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Soil Microbial Diversity and Nutrient Cycling in Loquat Orchards of Zhejiang Province

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Abstract Soil microbial diversity plays a crucial role in maintaining soil fertility and regulating nutrient cycling in orchard ecosystems. This study focuses on loquat orchards in Zhejiang Province, aiming to investigate the characteristics of soil microbial communities and their relationships with nutrient cycling processes. Field sampling and laboratory analyses, including high-throughput sequencing and soil physicochemical measurements, were conducted to assess microbial diversity, community structure, and soil nutrient status. The results reveal significant spatial variations in microbial diversity and identify key functional groups involved in carbon, nitrogen, and phosphorus transformations. Furthermore, strong correlations were observed between microbial diversity indices and soil nutrient availability, indicating a close coupling relationship. A case study of a typical loquat orchard further demonstrates how management practices influence microbial communities and soil ecological functions. This research provides a scientific basis for optimizing orchard management and improving soil health in subtropical fruit production systems.

Keywords Soil microbial diversity; Nutrient cycling; Loquat orchard; Zhejiang Province; Soil ecology

1 Introduction

Soil microbial diversity is increasingly recognized as a key determinant of soil fertility, ecosystem stability, and sustainable fruit production. Microorganisms such as bacteria, fungi, archaea, and protists drive nutrient cycling by decomposing organic matter, mineralizing and immobilizing nutrients, regulating soil structure, and suppressing soil-borne diseases, thereby exerting strong controls on crop growth and yield (Jiao et al., 2021). In perennial orchard systems, where inputs and disturbances accumulate over long periods, the structure and function of soil microbial communities are especially sensitive to management practices, microclimate, and soil physicochemical conditions (Xiang et al., 2023). Loquat (*Eriobotrya japonica* Lindl.) is an economically important subtropical fruit tree widely cultivated in southeastern China, and Zhejiang Province—particularly regions such as Ningbo and Ninghai-is a core production area with distinctive local varieties and high added value. Recent work in Zhejiang loquat orchards has shown that soil microbiomes are closely linked to fruit traits: the α- and β-diversity of bacteria and protists, together with composite indices of soil multi-nutrient cycling, correlate positively with average fruit weight, underscoring the pivotal role of belowground biodiversity in determining fruit yield and quality (Wang et al., 2024). However, the mechanisms by which soil microbial diversity and community composition regulate the cycling of key nutrients (e.g., C, N, P, K and microelements) under the specific environmental and management conditions of loquat orchards in Zhejiang remain insufficiently clarified. A deeper understanding of these mechanisms is of both scientific and practical significance for optimizing fertilization regimes, improving soil health, and supporting the high-quality development of the regional loquat industry.

Research from fruit orchards worldwide demonstrates that soil microbial communities respond sensitively to management measures, vegetation configuration, and soil physicochemical gradients, and that these responses translate into altered nutrient cycling and ecosystem functioning. In apple, citrus, mango and other orchards, cover crops, organic amendments, intercropping, and conservation tillage have been shown to increase microbial biomass, bacterial and fungal diversity, extracellular enzyme activities, and the abundance of functional groups involved in C, N and P cycling, thereby enhancing soil organic matter content, nutrient availability, and system sustainability (Xiang et al., 2023). Meta-analytical synthesis across Chinese orchards indicates that grass cover can significantly increase microbial biomass carbon, the abundances of bacteria, fungi and actinobacteria, Shannon diversity, and activities of key C-, N- and P-cycling enzymes in the top 0-40 cm of soil. In citrus and pomelo orchards, soil pH, available nutrients, and vertical soil profile strongly structure bacterial communities and their functional repertoires, with topsoil harboring higher diversity and higher relative abundance of taxa linked to C- and N-cycle processes (Muneer et al., 2022). Similarly, cover crops and organic or “green” management in citrus and apple systems tend to increase microbial diversity, network complexity, and the relative abundance of nutrient-cycling taxa, while also modifying soil organic carbon, ammonium, and available P and K (Janke et al., 2024; Zhang et al., 2025). At broader spatial scales, positive relationships between soil microbial multidiversity and multi-nutrient cycling indices have been detected across diverse terrestrial habitats, with community composition often explaining more variance in nutrient cycling than simple richness indices, highlighting the importance of community assembly processes and bacterial-fungal interactions for ecosystem functioning (Jiao et al., 2021).

Against this international backdrop, studies focused specifically on loquat orchards in Zhejiang Province are still limited but emerging. Recent investigations in Ningbo and Ninghai have revealed that, even under similar varieties and climatic conditions, loquat fruit quality varies markedly among orchards, a pattern that can be attributed to differences in soil physicochemical properties, microelement status, soil microbiomes, and field management measures (Wang et al., 2024). In these systems, soil pH, available phosphorus, available potassium, dissolved organic nitrogen, and microelements such as Mg and Cu have been identified as key edaphic drivers shaping bacterial, fungal, and protist communities, and these microbial communities, in turn, regulate multi-nutrient cycling indices that are closely associated with fruit weight and fruit mineral composition (Wang et al., 2024). Nevertheless, existing work has not yet systematically characterized the soil microbial diversity and nutrient cycling patterns in loquat orchards of Zhejiang Province, nor has it fully disentangled how different microbial groups jointly mediate macro- and micro-nutrient cycling under real production conditions. Therefore, the present study takes typical loquat orchards in Zhejiang as the research object, integrates high-throughput sequencing of bacteria, fungi, and protists with measurements of soil physicochemical properties, macro- and micro-nutrient pools, and enzyme activities, and constructs multi-nutrient cycling indices to: (i) characterize the diversity, composition, and assembly characteristics of soil microbial communities in loquat orchards; (ii) reveal the key soil factors controlling microbial community structure and nutrient cycling; and (iii) elucidate the quantitative relationships among soil properties, microbial diversity, nutrient cycling, and loquat fruit quality. On this basis, a technical framework is proposed that couples soil microbial indicators with nutrient management, aiming to provide a scientific reference for precise fertilization, soil quality improvement, and sustainable management of loquat orchards in Zhejiang Province.

2 Overview of the Study Area

2.1 Natural conditions of loquat-producing regions in Zhejiang

Loquat is a characteristic subtropical fruit of Zhejiang, with core production belts distributed in hilly and river-valley landscapes such as Ningbo, Lishui and surrounding mid-low mountain areas (Zhang et al., 2015). These regions typically have sufficient light, heat and water resources, with annual active accumulated temperature over 4500 °C and annual rainfall around or above 1600 mm, conditions that match the thermal and moisture demands of loquat growth (Jiang et al., 2022). River valleys and basins along major rivers, for example the Oujiang valley in southern Zhejiang, provide relatively flat terrain, deep weathered soils and mild microclimates, forming concentrated, high-quality loquat zones. In addition, complex small-scale topography in mountainous counties creates microclimate heterogeneity that further differentiates local suitability for loquat cultivation (Figure 1).

Figure 1 Zhejiang Ninghai Loquat Production Area (Photo by Qiaoyun Cao)

Meteorological risk factors also shape the natural conditions of Zhejiang's loquat areas. During the young fruit period, low-temperature and frost events can occur for more than 10 days in some locations, posing a threat to fruit set and yield stability (Jiang et al., 2022). Continuous overcast-rainy days are generally few, and extreme high-temperature events occur less than once per year on average, which is favorable for fruit enlargement and coloration. At the same time, pesticide-residue-based quality evaluation of characteristic fruits, including Lanxi loquat, shows that existing loquat belts in Zhejiang already support large-scale commercial production but face pressure to improve product stability and safety (Liu et al., 2023). These combined natural conditions—abundant heat and water, microclimate diversity, and manageable meteorological disasters—provide the environmental foundation for intensive loquat orchard development in Zhejiang.

2.2 Soil types and climatic characteristics

Loquat-producing regions in Zhejiang are mainly situated in subtropical monsoon climates, characterized by warm, humid conditions with distinct seasonal changes in temperature and rainfall (Jiang et al., 2022). Similar loquat regions in South China experience mean annual temperatures around 21-23 °C and rainfall above 1300 mm, reflecting a climatic background of long frost-free periods and high atmospheric humidity suitable for evergreen broad-leaved fruit trees (Zhang et al., 2025). In Zhejiang, the combination of high accumulated temperature, abundant precipitation and relatively few persistent meteorological extremes allows for stable flowering, fruit set and sugar-acid accumulation in loquat fruit. At the same time, inter-annual and intra-regional differences in precipitation and temperature can alter soil moisture regimes and erosion risk, indirectly affecting nutrient availability and microbial activity (Zhao et al., 2024).

The soils in Zhejiang's loquat areas are typically developed from weathered red and yellow parent materials on hilly landforms, forming acidic to weakly acidic soils rich in iron and aluminum oxides. In similar subtropical loquat bases, soils are classified as latosols or other highly weathered types, with relatively low inherent fertility but strong responsiveness to fertilization and organic matter inputs (Zhang et al., 2025). Studies on loquat orchards in mid-low mountain regions of central China show that available N, P and K display marked spatial heterogeneity under the combined influence of soil type, slope, erosion and mean annual precipitation. Fine-textured soils and sufficient rainfall favor ammonium storage and conversion, whereas erosion accelerates the loss of available P and N (Zhao et al., 2024). These patterns suggest that in Zhejiang, variations in soil texture, depth and erosion intensity across slopes and valleys are likely to cause strong within-region differences in soil nutrient supply capacity and microbial habitats, even under broadly similar climatic conditions (Jiang et al., 2022).

2.3 Cultivation patterns and management practices of loquat orchards

Loquat orchards in Zhejiang are generally established on sunny mid-slopes, lower hillsides and river terraces, forming a mosaic of smallholder plots and specialized production bases. Investigations in Ninghai and other key production counties show that, under the same variety and similar macro-climate, fruit quality differs significantly among orchards, reflecting heterogeneity in soil physicochemical properties and management measures (Wang et al., 2024). Long-term planting tends to increase soil bulk density while lowering pH, organic carbon and available nutrients, leading to a gradual decline in soil quality and multifunctionality indices as orchard age increases. These trends indicate that extensive, fertilizer-intensive patterns may not sustain soil health in old orchards, and that optimizing fertilization structure and frequency is critical for maintaining microbial activity and nutrient cycling (Cui et al., 2024).

Typical management in loquat germplasm nurseries and production orchards includes regular weeding, 2-3 fertilizations per year, irrigation as needed, foliar fertilization during flowering spikes, fruit-strengthening fertilization during fruit expansion, and the application of organic materials such as peanut bran after harvest (Cui et al., 2024; Zhang et al., 2025). In practice, however, differences in fertilization types, dosages and timing among growers lead to site-specific soil nutrient profiles and microbial community responses. Soil microbial and protist communities in Ningbo loquat orchards are strongly structured by pH, available P, available K and dissolved organic N, and these communities in turn regulate multi-nutrient cycling indices linked to average fruit weight (Figure 2) (Wang et al., 2024). At the same time, studies on pesticide residues in Lanxi loquat highlight the need to strengthen standardized management, especially rational pesticide use and pre-harvest interval control, to ensure both fruit safety and stable quality (Liu et al., 2023). Overall, current cultivation and management patterns in Zhejiang's loquat orchards provide an important context for understanding spatial variability in soil microbial diversity and nutrient cycling.

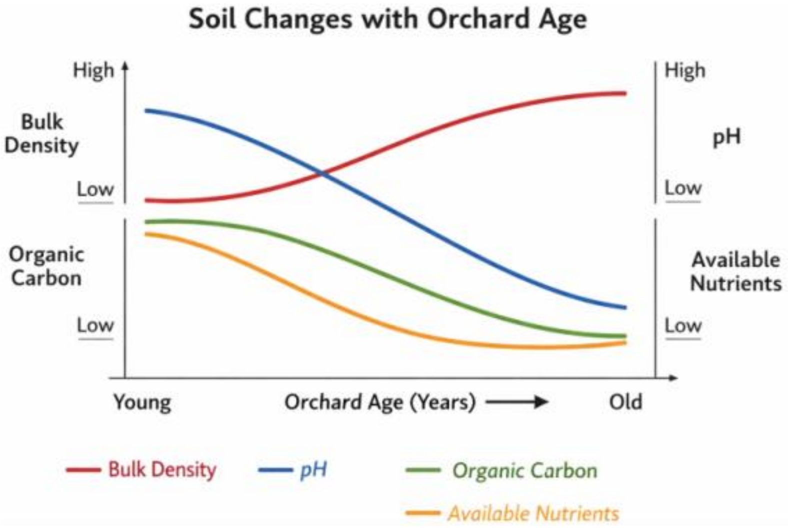

Figure 2 Conceptual trends of soil physicochemical properties with increasing orchard age, including bulk density, pH, organic carbon, and available nutrients (Adopted from Wang et al., 2024)

3 Theoretical Basis of Soil Microbial Diversity

3.1 Classification and functional groups of soil microorganisms

Soil harbors an enormous variety of microorganisms spanning all three domains of life, including bacteria, archaea, and eukaryotes such as fungi, algae, protozoa, and nematodes, each contributing differently to soil processes and plant growth (Kiprotich et al., 2025). Bacteria are typically the most abundant, driving rapid turnover of labile organic matter, transforming nitrogen and phosphorus, and producing phytohormones that support plant development. Fungi, with extensive hyphal networks, are crucial for decomposing recalcitrant plant residues such as lignin and cellulose, stabilizing soil aggregates, and forming symbiotic mycorrhizal associations that extend the root absorptive zone (Wang et al., 2024). Archaea participate in the transformation of low-molecular-weight organic substrates and play key roles in nitrogen cycling, including ammonia oxidation and other steps that influence soil N availability (Yadav et al., 2021). Protozoa and nematodes act mainly as microbial predators, regulating bacterial and fungal populations, recycling nutrients immobilized in microbial biomass, and shaping trophic interactions in the soil food web.

From a functional perspective, soil microorganisms can be divided into broad groups according to their ecological roles in nutrient acquisition and plant-soil interactions. One conceptual framework classifies them as “miners,” “scavengers,” and “carriers”: miners such as saprotrophic microbes, N_2 -fixing and phosphate-solubilizing bacteria, and ectomycorrhizal fungi liberate nutrients from organic matter and minerals; scavengers, notably arbuscular mycorrhizal fungi, efficiently take up soluble nutrients in collaboration with host plants; and carriers, including filamentous fungi, transport nutrients and bacteria across the soil matrix (Cao et al., 2023). In agricultural soils, additional functional groupings include plant growth-promoting rhizobacteria, nitrogen-fixing symbionts, phosphate-solubilizing microbes, decomposers, and biocontrol agents that suppress pathogens through competition or antibiotic production (Yadav et al., 2021). These overlapping and flexible roles create a division of labor that enhances substrate utilization, supports nutrient cycling, and underpins soil fertility and plant health, making functional grouping a useful theoretical basis for interpreting microbial diversity patterns in orchard systems (Sahu et al., 2019).

3.2 Indicators for evaluating microbial diversity

Quantifying soil microbial diversity relies on both taxonomic and functional indicators that capture different aspects of community structure. High-throughput sequencing of marker genes, such as 16S rRNA for bacteria and ITS regions for fungi, enables the estimation of α-diversity metrics and β-diversity based on dissimilarity measures like Bray-Curtis, revealing how communities differ across land uses and environmental gradients (Yoon et al., 2024). Studies comparing agricultural, grassland, and forest soils show that land-use type strongly structures microbial communities, with distinct taxonomic signatures and variable alpha diversity among ecosystems. Beyond taxonomic composition, functional diversity can be evaluated using enzyme activity profiles or community-level physiological profiling (CLPP), which infer the range and evenness of metabolic capabilities from patterns of substrate use and extracellular enzyme activities (Moscatelli et al., 2018). Enzyme-based and CLPP-based Shannon indices often respond differently to soil properties and land use, suggesting they reflect complementary components of functional diversity.

Microbial diversity is also assessed using indicators that link community structure to soil functioning. Functional gene abundances and predicted metabolic pathways, derived from sequencing data, help evaluate capacities for nitrogen fixation, phosphorus solubilization, carbon degradation, and greenhouse-gas related processes. For example, variation in soil pH can alter not only bacterial and fungal diversity but also the abundance of nitrogen-cycle genes and the potential for methane production and consumption (Xiong et al., 2024). At broader scales, meta-analyses show that shifts in microbial α-diversity under global change are largely explained by changes in soil pH, while soil functionality is more closely tied to community structure and biomass than to richness alone (Zhou et al., 2020). Therefore, an integrated evaluation framework for orchard soils should combine taxonomic indices (richness, Shannon, β-diversity), functional assays (enzyme activities, CLPP), and key functional gene or pathway indicators, allowing a more comprehensive assessment of how microbial diversity supports nutrient cycling and soil health (Yoon et al., 2024).

3.3 Key factors influencing microbial diversity

Soil microbial diversity is controlled by a suite of natural environmental factors and human-induced disturbances that interact across spatial and temporal scales. Among edaphic factors, soil pH consistently emerges as a dominant predictor of bacterial community composition and diversity, often showing unimodal relationships where diversity peaks at intermediate pH values (Xiong et al., 2024). Experimental pH amendments in contrasting agricultural soils demonstrate that bacterial communities are more tightly constrained by pH than fungal communities, and that pH influences microbial assemblages both directly, via physiological limits, and indirectly by modifying nutrient availability. Soil texture also exerts strong control over microbial diversity and community structure: fungal richness and Shannon diversity tend to increase with sand fraction, while finer-textured soils with higher silt and clay contents support distinct assemblages of filamentous bacteria and fungi and greater genetic potential for organic matter degradation (Xia et al., 2020). At landscape scales, gradients in temperature, precipitation, and soil nutrients produce spatially structured microbial communities, and different land uses along such gradients often harbor characteristic dominant phyla (Liu et al., 2022).

Agricultural management practices are another major driver of soil microbial diversity and function, particularly in orchards and other long-term systems. Organic and conservation-oriented practices generally increase microbial α-diversity and promote taxa associated with disease suppression and nutrient cycling, whereas intensive conventional practices can reduce diversity and simplify community networks (Zhou and Fong, 2021; Khmelevtsova et al., 2022). Global syntheses show that land-use change from natural ecosystems to croplands induces taxonomic homogenization of soil bacterial communities across continents, with large shifts in the relative abundances of major phyla and depletion of functional genes related to nitrogen fixation and phosphorus mineralization (Peng et al., 2024). At the same time, global change factors such as warming, altered precipitation, and nutrient deposition affect microbial communities in complex ways, with rare taxa often more sensitive than common ones and soil pH again mediating many responses (Wang et al., 2025). These findings highlight that in fruit orchards, management regimes (fertilization, tillage, cover crops), together with soil physicochemical properties and regional climate, jointly shape microbial diversity and thereby regulate nutrient cycling and ecosystem resilience (Narayana et al., 2022; Chen et al., 2024).

4 Nutrient Cycling Mechanisms in Loquat Orchard Soils

4.1 Soil carbon cycling processes

Soil carbon cycling in loquat orchards is driven by the input, transformation, and stabilization of organic matter derived from litterfall, pruned branches, root exudates, and organic amendments. In perennial orchards, repeated inputs of plant residues regulate soil organic carbon (SOC) dynamics by providing both labile and recalcitrant substrates that fuel microbial metabolism and aggregation processes (Figure 3) (Cai et al., 2025). The chemical quality of residues, particularly the C/N ratio and lignin content of roots and shoots, modulates decomposition rates and the incorporation of carbon into stable aggregates and mineral-associated fractions. In organic orchards, legume cover or mulched residues can enhance SOC and nitrate-N while simultaneously altering microbial co-occurrence networks, indicating that residue origin and placement affect both carbon turnover and the stability of decomposer communities (Wu et al., 2023). Over time, the balance between rapid mineralization and physical-chemical protection of carbon within aggregates determines SOC stocks and thus the capacity of loquat orchard soils to function as carbon sinks under different management regimes (Bhattacharyya et al., 2022).

Soil microorganisms mediate nearly all steps of carbon cycling, from the initial depolymerization of complex plant polymers to respiration and the formation of microbial necromass. Microbial communities decompose organic inputs through diverse metabolic pathways, with community composition and activity emerging as key drivers of variation in soil carbon storage potential (Wu et al., 2023). Reviews of microbial carbon cycling highlight that interactions among microbial taxa, their enzyme systems, and environmental filters such as pH and moisture shape both carbon mineralization and stabilization, linking microbial assembly processes to long-term SOC sequestration (Zhou et al., 2025). In orchard systems, management practices that increase organic inputs and reduce disturbance—such as organic fertilization, mulching, and cover cropping—tend to promote microbial biomass, enhance aggregate formation, and improve carbon retention, whereas intensive tillage and mineral-fertilizer-dominated regimes may accelerate SOC loss. These mechanisms imply that optimizing carbon inputs and microbial habitat quality is central to sustaining soil fertility and mitigating greenhouse gas emissions in loquat orchards.

4.2 Characteristics of nitrogen, phosphorus, and potassium cycles

Nitrogen (N), phosphorus (P), and potassium (K) cycles in orchard soils are tightly coupled to organic matter dynamics and fertilizer management, with perennial canopies and surface litter creating strong vertical and horizontal nutrient gradients. In loquat orchards of Zhejiang, multiple nutrient cycling indices integrating C, N, P and K transformations are significantly associated with fruit weight, suggesting that balanced and efficient nutrient cycling underpins high-quality production (Wang et al., 2024). In organic orchards, mulching with legume shoot and root litter supplies slow- and fast-release N sources, where fine roots with higher C/N ratios act as longer-term reservoirs and shoots decompose rapidly to meet immediate N demand (Wu et al., 2023). Nitrogen transformations in orchard soils involve mineralization of organic N, nitrification, and denitrification, all mediated by specialized microbial guilds whose gene abundances (e.g., nifH, amoA, nirS/nirK, nosZ) respond to soil moisture and organic carbon status (Morugán-Coronado et al., 2019). Moist zones near drip irrigation in citrus orchards show enhanced potential for N fixation and denitrification, indicating that fine-scale hydrological heterogeneity can strongly influence N availability and gaseous losses in tree-crop systems.

Phosphorus cycling in loquat and other orchard soils is characterized by substantial accumulation of both inorganic and organic P fractions due to long-term fertilization and litter inputs. Comparative studies of orchard species show that loquat soils often contain higher total and extractable P than citrus and guava, with residual and HCl-extractable forms dominating, but $NaHCO_3$- and H_2O- extractable pools determining short-term bioavailability (Bibi et al., 2022). Sequential fractionation demonstrates strong relationships between P forms and soil organic matter, clay content and cation-exchange capacity, highlighting the role of soil physical-chemical properties in regulating P sorption and release. Potassium cycling is closely linked to litter decomposition and cover management; in organic orchards, root litter can release over half of its K content within weeks, providing a rapid recycling pathway that supports tree demand during active growth (Wu et al., 2023). In addition, conservative, cover-crop-based management in plum orchards has been shown to enhance SOC and modify P and K dynamics relative to herbicide-based systems, indicating that management-induced changes in organic inputs drive long-term N, P and K distributions in orchard soils (Rusu et al., 2025).

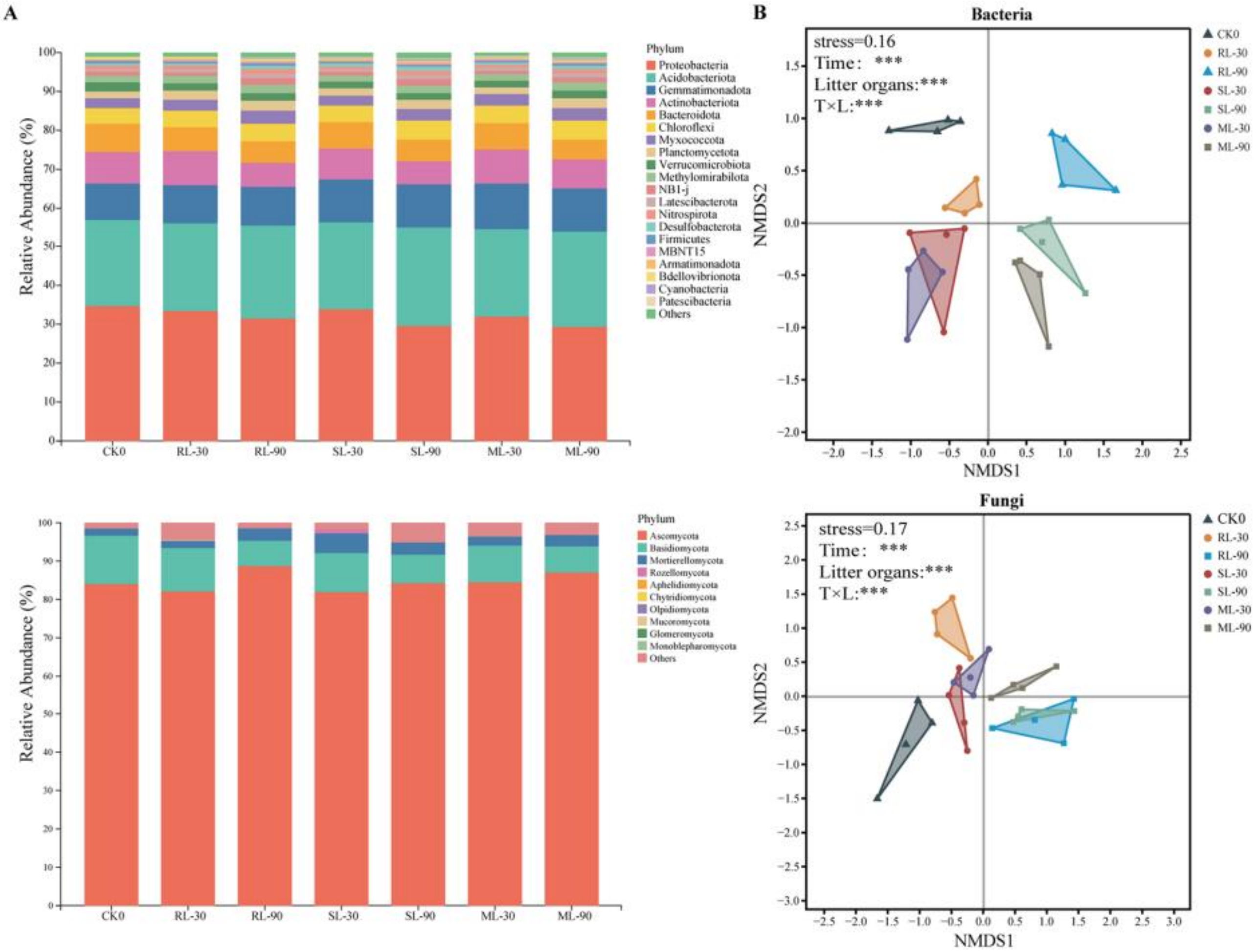

Figure 3 Composition of bacterial and fungal taxa (A) at the phylum level and NMDS of community (B). *** indicates significant impacts on microbial community structure due to litter organs, decomposition time, or their interactions ($P<0.001$, Adonis). Treatments including CK0 (the blank soil), RL (root litter), SL (shoot litter) and ML (mixed litter). Soil samples were taken at 0, 30 and 90 days post-residue addition (Adopted from Cai et al., 2025)

4.3 Roles of microorganisms in nutrient transformation

Microorganisms are central agents in nutrient transformations, coupling carbon use to nitrogen, phosphorus and potassium cycling through a wide suite of functional genes and ecological strategies. Metagenomic studies in perennial orchards reveal that long-term fertilization regimes sharply modify the relative abundance of genes associated with labile and recalcitrant carbon degradation, N degradation and dissimilatory nitrate reduction to ammonium (DNRA), and organic P mineralization and solubilization (Du et al., 2023). In walnut orchards, exclusive chemical fertilization increased genes for labile C degradation, whereas organic and biofertilizer additions reduced C-degradation potential but enhanced genes for N turnover (e.g., ureA, glnA) and P mobilization (e.g., phy, gcd), indicating a shift toward tighter nutrient recycling and potentially improved nutrient use efficiency. Across diverse Chinese agroecosystems, long-term N and P inputs have been shown to reconfigure P-transformation communities: sustained P additions increase microbial P immobilization by favoring low-affinity transporter genes, while chronic N enrichment acidifies soils and reduces the abundance and connectivity of P-solubilizing genes, challenging the assumption that N:P stoichiometry alone governs microbial P solubilization capacity (Dai et al., 2019). These findings underscore that fertilization strategies in loquat orchards will strongly influence the functional gene repertoire and, consequently, the efficiency and environmental footprint of nutrient cycling.

Within loquat orchards of Zhejiang, bacterial and protist communities are directly linked to multi-nutrient cycling and fruit yield, emphasizing that transformations of C, N, P and K are not only biochemical processes but also emergent properties of community composition and diversity (Wang et al., 2024). Orchard-scale analyses show that soil pH, available P and K, and dissolved organic N structure bacterial and protist assemblages, which in turn drive a composite nutrient-cycling index correlated with average fruit weight. In organic and intercropped fruit orchards, higher microbial diversity, respiration, and abundances of diazotrophs, denitrifiers and arbuscular mycorrhizal fungi have been reported, indicating that diversified management promotes microbial groups that regulate N acquisition, loss pathways and P uptake (Figure 4) (Janke et al., 2024). Microbial P-solubilizing communities and their phosphatase genes are also sensitive to over-fertilization and acidification in citrus orchards, where excess P accumulation suppresses phoD-harboring taxa and simplifies co-occurrence networks, thereby weakening biologically driven P mineralization (Zhou et al., 2025). Together, these results highlight that managing loquat orchards for high microbial diversity and functional redundancy—through moderated fertilization, organic amendments, and soil-conserving practices—is essential for sustaining robust nutrient transformation networks and resilient nutrient cycling.

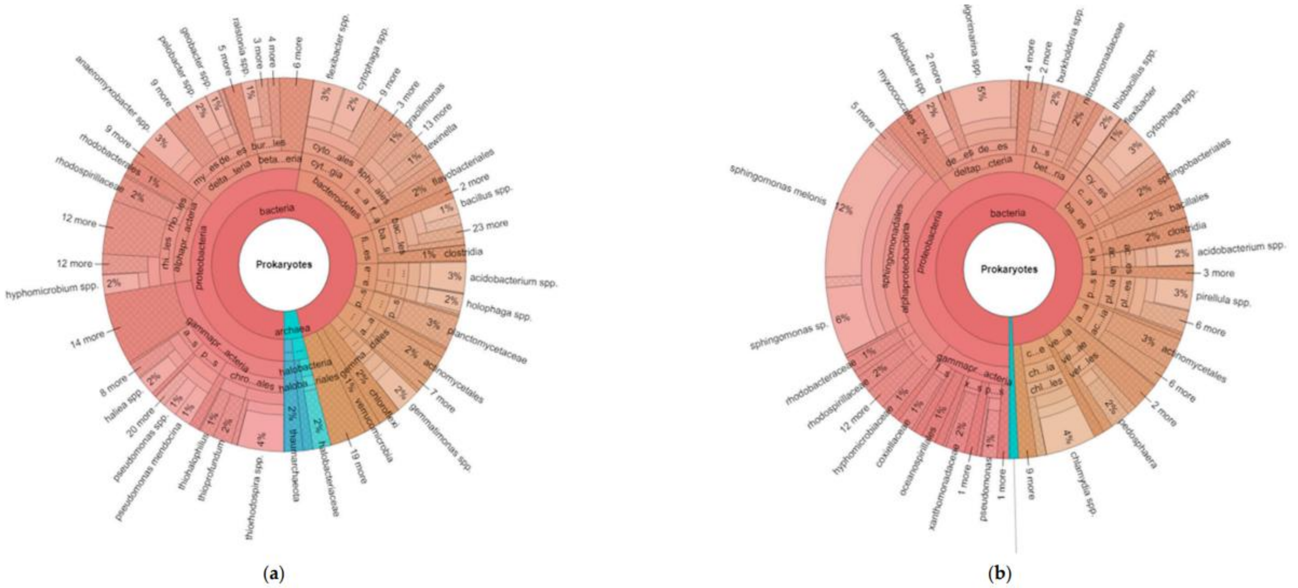

Figure 4 Hierarchical taxonomic abundance (from kingdom to genus) of prokaryotes based on 16S diverse treatments). Bacteria are represented in pink-brown sections of the chart, and archaea in the blue section. ribosomal RNA for organic (a) and conventional (b) soils (averaged across monoculture and diverse treatments). Bacteria are represented in pink-brown sections of the chart, and archaea in the blue section (Adopted from Janke et al., 2024)

5 Materials and Methods

5.1 Site selection and sample collection

Loquat orchards were selected in major production areas of Zhejiang Province to capture typical climatic and edaphic conditions, focusing on sites with similar parent material but contrasting management histories (conventional versus organic or reduced-input). Within each orchard, plots were established along tree rows and adjacent inter-row zones to account for small-scale spatial heterogeneity known to influence soil microbial communities in perennial systems (Deakin et al., 2018). Orchards with at least ten years of continuous loquat cultivation and no recent land-use change were prioritized to ensure that soil microbial assemblages and nutrient status reflected long-term management rather than short-term disturbance (Wang et al., 2021). Basic site information, including geographic coordinates, elevation, tree age, cultivar, fertilization regime, and groundcover management, was recorded during field surveys to support later interpretation of microbial and biochemical data (Taguali et al., 2025).

Soil sampling followed a stratified and partly composite design to balance spatial coverage and sequencing costs. At each orchard, soil cores (0-20 cm) were collected beneath the tree canopy at several points along a transect, with distances between points recorded to allow analysis of spatial structure in microbial communities. Individual cores from each plot were composited after thorough homogenization to provide representative samples for physicochemical and microbial analyses, while a subset of individual cores was retained to evaluate within-plot variability following recommendations for agricultural microbiome sampling (Castle et al., 2019). Visible roots and stones were removed, and samples were passed through a 2-mm sieve in the field. Subsamples for DNA extraction were placed in sterile bags, transported on ice, and stored at −80 °C, whereas portions for physicochemical and enzyme analyses were kept at 4 °C and processed within a short period to minimize biological changes (Yan et al., 2022).

5.2 Microbial community analysis methods

DNA was extracted from 0.25-0.50 g of sieved, frozen soil using a commercial soil DNA kit following the manufacturer's protocol, with minor modifications to improve lysis efficiency for mineral soils. DNA concentration and purity were measured fluorometrically, and extracts were normalized prior to PCR to reduce variation in amplification efficiency across samples (Sun et al., 2020). For bacterial communities, the V3-V4 or V4 region of the 16S rRNA gene was amplified using widely adopted primer pairs that provide broad coverage of major soil taxa, whereas fungal communities were characterized by sequencing the ITS2 region, enabling parallel analysis of both bacterial and fungal assemblages (McPherson et al., 2018). Amplicons were generated in triplicate PCR reactions per sample to reduce stochastic amplification bias, then pooled and purified using magnetic beads before library preparation.

Sequencing libraries were prepared according to Illumina protocols, including adapter ligation and indexing, and were sequenced on a MiSeq platform with paired-end reads, yielding sufficient depth to resolve differences in alpha and beta diversity among orchard soils (Taguali et al., 2025). Raw reads were processed using a quality-controlled amplicon pipeline based on QIIME2 and DADA2, which has been shown to outperform several alternative workflows in sequence recovery, taxonomic assignment, and diversity estimation for environmental microbiomes (Straub et al., 2020). After removal of low-quality reads, chimeras, and non-target sequences, amplicon sequence variants (ASVs) were inferred and assigned taxonomy using curated reference databases (e.g., SILVA for 16S, UNITE for ITS) (Schöler et al., 2017). Where quantitative comparisons of bacterial abundance were required, a subset of samples was spiked with a known amount of internal-standard DNA before extraction, allowing calculation of absolute 16S rRNA gene abundances from sequencing data (Smets et al., 2016). Downstream analyses included computation of richness and Shannon indices, ordination of community dissimilarities, and tests of relationships between microbial composition, soil properties, and enzyme activities.

5.3 Determination of soil physicochemical properties and enzyme activities

Soil physicochemical parameters were determined on air-dried, 2-mm-sieved subsamples using standard agronomic methods. Soil pH was measured potentiometrically in a 1:2.5 soil:water suspension, while total organic carbon and total nitrogen were quantified by dry combustion using an elemental analyzer, providing key indicators of soil fertility and microbial substrate supply (Deakin et al., 2018). Available phosphorus and potassium were extracted with appropriate reagents (e.g., bicarbonate for P, ammonium nitrate or ammonium acetate for K) and analyzed colorimetrically or by atomic absorption spectroscopy, following widely used protocols for orchard and arable soils (Piotrowska - Długosz et al., 2021). Bulk density was assessed with core cylinders, and particle-size distribution (sand, silt, clay) was determined by sieving and sedimentation or laser diffraction, enabling evaluation of texture effects on microbial communities and enzyme kinetics (Piotrowska - Długosz et al., 2022).

Enzyme activities associated with carbon, nitrogen, and phosphorus cycling were measured on fresh field-moist soils to characterize the functional potential of the microbial community. Urease, invertase (β-fructofuranosidase), alkaline phosphatase, and dehydrogenase activities were determined using colorimetric assays after incubation with specific substrates under controlled temperature and pH, reflecting common practice in studies linking enzyme activity to soil fertility and management (Ren et al., 2021). For example, urease activity was assessed using urea as substrate and quantifying released ammonium, whereas alkaline phosphatase was measured by the release of p-nitrophenol from p-nitrophenyl phosphate. Activities were expressed on both a soil mass basis and, where microbial biomass data were available, normalized to microbial biomass carbon to distinguish changes driven by biomass from those due to shifts in specific activity (Piotrowska - Długosz et al., 2022). These enzyme measurements, combined with microbial community profiles and soil properties, provided an integrated assessment of soil biochemical functioning in loquat orchards under contrasting management.

6 Characteristics of Soil Microbial Diversity in Zhejiang Loquat Orchards

6.1 Composition of microbial community structure

Soil microbial communities in Zhejiang loquat orchards are taxonomically rich and dominated by a core set of bacterial and fungal phyla typical of subtropical perennial systems. High-throughput sequencing of orchard soils in Ningbo revealed that bacteria, fungi, and protists form distinct yet coexisting assemblages that are tightly linked to local soil conditions and orchard location. At the bacterial phylum level, Proteobacteria, Actinobacteriota, Acidobacteriota, Chloroflexi, and Bacteroidota generally predominate, mirroring patterns reported for other fruit orchards and intercropping systems where these groups drive decomposition and nutrient turnover (Muneer et al., 2022). Fungal communities are typically dominated by Ascomycota and Basidiomycota, with additional contributions from Mortierellomycota, forming a functional continuum from saprotrophs to potential plant pathogens that respond sensitively to soil salinity and nutrient status.

Protists constitute an important but often overlooked component of loquat orchard microbiomes, acting as predators, primary producers, and parasites within the soil food web. In Ninghai County orchards, protistan communities showed strong compositional gradients along dissolved organic nitrogen and available potassium, indicating that labile N sources and base cation supply partly structure their distribution (Wang et al., 2024). Beyond loquat monocultures, metagenomic work in loquat-tea intercropping systems has shown that intercropping can substantially expand the taxonomic breadth of rhizosphere microbiota, with more than 160 phyla and thousands of genera detected and Actinobacteria, Proteobacteria, Acidobacteria, and Chloroflexi emerging as dominant groups (Zou et al., 2025). Together, these findings suggest that loquat orchards host complex multi-kingdom communities whose composition reflects both orchard-scale edaphic filters and broader management contexts.

6.2 Diversity indices and spatial variations

Microbial diversity in Zhejiang loquat orchards varies markedly among orchards and at finer spatial scales, reflecting the influence of location, soil chemistry, and management. In Ninghai orchards, bacterial and protist α-diversity, measured by richness and Shannon indices, differed significantly among sites and was closely associated with soil pH, available phosphorus, and available potassium, whereas cultivation time and fertilization intensity explained little of the variation (Wang et al., 2024). Similar patterns of strong spatial structuring have been observed in citrus and pomelo orchards, where microbial richness and diversity decrease with depth and co-occurrence network complexity weakens, indicating a shift from highly interactive topsoil communities to more filtered subsurface assemblages (Muneer et al., 2022). Within-field studies in other agricultural systems confirm that bacterial and fungal diversity exhibit spatial autocorrelation at tens of meters and are best predicted by gradients in soil organic carbon, clay content, and water retention, highlighting the need to account for micro-topography and texture when interpreting loquat orchard microbiomes (Naveed et al., 2016).

Horizontal spatial variability within individual orchards is also pronounced and can arise from differences between tree rows and inter-row vegetation, localized management, and microclimatic heterogeneity. Work in commercial apple orchards has shown that most variation in bacterial and fungal community structure occurs between orchards, but within-orchard distance-decay relationships and sharp differences between tree stations and adjacent grass aisles still emerge, emphasizing the role of vegetation type and associated management as local filters (Deakin et al., 2018). In Zhejiang loquat orchards, orchard location similarly dominates over cultivation time as a determinant of diversity, but the observed correlations between α- and β-diversity of bacteria and protists and fruit weight indicate that small-scale spatial patterns in diversity have agronomic consequences. Studies across land-use gradients in China further support that shifts from natural vegetation to intensive perennial cropping alter both bacterial and fungal diversity, generally increasing chemoheterotrophic and pathogenic groups at the expense of symbionts, which may also occur where loquat cultivation replaces former woodland (Labouyrie et al., 2023).

6.3 Dominant microbial taxa and their ecological functions

Several dominant microbial taxa in loquat orchard soils perform key ecological functions related to nutrient cycling, organic matter turnover, and plant health. In Ningbo loquat orchards, specific bacterial phyla, including Proteobacteria and Actinobacteriota, were positively associated with a composite multi-nutrient cycling index and with average fruit weight, indicating that these taxa contribute to processes that maintain soil fertility and yield (Wang et al., 2024). In pomelo orchards on red soils, Proteobacteria, Acidobacteria, Actinobacteria, and Chloroflexi were identified as the most abundant phyla, with predicted functions linked to carbon and nitrogen cycling, energy production, and other core metabolic processes that were especially enriched in biologically active topsoil horizons (Muneer et al., 2022). At finer taxonomic levels in loquat-tea intercropping systems, genera such as Bryobacter and Sphingomonas were strongly correlated with organic matter, alkali-hydrolyzed nitrogen, and available phosphorus and potassium, suggesting specialized roles in nutrient mineralization and mobilization under diversified perennial canopies (Zou et al., 2025).

Fungal and protistan taxa add additional layers of functional complexity. Ascomycota-dominated fungal assemblages in orchard soils include saprotrophic groups that drive litter decomposition as well as potential plant pathogens whose prevalence can increase under long-term orchard management, as shown after conversion of cropland to orchards on the Loess Plateau (Wang et al., 2021). Arbuscular mycorrhizal fungi (AMF) in loquat rhizospheres exhibit substantial colonization rates, with Glomus and Diversispora as dominant genera that respond sensitively to total carbon and soil organic matter, underscoring their role in enhancing phosphorus and micronutrient uptake while being suppressed by excessive nitrogen and potassium enrichment (Zhang et al., 2025). In Ninghai loquat orchards, many protistan genera correlated with microelement gradients, and microelements together with the microbiome emerged as leading predictors of fruit mineral composition and overall quality, revealing that protist-mediated grazing and nutrient regeneration likely influence both microbial community assembly and loquat fruit micronutrients. Collectively, these dominant bacterial, fungal, protistan, and mycorrhizal taxa form an integrated functional network that links soil chemistry, nutrient cycling, and loquat productivity in Zhejiang orchards.

7 Coupling Relationships Between Soil Microorganisms and Nutrient Cycling

7.1 Relationships between microbial diversity and soil nutrient content

In Zhejiang loquat orchards, overall microbial diversity is closely linked to soil nutrient status through multi-element cycling. Work in Ninghai showed that bacterial and protist α- and β-diversity were significantly correlated with a composite multiple nutrient cycling index that integrated C, N, P, and K processes, and this same index strongly related to average loquat fruit weight (Wang et al., 2024). Across diverse terrestrial habitats, multidiversity combining bacterial and fungal richness was positively associated with a similar multinutrient cycling index in most ecosystems, highlighting that community composition and not just α-diversity is a key predictor of nutrient cycling capacity (Jiao et al., 2021). These findings imply that in loquat soils, shifts in microbial diversity are likely reflected in altered nutrient availability and ultimately in fruit yield and quality.

Soil microbial diversity is itself shaped by the availability and balance of key nutrients, creating a feedback between community structure and nutrient pools. In apple orchards across different Chinese climate zones, increased bacterial diversity was positively associated with soil organic matter and pH, and higher diversity improved soil nutrient availability and leaf nutrient uptake through changes in ecological stoichiometry (Zhang et al., 2017). In Ninghai loquat orchards, heterogeneity in bacterial communities was driven mainly by soil pH and available P and K, whereas protists responded more strongly to dissolved organic nitrogen and available K, indicating that both macronutrients and labile N forms regulate multi-kingdom diversity and its functional consequences (Wang et al., 2024). Together, these patterns suggest that managing soil C and N supply, P and K fertility, and pH in Zhejiang loquat orchards will modify microbial diversity and, in turn, multi-nutrient cycling.

7.2 Nutrient transformation driven by key microorganisms

Specific microbial taxa and functional groups are central to the transformation of C, N, P, and S in orchard soils. In Ninghai loquat orchards, several bacterial phyla, including Proteobacteria and Actinobacteriota, were positively associated with the multi-nutrient cycling index and with fruit weight, indicating that these groups underpin coupled transformations of organic matter and mineral nutrients (Wang et al., 2024). Metagenomic work in long-term fertilization experiments further demonstrated that manure application enriches functional genes related to C, N, P, and S cycling, thereby increasing C and N turnover rates and providing substrates that sustain microbial growth and activity (Tang et al., 2023). Such functional enrichment suggests that loquat orchards with higher abundances of nutrient-cycling taxa may show faster organic matter decomposition, stronger N mineralization, and more dynamic P and S transformations.

Microbial functional genes provide a mechanistic link between taxonomic composition and observed nutrient fluxes. Under long-term P fertilization on the Loess Plateau, the abundance of genes involved in C cycling increased, whereas genes for P solubilization and mineralization decreased, and keystone taxa such as Actinobacteria, Proteobacteria, Bacteroidetes, and Chloroflexi were strongly correlated with C, N, P, and S cycling genes (Figure 5) (Liu et al., 2023). In a complementary synthesis, soil microorganisms were shown to enhance plant nutrition by decomposing organic residues, mineralizing N and P, and producing extracellular enzymes that regulate nutrient release and immobilization in agricultural soils (Chen et al., 2024). These results indicate that in Zhejiang loquat orchards, the dominance of particular bacterial and fungal groups, together with their encoded enzymes and transporters, likely determines the efficiency and stoichiometry of nutrient transformations.

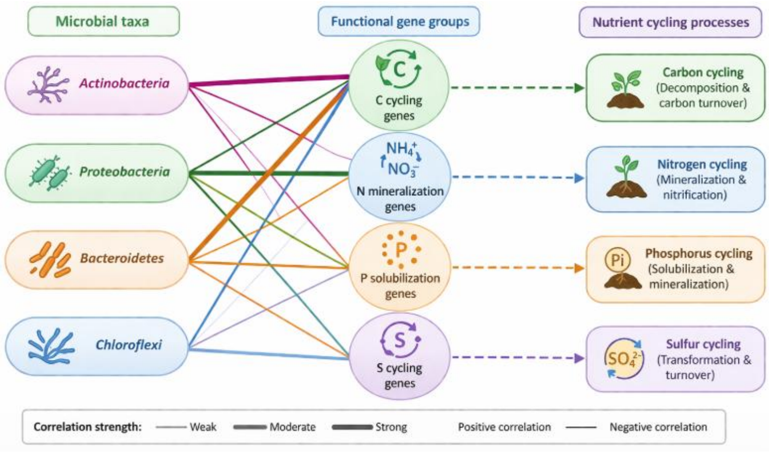

Figure 5 Network linking microbial functional genes and key taxa to C, N, P, and S cycling processes in agricultural soils (Adopted from Liu et al., 2023)

7.3 Regulatory effects of environmental factors on coupling relationships

Environmental factors strongly modulate how tightly soil microorganisms are coupled to nutrient cycling, both in loquat orchards and in broader agroecosystems. In Ninghai, orchard location—representing combined differences in climate, soil type, and management—was the main driver of soil physicochemical properties, microbial communities, and fruit quality, whereas cultivation time and fertilization showed much weaker effects (Wang et al., 2024). A large-scale survey across multiple habitats likewise found that the strength and even direction of the diversity-multinutrient cycling relationship depended on the balance between neutral processes and bacterial-fungal associations, with habitats showing stronger negative interactions exhibiting weaker or negative diversity-function links (Jiao et al., 2021). These findings imply that in Zhejiang loquat systems, local edaphic context and microbial interaction networks may either reinforce or dampen the benefits of high microbial diversity for nutrient cycling.

Soil nutrient stoichiometry and pH are particularly important regulators of the coupling between microbial communities and nutrient transformations. In long-term manure trials, variation partitioning revealed that soil C and N contents—especially dissolved organic C—explained more microbial community variation than P and S, and path analysis showed that dissolved organic C directly promoted C and S cycling, whereas N and P cycles were mediated indirectly through shifts in microbial composition (Tang et al., 2023). Experiments manipulating N and P inputs in forest and grassland soils further demonstrated that changes in P availability reshaped microbial functional genes and phosphatase activity, and that element-cycling rates were often controlled more by abiotic factors (pH, C availability) than by biomass alone (Widdig et al., 2020; Xiaomin et al., 2022). For Zhejiang loquat orchards, these results suggest that practices which adjust organic matter inputs, maintain moderate P fertility, and alleviate acidification will influence not only microbial diversity but also the tightness of its coupling to multi-element nutrient cycling.

8 Case Study: Soil Ecosystem Analysis of a Typical Loquat Orchard

8.1 Selection and basic description of the case study site

A representative loquat orchard in Ninghai County, Ningbo, Zhejiang Province can be selected as a typical case because this region is a core production area of the high-quality “Ninghai Bai” loquat and has been the focus of recent soil-microbiome-fruit quality research (Wang et al., 2024). The orchard is situated in a subtropical monsoon climate with warm, humid conditions and distinct wet and dry seasons, and loquat trees are generally planted on gently sloping hillsides with well-drained, acidic soils. Trees are usually of the same commercial cultivar and grafted onto similar rootstocks, which reduces genetic variation and allows differences in soil and microbial properties to be more clearly attributed to environmental and management drivers (Zhang et al., 2025).

In the Ninghai area, surface soils (0-20 cm) of loquat orchards typically exhibit decreased pH and declining organic carbon and available nutrient contents with increasing planting years, indicating progressive soil acidification and fertility loss under long-term cultivation (Cui et al., 2024). Bulk density tends to increase as planting years extend beyond 10-15 years, reflecting compaction from machinery traffic and reduced aggregation, while microbial biomass carbon and soluble organic C and N decline, signaling deterioration of biological activity alongside physical and chemical degradation. These characteristics make a mid- to late-stage commercial orchard (15-20 years) in Ninghai an appropriate case to analyze how soil microbial diversity, nutrient cycling, and management interact under realistic production conditions (Wang et al., 2024).

8.2 Analysis of microbial diversity and nutrient cycling characteristics

High-throughput sequencing of bacterial, fungal, and protist communities in Ninghai loquat orchards has shown that orchard location is the primary determinant of soil microbiomes and fruit quality, surpassing cultivation time and fertilization history (Wang et al., 2024). In the selected orchard, bacterial, fungal, and protist assemblages in the 0-20 cm layer are expected to be structured by local soil physicochemical conditions, including pH, electrical conductivity, and the availability of macro- and micro-nutrients such as P, K, Mg, and Cu. Bacterial community heterogeneity is mainly driven by soil pH and available P and K, fungal communities respond more strongly to electrical conductivity and K, while protists are particularly sensitive to dissolved organic nitrogen and available K, indicating differentiated ecological niches among the three groups.

From a functional perspective, microbial diversity in this orchard is closely linked to a composite multiple nutrient cycling index that integrates C, N, P, and K processes, and this index in turn correlates strongly with average fruit weight, a key yield indicator (Wang et al., 2024). Bacterial and protist α- and β-diversity exhibit significant positive relationships with the multinutrient cycling index, suggesting that richer and more heterogeneous communities support more efficient nutrient turnover and resource use in the rhizosphere. Microelements further modulate these relationships: variations in Mg and Cu contents explain a substantial fraction of the variance in community structure, and together with the microbiome they account for around one-fifth of the variation in loquat fruit quality, including mineral nutrient profiles. This indicates that in the case study orchard, microbial diversity, nutrient cycling, and fruit performance are tightly coupled through both macro- and micro-element availability.

8.3 Effects of management practices on soil ecological functions

Management practices in the typical Ninghai loquat orchard—especially fertilization intensity, groundcover handling, and tillage—strongly influence soil quality and, indirectly, microbial functions. Long-term surveys across planting-year gradients show that with continued loquat cultivation, soil quality indices and multifunctionality indices decline sharply, with reductions exceeding 35% after 15-20 years compared with younger orchards, largely due to losses of soluble N, available P and K, and total organic C and N (Cui et al., 2024). This trend reflects heavy reliance on mineral fertilizers combined with limited organic inputs and frequent soil disturbance, which together deplete soil organic matter and weaken the capacity of the soil to buffer nutrient fluctuations and support diverse microbial communities (Wang et al., 2024). In contrast, studies of fruit orchards under conservative management demonstrate that no-tillage, cover crops, and recycling of pruning residues increase soil organic carbon, microbial activity, and functional diversity, thereby enhancing nutrient supply and ecosystem resilience (Montanaro et al., 2017).

Within the Ninghai loquat orchard, nutrient management also interacts with the arbuscular mycorrhizal fungal (AMF) community, which contributes to P uptake and soil structure. Evidence from a loquat germplasm nursery indicates that long-term enrichment of N and K reduces AMF diversity and colonization, whereas higher total C and soil organic matter favor dominant AMF genera such as Glomus and Diversispora, highlighting the cost of excessive mineral fertilization for symbiotic fungi (Zhang et al., 2025). Microelement management is equally important: targeted Mg and Cu fertilization can shift bacterial, fungal, and protist community composition in ways that improve fruit micronutrient content, but imbalances or toxicities risk disrupting community assembly processes and weakening the link between microbial diversity and nutrient cycling. Drawing on broader orchard studies, integrating organic amendments, maintaining groundcover, and optimizing mineral fertilizer and microelement inputs would be expected to increase soil organic carbon, microbial biomass, and functional gene abundance, thereby strengthening soil ecological functions and sustaining high-quality loquat production over the long term (Zhao et al., 2024; Janke et al., 2024).

9 Conclusions and Prospects

Research on loquat orchards in Zhejiang, particularly Ninghai County, shows that soil microbial diversity is tightly coupled to multi-element nutrient cycling and fruit yield. Bacterial and protist α- and β-diversity are strongly associated with a composite nutrient cycling index and with average fruit weight, indicating that belowground biodiversity directly underpins productivity in these systems. At the same time, long-term planting progressively degrades soil quality: bulk density increases, pH declines, and organic C and available N, P, and K all decrease with orchard age, leading to sharp reductions in soil multifunctionality indices. Together, these findings highlight that maintaining a diverse, functionally rich microbiome while preventing physicochemical degradation is central to sustaining loquat production in Zhejiang. Soil chemical drivers of microbial communities and nutrient cycling are now better resolved for loquat orchards. Macro-nutrients (available P and K) and pH largely structure bacterial assemblages, while electrical conductivity and K are more important for fungi, and dissolved organic N and K regulate protists, revealing distinct ecological controls across microbial kingdoms. Microelements such as Mg and Cu have emerged as particularly influential, explaining more variation in microbial community structure than many macro-properties and jointly with the microbiome accounting for a significant share of fruit quality variation. Long-term management further alters symbiotic groups: high N and K enrichment reduces arbuscular mycorrhizal fungal diversity, whereas higher total C and soil organic matter favor beneficial AMF genera in loquat rhizospheres. Overall, the major advances lie in clarifying how macro- and micro-nutrients, soil quality decline, and community composition interact to control nutrient cycling and fruit quality in Zhejiang loquat systems.

Given the documented decline in soil quality with planting years, management in Zhejiang loquat orchards should prioritize slowing acidification and restoring organic matter. Evidence from Ninghai indicates that soluble N, available P and K, and total organic C and N are key determinants of soil quality and multifunctionality, which fall by more than one-third in 15-20-year orchards compared with younger stands. Introducing regular organic amendments, groundcover or sod culture, and reduced tillage can increase soil organic carbon, microbial biomass, and enzyme activities, thereby improving nutrient retention and buffering capacity in fruit orchards more broadly. These practices are likely to be particularly beneficial in mid- and late-stage loquat orchards where physical compaction and nutrient depletion are already evident. Fertilization strategies should be refined from both macro- and micro-nutrient perspectives to support microbial diversity and fruit quality. Work in Ninghai shows that soil microelements, especially available Mg and Cu, explain substantial variation in bacterial, fungal, and protist genera and act alongside the microbiome as top predictors of fruit micronutrient profiles. At the same time, long-term nutrient enrichment, particularly of N and K, suppresses AMF diversity and colonization in loquat roots, suggesting that balanced fertilization with moderated N and K rates is needed to protect symbiotic fungi. Orchard managers should therefore combine soil testing with targeted microelement inputs, avoid excessive mineral N and K, and integrate AMF-friendly practices such as reduced disturbance and organic inputs. Lessons from other fruit orchards, where organic and intercropping systems enhance microbial diversity, respiration, and nutrient cycling, provide a practical template for transitioning Zhejiang loquat orchards toward more sustainable, microbially driven management.

Future work should deepen mechanistic understanding of how specific microbial taxa and functional genes regulate C, N, P, and K cycles in loquat soils. Current research has established strong correlations between bacterial and protist diversity, multinutrient cycling, and fruit weight, but the causal pathways linking particular taxa or guilds to nutrient fluxes remain largely unresolved. Metagenomic and metatranscriptomic approaches, which have clarified nutrient-cycling gene networks in other perennial orchards, could be applied to loquat to track how functional genes for organic matter decomposition, N transformations, and P solubilization respond to management and soil gradients. In parallel, integrating AMF community profiling with measurements of root nutrient uptake and soil enzyme activities would clarify the specific contribution of mycorrhizal symbioses to nutrient efficiency under different fertilization regimes. Another priority is to evaluate the long-term impacts of alternative management systems—such as organic, green mulching, and intercropping—on soil multifunctionality and fruit quality in loquat orchards. Studies in citrus, persimmon, and other fruit systems show that leguminous mulching, sod culture, and organic management can enhance microbial diversity, increase C-, N-, and P-cycling enzyme activities, and strengthen microbial interaction networks, ultimately improving soil quality and yield stability. Translating these approaches to the humid subtropical context of Zhejiang loquat orchards will require multi-year field experiments that couple high-resolution microbiome analyses with soil health and fruit-quality assessments. Finally, linking loquat-specific findings to broader frameworks on microbial diversity-function relationships and environmental controls on available nutrients can help design precision fertilization and soil-ecological regulation strategies tailored to the complex topography and climate of East China's loquat-growing regions.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

Bhattacharyya S., Ros G., Furtak K., Iqbal H., and Parra-Saldívar R., 2022, Soil carbon sequestration: An interplay between soil microbial community and soil organic matter dynamics, Science of the Total Environment, 815: 152928.
https://doi.org/10.1016/j.scitotenv.2022.152928

Bibi S., Irshad M., Mohiuddin M., Sher S., Tariq M., and Ng A., 2022, Distribution of phosphorus fractions in orchard soils in relation to soil properties and foliar P contents, Sustainability, 14(7): 3966.
https://doi.org/10.3390/su14073966

Cai M., Chen H., Tan H., Chen J., He S., and Long M., 2025, Temporal dynamics of nutrient release from mulching of legume roots and shoots litter driven by microbial community during decomposition in organic orchards, BMC Plant Biology, 25(1): 92.
https://doi.org/10.1186/s12870-025-06392-2

Cao T., Luo Y., Shi M., Tian X., and Kuzyakov Y., 2023, Microbial interactions for nutrient acquisition in soil: Miners, scavengers, and carriers, Soil Biology and Biochemistry, 185: 109215.
https://doi.org/10.1016/j.soilbio.2023.109215

Castellano-Hinojosa A., Kanissery R., and Strauss S., 2023, Cover crops in citrus orchards impact soil nutrient cycling and the soil microbiome after three years but effects are site-specific, Biology and Fertility of Soils, 59(5): 659-678.
https://doi.org/10.1007/s00374-023-01729-1

Castle S.C., Samac D.A., Sadowsky M.J., Rosen C.J., Gutknecht J.L.M., and Kinkel L.L., 2019, Impacts of sampling design on estimates of microbial community diversity and composition in agricultural soils, Microbial Ecology, 78(3): 753-763.
https://doi.org/10.1007/s00248-019-01318-6

Chen Q., Song Y., An Y., Lu Y., and Zhong G., 2024, Soil microorganisms: Their role in enhancing crop nutrition and health, Diversity, 16(12): 734.
https://doi.org/10.3390/d16120734

Cui X., Xiao M., Zhao Y., Wu Y., Wu B., Qi L., Li H., Yu C., Lu S., Zhang Y., and Ge T., 2024, Soil health evaluation of loquat orchard based on soil quality index method, Chinese Journal of Applied Ecology, 35(10): 2775-2784.
https://doi.org/10.13287/j.1001-9332.202410.013

Dai Z., Liu G., Chen H., Chen C., Wang J., Ai S., Wei D., Li D., Tang C., Brookes P.C., and Xu J., 2019, Long-term nutrient inputs shift soil microbial functional profiles of phosphorus cycling in diverse agroecosystems, ISME Journal, 14(3): 757-770.
https://doi.org/10.1038/s41396-019-0567-9

Deakin G., Tilston E.L., Bennett J., Passey T., Harrison N., Fernández-Fernández F., and Xu X., 2018, Spatial structuring of soil microbial communities in commercial apple orchards, Applied Soil Ecology, 130: 1-12.
https://doi.org/10.1016/j.apsoil.2018.05.015

Du T., Hu Q., Mao W., Yang Z., Chen H., Sun L., and Zhai M., 2023, Metagenomics insights into the functional profiles of soil carbon, nitrogen, and phosphorus cycles in a walnut orchard under various regimes of long-term fertilisation, European Journal of Agronomy, 146: 126887.
https://doi.org/10.1016/j.eja.2023.126887

Janke R., Menezes-Blackburn D., Hamdi A., and Rehman A., 2024, Organic management and intercropping of fruit perennials increase soil microbial diversity and activity in arid zone orchard cropping systems, Sustainability, 16(21): 9391.
https://doi.org/10.3390/su16219391

Jiang Y., Huang A., Wu H., and Zhang X., 2022, GIS-based research on climate suitable region of loquat in Lishui, Zhejiang province of China, Environmental Research Communications, 4(2): 025001.
https://doi.org/10.1088/2515-7620/ac4a3c

Jiao S., Peng Z., Qi J., Gao J., and Wei G., 2021, Linking bacterial-fungal relationships to microbial diversity and soil nutrient cycling, mSystems, 6(1): e01052-20.
https://doi.org/10.1128/msystems.01052-20

Khmelevtsova L., Sazykin I., Azhogina T., and Sazykina M., 2022, Influence of agricultural practices on bacterial community of cultivated soils, Agriculture, 12(3): 371.
https://doi.org/10.3390/agriculture12030371

Kiprotich K., Muema E., Wekesa C., Ndombi T., Muoma J., Omayio D., Ochieno D., Motsi H., Mncedi S., and Tarus J., 2025, Unveiling the roles, mechanisms and prospects of soil microbial communities in sustainable agriculture, Discover Soil, 2(1): 37.
https://doi.org/10.1007/s44378-025-00037-4

Liu L., Gao Y., Yang W., Liu J., and Wang Z., 2023, Community metagenomics reveals the processes of nutrient cycling regulated by microbial functions in soils with P fertilizer input, Plant and Soil, 489(1-2): 1-16.
https://doi.org/10.1007/s11104-023-05875-1

Liu S., Sun Y., Shi F., Liu Y., Wang F., Dong S., and Li M., 2022, Composition and diversity of soil microbial community associated with land use types in the agro-pastoral area in the upper Yellow River Basin, Frontiers in Plant Science, 13: 819661.
https://doi.org/10.3389/fpls.2022.819661

Liu Y., Bei K., Zheng W., Yu G., and Sun C., 2023, Pesticide residues risk assessment and quality evaluation of four characteristic fruits in Zhejiang Province, China, Frontiers in Environmental Science, 11: 1124094.
https://doi.org/10.3389/fenvs.2023.1124094

McPherson M., Wang P., Marsh E.L., Mitchell R.B., and Schachtman D.P., 2018, Isolation and analysis of microbial communities in soil, rhizosphere, and roots in perennial grass experiments, Journal of Visualized Experiments, (140): e57932.
https://doi.org/10.3791/57932

Montanaro G., Xiloyannis C., Nuzzo V., and Dichio B., 2017, Orchard management, soil organic carbon and ecosystem services in Mediterranean fruit tree crops, Scientia Horticulturae, 217: 92-101.
https://doi.org/10.1016/j.scienta.2017.01.012

Morugán-Coronado A., García-Orenes F., McMillan M., and Pereg L., 2019, The effect of moisture on soil microbial properties and nitrogen cyclers in Mediterranean sweet orange orchards under organic and inorganic fertilization, Science of the Total Environment, 655: 158-167.
https://doi.org/10.1016/j.scitotenv.2018.11.174

Moscatelli M.C., Secondi L., Marabottini R., Papp R., Stazi S.R., Mania E., and Marinari S., 2018, Assessment of soil microbial functional diversity: land use and soil properties affect CLPP-MicroResp and enzymes responses, Pedobiologia, 66: 36-42.
https://doi.org/10.1016/j.pedobi.2018.01.001

Muneer M., Hou W., Li J., Huang X., Kayani M.U.R., Cai Y., Yang W., Wu L., Ji B., and Zheng C., 2022, Soil pH: a key edaphic factor regulating distribution and functions of bacterial community along vertical soil profiles in red soil of pomelo orchard, BMC Microbiology, 22(1): 52.
https://doi.org/10.1186/s12866-022-02452-x

Narayana N., Kingery W.L., Shankle M.W., and Shanmugam S.G., 2022, Differential response of soil microbial diversity and community composition influenced by cover crops and fertilizer treatments in a dryland soybean production system, Agronomy, 12(3): 618.
https://doi.org/10.3390/agronomy12030618

Naveed M., Herath L., Moldrup P., Arthur E., Nicolaisen M., Norgaard T., Ferre T.P.A., and de Jonge L.W., 2016, Spatial variability of microbial richness and diversity and relationships with soil organic carbon, texture and structure across an agricultural field, Applied Soil Ecology, 103: 44-55.
https://doi.org/10.1016/j.apsoil.2016.03.004

Peng Z., Qian X., Liu Y., Li X., Gao H., An Y., Qi J., Jiang L., Zhang Y., Chen S., Pan H., Chen B., Liang C., van der Heijden M.G.A., Wei G., and Jiao S., 2024, Land conversion to agriculture induces taxonomic homogenization of soil microbial communities globally, Nature Communications, 15(1): 47348.
https://doi.org/10.1038/s41467-024-47348-8

Piotrowska-Długosz A., Długosz J., Frąc M., Gryta A., and Breza-Boruta B., 2022, Enzymatic activity and functional diversity of soil microorganisms along the soil profile - A matter of soil depth and soil-forming processes, Geoderma, 406: 115779.
https://doi.org/10.1016/j.geoderma.2022.115779

Piotrowska-Długosz A., Kobierski M., and Długosz J., 2021, Enzymatic activity and physicochemical properties of soil profiles of Luvisols, Materials, 14(21): 6364.
https://doi.org/10.3390/ma14216364

Ren J., Liu X., Yang W., Yang X., Li W., Xia Q., Li J., Gao Z., and Yang Z., 2021, Rhizosphere soil properties, microbial community, and enzyme activities: short-term responses to partial substitution of chemical fertilizer with organic manure, Journal of Environmental Management, 299: 113650.
https://doi.org/10.1016/j.jenvman.2021.113650

Rusu M., Filip M., Cara I., Ţopa D., and Jitareanu G., 2025, Soil nutrient dynamics and farming sustainability under different plum orchard management practices in the pedoclimatical conditions of Moldavian Plateau, Agriculture, 15(5): 509.
https://doi.org/10.3390/agriculture15050509

Sahu P.K., Singh D.P., Prabha R., Meena K.K., and Abhilash P.C., 2019, Connecting microbial capabilities with the soil and plant health: options for agricultural sustainability, Ecological Indicators, 105: 601-612.
https://doi.org/10.1016/j.ecolind.2018.05.084

Schöler A., Jacquiod S., Vestergaard G., Schulz S., and Schloter M., 2017, Analysis of soil microbial communities based on amplicon sequencing of marker genes, Biology and Fertility of Soils, 53(5): 485-489.
https://doi.org/10.1007/s00374-017-1205-1

Smets W., Leff J.W., Bradford M.A., McCulley R.L., Lebeer S., and Fierer N., 2016, A method for simultaneous measurement of soil bacterial abundances and community composition via 16S rRNA gene sequencing, Soil Biology and Biochemistry, 96: 145-151.
https://doi.org/10.1016/j.soilbio.2016.02.003

Straub D., Blackwell N., Langarica-Fuentes A., Peltzer A., Nahnsen S., and Kleindienst S., 2020, Interpretations of environmental microbial community studies are biased by the selected 16S rRNA (gene) amplicon sequencing pipeline, Frontiers in Microbiology, 11: 550420.
https://doi.org/10.3389/fmicb.2020.550420

Sun J., Yang L., Wei J., Quan J., and Yang X., 2020, The responses of soil bacterial communities and enzyme activities to the edaphic properties of coal mining areas in central China, PLoS One, 15(3): e0231198.
https://doi.org/10.1371/journal.pone.0231198

Taguali S., Pöter R., Aloi F., Fernández-Trujillo C., Acedo A., La Spada F., Nicosia M., Pane A., Schena L., and Cacciola S.O., 2025, Influence of environmental and agronomic variables on soil microbiome in citrus orchards: a comparative analysis of organic and conventional farming systems, Microbiological Research, 299: 128260.
https://doi.org/10.1016/j.micres.2025.128260

Tang S., Qiu Q., Marsden K.A., Chadwick D.R., Luo Y., Kuzyakov Y., Wu L., and Jones D.L., 2023, Microbial community succession in soil is mainly driven by carbon and nitrogen contents rather than phosphorus and sulphur contents, Soil Biology and Biochemistry, 184: 109019.
https://doi.org/10.1016/j.soilbio.2023.109019

Wang L., Ji J., Zhou F., Wu B., Zhong Y., Qi L., Wang M., Wu Y., Cui X., Ge T., and Zhu Z., 2024, Soil bacterial and protist communities from loquat orchards drive nutrient cycling and fruit yield, Soil Ecology Letters, 6(2): 232-244.
https://doi.org/10.1007/s42832-024-0232-8

Wang R., Wang Y., Zheng W., Hou F., Hu Y., and Guo S., 2021, Converting croplands to orchards changes soil microbial community composition and co-occurrence patterns, Land Degradation and Development, 32(8): 2509-2519.
https://doi.org/10.1002/ldr.3875

Wang X., Chi Y., and Song S., 2024, Important soil microbiota's effects on plants and soils: a comprehensive 30-year systematic literature review, Frontiers in Microbiology, 15: 1347745.
https://doi.org/10.3389/fmicb.2024.1347745

Wang X., Wang L., Wu B., Yuan Z., Zhong Y., Qi L., Wang M., Wu Y., Ge T., and Zhu Z., 2024, Neglected role of microelements in determining soil microbial communities and fruit micronutrients in loquat orchards, Frontiers in Microbiology, 15: 1447921.
https://doi.org/10.3389/fmicb.2024.1447921

Wang X., Wu W., Ao G., Han M., Liu M., Yin R., Feng J., and Zhu B., 2025, Minor effects of warming on soil microbial diversity, richness and community structure, Global Change Biology, 31(2): e70104.
https://doi.org/10.1111/gcb.70104

Wang Y., Liu L., Yang J., Duan Y., Luo Y., Taherzadeh M.J., Li Y., Li H., Awasthi M.K., and Zhao Z., 2020, The diversity of microbial community and function varied in response to different agricultural residues composting, Science of the Total Environment, 715: 136983.
https://doi.org/10.1016/j.scitotenv.2020.136983

Widdig M., Heintz-Buschart A., Schleuss P.M., Guhr A., Borer E.T., Seabloom E.W., and Spohn M., 2020, Effects of nitrogen and phosphorus addition on microbial community composition and element cycling in a grassland soil, Soil Biology and Biochemistry, 148: 107841.
https://doi.org/10.1016/j.soilbio.2020.107841

Wu H., Cui H., Fu C., Li R., Qi F., Liu Z., Yang G., Xiao K., and Qiao M., 2023, Unveiling the crucial role of soil microorganisms in carbon cycling: a review, Science of the Total Environment, 890: 168627.
https://doi.org/10.1016/j.scitotenv.2023.168627

Xia Q., Rufty T.W., and Shi W., 2020, Soil microbial diversity and composition: links to soil texture and associated properties, Soil Biology and Biochemistry, 149: 107953.
https://doi.org/10.1016/j.soilbio.2020.107953

Xiang Y., Chang S.X., Shen Y., Chen G., Liu Y., Yao B., Xue J., and Li Y., 2023, Grass cover increases soil microbial abundance and diversity and extracellular enzyme activities in orchards: a synthesis across China, Applied Soil Ecology, 184: 104720.
https://doi.org/10.1016/j.apsoil.2022.104720

Xiong R., He X., Gao N., Li Q., Qiu Z., Hou Y., and Shen W., 2024, Soil pH amendment alters the abundance, diversity, and composition of microbial communities in two contrasting agricultural soils, Microbiology Spectrum, 12(2): e04165-23.
https://doi.org/10.1128/spectrum.04165-23

Yadav A.N., Kour D., Kaur T., Devi R., Yadav A., Dikilitas M., Abdel-Azeem A.M., Ahluwalia A.S., and Saxena A.K., 2021, Biodiversity and biotechnological contribution of beneficial soil microbiomes for nutrient cycling, plant growth improvement and nutrient uptake, Biocatalysis and Agricultural Biotechnology, 33: 102009.
https://doi.org/10.1016/j.bcab.2021.102009

Yan K., Zhou J., Feng C., Wang S., Haegeman B., Zhang W., Chen J., Zhao S., Zhou J., Xu J., and Wang H., 2022, Abundant fungi dominate the complexity of microbial networks in soil of contaminated site: high-precision community analysis by full-length sequencing, Science of the Total Environment, 817: 160563.
https://doi.org/10.1016/j.scitotenv.2022.160563

Yoon J., Adhikari M., Jeong S., Lee S., Kim H., Lee G., Park D., Kim H., and Yang J., 2024, Microbial diversity of soils under different land use and chemical conditions, Applied Biological Chemistry, 67(1): 70.
https://doi.org/10.1186/s13765-024-00970-y

Zhang D., Wang C., Li X., Yang X., Zhao L., Liu L., Zhu C., and Li R., 2017, Linking plant ecological stoichiometry with soil nutrient and bacterial communities in apple orchards, Applied Soil Ecology, 126: 1-10.
https://doi.org/10.1016/j.apsoil.2017.12.017

Zhang G., Wang Z., Zhang H., Li X., Liu K., Yu K., Zheng Z., and Zhao F., 2025, Influence of agricultural practices on soil physicochemical properties and rhizosphere microbial communities in apple orchards in Xinjiang, China, Horticulturae, 11(8): 891.
https://doi.org/10.3390/horticulturae11080891

Zhang W., Zhao X., Sun C., Li X., and Chen K., 2015, Phenolic composition from different loquat (Eriobotrya japonica Lindl.) cultivars grown in China and their antioxidant properties, Molecules, 20(1): 542-555.
https://doi.org/10.3390/molecules20010542

Zhang Y., Liang Z., Zheng L., Wang X., Chen H., Xu T., and Tang M., 2025, Impact of long-term loquat cultivation on rhizosphere soil characteristics and AMF community structure: implications for fertilizer management, Frontiers in Plant Science, 16: 1549384.
https://doi.org/10.3389/fpls.2025.1549384

Zhao Y., Gong L., Wang F., Liu Y., Ai X., Zhu W., Zhang Y., Gan Z., He H., and Wang H., 2024, Preliminary study of distribution of soil available nutrients in loquat orchards and their responses to environmental factors based on path analysis model, Agronomy, 14(12): 2970.

Zhou J., and Fong J.J., 2021, Strong agricultural management effects on soil microbial community in a non-experimental agroecosystem, Applied Soil Ecology, 165: 103970.
https://doi.org/10.1016/j.apsoil.2021.103970

Zhou Q., Zhou L., Zhang H., Li J., and Zeng Q., 2025, Microbial phosphorus cycling shaped by citrus-induced soil acidification and phosphorus accumulation in fertilized orchards, Journal of Environmental Management, 395: 127885.
https://doi.org/10.1016/j.jenvman.2025.127885

Zhou Z., Wang C., and Luo Y., 2020, Meta-analysis of the impacts of global change factors on soil microbial diversity and functionality, Nature Communications, 11(1): 3072.
https://doi.org/10.1038/s41467-020-16881-7

Zou C., Dai T., Liang Z., Li M., Meng L., Zhao X., Li N., Wei Q., Elhamid M.A., Atif A., Soaud S., Wen M., Yan K., and El-Sappah A., 2025, Loquat-tea intercropping enhances rhizosphere microbial diversity and functional profiles in tea soil ecosystems, Frontiers in Microbiology, 16: 1651997.
https://doi.org/10.3389/fmicb.2025.1651997