.

Literature Search Strategy

A literature search was conducted using Google Scholar, Scopus, ScienceDirect, and Google to identify studies on herbicide effects on bacterial communities and soil functions in rice agroecosystems. The search covered publications from 2018 to 2026 and used terms including “herbicide,” “herbicide exposure,” “rice,” “paddy soil,” “soil bacteria,” “bacterial community,” “microbial diversity,” “soil functions,” “microbiome,” and “microbial resilience.” Studies were included when they examined herbicide effects on bacterial abundance, community composition, diversity, microbial biomass, functional genes, soil enzymatic activities, and nutrient cycling. Studies involving pesticide mixtures were retained but distinguished from herbicide-specific evidence, while non-rice studies were considered only as comparative evidence. Studies unrelated to herbicide exposure, microbial and soil responses, or the objectives of the review were excluded. The review followed a critical narrative approach and emphasized herbicide type, application rate, environmental and soil conditions, rice establishment systems, exposure history, bacterial responses, functional effects, and ecological resilience.

Patterns of Bacterial Abundance and Diversity

Many field studies report an initial decline in total bacterial numbers and microbial biomass after herbicide application, followed by partial or full recovery over weeks as residues dissipate (Bhardwaj et al., 2023; Bhardwaj et al., 2024a). In direct-seeded and zero-tillage rice, pendimethalin, pretilachlor, bispyribac-sodium and other common herbicides reduced microbial biomass C and N and key enzyme activities, with negative correlations between herbicide residues and microbial parameters. Broader pesticide uses in irrigated rice fields similarly decreased bacterial abundance and diversity, with lower Shannon and Simpson indices in exposed soils (Onwona-Kwakye et al., 2020). Yet at recommended doses, several studies in direct-seeded and wet-seeded rice found that overall bacterial populations and actinomycetes could recover or even increase by mid-to late season, suggesting largely transient effects under standard use rates (Dubey et al., 2023; Mathew et al., 2023).

Herbicide Effects on Bacterial Community Structure

High-throughput 16S rRNA sequencing in flooded rice soils shows that herbicides alter the relative abundance of specific bacterial taxa more than the dominance of major phyla. Proteobacteria, Acidobacteria, Chloroflexi, Actinobacteria and Firmicutes remain core groups, but sensitive oligotrophic and nutrient-cycling taxa may decline, while copiotrophic genera (e.g. *Bacillus*, some Actinobacteria) increase (Bhardwaj et al., 2024b; Wang et al., 2025). Herbicide use can reduce ammonia-oxidizing and nitrifying groups or suppress nitrification potential, indicating functional shifts in nitrogen cycling (Vishwakarma et al., 2020). In lateritic paddy soils, combined glyphosate and diquat exposure increased Actinobacteria but inhibited Proteobacteria, yet did not strongly reduce overall bacterial richness at recommended to 10-fold doses (He et al., 2023). In the rice rhizosphere, the selective herbicide diclofop-methyl increased microbial richness and diversity, coupled with enhanced root exudation of amino acids, sugars and fatty acids, and stimulated denitrification gene expression and activity, illustrating an indirect plant-mediated pathway by which herbicides reshape rhizosphere microbiota and N loss processes (Qian et al., 2018).

Functional Consequences for Soil Processes

Across irrigated rice systems, pesticide and herbicide exposure is consistently associated with disruption of microbial functions central to nutrient cycling. Studies report reduced activities of dehydrogenase, phosphatase, urease and other enzymes, especially shortly after application, with effects generally weakening as herbicides degrade (Vischetti et al., 2020; Li et al., 2021a). Suppression of nitrification and changes in denitrification and dissimilatory nitrate reduction genes suggest altered nitrogen fluxes and potential accumulation of nitrate/nitrite in heavily treated paddies (Pan et al., 2025). Long-term pesticide use under flooded conditions can shift communities toward deterministic assembly, reduce network connectivity, decrease genes linked to nitrogen cycling and cellulolysis, and increase

human-disease-related functions, pointing to weakened soil multifunctionality and heightened disease risk (Wang et al., 2025).

At the field scale, some herbicide regimes in direct-seeded rice increased actinomycete populations and coincided with high grain yield, possibly because certain bacteria can use herbicide metabolites as carbon sources or degrade residues, partially offsetting early toxicity (Dubey et al., 2023; Dubey et al., 2018). However, pesticide-exposed fields also lost many beneficial genera involved in nutrient mobilization and plant growth promotion, raising concerns about long-term fertility (Deka et al., 2025).

Mitigation, Alternatives, and Sustainable Weed Management

Several lines of work explore ways to control weeds while minimizing harm to bacterial communities. Bioorganic fertilizers (BIO) containing natural herbicidal organic acids achieved weed control comparable to synthetic herbicides without significantly altering overall bacterial diversity, dominant phyla across multiple rice regions and in long-term trials (Pattanayak et al., 2022). BIO slightly shifted specific genera and soil chemical properties (pH, K, P). Overall, it was characterised as “not harmful” to soil bacteria and enzymes, supporting its role as a sustainable weed-biocontrol strategy (Li et al., 2021b).

Complementary strategies include integrating organic amendments and nature-based solutions. In rice systems receiving constant herbicide but different nitrogen sources, vermicompost plus inorganic N enhanced beneficial bacterial phyla and increased yield, helping buffer against chemical build-up and fostering favorable niches for beneficial bacteria (Deka et al., 2025). Weed management based on organic methods and reduced herbicide reliance in unpuddled transplanted rice improved microbial populations and enzyme activities compared with purely chemical control (Yasir et al., 2025). Biological control agents (*Pseudomonas* and *Bacillus* strains) tolerant to common rice pesticides have also shown potential to maintain or increase microbial biomass while fitting within integrated pest management (Moccellin et al., 2023).

Broader Ecological and Multi-Pesticide Context

Work at continental and conceptual scales emphasizes that rice paddies are exposed to complex pesticide cocktails, including herbicides, fungicides and insecticides, which jointly shape bacterial communities and functions (Ruuskanen et al., 2022). Multi-omics analyses show that high-risk sites with many co-occurring residues have reduced microbial network robustness but enriched xenobiotic degradation potential, often in bacteria that also carry nitrogen-cycling genes, indicating a trade-off between detoxification and nutrient-cycling efficiency. Reviews highlight that herbicide-altered microbiomes can cascade to plant performance, soil processes, and higher trophic levels, suggesting ecosystem-level and even evolutionary consequences of chronic herbicide exposure (Pan et al., 2025).

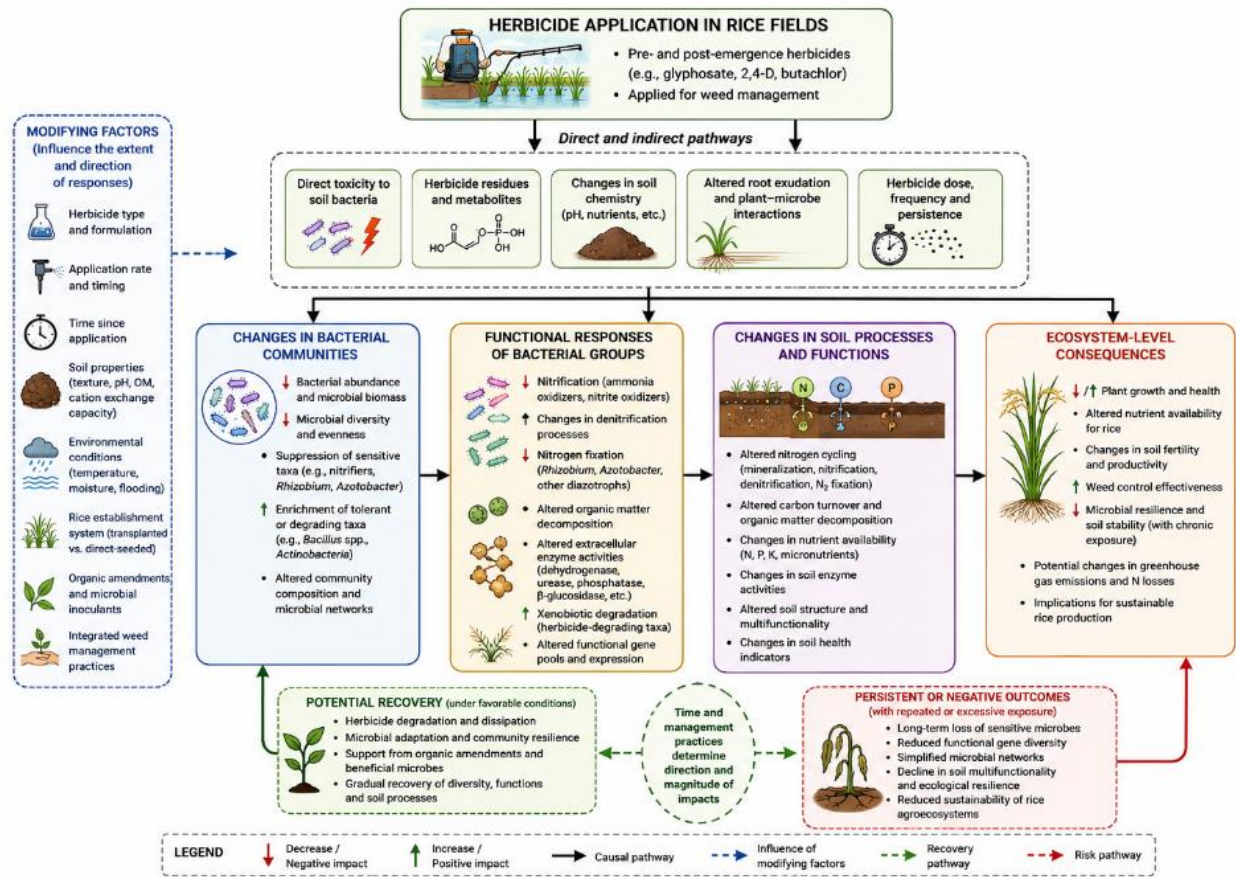


Figure. Conceptual framework showing the pathways linking herbicide application, changes in bacterial communities, functional responses, soil processes, and ecosystem-level consequences in rice agroecosystems.

Figure 1. Illustrates the proposed pathways linking herbicide application, changes in bacterial communities, functional responses, soil processes, and ecosystem-level consequences.

Bacterial Community Responses in Different Rice Establishment Systems

Rice establishment method modifies how herbicides influence bacterial populations. In direct-seeded and zero-tillage systems, where herbicide reliance is high, consistent negative correlations between herbicide residues and microbial biomass C, N, and diversity have been documented, even when total populations later recover (Bhardwaj et al., 2023). In transplanted systems, chemical weed control causes an initial decline in bacteria and actinomycetes. Still, microbial counts and enzyme activities often rebound as microbes degrade herbicides and use breakdown products as carbon sources (Mathew et al., 2023). Flooded, pesticide-free paddies maintain higher bacterial diversity in both generalist and specialist subcommunities than long-term pesticide-treated fields, and pesticide-treated soils show reduced co-occurrence network complexity and specialised taxa that are particularly vulnerable to environmental filtering (Wang et al., 2025).

Comparative evidence from rice agroecosystems. The available literature indicates that bacterial responses to herbicide exposure are highly context-dependent, with effects ranging from short-term

reductions in microbial abundance and enzyme activity to recovery or enrichment of particular bacterial groups. Herbicide-specific studies conducted in direct-seeded, wet-seeded, transplanted, zero-tillage and rhizosphere systems provide the strongest basis for evaluating these responses. However, studies involving multiple pesticides or other agrochemicals are considered separately because their findings cannot be attributed exclusively to herbicides. Table 1 summarizes herbicide-specific and herbicide-mixture evidence from rice agroecosystems, whereas Table 2 presents mixed-pesticide and comparative evidence.

Table 1. Comparative summary of herbicide-specific evidence on bacterial communities in rice agroecosystems

Study	Rice establishment/system	Herbicide(s) reported	Application rate	Sampling period/duration	Bacterial response	Functional/soil response	Major conclusion
Bhardwaj et al. (2023)	Zero-tillage / direct-seeded tropical rice	Pendimethalin, pretilachlor, bispyribac-sodium and other herbicides	NR	Responses following application	Herbicide residues were negatively associated with microbial biomass C, N and bacterial diversity; total populations could subsequently recover.	Reduced microbial biomass and enzyme activities were reported following herbicide exposure.	Herbicide effects were initially suppressive but could be transient, with responses influenced by herbicide residues and rice establishment system.
Bhardwaj et al. (2024a)	Flooded rice field	Herbicide exposure; specific compound not stated in the relevant manuscript passage	NR	NR	Herbicides altered relative abundance of bacterial taxa while major phyla remained comparatively stable. Proteobacteria, Acidobacteria, Chloroflexi, Actinobacteria and Firmicutes remained dominant.	Changes were associated with alterations in nitrifying groups and nitrogen-cycling processes.	Herbicides primarily modified community structure and relative abundance of particular taxa, rather than eliminating dominant bacterial phyla.
Bhardwaj et al. (2024b)	Irrigated tropical rice/rhizosphere	Herbicide exposure; specific compound not stated in the relevant passage	NR	NR	Herbicide-treated rhizospheres showed slightly lower microbial biomass and altered community composition; dominant bacterial genera remained present but changed in relative abundance.	Potential effects on nitrification, methanogenesis and other soil processes.	Herbicide effects extend to the rhizosphere and can alter bacterial community structure without completely replacing dominant taxa.
Dubey et al. (2018)	Direct-seeded rice	Six herbicides; individual compounds are not specified in the manuscript text.	NR	NR	Soil microbial populations were evaluated following herbicide application. The manuscript uses this study as evidence that some herbicide regimes can increase actinomycete populations.	Microbial responses occurred alongside rice yield responses.	Herbicide effects were not uniformly negative; some bacterial groups, particularly actinomycetes, may tolerate or benefit from particular herbicide regimes.

Study	Rice establishment/system	Herbicide(s) reported	Application rate	Sampling period/duration	Bacterial response	Functional/soil response	Major conclusion
Dubey et al. (2023)	Direct-seeded rice	Herbicides; specific compounds not detailed in manuscript discussion	NR	Mid- to late-season response reported; exact sampling dates.	Bacterial populations and actinomycetes could recover or increase by mid- to late season.	Some herbicide regimes were associated with high grain yield; possible use of herbicide metabolites as carbon sources was proposed.	At recommended use conditions, some bacterial responses may be transient, and tolerant/degrading bacteria may contribute to recovery.
Mathew et al. (2023)	Direct wet-seeded rice	Pre- and post-emergence herbicide combinations	NR	55 days after sowing reported for recovery	Bacterial counts decreased shortly after application but returned to or near control levels by 55 days after sowing.	Microbial recovery occurred as herbicide toxicity declined; enzyme activities also increased later in the season in comparable systems.	Herbicide effects on overall bacterial abundance can be temporary, with recovery following residue degradation/sorption.
Pattanayak et al. (2022)	Transplanted, unpuddled and other rice establishment systems	Chemical herbicide-based weed management	NR	Initial decline up to approximately 2 weeks, followed by later-season recovery	Bacterial and actinomycete populations initially declined but increased later in the season.	Microbial enzyme activities also recovered/increased; organic or reduced-herbicide management supported higher microbial activity.	Rice establishment and weed-management strategy modify microbial responses; effects may be reduced under less intensive chemical management.
Qian et al. (2018)	Rice rhizosphere	Diclofop-methyl	NR	NR	Diclofop-methyl increased microbial richness and diversity and stimulated denitrifying bacteria.	Increased root exudation of amino acids, sugars and fatty acids; increased denitrification gene expression and denitrification rates.	Demonstrates that herbicides may indirectly restructure bacterial communities through plant-mediated changes in root exudation, rather than through direct toxicity alone.
He et al. (2023)	Lateritic paddy soil	Glyphosate + diquat	Up to 10–100× recommended dose reported in manuscript	NR	Actinobacteria increased while Proteobacteria decreased; bacterial richness was not strongly reduced even at high exposure levels.	Differential sensitivity was observed between bacterial and fungal communities.	Bacterial responses can be taxon-specific and dose-dependent; higher herbicide concentrations do not necessarily produce proportional reductions in overall bacterial richness.

NR = not reported

Table 2. Comparative summary of mixed-pesticide and comparative evidence

Study	Agroecosystem	Chemical exposure	Evidence category	Bacterial response	Functional/network response
Onwona-Kwakye et al. (2020)	Irrigated rice fields	Multiple pesticides; not herbicide-specific	Multi-pesticide rice evidence	Reduced bacterial abundance and diversity; lower Shannon and Simpson diversity indices.	Changes in community structure were observed.
Wang et al. (2025)	Flooded paddy fields	Long-term pesticide exposure versus non-pesticide systems	Multi-pesticide rice evidence	Reduced diversity in generalist and specialist bacterial subcommunities; specialist taxa were particularly vulnerable.	Reduced network complexity, lower network robustness and changes in functional genes related to nitrogen cycling and cellulolysis.
Pan et al. (2025)	Paddy soils across a broad geographic scale	Pesticide cocktails containing herbicides, fungicides and insecticides	Multi-pesticide rice evidence	Complex pesticide mixtures were associated with altered bacterial community structure.	Reduced microbial network robustness; enrichment of xenobiotic degradation potential; changes in nitrogen-cycling functions.
Deka et al. (2025)	Rice ecosystem	Herbicide/pesticide exposure with different nitrogen/organic amendments	Mixed-management evidence	Some beneficial bacterial groups associated with nutrient mobilization, mineralization and plant growth promotion declined under pesticide exposure. Organic amendments supported more beneficial bacterial groups.	Organic N sources and vermicompost appeared to buffer microbial stress and improve yield.
Meena et al. (2020)	Agricultural/rice systems and broader agroecosystems	Agrochemicals; includes pesticides beyond herbicides	Broader agrochemical evidence	Evidence of effects on soil microbiota.	Reduced nitrification potential and effects on nitrifiers/N-fixing bacteria.
Feng et al. (2025)	Proso millet, <i>Panicum miliaceum</i>	Herbicide + safener	Non-rice comparative evidence	Herbicide–safener co-application altered rhizosphere microbiota and community assembly.	Co-application shifted assembly toward more stochastic processes and strengthened positive interactions.
Michael et al. (2024)	Review / broader agricultural systems; includes paddy-related evidence	Herbicides	Comparative/review evidence	Synthesizes effects of herbicides on soil microbial processes.	Discusses impacts on soil functions and nutrient cycling.
Daisley et al. (2022)	Agricultural soils	Pesticides broadly	Broader pesticide evidence	Reports deterioration of agricultural microbiomes and loss of functionally beneficial microorganisms.	Implications for nutrient mobilization and plant growth promotion.

Bacterial Taxa

Across rice paddies, some bacterial groups emerge as relatively tolerant or even enriched under herbicide regimes, while others decline. Copiotrophic and potentially pesticide-degrading genera such as some *Bacillus*, *Actinobacteria* and *Clostridium sensu stricto* often increase and may contribute to residue breakdown and carbon cycling (Daisley et al., 2022; Bhardwaj et al., 2024b). In contrast, oligotrophic groups and key nutrient cyclers, including certain nitrifiers and cyanobacteria, can be suppressed, with documented reductions in nitrification potential and shifts away from ammonia-oxidizing communities (Onwona-Kwakye et al., 2020). In pesticide-exposed irrigated fields, multiple genera involved in nutrient mobilization, mineralization and plant growth promotion declined, suggesting loss of important ecosystem services (Deka et al., 2025).

Temporal Dynamics and Dose Effects

Time since application and dose strongly modulate bacterial responses. Many studies using recommended field rates report that inhibitory effects on bacterial counts and enzyme activities are strongest in the first 7–15 days, then diminish as microbes adapt and degrade residues, sometimes restoring initial populations by mid-season or harvest (Pattanayak et al., 2022; He et al., 2023). Chronic multi-pesticide exposure, however, is associated with longer-lasting diversity reductions, functional suppression of nitrogen cycling genes, and structurally simplified bacterial networks (Dubey et al., 2023). Experiments with glyphosate and diquat up to 100-fold recommended doses in lateritic paddy soil found that even very high concentrations did not further depress bacterial richness compared with single-herbicide exposures. However, fungal diversity decreased at high levels, highlighting differential sensitivity among microbial groups (Dubey et al., 2018).

Interaction with Plant Roots and Rhizosphere Processes

The rhizosphere is a key interface where herbicides, plants and bacteria interact. Herbicides can indirectly reshape rhizosphere bacteria by altering root exudation patterns; for example, diclofop-methyl triggered increased exudation of labile carbon compounds, stimulated denitrifying bacteria, and enhanced denitrification rates (Qian et al., 2018). Field studies consistently find that rhizospheric bacterial abundance peaks around flowering, and that herbicide-treated rhizospheres exhibit slightly lower microbial biomass and altered community composition relative to untreated controls (Bhardwaj et al., 2023). Dominant archaea (e.g. *Nitrososphaera*, *Nitrosocosmicus*, *Methanosarcina*) and bacterial genera (e.g. *Bacillus*, *Nitrospira*, *Azospira*, *Neobacillus*) remain important players in both treated and untreated soils, but relative abundances shift under herbicide pressure, with potential consequences for nitrification, methanogenesis and other key processes (Bhardwaj et al., 2024a).

Microbiome-Mediated Risks and Opportunities

Conceptual work positions herbicides as microbiome-modulating agents whose impacts extend beyond target weeds. By altering bacterial diversity, composition and functional gene pools in rice soils and rhizospheres, herbicides can influence nutrient cycling, greenhouse gas emissions, plant health and resilience to biotic and abiotic stress (Ruuskanen et al., 2022). While some bacterial taxa can adapt and even exploit herbicide-derived carbon, chronic exposure risks eroding functional redundancy, increasing disease-related functions, and weakening the ecological buffering capacity of paddy microbiomes (Wang et al., 2025). At the same time, these microbial responses open opportunities: selecting or engineering bacterial consortia that degrade herbicides, harnessing bioorganic amendments that suppress weeds without harming bacteria, and designing weed-management strategies that explicitly protect microbial diversity and function (Moccellin et al., 2023).

Bacterial Responses to Herbicides in Rice Fields

Short-Term Impacts and Recovery

In the short term after herbicide application, bacterial populations in rice soils commonly exhibit stress responses. Field trials with pendimethalin, pretilachlor, bispyribac-sodium, and related compounds in direct-seeded and wet-seeded rice show initial reductions in total bacteria, fungi, and actinomycetes, along with decreases in microbial biomass carbon and nitrogen and lower activities of key enzymes such as dehydrogenase, phosphatase, and urease (Bhardwaj et al., 2023). Pesticide-exposed irrigated rice soils also show reduced bacterial diversity and altered composition compared with unexposed areas (Onwona-Kwakye et al., 2020). These early responses reflect both direct toxicity and indirect changes in soil chemistry and root exudation.

Over weeks, however, many studies report microbial recovery as herbicides degrade or sorb. For example, in direct wet-seeded rice, pre- and post-emergence herbicide combinations decreased bacterial counts shortly after application, but populations returned to or near control levels by 55 days after sowing, indicating reduction in toxicity over time (Mathew et al., 2023). Similar temporal patterns appear in transplanted and unpuddled systems, where declines up to about two weeks are followed by increasing bacterial numbers and enzyme activities later in the season (Pattanayak et al., 2022). These dynamics suggest that, at recommended doses, herbicides in many rice systems have predominantly transient, rather than permanently suppressive, effects on overall bacterial abundance.

Community Composition and Sensitive Functions

Beyond total abundance, herbicides can restructure bacterial communities and selectively impair sensitive functional groups. In paddy fields under long-term pesticide use, bacterial diversity in both generalist and specialist subcommunities is reduced compared with pesticide-free fields, especially

among specialists with narrow niches and high resource specificity (Wang et al., 2025). Copiotrophic bacteria, which thrive in resource-rich environments, increase under pesticide treatments, while oligotrophic taxa that specialize in low-nutrient conditions decline (Baćmaga et al., 2024).

Functional predictions and gene assays indicate that nitrogen cycling processes are particularly vulnerable. Multi-pesticide surveys across Chinese paddies show correlations between certain fungicides and suppression of nitrification, denitrification and dissimilatory nitrate reduction genes, implying altered nitrogen fluxes and possible accumulation of reactive nitrogen forms (Pan et al., 2025). Experimental studies in paddy microcosms and field soils link specific herbicides, such as bispyribac-sodium and mixtures including bensulfuron-methyl, to decreased nitrification potential and reduced abundances of nitrifiers and N-fixing bacteria (Meena et al., 2020; Li et al., 2021b). In the rice rhizosphere, diclofop-methyl exposure increased denitrification gene transcription and denitrification rates, illustrating that herbicides can amplify N losses from flooded soils via microbiome–plant–process interactions (Qian et al., 2018).

RICE ESTABLISHMENT SYSTEMS AND MANAGEMENT CONTEXT

The influence of herbicides on bacterial populations is shaped by rice establishment methods and weed-management strategies. Direct-seeded and zero-tillage rice rely more heavily on herbicides, and studies in these systems document stronger negative correlations between herbicide residues and microbial biomass, as well as more pronounced shifts in community composition (Bhardwaj et al., 2023; Bhardwaj et al., 2024b). In transplanted rice with organic weed management (e.g., mechanical weeding, green manuring), microbial populations and enzyme activities are higher and less perturbed, underscoring the benefits of reduced synthetic herbicide use (Pattanayak et al., 2022).

Management experiments combining herbicides with different nitrogen and organic sources show that the surrounding soil environment modulates bacterial responses. In rice–rice sequences with constant herbicide application, plots receiving vermicompost plus inorganic N supported higher beneficial bacterial phyla and produced greater yields than plots under purely mineral fertilization, suggesting that organic inputs can offset some microbiome stress from herbicides and fertilizers (Deka et al., 2025). Integrated practices that combine lower herbicide doses with hand weeding also achieved good weed control and high yields while maintaining or enhancing actinomycete populations, indicating that careful dosing and mixed strategies can temper impacts on soil bacteria (Dubey et al., 2023).

Alternatives and Microbiome-Friendly Weed Control

Due to the central role of bacteria in rice soil health, alternative weed management approaches aim to minimize negative impacts on microbial communities. Bioorganic fertilizers (BIO), formulated from organic materials that release natural herbicidal compounds, have emerged as promising tools.

Multi-site and long-term field trials show that BIO effectively suppresses weeds and supports rice yields while causing only slight shifts in bacterial community structure and enzyme activities, with no major changes in dominant phyla or diversity indices at most application rates (Li et al., 2023). Correlations between specific bacterial genera, soil pH, and nutrient status suggest that BIO influences bacterial communities indirectly via changes in soil chemistry rather than broad toxicity (Li et al., 2021a).

Biocontrol agents, particularly *Pseudomonas* and *Bacillus* strains adapted to rice paddies, offer another avenue. These bacteria can be compatible with common herbicides and fungicides, retain activity in treated fields, and in some cases increase microbial biomass and metabolic quotient, making them suitable components of integrated pest management that support, rather than erode, rhizosphere bacterial function (Moccellin et al., 2023). At the same time, synthetic herbicide mixtures remain important in many systems, and recent work has begun to assemble tailored bacterial consortia capable of degrading herbicide cocktails while alleviating phytotoxicity, pointing toward microbiome-based remediation strategies (Michael et al., 2024).

Ecosystem-Level Perspective

Rice paddies exemplify how herbicide use shapes bacterial communities in ways that reverberate through ecosystem processes. Conceptual syntheses emphasize that microbiome-mediated pathway changes in nutrient cycling, plant interactions, and food-web dynamics are central to the ecosystem consequences of herbicides (Ruuskanen et al., 2022). Continental-scale surveys of pesticide residues in paddy soils demonstrate that most sites harbor complex mixtures, with many bacterial genomes carrying both xenobiotic degradation and nitrogen-cycling genes, highlighting the dual roles of bacteria as both buffers against chemical stress and maintainers of soil fertility. Where pesticide pressure is high, bacterial networks become less robust and functionally rich, especially among specialist taxa that underpin niche processes (Wang et al., 2025).

Effects of Herbicides on Bacterial Composition and Function in Rice Ecosystems

Shifts in Core Bacterial Groups. Across varied rice agroecosystems, herbicides tend to modify the relative abundance of core bacterial groups rather than replacing them entirely. Sequencing studies in transplanted, direct-seeded, and zero-tillage rice identify Proteobacteria, Acidobacteria, Actinobacteria, Chloroflexi, and Firmicutes as dominant phyla in both treated and untreated soils (Bearson et al., 2024). Within this stable phylum-level framework, however, herbicides change the representation of specific genera and lineages, with implications for nitrogen transformations, carbon turnover, and plant associations. For example, nitrifying and ammonia-oxidizing archaea such as *Candidatus Nitrososphaera* remain important under herbicide regimes, but their relative abundances can shift compared with methanogenic or other archaeal groups (Chaudhary et al., 2023). Bacterial nitrifiers like

Nitrospira and Azospira appear in both control and treated soils, though their functional contribution may be reduced where herbicide or pesticide cocktails suppress nitrification genes (Pan et al., 2025).

In pesticide-exposed irrigated fields, several genera associated with nutrient mobilization, plant growth promotion, and organic compound metabolism were depleted, suggesting that herbicides and other pesticides disproportionately affect functionally beneficial bacteria (Daisley et al., 2022). Conversely, genera such as Bacillus, Domibacillus, and some Clostridia were more abundant in treated soils, hinting at tolerance or even utilization of pesticide-derived substrates (Feng et al., 2025). Some Actinobacteria increased in lateritic paddy soils under glyphosate and diquat mixtures, again indicating that particular lineages can thrive under herbicide exposure, potentially contributing to residue breakdown or altered carbon cycling (He et al., 2023).

Functional Gene Pools and Biogeochemical Cycling

The impacts of herbicides on rice-field bacteria are especially evident in functional gene pools related to biogeochemical cycles. Multi-omics and functional prediction approaches show that pesticide-rich paddy soils often have reduced gene abundances for nitrification, denitrification, and other nitrogen transformations, while genes involved in xenobiotic degradation are enriched (Johnsen et al., 2001; Wang et al., 2025). Bacterial taxa like Chitinophagales and Gemmatimonadales frequently carry both sets of functions, creating a trade-off where the capacity to detoxify pesticides co-exists with, and may compete with, roles in nutrient cycling (Karpouzas et al., 2022).

Experimentally, herbicide mixtures in maize systems and specific herbicides in paddy microcosms have been shown to inhibit key nitrogen-cycle genes (AOA-amoA, AOB-amoA, nifH) and suppress nitrification potential, suggesting similar risks in rice fields where related compounds and application regimes are used (Michael et al., 2024). In rice rhizospheres, herbicide-induced changes in root exudation alter the availability of labile carbon and nitrogen to bacteria, thereby reshaping denitrifier communities and increasing N-loss pathways under certain exposures (Qian et al., 2018). Collectively, these findings indicate that even when total bacterial abundance recovers after herbicide application, the functional architecture of bacterial communities and thus soil nutrient dynamics may remain altered.

Microbial Networks, Resilience, and Specialization

Network and assembly analyses provide further insight into how herbicides affect bacterial community organization in rice soils. Under long-term pesticide regimes, bacterial networks in flooded paddies display lower node degree and closeness centrality, signaling a loss of complex interactions that underpin functional redundancy and resilience (Moccellin et al., 2023). Specialist bacterial subcommunities with narrow niches are especially sensitive, being shaped predominantly by

deterministic processes such as strong environmental filtering and limited dispersal, which reduce their diversity under chemical stress (Shafiq et al., 2024).

In contrast, management strategies that incorporate bioorganic fertilizers or reduce synthetic herbicide reliance tend to preserve or enhance network complexity, support a broader range of bacterial taxa, and maintain more balanced positive and negative interactions (Li et al., 2021a). In non-rice systems, co-application of safeners has been shown to steer microbial community assembly towards more stochastic processes and strengthen positive interactions, thereby improving resilience to herbicide disturbances; these mechanisms may be instructive for designing more microbiome-friendly weed management in rice (Feng et al., 2025).

HERBICIDE FATE IN RICE SYSTEMS

Herbicide persistence, leaching, and phytotoxicity are governed by the interplay of intrinsic herbicide chemistry, application rate, soil physicochemical properties, and environmental conditions. Herbicide molecular properties solubility, adsorption affinity, and degradation pathway fundamentally determine mobility; for instance, diuron is retained in superficial soil layers whereas hexazinone and sulfometuron-methyl leach into deeper profiles, and commercial formulation additives can enhance this leaching relative to analytical standards (De Cássia Araújo De Medeiros et al., 2024). Application rate directly modulates persistence: doubling the agronomic dose of aminopyralid and iodosulfuron-methyl-sodium increased their half-lives (DT50) by up to 2.6- and 1.9-fold, respectively, raising carryover risk for rotational crops (Marín-Benito et al., 2025), and cinmethylin half-lives ranged from 26 to 52 days depending on whether applied at 1-, 10-, or 100-fold the recommended rate (Yu et al., 2024). Soil texture and organic carbon exert strong control: sandy loam soils exhibited more rapid herbicide dissipation than silt loams, giving finer-textured soils greater flexibility in application timing but increasing carryover risk in coarse soils (Chudzik et al., 2026), while higher organic carbon and silt content were associated with improved forage performance and reduced residual phytotoxicity from imidazolinones (Rodríguez-De-Barbieri et al., 2025).

Soil pH emerged as a dominant mediator of pesticide effects on microbial communities, explaining over 60% of bacterial community variability more than soil type or pesticide identity (Némethová et al., 2026). Environmental conditions further modify these outcomes: low soil moisture (25% vs. 50% water-holding capacity) slowed aminopyralid degradation by up to 2.3-fold (Marín-Benito et al., 2025), and dry conditions generally reduced herbicide efficacy by limiting solubility and root uptake (deNux et al., 2024). Notably, one large-scale monitoring study found no significant correlation between soil properties and herbicide residue occurrence, attributing residue presence instead to active-ingredient chemistry, application timing, and local climate (Šunjka et al., 2024), underscoring that the relative weight of each factor may itself be context-dependent.

Rice establishment systems and previous herbicide exposure history introduce additional layers of variation that explain divergent findings across studies. Direct-seeded rice (DSR) systems, particularly under zero-tillage, demand different herbicide strategies than conventional puddled transplanting, and the ready-mix penoxsulam–pendimethalin combination produced distinct rhizobacterial community shifts depending on whether rice was established under zero-tillage or conventional tillage, with zero-tillage soils showing higher nutrient levels and enzymatic recovery after an initial microbial decline (Karubakee et al., 2026). Under rice–barnyardgrass co-cultivation, herbicides considered selective to rice triggered context-dependent growth suppression up to 17.8% lower root lengths and 24.8% lower shoot fresh weights that did not occur under herbicide exposure or co-cultivation alone, identifying an emergent interaction between establishment pattern and herbicide response (Li et al., 2026). Previous exposure history shapes both residue persistence and ecological outcomes: imidazolinone residues applied one season prior reduced forage shoot biomass by up to 60%, with effects detectable more than 17 months after the last application and varying by species and soil depth (Rodríguez-De-Barbieri et al., 2025), while long-term (8-year) pesticide application in flooded paddies shifted microbial assembly toward deterministic processes, reduced specialist subcommunity diversity, and increased pathogenic *Fusarium* abundance (Wang et al., 2025).

In California rice, oxyfluorfen—proposed for pre-flood use with tolerant rice strains was predicted to concentrate in sediment and persist, with risks to aquatic plants and benthic invertebrates exceeding levels of concern under all evaluated conditions, though California-specific soil conditions were associated with lower risk than standard scenarios (Bonnar & Tjeerdema, 2025). Together, these findings indicate that reported differences in herbicide performance and ecological impact reflect multifactorial interactions among herbicide chemistry, dose, soil texture and pH, moisture, establishment method, and cumulative exposure history, making site-specific management essential rather than reliance on generalized recommendations.

MICROBIOME-CENTRIC RISK ASSESSMENT AND MANAGEMENT

Microbiome-centric risk assessment integrates four complementary tiers of indicators to detect and manage environmental disturbance. At the taxonomic level, indicator taxa identified through sequencing and machine learning such as pollutant-degrading specialists, putative pathogens, and oligotrophic taxa differentiate impacted from reference conditions across soil, freshwater, and marine systems (Li et al., 2022; Zárate et al., 2025). Threshold analyses pinpoint ecological breakpoints along stress gradients where specific taxa respond, enabling early detection of community shifts before macroscopic damage occurs (Thorpe et al., 2026). Functional indicators extend beyond composition by profiling metabolic potential chemoheterotrophy, nitrate reduction, pollutant degradation pathways, and stress-tolerance traits that reveal the community's capacity to process or withstand contaminants (Thorpe

et al., 2026; Laroche et al., 2018). Functional profiles often diverge from taxonomic profiles, and their combined use estimates functional redundancy, a key dimension of ecosystem resilience (Laroche et al., 2018). At the network level, co-occurrence network topology modularity, connectance, average degree, robustness, and vulnerability detect subtle perturbations that conventional diversity indices miss, with network metrics varying 10–50% under minor stress while diversity remains stable (Codello et al., 2022). Environmental stress destabilizes networks by reducing modularity and shifting the ratio of negative to positive cohesion, with stress explaining 51–78% of variation in these stability properties (Hernandez et al., 2021).

Keystone taxa identified through network topology link community integrity to environmental sensitivity and represent promising sentinels of ecosystem condition (Layeghifard et al., 2016; Zárate et al., 2025). At the ecosystem level, microbiome-based indices such as microgAMBI correlate with contaminant pressure and integrate community-wide responses into operational monitoring tools (Bourhane et al., 2021). Stability-landscape frameworks infer basins of attraction and hysteresis along environmental gradients, enabling forecasting of abrupt transitions into dysfunctional states and informing management thresholds to prevent irreversible shifts (Toju et al., 2026). The microbiome serves as an early-warning indicator because community changes precede conventional health signals, allowing timely assessment of management interventions (Ribas et al., 2023). Integrating all four tiers strengthens the robustness and interoperability of microbial indicators, though realizing their full potential requires standardized methodologies, baseline reference databases, and validated diagnostic performance relative to established biotic indices (Thorpe et al., 2026; Debode et al., 2024).

RESEARCH GAPS AND FUTURE PERSPECTIVES

Although numerous studies have investigated the effects of herbicides on soil microbial communities, several important knowledge gaps remain. Most existing research focuses on short-term changes in bacterial abundance and enzyme activities following herbicide application, whereas information on long-term impacts on bacterial community structure, functional diversity, and ecosystem resilience remains limited. Furthermore, many studies have been conducted under controlled laboratory or greenhouse conditions, which may not accurately reflect the complexity of field environments in rice production systems.

Current evidence also indicates that bacterial responses vary considerably depending on herbicide type, soil properties, climatic conditions, and management practices; however, the mechanisms underlying these variations are not yet fully understood. In addition, most studies emphasize taxonomic diversity while providing limited information on functional genes involved in nutrient cycling, organic matter decomposition, herbicide degradation, and plant growth promotion.

Another significant gap is the limited understanding of the cumulative and interactive effects of multiple pesticide residues, including herbicides, insecticides, and fungicides, which commonly occur together in rice fields. Research exploring the influence of herbicides on microbial network interactions, microbiome stability, and the spread of antimicrobial resistance genes is also still emerging. Moreover, there is insufficient information on the potential of microbial consortia, biofertilizers, and microbiome-based remediation strategies to mitigate herbicide-induced disturbances in rice ecosystems.

Future studies should employ advanced molecular approaches such as metagenomics, metatranscriptomics, metabolomics, and multi-omics integration to better understand the functional responses of bacterial communities to herbicide exposure. Long-term field investigations across diverse rice-growing regions are needed to evaluate the sustainability of herbicide use and to develop microbiome-friendly weed management strategies that maintain soil health, ecosystem functioning, and crop productivity.

CONCLUSION

Herbicides remain indispensable tools for weed management in modern rice production systems, but their impacts on soil bacterial communities are significant and multifaceted. Current evidence indicates that herbicide application can temporarily reduce bacterial abundance, diversity, and enzymatic activity while altering the composition of key functional groups involved in nutrient cycling and soil fertility. Although many bacterial populations recover after herbicide degradation, repeated or excessive applications may lead to persistent changes in microbial community structure, functional gene composition, and ecological network stability. Such alterations can affect nitrogen cycling, organic matter decomposition, plant health, and overall soil productivity. The magnitude of these effects depends on herbicide type, application rate, soil characteristics, environmental conditions, and rice management practices. Sustainable alternatives, including bioorganic fertilizers, microbial inoculants, organic amendments, and integrated weed management approaches, offer promising opportunities to reduce negative impacts while maintaining crop yields. Therefore, future rice production strategies should prioritize microbiome-friendly weed management practices and incorporate advanced molecular tools to monitor microbial responses, ensuring long-term soil health, ecosystem resilience, and sustainable agricultural productivity.

Additional Declarations

Authors Contributions

Author 1: Conceptualization, literature review, manuscript preparation (40%).

Author 2: Literature review and manuscript editing (20%).

Author 3: Data collection and validation (15%).

Author 4: Critical revision of manuscript (10%).

Author 5: Referencing, formatting, and proofreading (15%).

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Conflict of Interest Statement

The authors declare that there are no conflicts of interest related to the publication of this study.

Ethical Declaration

All processes related to this study have been conducted in accordance with the principles of the Pen Academic Publishing Research Ethics Policy. Since this study is a narrative review based exclusively on published literature, ethical committee approval was not required.

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