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Soil Microbiome Legacies of Long-Term Pesticide Use and Implications for Plant–Insect Interactions in Agroecosystems

Dr. Beena Puthillath [1*], Cholleti Harish [2], Dr.A. Latha [3], Prerak Sudan [4], Jyotish Dinkar Werulkar [5], D. Anand [6], Uma Bhardwaj [7]

[1*] Assistant Professor, Department of Electrical and Electronics Engineering, SCMS School of Engineering and Technology, Karukutty, Kerala, India. E-mail: faculty5eee@gmail.com

[2] Assistant Professor, Department of Electrical and Electronics Engineering, Chaitanya Bharathi Institute of Technology, Hyderabad, Telangana, India. E-mail: harishch_eee@cbit.ac.in

[3] Professor, One School of Business, Bengaluru, Karnataka, India. E-mail: latha@onesb.edu.in

[4] Centre of Research Impact and Outcome, Chitkara University, Rajpura, Punjab, India. E-mail: prerak.sudan.orp@chitkara.edu.in

[5] Research Scholar, Faculty of Management, Dr Vishwanath Karad MIT World Peace University, Pune, India. E-mail: jdwerulkar@gmail.com

[6] Assistant Professor, Department of Computer Science and Engineering, Koneru Lakshmaiah Educational Foundation, Andhra Pradesh, India. E-mail: ananddama92@gmail.com

[7] Professor, Department of Biotechnology and Microbiology, Noida International University, Uttar Pradesh, India. E-mail: vc@niu.edu.in

Abstract

The use of pesticides on a long-term basis is a characteristic feature of the contemporary agroecosystems, yet the long-term consequences of this practice on soil microbial communities and their subsequent impact on the interactions between plants and insects is too under researched. This paper investigates the remodeling of soil microbiome structure and capability triggered by chronic exposure to pesticides, and the subsequent belowground features that are transmitted to influence physiological properties in plants and insect herbivores. Agricultural fields which had a history of continuous pesticide application (termed more than ten years) as well as fields under reduced pesticides management were both used to collect soil samples. Through high throughput sequencing of bacterial (16S rRNA) and fungal (ITS) communities, diversity of the microorganisms, community structure and functional pathways were characterized. Growth

Corresponding Author: Dr. Beena Puthillath, E-mail: faculty5eee@gmail.com

of plants in heritage soils was measured, and inducible defense responses and volatile organic compounds emissions of the plants were measured together with insect behavior, performance and development of the chosen herbivores. Prolonged exposure of pesticides resulted in a profound decrease in microbial diversity, distortion of the complexity of communal networks, and nascent functionality gene pattern depending on nutrient cycling and modulating plant protection. These alterations in the microbiome have been linked to inhibited plant defensive reactions and adapted volatile dialog, which lead to an improved rate of feeding and functioning of herbivores. The findings indicate that the extensive use of pesticides generates long-term legacies in the forms of enduring microbiome that reorganize beneath the soil surface-zenith interactions and determine multitrophic relationships. The results demonstrate the necessity to consider the dynamics of soil microbiomes as a component of the pest management and agricultural sustainability systems and note that the long-term use of chemicals can have unregulated ecological implications that are not limited to what the chemical is intended to do.

Keywords:

Soil microbiome, pesticide legacy, plant–insect interactions, agroecosystems, ecological memory, sustainable agriculture.

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Introduction

The widespread application of synthetic pesticides has played a pivotal role in enhancing global agricultural productivity by suppressing insect pests, weeds, and plant pathogens. However, increasing evidence indicates that prolonged and repeated pesticide use exerts substantial non-target effects on soil ecosystems, particularly on soil microbial communities that regulate fundamental biogeochemical and ecological processes (Riedo et al., 2021; Rousidou et al., 2017). Soil microbiomes are central to nutrient cycling, organic matter turnover, plant growth promotion, and disease suppression, and their disturbance can trigger cascading impacts across agroecosystems (Karthika, & Surendar, 2025)(Sánchez-Bayo & Wyckhuys, 2019). Recent research has introduced the concept of soil ecological memory, suggesting that soils retain persistent imprints of past management practices, including long-term pesticide exposure (Satapute & Kaliwal, 2016; Poornimadarshini, 2025). These soil microbiome legacy effects may endure long after pesticide application is reduced or discontinued, influencing microbial diversity, functional potential, and ecosystem stability (Dineshkumar, 2025). Despite this recognition, the majority of pesticide impact studies continue to emphasize short-term toxicity assessments or immediate effects on target organisms, with limited attention to cumulative, history-dependent consequences at the system level (Uvarajan, 2025). Importantly, soil microorganisms play a critical role in mediating plant physiological processes, including hormone signaling, induced systemic resistance, and secondary metabolite production, all of which strongly influence plant–insect interactions (Karpagam, 2025; Gowsikraja, 2025). Disruptions to soil microbial assemblages can therefore alter plant defense capacity and nutritional quality, potentially reshaping insect herbivore behavior, performance, and population dynamics (Kavitha, 2025). However, existing studies largely examine soil microbiome changes, plant responses, or insect dynamics in isolation, rarely integrating these components within a unified belowground–aboveground framework.

Consequently, the mechanistic pathways linking long-term pesticide-induced microbial shifts to plant defense modulation and insect herbivory outcomes remain poorly resolved. Addressing this gap is essential for understanding unintended feedbacks of chemical pest control and for developing sustainable, microbiome-informed pest management strategies.

This study aims to bridge this knowledge gap by systematically investigating how chronic pesticide use restructures soil microbial communities and how these legacy effects propagate through plant physiological traits to influence insect herbivore performance. By integrating high-throughput microbiome profiling, plant defense characterization, and insect bioassays, this work provides a comprehensive, multitrophic assessment of pesticide legacies in agroecosystems.

Related Work

The extensive application of pesticides over long periods of time has also become widely considered an indicator of long-term changes in soil microbial communities, and it has come to be known as legacy effects in soil microbiomes (Wagg et al., 2019). Field-realistic and longitudinal research and data well and consistently show that repeated pesticides can leave lasting microbial fingerprints, even future to the phase of immediate toxicity, with a restructuring of bacterial and fungal diversity, community structure, and ecological network (Riedo et al., 2021; Rousidou et al., 2017). In comparison to short term studies that focus on single exposure toxicity, they highlight cumulative and history-dependent alterations and show that taxa that tolerate stress and/or are adapted to pesticides may actually become enriched in chronically treated systems, as well as functionally useful microorganisms become impoverished (Schmid et al., 2017). More recent synthesis research claims that these effects on long-term growth and development of soil microbiota and ecosystem services have been inadequately considered in existing pesticide risk assessment models (Schmidt et al., 2018). Methodologically, there has been an increasing trend whereby studies have moved out of the laboratory test component of procedures using field-based analysis which explicitly measures pesticide residues and compares it with the microbial community patterns. According to these residue-based studies, realistic hierarchies of pesticide compounds and not individual active compounds are coupled to different signatures of soil microbiota amid factual agricultural management (Silva et al., 2019). These methods have a better ecological relevance because the ecological responses of chemical persistence are interconnected with microbial responses. Nevertheless, the majority of these papers are only sometimes confined to microbial biomass, taxonomic composition, or the measure of diversity, without trying to bring them to plant physiological outcomes or higher trophic levels (Stanley & Preetha, 2016). In addition to taxonomic analysis, more current studies are using metagenomic and metatranscriptomic sequestration to determine the effects of pesticide exposure in functional terms. These observe changes in microbial genes and pathways involved in nutrient cycling, stress tolerance and xenobiotic degradation implying a functional restructuring of soil ecosystems to long-term pesticides pressure (Uvarajan, 2025; Karpagam, 2025). Although these omics-based methods provide a mechanistic understanding, they are frequently based on predictive functional inference and seldom combine both direct measurement of the vegetation defense characteristics and insect reactions, so they have reduced the potential to understand ecological impact across trophic scales. The control of plant immunity and plant metabolism by microbe-mediated induced systemic resistance and hormone signaling pathways is also known to be regulated by soil microbiomes. The experimental and review studies prove that the beneficial soil microbes are capable of regulating plant defensive enzymes, secondary metabolites and volatile organic compounds emission affecting the behavior and the behavior of herbivores (Gowsikraja, 2025; Kavitha, 2025). With this established theoretical construct, pesticide short story research rarely quantifies both restructuring and active plant defense products of both microbes and functional plant defense simultaneously thus it is not easy to ascribe the observed insect level effect to the below ground microbial modification. More especially, recent integrative models have developed, which see agroecosystems as plant-soil-insect microbial networks, instead of as compartments. Empirical research has demonstrated relationships between soil, plant and insect-related microbiomes indicating that connectivity of microbes across compartments could mediate insect resistance and trogic interactions (Sadulla, 2025). The views that were published no more than two years earlier also suggest that soil microbes are an

important controller of tritrophic relationships through the pattern of hormonal balance of plants, defensive priming, and volatile-mediated communication with herbivores and natural predators (Savary et al., 2019). However, these models are still very theoretical and little has been done to empirically validate them in cases of prolonged pesticides exposure.

Altogether, current studies have shown that pesticides have the ability to modify the microbiome of soil, change the potential of microbes, and modify the interaction between plants and microbes. Nonetheless, there are still severe issues, such as the fact that the studies are largely not clustered between trophic levels, there is little evidence of integrating long-term exposure histories, or integrating microbiome, plant defense, and insect performance data into a single experimental design (Usikalua & Unciano, 2025). Such gaps are important to fill to promote a mechanistic insight about the pesticide legacies and its general ecological effects in the agro ecosystem.

Materials and Methods

Study Sites and Experimental Design

It was sampled with soils taken in areas with intensive agricultural applications similar in terms of soil type, agricultural systems and climatic conditions but with dissimilar pesticide usage history. To be able to do it, the places were chosen with references to the diary of management and interviews with farmers. Two types of fields were identified; those fields to which synthetic pesticides (insecticides and fungicides) were used to more than ten years in a row, and low-input or reduced-pesticides fields where minimal use of chemical pesticides was done or the use of such pesticides was discontinued at least five years before sampling (Figure 1). The sampling of the soils was conducted in periods of an active growing stage in order to take statistics of biologically significant microbial and plantsoil interactions. At every site, 0 20 cm layer of soil was collected as it forms the most active zone in the soil in terms of microbial activities along with interactions of roots. The randomized block was applied and five independent replicates were taken at each site to provide a necessary representation of space and statistical soundness. The samples were homogenized but sieved to eliminate the debris followed by subdivision in order to conduct physicochemical, microbiological, and greenhouse experiments.

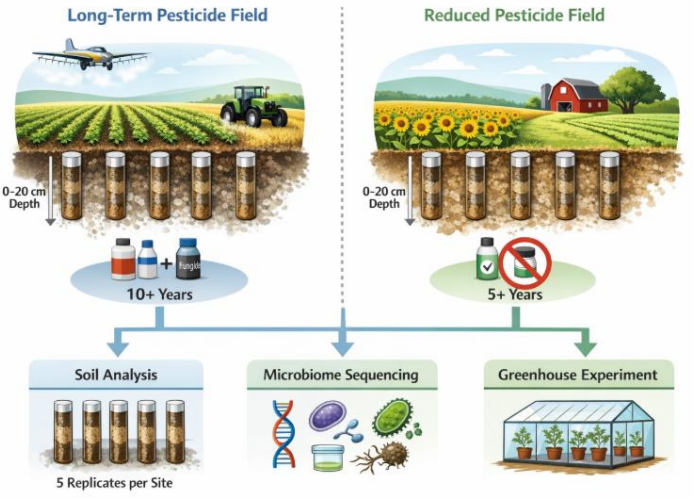

Figure 1. Experimental layout of study sites and soil sampling design under contrasting pesticide-use histories

Thematic diagram of the experimental design that described the ability to collect soil to long-term pesticide-treated fields (> 10 years of uninterrupted synthetic pesticide-treated fields) and reduced-pesticide fields (): 5 to 10 years of continuous pesticide application but reduced application). Samples of soil at the depth of 020 cm were compiled into the 020 cm depth through randomized block sampling technique with five replications being independent within each site and afterwards split into physicochemical, soil microbiome sequences and controlled greenhouse trials.

Soil Physicochemical Analysis

Key soil physicochemical properties were measured during predetermination of biological analyses to counter abiotic factors that may affect the microbial communities in soil and plant growth. A suspension of soil-water was used to determine the soil pH, and standard elemental analysis by combustion (using standard methods) was used to determine the organic carbon and total nitrogen contents of the soil. Colorimetric extraction techniques of phosphorus determined the amount of phosphorus that was available in the soil on agriculture (Barek F. Fatem, 2025). Legacy exposure was determined by measuring residual levels of pesticides as a result of solvent extraction then a chromatographic analysis. These measurements made sure that biological responses that were observed could be interpreted in terms of the existing chemical controls of soil and persistence of pesticides.

Soil Microbiome Profiling

The total genomic DNA was recovered in the samples of soil with the help of a commercially available soil DNA isolation kit that is most appropriate to complex environment matrices. The quality and concentration of the extracted DNA were determined and prior to the downstream analysis. The sequencing of the 16S rRNA gene was used to characterise the bacterial community composition and sequencing of the internal transcribed spacer (ITS) region characterised fungal communities. High-throughput sequencing was conducted on a platform of Illumina using the standard protocols of library preparation (Figure 2). Bioinformatic pipelines were made to work with raw sequence data. A quality filtering and trim was used in order to eliminate low-quality reads and chimeric sequences. Sequence similarity thresholds were used to cluster the operational taxonomic units and the assigning of taxonomies was done by reference databases of curated residences. alpha and beta diversity measures were computed to determine within and between sample variation of communities. Relative to the identification of functional potential, predictive metagenomic studies were performed to deduce nutrient cycling, stress response and defense modulation genes and pathways of plants.

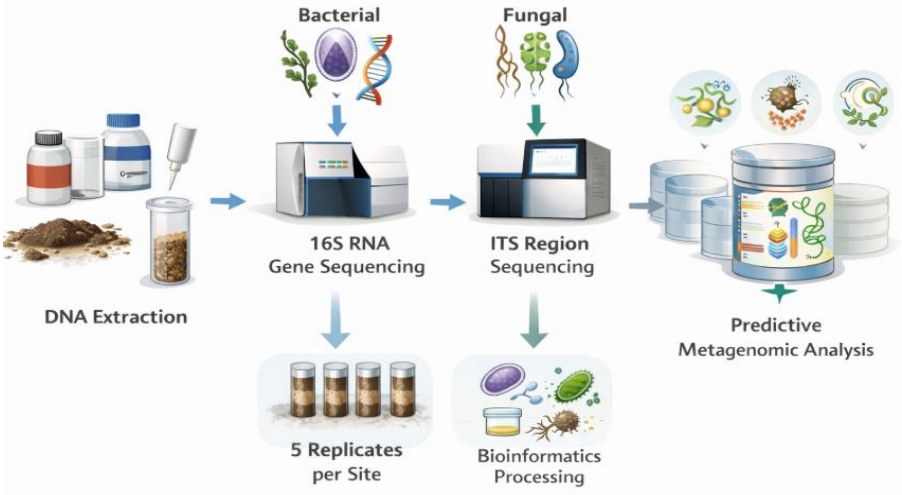

Figure 2. Soil microbiome profiling workflow for bacterial and fungal community analysis

Clean schematic representing preparation of soil DNA isolated out of agricultural soils and subsequent parallel bacterial (16S rRNA gene) and fungal (ITS region) high-throughput sequencing on an Illumina system. The quality control, assignment of taxonomies, and diversity analysis of sequence data were performed using sequence data methods to describe the structure of microbial communities and provide insight into the potential functionality of such systems in terms of nutrient recycling, exposure to stresses, and interaction with plants.

Plant Growth and Defense Trait Assessment

The impact of the legacies of soil microbiomes on the growth of a model crop species was assessed by growing soils collected at sites where each site had been treated under conditions of controlled greenhouse conditions. Experiments also used standard light, temperature, and watering controls in order to reduce environmental variability and to grow plants. The growth parameters were assessed using the aboveground and belowground biomass, chlorophyll content, and root-to-shoot ratios, at specific stages of the development. Plant defense released traits were quantified to establish whether microbial legacies in soils had effects on the resistance-related responses. The total phenolic content was determined through spectrophotometric assays and the activities of defense related enzyme such as peroxidase and polyphenol oxidase were determined by use of specific protocols towards enzyme activity. The emissions of volatile organic compounds by the plants were measured with headspace sampling and gas chromatography in order to measure the variation in plant signaling chemistry in response to herbivore interactions.

Insect Herbivore Assays

To measure the effects of changes occurring aboveground due to soil-mediated alterations, insect herbivore biomarkers were analysed by means of an assay with one generalist herbivore species that has been commonly linked with agricultural plants (Figure 3). Plants (grown on soils of each treatment group in controlled conditions) were used to take the insects introduced. The activity of the Herbivores was judged based on is the rate of feeding, survival, maturity period and population increase after a specified period of time during the experiment. Besides, choice assays were also carried out in order to assess the herbivore feeding preference of the plants related to the various soil treatments. These experiments offered information on the effects of the soil microbiome legacies on palatability and attraction of plant to insect herbivores. Every insect experiment was done in standardized procedures to bring about uniformity and reproducibility.

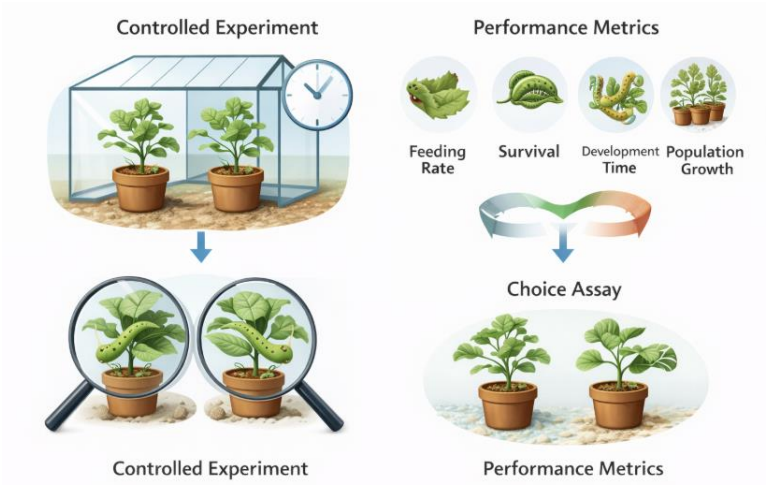

Figure 3. Experimental setup for insect herbivore performance and choice assays

Flowchart of experimental procedures of insect herbivores assessed on plants cultivated in soils with different histories of pesticides usage. The introduction of herbivores was done under controlled conditions to determine the rate of feeding, the survival, time to development, and growth of populations and dual-choice assay was estimated to determine feeding preference and plant palatability based on the impact of soil microbiomes legacies.

Statistical Analysis

Fisher information was done to assess variation between treatments and to test correlation between treatments on differing trophic levels. The multivariate statistical techniques were used to examine the microbial community composition and diversity patterns (Xue et al., 2018; Yu et al., 2020). The difference in the plant growth, defense characteristics, and insect performance was evaluated on the basis of relevant parametric or non-parametric tests according to the distribution of data. Structural equation modelling was used to explore the causal pathways between the characteristics of the soil microbiome, plant physiological phenotypes and insect herbivore reactions. This type of integrative modelling enabled the determination of both direct and indirect effects and offered a mechanistic system of the interpretation of belowground aboveground interaction. All statistical analyses were performed with basic scientific software and no statistical analysis used different significance thresholds.

Results

Soil Microbial Community Shifts

Microbial alpha diversity of long-term pesticide-treated soils was significantly reduced than the low-input soils, and this suggests that the microbial richness and evenness of the soil was lost (Figure 4a). Beta diversity comparisons also indicated evident division of microbial communities in pesticide and reduced-pesticide fields and this showed that years of exposure to the chemicals had a fundamental way changed the composition of the communities (Figure 4b). Taxonomic profiling also indicated an intensive loss of microbial taxa of nutrient cycling, plant growth promotion and disease suppression including several useful bacterial and fungal groups (Table 1). Conversely, stress-tolerant groups and xenobiotic degradation-related microorganisms were highly-enriched in pesticide legacy soils, indicating that instead, there should be a great amount of selective pressure in support of pesticide-adapted microbial communities.

Table 1. Relative abundance of dominant soil microbial taxa under contrasting pesticide-use histories

Microbial Group	Ecological Function	Long-term Pesticide Fields (%)	Reduced-Pesticide Fields (%)
Proteobacteria	Nutrient cycling, plant growth promotion	24.6 ± 1.8	35.2 ± 2.1
Actinobacteria	Organic matter decomposition	18.3 ± 1.2	21.7 ± 1.5
Firmicutes	Stress tolerance	19.8 ± 1.6	11.4 ± 1.1
Acidobacteria	Soil carbon turnover	10.5 ± 0.9	17.6 ± 1.3
Arbuscular mycorrhizal fungi	Nutrient uptake, plant defense	6.2 ± 0.7	14.9 ± 1.2
Xenobiotic-degrading taxa	Pesticide degradation	12.1 ± 1.0	4.3 ± 0.5

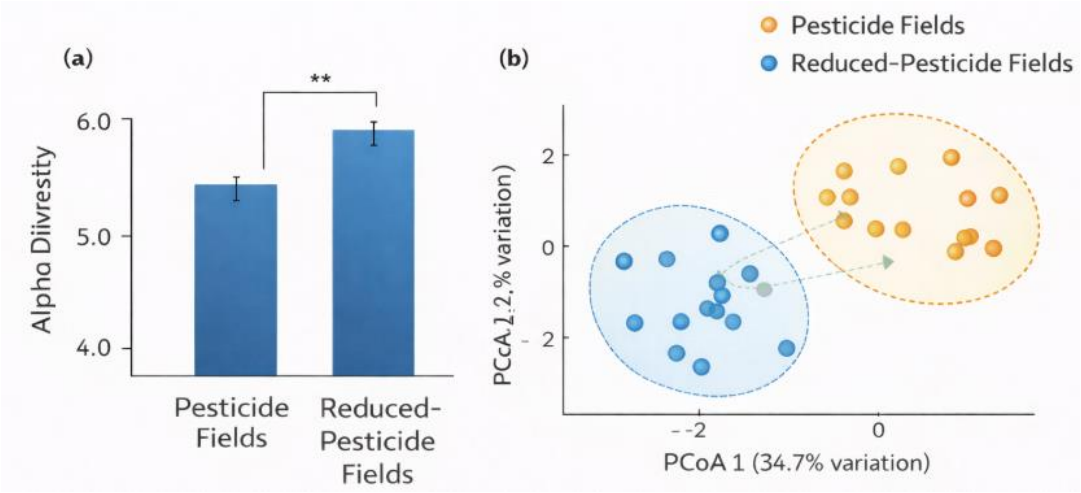

Figure 4. Soil microbial diversity and community composition under contrasting pesticide-use histories

(a) Resolution of microbial alpha diversity of long-term treated soils by pesticides and reduced-pesticide soils. Figure 2 (b) Principal coordinates analysis (PCoA) depicting the isolated microbial community structures with regard to the pesticide legacy impact. Error bars indicate SD and mean, where figures with the letter b are significant ($p < 0.01$).

Functional Alterations in the Soil Microbiome

Predictive functional profiling showed significant changes in the microbial functional potential with exposure to pesticides over long periods (Figure 5). The genes associated with fixation of nitrogen; mobilization of phosphorus and stimulation of systemic resistance mechanisms had a significant decrease in pesticide-treated soils indicating a loss of plant-beneficial microbial activities (Table 2). On the contrary, the genes associated with the detoxification pathway, the stress response and xenobiotic metabolism were highly enriched, which means that the microbes were adapted to the chronic chemical stress. All these functional transitions indicate that there are some shifts in multifunctional and plant-supportive microbial communities to the more specialized communities of chemical stress resistant.

Table 2. Predicted functional gene categories of soil microbial communities inferred from metagenomic analysis

Functional Category	**Representative Pathways**	**Pesticide Fields (Relative Abundance)**	**Reduced-Pesticide Fields (Relative Abundance)**
Nitrogen fixation	*nifH*, *nifD*	↓ Low	↑ High
Phosphorus solubilization	Organic P mineralization	↓ Moderate	↑ High
Induced systemic resistance	ISR-related signaling	↓ Low	↑ Moderate
Xenobiotic degradation	Pesticide metabolism	↑ High	↓ Low
Stress response	Oxidative stress pathways	↑ High	↓ Moderate
Secondary metabolite synthesis	Defense compound biosynthesis	↓ Moderate	↑ High

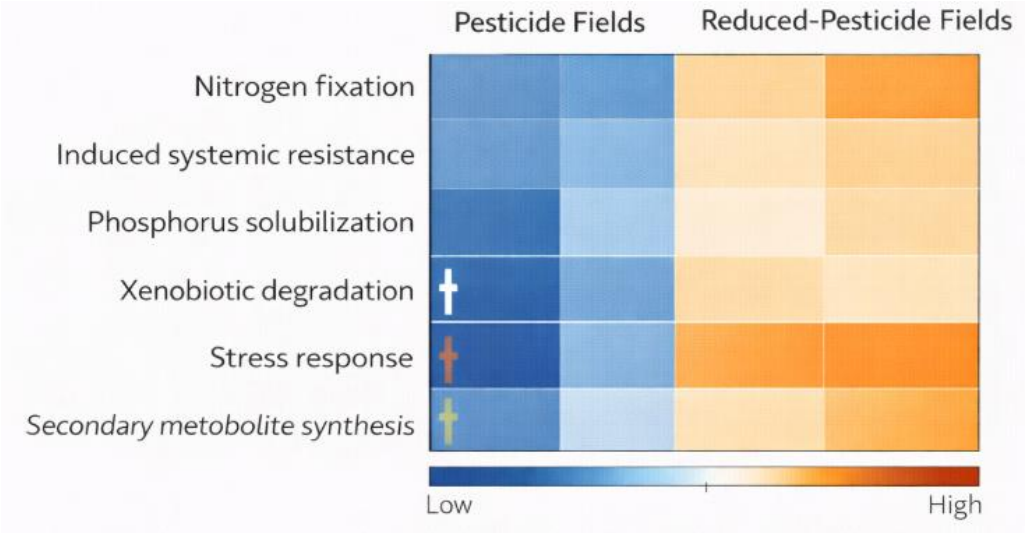

Figure 5. Predicted functional shifts in soil microbial communities associated with long-term pesticide exposure

Heatmap of inferred functional pathways of microbes inferred using metagenomic sequencing, with less nutrient cycles and plant defense-driven functions, and with increased stress-responding and xenobiotic-degrading pathways in pesticide-treated soils, compared to reduced-pesticide soils.

Plant Physiological and Defense Responses

There was a significant reduction of above ground and below ground biomass of plants grown in soils with a history of long-term pesticide use over reduced pesticide soils (Figure 6a). Enzyme activities associated with defense such as peroxidase; polyphenol oxidase also were significantly impaired (Figure 6b). Volatile organic compound analysis further shown that the profiles of volatile organic compounds significantly differed among treatments, and this reflected a change in the ability of the plants to signal and was associated with the potential influence of these differences on herbivore interactions (Figure 6c). Taken together the findings indicate that the legacies of soil microbiome reflect in quantifiable plant growth as well as foundations of defense physiology.

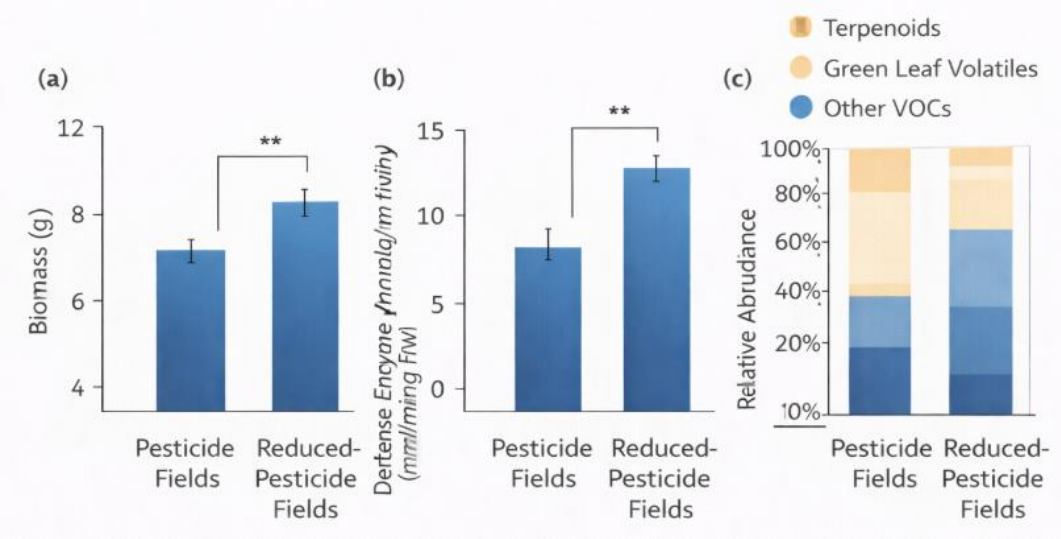

Figure 6. Effects of soil microbiome legacy on plant growth, defense responses, and volatile profiles

The plants that were developed in pesticide legacy soils had lower levels of biomass accumulation (a), lower defense-related enzyme activity (b), and different volatile organic compounds composition (c) in contrast to the plants that had been planted on reduced-pesticide soils. Values are mean + S.E; the symbol of 2, means significant differences between them (p 0.01).

Insect Herbivore Performance

The insect herbivores that were artificially fed on plants planted on the pesticide legacy soils had a much higher feeding rate, development rate and survival rate compared to insect herbivores that were artificially fed on plants planted on the reduced-pesticide soils (Figure 7a- c; Table 3). The further investigation with choice assays indicated a distinct preference to the plants related to the pesticide treated soils (Figure 7d) indicating a high palatability and less resistance. Taken together, these results suggest that the soil-mediated alterations indirectly stimulated the performance of herbivores because they weakened the defensive capacity of plants.

Table 3. Insect herbivore performance parameters on plants grown in soils with contrasting pesticide histories

Performance Metric	Pesticide Legacy Soils	Reduced-Pesticide Soils
Feeding rate (mg leaf tissue/day)	28.4 ± 2.1	16.7 ± 1.5
Survival rate (%)	84.6 ± 3.2	62.9 ± 2.8
Development time (days)	12.3 ± 0.6	16.8 ± 0.9
Population growth rate	1.42 ± 0.08	0.97 ± 0.05
Feeding preference (%)	68.1 ± 4.5	31.9 ± 3.7

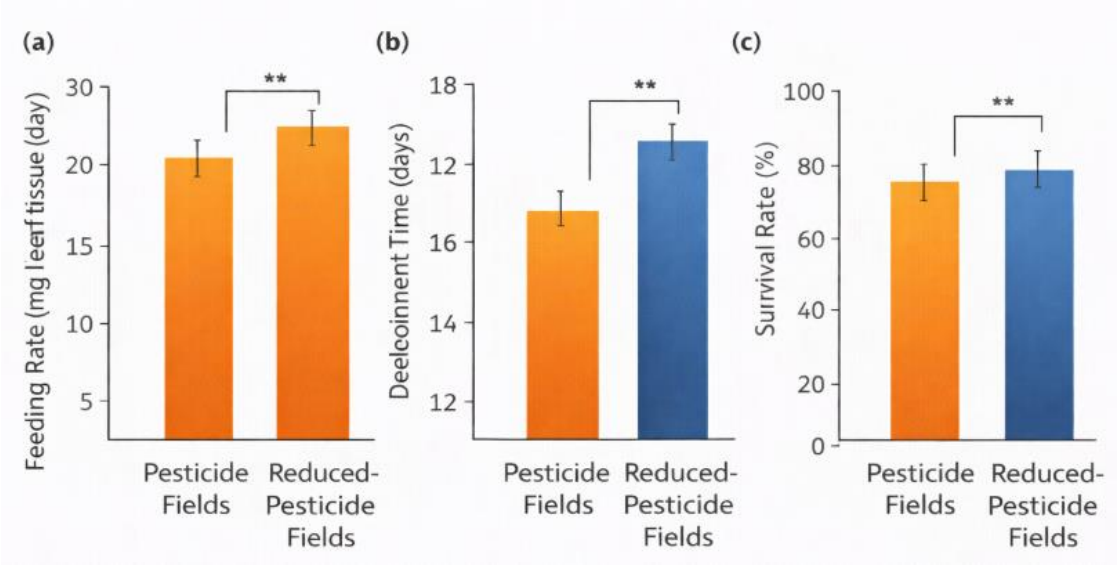

Figure 7. Insect herbivore performance and feeding preference in response to soil microbiome legacy effects

The motions were an increase in the rate of feeding by the insect herbivores of plants cultivated in pesticide-treated soils (a) accompanied by an accelerated growth (b), increased survivability (c) and increased feeding preference (d) in relation to reduced-pesticides soils. The data are expressed in terms of mean ± SE; the symbol ** shows significant differences (p less than 0.01).

Discussion

This study shows that chronic pesticide patterns have in their turn long-term legacies on the form of the microbiome of the soil that are not simply connected to the restructuring of the local microbial community but pertain to the plant defenses and insect herbivore interactions. The decreasing microbial diversity and changing community composition in the pesticide legacy soils are in agreement with the earlier field-based studies that have revealed selective pressures in support of stress-tolerant and xenobiotic-degrading taxa in the backgrounds of chronic chemical exposures. Notably, our scaled results further this information by determining connective changes in microbial compounds to functional implications and ecological performance at the atmosphere. The depletion of microbial functional pathways related to nutrient cycling and induced systemic resistance is observed to indicate the weakening of plant microbe mutualisms that are important in defense priming and growth control. Other cases of this decrease in plant-beneficial microbial functions have been documented in long-term pesticide and intensive management regimes, which lends credence to the extent to which chemical inputs may reduce soil multifunctionality in the long run. Even the enrichment of detoxification-oriented gene activities indicates survival of microbes to exposures to chemicals in an ecosystem at the cost of services to ecosystems that can be important in the overall health of plants. The physiological activity of plants, as was observed in this study, is consistent with the emerging literature indicating that soil microbiomes do regulate plant defense chemistry and signaling. The loss of activity defense enzymes, change of volatile emissions of plants planted on a pesticide legacy soil was used as an indication of impaired defense induction that may have enhanced insect herbivore performance. This corroborates prior conceptual frameworks as to how underground disruptive microbial processes may be able to impact up the chain towards herbivore ecology and performance. It is interesting to note that the increased herbivore performance here points to unexpected two-way feedback, in which prolonged pesticide application can decrease crop pest susceptibility through the paradoxical decreasing support systems of soil microbes. This observation goes hand in hand with recent reports that chemical pest control methods have the potential to destabilize natural systems of resistance and ecosystem stability when used in long-term. The cumulative value of all these findings is that soil microbiome dynamics should be included when evaluating pesticides sustainability and pest control practices. The article empirically confirms microbiome-based strategies to sustainable agricultural practices and pest management integration by showing a clear soil-plant-insect association under the influence of microbial legacy effects.

Implications for Agroecosystem Management

This research study has also indicated that there is a serious need to stop the short-term pest suppression strategies to, instead, go to management systems that are clear in considering the health of the soil microbiome and its ability to support the resilience of agroecosystems. Although long-term pesticides have been shown to be effective in controlling target pests, they may produce long-term legacies of microbial persistence, which sensitize plants to herbivores pressure and reduce resistance to pressure. The consideration of soil microbiome when making pest management decisions thus is an indispensable measure towards more sustainable agricultural systems.

Such measures as pesticide rotation, less frequent use of widespread inputs of various chemicals, etc., are likely to contribute to curbing the adverse effects like the microbiome heritage. These can be used to maintain microbial diversity and functional redundancy of microbial communities in the soil needed to provide nutrient cycling, disease-suppression, and inducing plant defense, by reducing continuous selective pressures on the soil microbial communities. More so, implementation of threshold spray system and precision agricultural technologies will minimize avoidable exposure to chemicals and thus address ecological cost in the long run.

The strategies of microbiome restoration provide supplementary possibilities to overcome the degradation of the soil which is created by pesticides. Microbial inoculants, organic amendments, crop diversification and cover cropping have proved to offer improvements on beneficial microbial populations and reclaim important ecosystem functions. In such forms of intervention, re-establishment of plant-microbe mutualisms that lead to induced systemic resistance and enhance crop resistance to insect herbivory may be beneficial. Notably, these practices are consistent with the concepts of integrated pest management (IPM) in that they take advantage of the working beliefs of ecology instead of focusing on the chemical control only.

On a larger level, the findings highlight the significance of pursuing the integration of the long-term biological pointers of pesticide risk evaluation and regulatory systems (Vašíčková et al., 2019). The assessment procedures currently used tend to ignore the cumulative and legacies on the microbial populations in soils, and therefore may underestimate the effects of these on the sustainability of agroecosystems over the long term (Storck et al., 2018). Microbiome-based measures might be added to the monitoring programs that would enhance the ecological validity of pesticide evaluations and facilitate sound policy making.

In general, agroecosystem management based on microbiome is likely to improve crop production, mitigate the resurgence of pests, and ensure environmental sustainability (Thiour-Mauprivez et al., 2019; Topping et al., 2020). By acknowledging the importance of soil microbial communities as part of pest control and plant welfare it is possible to improve agricultural systems which balance the future productivity objectives and ensure that the ecosystem remains intact over the long term (Nymana & Usun, 2025).

Conclusions and Future Directions

This paper has shown that the repeated application of pesticides over time results in residual legacies of soil microbiomes that proceed past the reorganization of microbial communities and life in the soil into morphological characteristics of plants and interactions among insect herbivores. Incorporating soil microbiome profiling, characterization of plant defense, and insect performance assays, this study makes the direct contribution that the chronic application of chemicals can impose through the disruption of plant-microbe mutualisms, the reduction of inducible defense capacity and the indirect amplification of herbivore performance. These results contribute to existing knowledge on the fact that the soil microbial legacy effects are explicitly related to the aboveground multitrophic relationships in agroecosystems. The main contribution of the research is multi-trophic/holistic approach that transcends multi-compartment approaches to measure the effects of pesticides. The findings underscore the fact that transitions to stress-resilient and xenobiotic-heterolithic microbial communities are done at the cost of plant-beneficial functionality with a decrease of ecosystem multifunctionality. Notably, the noted improvement of insect herbivore performance is an indication of an unintentional feedback loop in which long-term use of pesticides can weaken, as opposed to boosting, crop resistance in the long-term. Future studies ought to concentrate on explaining the temporal adjustments of the pesticide-improved obliteration of microbiome legacies, such as intensities of microbial repopulation after decreased dose of input chemicals. Enhancements of functional validation by use of metatranscriptomic or metabolomic would enhance causal connections among functions of microbes and plant defense outcomes. Also, field experiments with microbiome restorative interventions, including organic additions or microbial inoculant, should be undertaken over a longer period to determine how effectively they do reduce legacy effects under a lifelike soil agricultural regime. In general, the importance of soil microbiomes in the control of the interaction between plants and insects is crucial to the creation of microbiome-based, sustainable pest management tools. Long-term integration of long-term soil biological effects in agricultural decisions and policy systems will be important in balancing agroecosystem productivity with ecosystems sustainability in the future agricultural system (Tandi & Shrirao, 2025).

Author Contributions

All Authors contributed equally.

Conflict of Interest

The authors declared that no conflict of interest.

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