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IMPACT OF PESTICIDES USE ON SOIL MICROBIAL COMMUNITIES

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Abstract

The increasing global use of agrochemicals in ensuring food security has posed severe ecotoxicological risks to agricultural soil ecosystems. Soil microbes are foundation of soil fertility, playing critical roles in vital biogeochemical processes like carbon sequestration, nitrogen fixation, phosphorus solubilization, and sulfur cycling. However, continuous use and accumulation of diverse pesticide active ingredients have posed severe risks on microbial diversity assembly and stability. Classical pesticide risk assessments have traditionally been based on single active ingredient-based assessments under extremely controlled laboratory conditions. However, modern-day agricultural ecosystems are characterized by high pesticide diversity where co-occurrence of multiple active ingredients like herbicides, insecticides and fungicides poses complex multi-stressor conditions. These chemical cocktails have potential to act synergistically thus increasing the overall ecological stress while reshaping fundamental microbial network topologies. Advances in high-throughput sequencing technologies and metagenomic studies clearly demonstrated that high pesticide diversity leads to reduced stochastic microbial assembly, favoring growth of deterministic specialists and opportunistic microbes with ability to degrade xenobiotics. Consequently, evolutionary forces like genome streamlining led to enhanced expressions of specific functional genes which are associated with rapid nutrient cycling, thus paradoxically accelerating depletion of critical soil resources. This comprehensive review critically evaluates distinct impacts of herbicides, insecticides, and fungicides on soil microbiomes, emphasizing disruption of enzymatic activities such as those of dehydrogenase, urease, and nitrogenase. Furthermore, it explores utility of molecular biomarkers and proposes agronomic interventions specifically nitrogen fertilization and conservation tillage to mitigate Eco toxicological risks. By integrating these molecular insights with agronomic management, this review provides framework for preserving long-term soil health and redefining regulatory pesticide risk assessments

INTRODUCTION

The evaluation of the impact of pesticides on soil microorganisms, as well as the concept of soil fertility, represents an integral and fundamental component of the overall process of approval of agrochemicals worldwide by Ernakovich, J.G. (2023). The biological potential of soil microorganisms, which include an incredibly complex and dynamic array of microscopic life, including bacteria, fungi, archaea, and protozoa, represents the fundamental bedrock of agricultural soil health. These microscopic entities are directly responsible for the orchestration of several fundamental processes, including the cycling of essential elemental nutrients and the degradation of organic matter by Mackay et al., (2023). While these microscopic entities are absolutely essential for the proper functioning of the ecosystem, the constant and ever-expanding need for pesticides worldwide, in order to ensure optimal crop production, ultimately leads to the accumulation of complex, bioactive molecules in the soil matrix. When pesticides are applied to crops, 30% to 50% of the overall active ingredient does not reach the target site but rather directly lands on the surface of the soil, where these molecules intimately interact with the resident microflora (Mackay et al., 2023).

Although it is still a formidable task for science to precisely forecast the type of relationships between unique molecular pesticide structures and resultant ecological consequences on varied taxonomic classes of soil microbiota, it is evident that such relationships occur on a very broad spectrum of ecological consequences for example Streletskii et al., (2010) These consequences range from localized induction of unique classes of microbial metabolism and enhancement of pesticide-degrading populations to severe depressive, toxic, and even lethal ecological consequences that result in the complete annihilation of sensitive keystone populations. In the past, traditional approaches such as those of the Organization for Economic Co-operation and Development (OECD) have heavily relied on basic integral approaches such as carbon and nitrogen mineralization assays as a means of assessing ecological damage. Due to the highly complex Eco toxicological phenomena observed in contemporary soils, assessments are increasingly shifting away from basic functional assays and traditional plate counts by Ni et al., (2025). Rather, researchers currently rely on the latest advances in molecular genetic analysis, such as high-throughput next-generation sequencing (NGS) and denaturing gradient gel electrophoresis (DGGE), to accurately quantify responses in terms of structure, function, and life strategy patterns in soil microbiomes (Streletskii et al., 2010).

Theoretical Background

The theoretical basis for understanding the impact of complex pesticide mixtures on soil microbiomes is highly influenced by and based on the understanding of microbial community assembly and evolutionary genome dynamics under environmental stress. In understanding community assembly from an ecological perspective, there is a balance between deterministic and stochastic processes by (Chen et al., 2007). However, under environmental stress, such as pesticide diversity, it is understood that deterministic processes are favored. Pesticide diversity is a strong selective pressure on soil ecosystems and filters out the stochastic nature of the community, highly favoring those microbes that are specialists and opportunistic and have specific traits for tolerating and degrading xenobiotic compounds for examples (Ni et al., 2025).

As habitat generalists become less prevalent, niche widths of bacterial communities become narrower, leading to a highly interdependent community and a highly complex network of multitrophic interactions (Ni et al., 2025).

At the same time, the morphological and genetic adaptations of these communities can also be explained by Genome Streamlining Theory and Black Queen Hypothesis. The Genome Streamlining Theory suggests that under high stress conditions, maintaining a high genome size would result in very high biological costs in terms of energy expenditure for maintaining cells, replicating DNA, and regulating genes by (Chen et al., 2007) Thus, under high selective pressure due to high pesticide diversity, bacteria are forced to optimize and minimize their average genome size in order to conserve energy. It is ironic to note that while the size of the genomes is reduced, the microbial community also maximizes and optimizes the expression of some functional genes, (Ni et al., 2025) which are essential for their survival and metabolism, especially those involved in the rapid metabolism of carbon, nitrogen, phosphorus, and sulfur compounds. This high and specialized rate of metabolism, while ensuring the survival of the microbial population, also results in the rapid exhaustion and depletion of essential nutrients in the soil, leading to adverse effects on the fertility and structural integrity of the soil (Ni et al., 2025).

The methodology for this extensive review process is based on a meticulous synthesis of empirical data, reviews, and experimental research from the literature corpus provided.

The source materials for this process by (Lo et al., 2010). Include a wide range of experimental designs aimed at evaluating pesticide effects on microbiomes in soils. For example, the literature includes long-term field experiments to evaluate the combined effects of pesticide seed treatments (PSTs) and tillage practices such as conventional, strip, and no-till on soybean-corn rotation in New England. The literature also includes controlled laboratory microcosm experiments using BIOLOG GN2 microplates to monitor 90-day microbiological profile shifts in soils from the Changshu, Changwu, and Luancheng agricultural stations subjected to combined inorganic fertilizer and pesticide stress (Chen et al., 2007).

Furthermore, the data synthesize advanced molecular approaches, which include the study using next-generation sequencing (NGS) techniques targeting the 16S and 18S rRNA genes to examine the taxonomic restructurings of the microbiomes exposed to single and tenfold concentrations of the pesticides imidacloprid, benomyl, and metribuzin, with and without starch-mineral mixture successional triggers by (Lo et al., 2010). The review will also synthesize large-scale field studies conducted in the Erguna Forest-Steppe Ecotone to examine the effects of pesticide diversity gradients (0 to 4 simultaneous pesticides) with different nitrogen fertilizer regimes, employing the metagenomics Community Aggregated Traits (CATs) approach to inform life history strategies, and finally, comparative critical reviews on the limitations of traditional cultivation approaches versus molecular approaches such as PCR-DGGE for different chemical classes (herbicides, insecticides, and fungicides) that form the basis of the analysis (Lo et al., 2010).

Comparison of Single and Multiple Pesticide Stress

Pesticides interact with the complex matrix of soil in a multitude of direct and indirect routes, leading to paradigm shifts in microbial biodiversity, community structure, and functionality of biogeochemistry. Until recently, Eco toxicological studies have heavily focused on the exclusive role of individual pesticide formulations by (Lo et al., 2010). However, it is a universally recognized fact that contemporary agroecosystems are always dominated by high levels of pesticide diversity the concurrent application and accumulation of multiple classes of chemicals. This high pesticide diversity acts as a severe stress factor that alters the ecological network fundamentally. Studies have shown that as pesticide diversity increases by (Ni et al., 2025). The abundance of network motifs of facilitative interactions such as cycle facilitation, cycad declines and shifts to indirect competition structures such as facilitation-mediated competition, Famcom, (lab). illustrated in Fig. 01 (Ni et al., 2025).

The presence of different pesticides in the community thus pushes it away from stochastic and random assembly and towards deterministic survival topologies. In empirical field studies on the gradients of pesticide diversity (ranging from zero to four different applications of omethoate, chlorpyrifos, azoxystrobin, propiconazole, mefenoxam, and mancozeb), Zwieten, L.V. (2006). It was determined that in the absence of nutrient mitigation, pesticide diversity directly correlates with increased complexity and modularity in microbial networks. This increased complexity, however, is not indicative of a healthy community, as it is more indicative of a stressed community that has become interdependent on other specialized organisms in order to survive the pesticide environment by Zwieten, L.V. (2006). Moreover, the combined effects of inorganic fertilizer and complex pesticide mixtures have been shown to induce massive and long-term variations in the way that microbial communities utilize sole carbon sources, as determined by BIOLOG metabolic profiling (Ni et al., 2025).

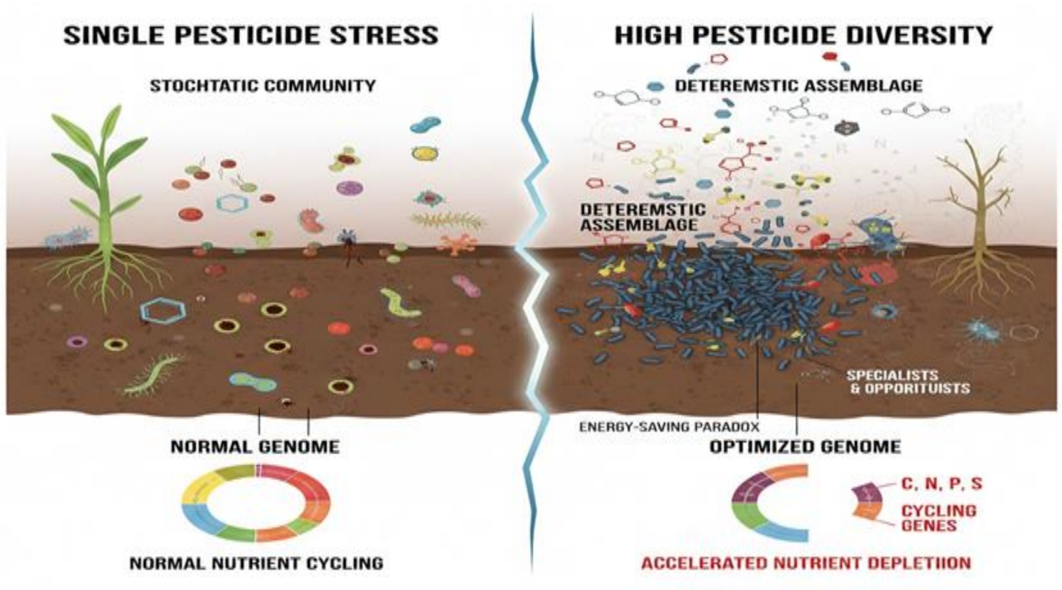

Fig. 01. Comparison of Single and Multiple Pesticide Stress

Impact of Specific Pesticide Classes on Soil Microorganisms

Herbicides

Herbicides are designed to target physiological processes that are essential for the normal growth of plants, like photosynthesis or the production of essential amino acids. But they often cause tremendous collateral damage to non-target bacteria and fungi in the soil that have similar physiological processes by Rodríguez-Cruz, M.S. (2007) For instance, the pre-emergent herbicide butachlor has been reported to have a profound impact on the population of nitrogen-fixing bacteria. Its application has been reported to cause a significant reduction in the population of beneficial bacteria like Azospirillum in non-flooded soil with sandy loam texture at recommended rates. The sulfonylurea herbicides that have been reported to cause damage to non-target bacteria include metsulfuron methyl, chlorsulfuron, and thifensulfuron methyl. The mechanism of action of these herbicides includes the inhibition of the enzyme acetolactate synthase (ALS) by Rodríguez-Cruz, M.S. (2007). Bacteria also use this enzyme to produce branched-chain amino acids like valine, leucine, and isoleucine. The application of these herbicides has been reported to cause severe toxicological effects on the growth of beneficial bacteria like fluorescent pseudomonads. But the sensitivity of the bacteria depends on the genetic makeup of the bacterial ALS (Lo et al., 2010).

Prolonged use of phenyl urea herbicides like diuron, linuron, chlorotoluron, etc., has a drastic impact on bacterial diversity. Interestingly, continuous exposure to phenylurea herbicides can cause the rapid evolutionary adaptation of certain microorganisms. For instance, in the sub-soil environment treated with isoproturon, there is an enhanced rate of degradation that is intimately associated with the rapid proliferation of certain Sphingomonas species. In contrast to this, glyphosate, an inhibitor of the shikimic acid biosynthesis pathway, has a relatively minor impact on the overall microbial community structure at recommended rates for agricultural purposes by Rodríguez-Cruz, M.S. (2007). However, at 100 times the recommended rate in the context of an accidental spill, glyphosate can cause a massive non-specific enrichment of culturable bacteria, thereby fundamentally altering the critical bacterial-to-fungal biomass ratio in the soil (Lo et al., 2010).

Insecticides

Insecticides have a variety of different and distinct chemical properties and neurotoxicity modes of action specifically tailored for eradication of target pests, yet they consistently disrupt non-target microbial ecologies and essential biological cycles. In particular, organophosphorus insecticides, by Zwieten, L.V. (2006). Which are highly utilized globally, play a significant role in the nitrogen cycle. Methylpyrimifos and chlorpyrifos chemicals have a strong inhibitory effect on nitrogen-cycling microflora, leading to highly significant reductions of aerobic dinitrogen-fixing bacteria and overall nitrification rates at different concentrations by Lo et al., (2010). Another insecticide, methamidophos, is a broad-spectrum insecticide with a paradoxical dual effect on the soil matrix, acting as a harsh environment filter leading to a drastic 41% to 83% reduction of total biomass carbon, yet forcing a significant increase of functional diversity and substrate richness as it highly favors the proliferation of highly specialized strains of bacteria metabolizing methamidophos (Lo et al., 2010).

Other insecticides, such as halogenated pyrethroids, i.e., cypermethrin and fenvalerate, are also known to interact with soil bacteria, though these interactions can exhibit a broad range of toxicity, from highly toxic to mildly suppressive Arora et al., (2016). Highly toxic insecticides, such as imidacloprid (a member of the class of neonicotinoids), exhibit a significant level of inhibition of basic soil respiration and enzymatic activities, even when applied at single-dose recommended rates for specific soils, i.e., loamy sand, (Arora et al., 2016). Furthermore, it is evident from high-throughput sequencing techniques that highly toxic insecticides, i.e., imidacloprid, drastically reduce the total number of Operational Taxonomic Units (OTUs) present in soil, leading to the total elimination of specific genera, i.e., Gemmata, and enriching stress-tolerating species of the class Phycisphaerae. Insecticides such as DDT and Aldrin, though extensively and inexplicably increasing total plate counts of microbes present in soil, exhibit a highly disruptive effect on the natural balance of the ecosystem (Arora et al., 2016).

Fungicides

As their primary biochemical targets are eukaryotic fungi, they are uniquely destructive to the extremely sensitive and vital fungal-bacterial balance in the soil microbiota. Chemical control or elimination of dominant fungal saprotrophs and mycorrhizal symbionts can inadvertently initiate a major secondary outgrowth of opportunistic bacteria in the soil microbiota. For example, Johnsen, K. (2000) the systemic fungicide fenpropimorph initiates an immediate and precipitous decline in actively growing fungal hyphae and protozoa in the first 10 to 20 days of treatment, which is rapidly followed by a sharp and sudden increase in the rate of increase of bacteria (Lo et al., 2010).

The toxicological profiles of these fungicides also differ significantly from each other based on their respective modes of action. For instance, broad-spectrum contact fungicides such as chlorothalonil cause severe and long-term adverse impacts on populations of protozoan as well as fungal organisms through inhibition of thiol conjugation and a consequent reduction in total dehydrogenase activity by Johnsen, K. (2000). Benomyl is also exceptionally known for its severe toxicity to arbuscular mycorrhizal fungi, causing a dramatic reduction in symbiotic colonization and affecting plant nutrition severely. Modern agricultural practices heavily rely on Pesticide Seed Treatments (PSTs) consisting of coatings of systemic fungicides such as metalaxyl and fludioxonil, and also insecticides such as thiamethoxam and imidacloprid applied directly onto seeds of crops. NGS-based studies clearly demonstrate that PSTs cause significant changes in the relative abundance of specific fungal phyla in bulk soil by artificially increasing populations of Chytridiomycota and Rhizophlyctidomycetes and also suppress populations of Leotiomycetes in a chemically induced manner by Johnsen, K. (2000). This restructuring of microbial populations also causes a shift in substrate preference from carbohydrates to amino acids and clearly provides evidence of systemic Eco toxicological impacts of seed-applied fungicides on microorganisms in soil beyond the immediate rhizosphere of plants (Arora et al., 2016).

Effects on Soil Enzymatic Activity and Nutrient Cycling

Soil extracellular and intracellular enzymes are the most critical biological parameters to determine the state of equilibrium, fertility, and pollution stress in the soil. Pesticides that penetrate the soil matrix can cause a major disruption in the local metabolism of the soil microbiota and inhibit particular enzymatic processes directly, (Arora et al., 2010). For instance, the organophosphorus nematicide fenamiphos is extremely detrimental to the potential nitrification process in the soil and directly inhibits this process in a proportionality that is directly correlated to its concentration by (Stretletskii et al., 2022). Moreover, the continued and prolonged use of agrochemicals in the soil will inevitably lead to a drastic reduction in dehydrogenase activity, which is an intracellular oxidoreductase enzyme and the primary biochemical parameter to determine the vitality of total microbial respiration in the soil (Arora et al., 2010).

Significantly, a number of common pesticides are potent inhibitors of the intricate molecular mechanisms that enable the symbiotic functioning of nitrogen-fixing bacteria, such as Rhizobium, in leguminous plant nodules, (Stretletskii et al., 2022). Chemical disruption of this symbiotic relationship significantly compromises the efficiency of atmospheric nitrogen fixation, leading to reduced levels of natural soil nitrogen and consequently lowering global crop yields. In addition to direct enzymatic inhibition, metagenomic analysis has shown that increased pesticide diversity significantly affects the level of functional genes involved in all major biogeochemical processes in the environment. In the absence of supplemental nitrogen, increased pesticide diversity significantly upregulates genes involved in carbon cycling processes, specifically aerobic respiration genes such as coxA and coxB, and nitrogen cycling genes involved in denitrification processes by (Stretletskii et al., 2022). Specifically narG and norC, while simultaneously downregulating genes involved in ammonia oxidation, specifically amoA. This chemical disruption of enzymatic processes causes the rapid metabolism and mineralization of all soil resources, leading to the rapid depletion of all soil carbon and nitrogen reserves (Arora et al., 2016).

Biomarkers and Advanced Molecular Profiling

This is because classical cultivation techniques are only able to culture 1% of total bacteria and an equally small percentage of total fungi present in soil. Thus, classical plate counting with agar plates grossly underestimates and misinterprets the extent of ecological damage caused by pesticide accumulation. Accordingly, ecotoxicology has pivotally turned towards molecular genetics techniques. Techniques such as Polymerase Chain Reaction Denaturing Gradient Gel Electrophoresis (PCR-DGGE) were highly useful initially, (Stretletskii et al., 2022). However, it is evident that DGGE is highly limited, as a single species with multiple copies of 16S rRNA can exhibit multiple false bands. Thus, High Throughput Next Generation Sequencing (NGS) of 16S and 18S rRNA is of prime importance (Stretletskii et al., 2022).

These highly sensitive molecular techniques have led to the identification of specific microbial "biomarkers" that are highly indicative of pesticide pollution. For example, high levels of pesticides have a profound effect on the composition of the fungal population, causing a significant decrease in Mucoromycota, but causing a statistically significant proliferation of Basidiomycota by (Ni et al., 2025). Metagenomic analysis has shown that certain genera within Basidiomycota, together with bacterial genera such as Terrabacter, Kitasatospora, Streptomyces, and Sphingomonas, have the unique genetic composition to actively resist or degrade complex organochlorines, pyrethroids, and fungicides (Ni et al., 2025). When the sensitive species die off because of the toxicity of the chemicals, the resilient species will quickly occupy the vacant ecological niches, acting as vital biological indicators of pesticide-mediated extreme stress within the ecosystem (Stretletskii et al., 2022).

A comparative evaluation of the literature reveals the intricate relationship between soil nutrient status and pesticide toxicity. For example, Streletskii et al. (2022) showed, using artificial microcosm experiments, that initiating artificial microbial successions with a starch-mineral mixture (SMM) had a dramatic effect on the baseline architecture of the microbiome, leading to a significant decline in alpha diversity (Shannon index), dominated by copiotrophs and Actinobacteria. Under these hyper-active conditions, the application of extreme pesticide doses (10x benomyl, imidacloprid, metribuzin) led to an avalanche of changes in the fungal community, virtually eliminating the starch-degrader Humicola and opening the door for massive blooms of stress-tolerant yeasts such as Apiotrichum and Solicoccozyma (Stretletskii et a., 2022).

On the contrary, field-based studies undertaken by Ni et al. (2025) on pesticide diversity gradient responses revealed that the addition of nitrogen fertilizer served as a potent mitigating buffer against chemical-induced stress. Unlike the artificial addition of carbon in microcosm experiments, the addition of high nitrogen fertilizer served to satiate the nutrient demand of the microbiome community such that it could maintain its structural constancy even in the presence of severe chemical toxicity. Furthermore, unlike approaches and unlike the BIOLOG-based approach undertaken by Chen et al. (2007) and spanning 90 days of monitoring, the approach undertaken by Ni et al. (2025) also served as a testament to a fundamental truth: complex combinations of pesticides irrevocably force the microbiome community in soil into highly specialized states of survival that significantly alter its natural state of functioning (Ni et al., 2025).

Mitigating Ecotoxicological Risks via Agronomic Interventions

Considering the serious ecotoxicological hazards of chronic pesticide accumulation, it is absolutely crucial that specific agronomic strategies are implemented to ensure the functionality and health of the microbiome of the soil, Berbee, M.L. (2001). This is because it has already been proven through intensive network analysis that the strategic application of nitrogen fertilizer is highly effective in counteracting the negative detriments of high pesticide diversity. This is because adequate nitrogen provisioning directly counteracts forced microbial niche differentiation and multitudes of competition caused by chemical stress Ni et al., (2025).

This prevents the microbiome from undergoing extreme genome streamlining and thus halts the rapid and hyper-accelerated expression of carbon and nitrogen metabolism genes and, in turn, alleviates the rapid and unsustainable depletion of carbon and nitrogen reserves in the soil (Ni et al., 2025).

Furthermore, physical conservation methods, such as strip tillage, are very effective at providing structural habitat protection. This is in contrast to conventional, completely invasive moldboard plowing, where the entire soil profile is overturned, and there is complete mixing of soil layers, as well as increased exposure to chemical applications (Mackay et al., 2023). Strip tillage, on the other hand, only disrupts the soil in the very narrow strips where the seeds are placed, leaving the vast majority of the soil surface protected by crop residue (Ni et al., 2025). Physical assessments have demonstrated that strip tillage maintains soil physicochemical properties such as pH, Electrical Conductivity, and Potentially Mineralizable Nitrogen, as well as maintaining the complex microbial community structure and substrate preference profile, much closer to completely undisturbed no-till soils than conventional moldboard plowing. This is very important, as it acts as a spatial buffer protecting the resident microbiome from the extreme, local stress of pesticide seed treatments, summarized in Table 01 (Mackay et al., 2023).

Table 01: Pesticide Effects, Microbial Dynamics and Mitigation Strategies

Domain	Factor / Indicator	Primary Effect	System-Level Outcome	Key Reference(s)
Soil Enzymatic Activity	Fenamiphos	Concentration-dependent inhibition of nitrification	Reduced nitrogen transformation efficiency	Arora & Sahni (2016); Lo (2010)
	Repeated agrochemical exposure	↓ Dehydrogenase activity	Suppressed microbial respiration & biomass vitality	Arora & Sahni (2016)
Nitrogen Fixation	Disruption of *Rhizobium* symbiosis	Impaired root nodule signaling	Reduced atmospheric N_2 fixation; lower soil N	Arora & Sahni (2016)
Functional Gene Shifts	High pesticide diversity	↑ coxA, coxB (C cycling); ↑ narG, norC (denitrification); ↓ amoA (ammonia oxidation)	Hyper-metabolic state; accelerated C & N mineralization	Ni et al. (2025)
Soil Nutrient Pools	Enzymatic overdrive	Rapid C & N depletion	Long-term soil fertility decline	Ni et al. (2025)
Molecular Profiling Tools	PCR-DGGE	Limited resolution; diversity overestimation	Inaccurate ecological representation	Lo (2010)

Limitations in Current Literature

Yet, despite these advances in methodology, there exist a number of critical limitations within the current body of research. The current set of international regulatory guidelines, as defined by the current OECD protocols for pesticide registration, absolutely require only the most elementary carbon and nitrogen mineralization tests McLachlan, J.A. (2007) The antiquated nature of these measures is made all the more egregious by the fact that the current body of research, as made evident by the molecular techniques currently employed, utterly ignores the massive degree of restructuring and loss of genetic diversity by McLachlan, J.A. (2007) Moreover, the current body of knowledge regarding this area of study is based upon a set of highly artificial and short-term microcosms, as well as the application of single chemicals at high doses, which utterly fail to mimic the chronic and low-dose multi-chemical stress profile of the actual agricultural fields. There also seems to be a lack of comprehensive data regarding the current impact of pesticide diversity upon the dynamics of phosphorus cycling, particularly as it pertains to the arable lands as compared to the natural grasslands (Stretletskii et al., 2022).

Future Perspectives and Recommendations

For the future sustainability of global agricultural systems, it is essential that pesticide risk assessment methodologies urgently move from traditional culture- and compound-specific evaluations toward more holistic, metagenomic-based approaches. For example, (Stretletskii et al., 2022). Future pesticide regulatory frameworks will require the monitoring of specific microbial biomarker groups, such as the relative abundance of Sphingomonas, Basidiomycota or Terrabacter, as early warning indicators of severe pesticide induced ecosystem stress. Another area for future research will be the implementation of long-term, multi-stressor field experiments that accurately reflect the complexity of current agricultural systems, including the combined effects of various pesticide mixtures, as well as climate and nutrient factors by Stretletskii et al., (2022). The universal adoption of integrated agronomic management strategies, such as the judicious management of nitrogen fertilizer application and minimal disturbance tillage systems, will be required as a set of universally effective strategies for protecting sensitive microbiomes from the inevitable impact of chemical pesticides (Stretletskii et al., 2022).

Conclusion

The precise quantification of single and combined pesticide effects on microbial populations in the soil is an absolutely essential metric in terms of modern sustainability in agriculture by Bueno de Mesquita, C.P. (2020). A rapidly expanding body of irrefutable scientific evidence clearly illustrates that increasing pesticide diversity universally represents a severe and chronic environmental stress factor by (Ni et al., 2025). This chemical burden artificially simplifies the genome of the average bacterium, aggressively reorganizes all complex trophic structures from cooperative to competitive forms, and inadvertently initiates hyper-metabolic processes that rapidly and unsustainable rates deplete vital nutrient reserves in the soil by Bueno de Mesquita, C.P. (2020). While particular chemical classes, including sulfonylurea herbicides, organophosphate insecticides, and systemic fungicides, selectively target, inhibit, or artificially promote extremely disparate taxonomic groups, their cumulative and ultimate effect is the profound disruption of global biogeochemical processes for examples, (Ni et al., 2025). Recent monumental advances in molecular biology, as represented by High-Throughput Sequencing and Metagenomics, have successfully circumvented the severe limitations of traditional culturing and have enabled the high-resolution detection of vital biomarkers such as Basidiomycota and Sphingomonas that rapidly adapt to degrade this persistent toxicant by (Ni et al., 2025). Ultimately, the seamless fusion of advanced molecular profiling technologies and highly informed agronomic management, such as the strategic optimization of nitrogen fertilizer applications to alleviate metabolic stress and the application of conservation strip tillage to preserve spatial habitat integrity, is arguably the most critical, tangible, and effective methodology to mitigate the ecotoxicological risks of agrochemicals and establish long-term soil health (Ni et al., 2025).

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