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Rhizosphere Biological Activity during Different Growth Stages of Rapeseed

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Abstract The rhizosphere of rapeseed (*Brassica napus*) serves as a critical interface connecting plant roots with soil microorganisms and nutrient cycling processes, playing a pivotal role in regulating crop productivity and soil ecological functions. This review systematically examines the rapeseed rhizosphere ecosystem, covering its formation mechanisms, root development, rhizosphere assembly, and the characteristics of carbon input and organic matter transformation driven by root exudates. Particular emphasis is placed on the assembly patterns and successional dynamics of rhizosphere microbial communities across different growth stages, highlighting the functional roles of key bacterial and fungal taxa in facilitating nutrient cycling. Furthermore, the dynamic changes in rhizosphere functional genes—specifically those related to nitrogen and phosphorus cycling—and their impact on nutrient use efficiency are discussed. Case studies within rapeseed rotation systems illustrate the mechanisms underlying enhanced soil enzyme activity, shifts in microbial diversity, and improved soil disease suppressiveness under long-term cultivation. Additionally, the regulatory effects of practices such as organic amendments, straw mulching, and integrated nutrient management on rhizosphere functions are summarized. Finally, the review identifies current challenges regarding the elucidation of rhizosphere signaling mechanisms, the application of multi-omics integration, and adaptive management in the context of climate change, while outlining future research directions. This review aims to provide a theoretical basis and scientific reference for enhancing rapeseed productivity and optimizing soil ecological functions in agricultural systems.

Keywords Rapeseed; Rhizosphere ecosystem; Microbial community; Nutrient cycling; Soil enzyme activity

1 Introduction

Rapeseed (*Brassica napus* L.) is a major oilseed crop that underpins both global food and energy security. It is cultivated worldwide for edible oil, high-protein meal, and biofuel feedstock, and also contributes to phytoremediation of contaminated soils and diversification of cereal-dominated rotations, thereby supporting soil fertility and farm income in many regions (Bell et al., 2022). Over recent decades, the global production of B. napus has risen steeply, driven by demand for a stable source of vegetable oil and by intensive breeding and management programs that have increased yields more than 450-fold since the late 1970s (Zandberg et al., 2022). As production areas expand and intensify, there is growing interest in understanding belowground ecological processes that sustain yield and resilience in rapeseed-based agroecosystems.

Within these systems, the rhizosphere-the narrow soil zone directly influenced by roots-is a key hotspot controlling nutrient cycling, carbon fluxes, and plant health. The rhizosphere is shaped by root respiration and exudation, which alter pH, redox conditions, and nutrient availability, and by intense interactions with a dense and functionally diverse microbiota. Comparative analyses across ecosystems show that rhizosphere soils host higher enzyme activities and are selectively enriched in copiotrophic bacterial groups and genes involved in organic carbon turnover, nitrogen fixation, and denitrification relative to bulk soil, underscoring their central role in biogeochemical cycling and plant nutrition (Ling et al., 2022). In B. napus, a substantial fraction of photoassimilated carbon is routed belowground and released into the rhizosphere, fueling bacterial and fungal communities that can either support or constrain crop performance.

Recent work has begun to characterize rapeseed rhizosphere microbiomes and their activity. High-throughput sequencing of rapeseed rhizosphere soil at flowering and fruiting identified over 400 bacterial and nearly 50 fungal species, with significant shifts in community composition between growth stages and abundant plant-growth-promoting rhizobacteria possessing phosphorus and silicate-solubilizing and auxin-producing capacities (Wang et al., 2024). RNA-stable isotope probing in oilseed rape further distinguished active root- and rhizosphere-associated bacterial and fungal taxa assimilating recently fixed carbon, revealing that distinct groups dominate roots versus rhizosphere soil and that certain lineages are superior competitors for plant-derived carbon. These studies highlight that *B. napus* hosts complex, dynamic microbial consortia and suggest that growth stage-dependent changes in carbon allocation and root exudation play a key role in structuring rhizosphere biological activity (Wang et al., 2024).

Despite these advances, major gaps remain in understanding how rhizosphere biological processes in rapeseed change over the crop's ontogeny. Global syntheses show that rhizosphere size, gradients of enzymes and nutrients, and microbial community structure are highly dynamic in time, with sharp spatial-temporal gradients forming within days but reaching quasi-stationary patterns as opposing formation and consumption processes balance each other. Field studies in other crops demonstrate marked, stage-specific shifts in rhizosphere microbial diversity and activity, with communities at the same developmental stage more similar across plant species than communities at different stages of the same species. However, for *B. napus*, systematic characterization of rhizosphere enzyme activities, microbial functional potential, and their coupling to plant growth and nutrient demand across defined growth stages is still scarce. Addressing these gaps by tracking rhizosphere biological activity over the rapeseed growing season is essential for mechanistically linking plant development, root-microbe interactions, and nutrient cycling in this globally important crop.

2 Root Development and Rhizosphere Formation in Rapeseed

2.1 Taproot architecture and lateral root dynamics

Rapeseed possesses a taproot system composed of a prominent primary root with an extensive network of lateral roots and fine roots, which together determine water and nutrient capture as well as anchorage. Lateral roots constitute the major portion of total root length and surface area, and their spatial distribution in soil strongly affects resource uptake and mechanical support (Zhang et al., 2023). Genome-wide association studies and linkage mapping show broad natural variation in traits such as taproot diameter, lateral root number, lateral root length and density, indicating that rapeseed root system architecture is quantitatively controlled and amenable to genetic improvement.

Dynamic studies across the growing season reveal that lateral root morphological parameters scale tightly with root biomass. Biomass-based models relating lateral root length, average diameter, surface area and volume to organ biomass were able to predict lateral root traits of two rapeseed cultivars with high accuracy ($r>0.9$), capturing temporal changes from early vegetative stages through flowering (Zhang et al., 2023). At seedling stage, comparisons of accessions with contrasting root systems combined with transcriptomics have identified key regulatory pathways involving phytohormone response, cell cycle progression and cell wall organization, as well as specific genes (e.g. *BnaA06.CIPK25*, *BnaA08.AGL21*) that differentially control primary root elongation and lateral root development (Song et al., 2025).

2.2 Root exudation patterns across developmental stages

Although detailed developmental exudation profiles are not yet available for rapeseed, broader work in other species demonstrates that root exudation is strongly stage-dependent. In Arabidopsis, cumulative secretion of sugars and sugar alcohols is highest at early stages and declines over time, whereas amino acids and phenolics increase as plants age, with gene expression in roots mirroring these shifts. Metatranscriptomic analyses showed that these developmental changes in exudates correlate with changing microbial functions in the rhizosphere, suggesting a programmed adjustment of rhizosphere chemistry as roots and shoots develop.

Field studies with maize further highlight developmental control of exudation quantity and composition. Over successive stages from early vegetative to reproductive growth, total carbon exudation per plant increased with biomass, but exudation rate per unit root surface decreased, and metabolite profiles shifted as plants matured. Exudation rates were also higher in substrates with lower nutrient mobility, emphasizing that both plant ontogeny and soil environment modulate carbon release to the rhizosphere (Santangeli et al., 2023). Together, these findings imply that rapeseed likely exhibits analogous, developmentally programmed shifts in exudate composition-particularly in sugars, organic acids and phenolics-that underpin changing rhizosphere activity across growth stages.

2.3 Rhizosphere boundary formation and microbial recruitment

The establishment of a rapeseed rhizosphere involves both physical root proliferation and chemical signaling to selectively recruit microorganisms. Reviews of root exudate-microbiome interactions emphasize that rhizosphere metabolites function as signals and nutrients that guide microbiome assembly, enabling plants to attract beneficial taxa and modulate ecosystem functions. Exudate composition responds to plant genotype, developmental stage and environmental cues, so that roots can adjust rhizosphere boundaries and microbial partners as growth progresses (Fan et al., 2025).

Mechanistic studies in other model systems reveal how developmental exudation patterns drive microbial recruitment at the root-soil interface. In Avena and Arabidopsis, pre-programmed successions in exuded sugars, amino acids and aromatic organic acids interact with microbial substrate preferences to structure rhizosphere communities over time, with early sugar-rich exudates attracting broad microbial groups and later phenolic-rich exudates selecting more specialized taxa. More broadly, root exudates such as organic acids, amino acids, sugars and secondary metabolites have been shown to mediate colonization by beneficial rhizobacteria and mycorrhizal fungi, alter soil pH and nutrient solubility, and exclude pathogens, thereby functionally defining the rhizosphere boundary and the composition of rapeseed-associated microbiomes across developmental stages (Chen and Liu, 2024).

3 Soil Organic Matter Transformation during Rapeseed Growth

3.1 Carbon input via root exudates and residue turnover

During rapeseed growth, soil organic matter (SOM) is strongly influenced by carbon (C) inputs from rhizodeposition, including root exudates, sloughed cells and mucilage. A global synthesis of crops and grasslands showed that annual crops allocate on average about 21% of assimilated C belowground, with belowground allocation peaking in the first 1-2 months and then declining rapidly, indicating that early growth stages are critical for rhizosphere C inputs and SOM dynamics. A specific pot study on rapeseed and wheat quantified root-exuded C over the full growth period and reported cumulative exudation of 14.09 g C plant^{-1} in rapeseed, almost twice that of wheat, highlighting the high rhizodeposition potential of B. napus in cropping systems (Tang et al., 2021).

Root traits tightly regulate temporal patterns of exudation and thus C supply to the rhizosphere. For rapeseed, exudation intensity per root biomass was higher than wheat in early growth but lower at later stages, and showed exponential relationships with specific root length, root surface area and root volume, as well as with root C/N ratio and soluble sugar content (Tang et al., 2021). Beyond individual crops, a recent review emphasized that not only the quantity but also the quality of root exudates is decisive for SOC input and efflux, because exudate composition controls microbial use efficiency, priming of existing SOM, and the balance between stabilization and mineralization in rhizosphere soils (Lei et al., 2023).

3.2 Enzymatic decomposition of organic matter

The conversion of rhizodeposited and residue-derived C into SOM pools is mediated by rhizosphere enzymes produced by roots and microorganisms. Conceptual work on rhizosphere enzymes shows that activities of C-, N-, P- and S-acquiring enzymes are generally higher in rhizosphere than bulk soil because of the continuous supply of labile C substrates, and that enzyme production is stimulated by root exudates, which can induce priming of SOM decomposition. Experimental imaging of enzyme activities in rice rhizospheres further demonstrated that chitinase and phosphatase hotspots closely track root distribution and that overall activities increase with plant growth, indicating that plant development and associated exudation dynamics are primary drivers of rhizosphere enzymatic patterns.

Soil fertility and organic matter availability modulate how microbial communities respond to rhizodeposits and govern enzyme kinetics. In soils contrasting in organic matter and nutrient status, hotspots around maize roots exhibited 1.2-fold higher specific microbial growth rates and greater growing biomass in low-fertility soil than in high-fertility soil, with β-glucosidase showing 1.7-2.1 times higher potential activity (Vmax) in hotspots than in bulk soil, underscoring that labile organics increase capacity for C acquisition (Tian et al., 2020). In saline-alkali rhizospheres, activities of catalase, invertase, amylase and β-glucosidase decreased with rising salinity, but β-glucosidase and amylase remained positively correlated with SOC, indicating that these enzymes are sensitive indicators of SOM turnover and C sequestration potential under stress (Qu et al., 2021).

3.3 Role of rapeseed residues in post-harvest soil legacy effects

After harvest, rapeseed residues represent a major above- and belowground C input that shapes SOM and microbial legacies into subsequent crops. In rice-rapeseed rotations, incorporation of crop straw increased SOC and total N, with the greatest gains in high-fertility soils, and microbial biomass C and N (MBC, MBN) showed strong seasonal dynamics, being higher in the rapeseed than rice season, indicating that residue-driven C and N inputs interact with crop phase to control microbial pools (Wang et al., 2023). For winter oilseed rape specifically, detailed mass-balance work across six N rates showed that stubble, chaff and fine root biomass C were relatively stable with fertilization, whereas straw C scaled with yield, implying that residue-C inputs to SOM models should be component-specific rather than based on simple allometric ratios (Ozkiper et al., 2026).

Rapeseed residues also influence microbial community assembly and soil functioning over time, including in rotation systems. In a wheat-oilseed rape rotation studied over multiple years, metabarcoding of 150 residue samples revealed that crop residues form a distinct microbial ecosystem in which plant-specific oligotrophic genera (often pathogens) are progressively replaced by more generalist, copiotrophic taxa of likely soil origin as decomposition proceeds. Application of rapeseed residues to paddy fields increased soil organic matter, microbial biomass C and N, and activities of urease, acid phosphatase and dehydrogenase, while simultaneously shifting cadmium from more labile to more reducible fractions and reducing Cd accumulation in rice tissues, demonstrating that rapeseed residues can leave beneficial biochemical and environmental legacies beyond simple C and nutrient additions (Yang et al., 2020).

4 Microbial Community Assembly in Rapeseed Rhizosphere

4.1 Bacterial and fungal succession patterns

Rhizosphere microbial communities of rapeseed show clear shifts over plant development and between soil compartments. At seedling, flowering, and maturity, dominant bacterial phyla in the rhizosphere include Proteobacteria, Actinobacteria, Acidobacteria, Bacteroidetes, and Cyanobacteria, while Ascomycota, Olpidiomycota, and Basidiomycota dominate fungi; nitrogen level alters community structure but not the identity of dominant groups, and diversity tends to be higher at flowering under high N (Xing et al., 2021). At flowering versus fruiting, high-throughput sequencing revealed 401 bacterial and 49 fungal species, with significant differences in alpha and beta diversity between stages, indicating that rapeseed development strongly structures rhizosphere communities (Wang et al., 2024).

Temporal dynamics also emerge when microbial activity and carbon flow are tracked. In a ^$14CO_2$ pulse-labeling study across three rapeseed growth stages, fungal ITS copy numbers were consistently higher in the rhizosphere and decreased with plant age, whereas bacterial 16S abundance increased markedly in the rhizosphere at flowering, suggesting a shift from fungal to more bacterial dominance in utilizing root-derived C as plants mature (Ruggaber et al., 2024). RNA-SIP work with ^$13CO_2$ showed that active bacterial and fungal communities in roots and rhizosphere differ strongly, with specific taxa in each compartment heavily enriched in plant-derived carbon, highlighting that successional patterns involve both compositional turnover and changing activity of carbon-assimilating taxa.

4.2 Keystone taxa associated with rapeseed roots

Network-based analyses have begun to identify keystone microorganisms that structure rapeseed rhizosphere communities. In feral B. napus grown at five grassland sites, rhizosphere prokaryotic, fungal, and eukaryotic communities were distinct from bulk soil and had lower diversity; *Pseudomonas brassicacearum*, *Olpidium brassicae*, and *Glissomonadida* were predominant, and network keystone species bridged otherwise weakly connected inter- and intra-kingdom associations, thereby maintaining diversity and stability (Cui et al., 2025). A multi-site, temporally intensive field study of B. napus roots and rhizosphere identified a fungal core microbiome of 38 ASVs dominated by Olpidium, Fusicola, Fusarium, Gibberella, Mortierella, and Cutaneotrichosporon, some of which were strongly associated with yield across growth stages, implying functional keystone roles in plant performance (Bazghaleh et al., 2022).

Keystone bacteria in the rapeseed rhizosphere also show crop-specific signatures. Comparing close and distant rhizosphere compartments of wheat, barley, rye, and oilseed rape, co-association network analysis identified an unclassified Chloroflexi group “KD4-96” as a keystone bacterial taxon in oilseed rape core microbiota, distinguishing its network from cereals (Lewin et al., 2021). Domestication studies further indicate that synthetic B. napus lines harbor distinct co-occurrence networks in which certain taxa act as hub nodes enriching nitrogen-metabolism pathways, suggesting that breeding and domestication can indirectly select rhizosphere hub taxa that influence nutrient cycling and plant health (Figure 1) (Zhang et al., 2023).

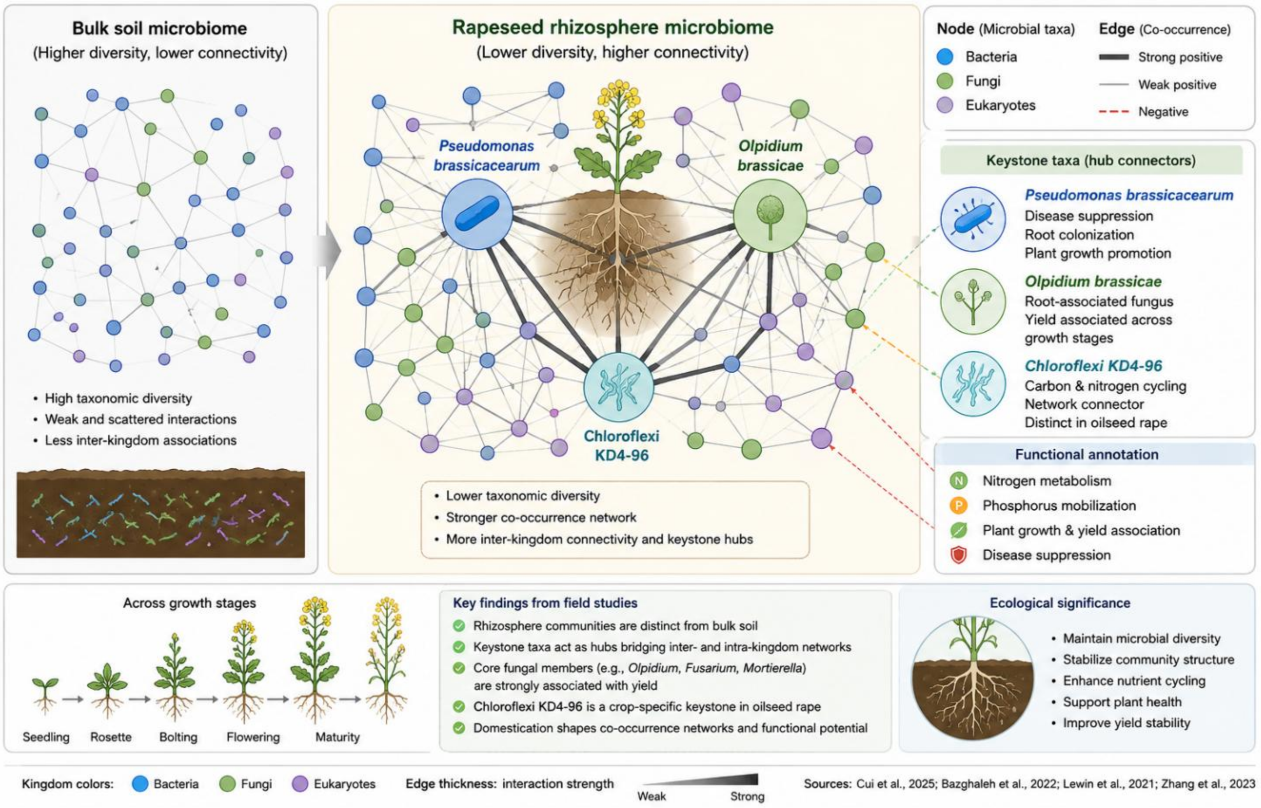

Figure 1 Keystone microbial network structure in the Brassica napus rhizosphere

4.3 Influence of root exudates on microbial selection

Root exudates are central drivers of microbial selection in the rapeseed rhizosphere. Conceptual and experimental work shows that rhizosphere metabolites serve as both nutrients and signals governing microbiome assembly, with plants “meticulously” attracting particular taxa from bulk soil via exuded organic acids, amino acids, sugars, and secondary metabolites (Fan et al., 2025). In oilseed rape, stable-isotope labeling demonstrated that 20%-50% of photoassimilated carbon is transferred belowground and about half released as exudates, which in turn shape distinct active bacterial and fungal communities in roots versus rhizosphere soil and select taxa that are superior competitors for plant-derived carbon.

Mechanistic studies in other species provide a template for how dynamic exudation during plant development may structure rapeseed communities. In Avena barbata, pre-programmed changes in exudate chemistry-transitioning from sugar-rich to phenolic- and aromatic-acid-rich profiles-interacted with microbial substrate preferences to drive predictable patterns of rhizosphere assembly, with bacteria preferentially consuming aromatic organic acids such as salicylic and indole-3-acetic acid. Broader reviews and cross-crop analyses underscore that root exudate composition is strongly affected by plant genotype and by biotic stresses, and that shifts in amino and organic acids under nutrient or stress conditions can reconfigure rhizosphere networks, alter keystone taxa, and ultimately modify plant stress tolerance, patterns likely relevant to rapeseed across its growth stages (Gong et al., 2023; Sharma et al., 2023).

5 Nutrient Cycling and Functional Gene Dynamics

5.1 Nitrogen cycling (fixation, nitrification, denitrification)

Nitrogen cycling in rapeseed systems is strongly shaped by fertilization strategy and associated shifts in rhizosphere N-cycling genes. In a field study with winter oilseed rape, root-zone N fertilization (localized placement) increased seed yield and aboveground N uptake while enriching rhizosphere NH_4^+ and NO_3^- pools compared with conventional broadcasting at the same N rate. Shotgun metagenomics showed that root-zone fertilization enhanced the functional potential for nitrogen fixation and assimilatory nitrate reduction, while reducing genes linked to nitrification and denitrification, indicating a reprogramming of N cycling toward retention and assimilation and away from gaseous N losses (Cheng et al., 2026).

Fertilizer formulation can further tune the balance among nitrifiers and denitrifiers. In a pot experiment with oilseed rape, a biochar-based controlled-release N fertilizer increased yield by ~16.6% and N-use efficiency by ~58.8% compared with urea alone, through gradual N release and modulation of N-cycling microbes. This treatment raised bacterial amoA gene copy numbers (stimulating nitrification) while decreasing nirS and nirK gene abundance (limiting denitrification), and significantly increased soil NO_3^-, thereby supporting higher N uptake and plant growth (Liao et al., 2020). Together, these studies highlight that both spatial N placement and fertilizer type can shift functional N-cycling gene profiles to favor crop N acquisition in rapeseed systems.

5.2 Phosphorus mobilization in rapeseed rhizosphere

Rapeseed is highly sensitive to P deficiency, and its rhizosphere P dynamics are strongly influenced by neighboring species and microbial partners. In intercropping systems with white lupin, soil available P, microbial biomass, and P content in the oilseed rape rhizosphere were all higher than in rapeseed monoculture, and P-solubilizing bacteria and fungi were significantly enriched around rapeseed roots under intercropping. Intercropping also increased organic acids and other metabolites in rapeseed root exudates, suggesting that altered exudation and P-solubilizing microbiomes jointly enhance P availability and uptake in the rapeseed rhizosphere (Chen et al., 2023).

Management of P and N fertilization levels can strongly condition the performance of phosphate-solubilizing bacteria (PSB) inoculants. In rhizotron experiments with rapeseed, a Pseudomonas strain with strong in vitro P-solubilizing capacity enhanced root and shoot biomass and increased root P and N content under complexed P conditions, but only when N supply was adequate (N80). Under lower N fertilization, these positive effects disappeared, implying that sufficient N is required for PSB to express P-solubilizing traits and to contribute effectively to rapeseed nutrition (Amy et al., 2024). This interaction between P form, N supply, and PSB activity is central to optimizing rhizosphere P mobilization strategies in rapeseed.

5.3 Functional genes linked to nutrient acquisition efficiency

Functional gene profiles in rhizosphere and root microbiomes provide mechanistic links between microbial communities and nutrient acquisition in oilseed crops. A global meta-analysis of rhizosphere bacteriomes showed that genes involved in organic compound conversion, nitrogen fixation, and denitrification were enriched by 11%-182% in rhizosphere versus bulk soil, whereas nitrification genes were strongly depleted, indicating that plant-influenced zones favor functions related to nutrient transformation and retention. This functional skew suggests that rapeseed roots, like those of other crops, select microbial guilds and gene repertoires that can support nutrient acquisition while modulating N-loss pathways (Ling et al., 2022).

At finer resolution, multi-omics analysis of 175 Brassica napus ecotypes across two field sites linked root transcriptomes, rhizosphere bacterial ASVs, and root ionomes to N uptake traits. Host gene expression together with specific bacterial ASVs explained up to 45% of natural variation in root N, and genome-wide association revealed host loci regulating the abundance of key taxa, many under eQTL hotspots related to C and N metabolism. The dominant, genetically regulated genus Sphingopyxis promoted lateral root development, auxin biosynthesis, and improved N acquisition under stress, illustrating how host-microbe-gene interactions can be harnessed to breed rapeseed genotypes with superior nutrient acquisition efficiency via targeted functional microbiomes (Li et al., 2026).

6 Case Study: Rhizosphere Biological Responses under Rapeseed-Crop Rotation Systems

6.1 Long-term rapeseed-wheat or rapeseed-maize rotation systems

Long-term rotation experiments with canola (rapeseed) and cereals demonstrate strong legacy effects on plant performance and belowground processes. A 12-year study comparing continuous canola with canola-wheat and canola-pea-barley rotations across three Canadian sites showed that diversification consistently increased yield and oil content while reducing disease pressure from Leptosphaeria and Alternaria, though effects on soil nutrient fluxes were site- and year-dependent (Town et al., 2023). In winter wheat rotations, rhizotron work comparing wheat after oilseed rape versus wheat in self-succession found higher subsoil nitrate and altered N-cycling gene abundances under the oilseed rape-preceded treatment, indicating a beneficial soil legacy for the following cereal (Kaloterakis et al., 2025).

In paddy-upland systems, seven years of rice-rapeseed rotation with rice straw return modified rapeseed rhizosphere microbial communities and enhanced microbial metabolic potential relative to non-straw controls. Across two sites, straw application altered the balance between fungi and Gram-negative bacteria and shifted key soil factors (e.g., available N, K, P, total C) that regulate rhizosphere enzyme activities, illustrating how long-term rotation plus residue management co-shape rapeseed rhizosphere functioning.

6.2 Changes in microbial diversity and enzyme activity under rotation

Rotation patterns preceding rapeseed markedly alter rhizosphere microbial diversity and enzyme activities compared with continuous rapeseed. In a two-year field study with six preceding crops, rapeseed after wheat (TaBn) showed the highest activities of key soil enzymes and higher bacterial and fungal richness (Chao1) and evenness (Simpson) than continuous rapeseed, with distinct bacterial and fungal OTU composition separating TaBn and sugar beet-rapeseed (BvBn) from monoculture (Tian et al., 2025). All non-rapeseed precedents increased Ascomycota and decreased Mucoromycota, while TaBn enriched Pseudomonadota and Actinomycetota, indicating rotation-specific restructuring of rhizosphere communities and functions (Figure 2) (Tian et al., 2025).

At broader scales, a meta-analysis of 76 studies showed that crop rotation generally increases soil microbial biomass C and N by ~13%-16% and enhances bacterial Shannon diversity by ~8% relative to monoculture, especially when rotations include legumes, reduced tillage, and favorable temperature and precipitation regimes (Liu et al., 2023). However, rotation effects on phosphatase and β-glucosidase activities were not universally significant, suggesting that enzyme responses depend on specific crop sequences and management contexts rather than rotation per se (Liu et al., 2023).

6.3 Impacts on soil suppressiveness and rapeseed yield stability

Rotation strongly influences soil suppressiveness to diseases relevant for rapeseed and associated crops. In long-term canola rotations, fungal communities were more responsive than bacterial ones, and monocropped canola harbored specific *Olpidium brassicae* lineages whose abundance correlated negatively with yield, implying reduced suppressiveness and heightened pathogen risk under continuous canola (Town et al., 2023). A global field experiment across crops showed that increasing rotational diversity enhanced the abundance of *prnD*-harboring bacteria producing antifungal compounds and maintained higher disease-suppressive potential than non-cropped fallow, even though total bacterial diversity slightly decreased, emphasizing the importance of functional composition over richness alone.

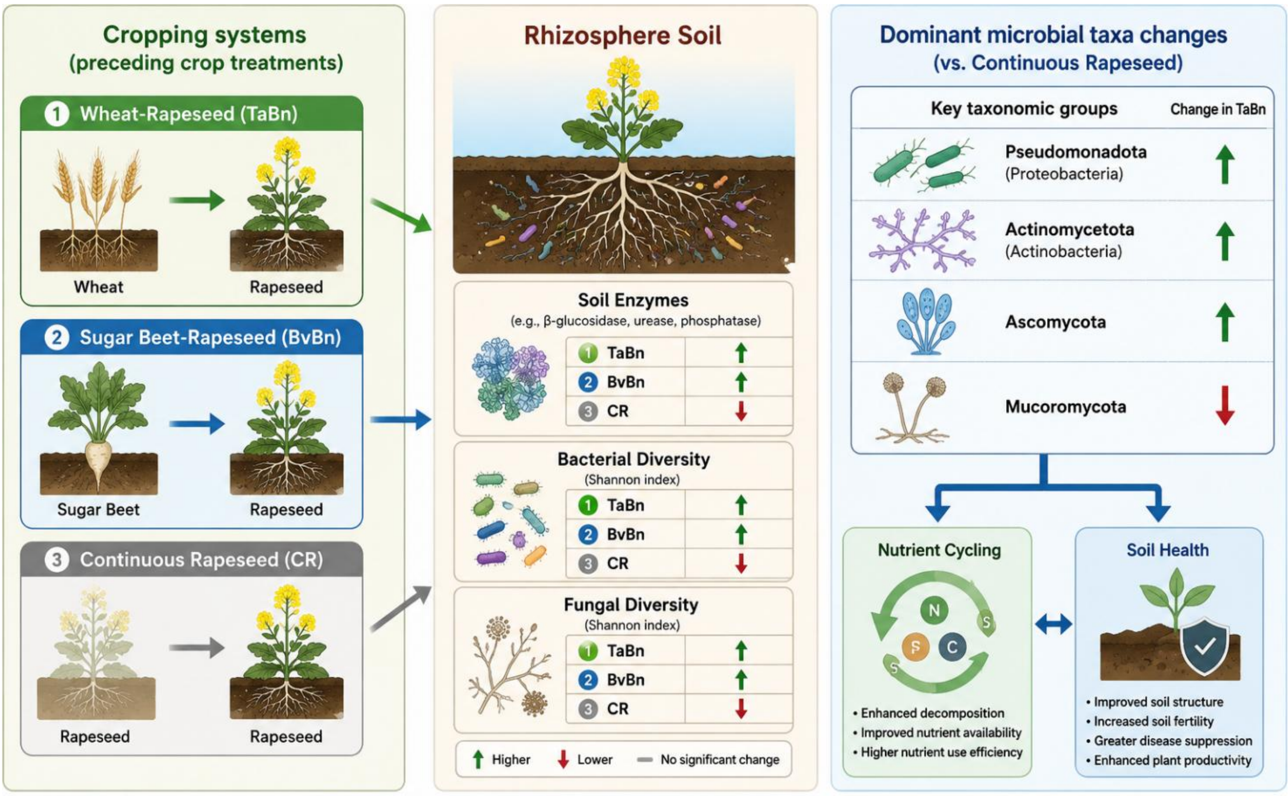

Figure 2 Conceptual framework illustrating the effects of different preceding crops on rhizosphere microbial communities, enzyme activities, and ecological functions in rapeseed systems

Rotation legacies also shape multifunctionality and disease outcomes in systems including rapeseed. In four rice-based rotations, crop rotation history explained most of the variation in bacterial richness, community composition and soil multifunctionality, with rice-rapeseed rotations showing the strongest positive link between bacterial diversity and multi-enzyme activity related to C cycling (Li et al., 2021). Field comparisons of winter rapeseed grown in five-year monoculture versus rotation (rapeseed-wheat-peas-wheat-rapeseed) further revealed lower severity of dark spot on leaves and dry rot on stems, and generally higher yields, for rapeseed following a four-year break, highlighting that diversified rotations contribute to both disease mitigation and yield stability.

7 Management Practices Regulating Rapeseed Rhizosphere Function

7.1 Organic amendments and biofertilizers in rapeseed systems

Organic amendments can substantially modify rapeseed rhizosphere functioning by improving plant physiology and reshaping soil microbiota. In a rapeseed system fertilized with poultry and plant-based organic amendments, plant growth and leaf biomass doubled, supported by enhanced CO_2 assimilation, carbohydrate and amino acid production, and upregulation of stress-related proteins and antioxidants; the amendments also promoted Actinobacteria in soil, indicating shifts in rhizosphere bacterial structure and potential functionality (Picazo et al., 2025). A global meta-analysis across crops further showed that organic amendments consistently increased microbial Shannon diversity, richness and phylogenetic diversity, shifted community composition, and that higher microbial diversity and functionality were positively associated with crop yields, underscoring the potential of organic inputs to enhance rhizosphere processes and productivity in rapeseed-based systems (Shu et al., 2022).

Biofertilizers based on plant growth-promoting rhizobacteria (PGPR) and symbiotic fungi also strongly influence Brassica rhizosphere performance. In canola, seed priming with *Rhizobium*, *Bacillus*, *Pseudomonas* or their consortium markedly increased root and shoot biomass, antioxidant enzyme activity, and seed yield, indicating that inoculated PGPR can intensify nutrient acquisition and stress protection during vegetative and reproductive stages (Farhat et al., 2023). Similarly, combined inoculation of *Enterobacter*, *Bacillus* and the endophytic fungus *Piriformospora indica* in canola enhanced growth, nutrient uptake, soil microbiological attributes and auxin pools, with *Bacillus* + P. *indica* showing up to 100% increases in shoot biomass and major gains in pod number, highlighting how microbial consortia can reprogram root proliferation and rhizosphere nutrient cycling in rapeseed systems (Iqbal et al., 2022).

7.2 Tillage and mulching effects on rhizosphere activity

Tillage and mulching regimes modify soil physical conditions and thereby rapeseed rhizosphere biology. Under arid and semiarid conditions, a three-year field experiment comparing ridge film mulching with furrow planting (RFMF) to flat planting showed that RFMF increased rhizosphere soil moisture by up to 5.6% and temperature by up to 3.0 °C, and significantly enhanced rhizosphere enzyme activities and microbial abundance, leading to improved root growth, nutrient uptake and seed yield of winter oilseed rape. Optimal N rates under RFMF (240 kg N ha^{-1}) further boosted rhizosphere microbial activity and root traits without yield gains beyond this level at 300 kg N ha^{-1}, indicating that mulching-fertilizer interactions jointly regulate rhizosphere processes and productivity.

Film mulching within ridge-furrow systems also alters microbial carbon utilization and diversity in rapeseed rhizosphere soils. Compared with flat planting and no-mulch controls, white, black and biodegradable polyethylene films under a ridge-furrow with film mulching (RFFM) system increased soil water storage, rhizosphere microbial metabolic activity (average well color development) and utilization of carbohydrate and amino acid C sources, particularly with wider furrows (80 cm). Shannon and Simpson diversity indices, as well as evenness, were significantly higher under several film treatments (e.g., biodegradable, black film), and RFFM increased rapeseed yield by 9.6%-86.1% relative to flat planting, demonstrating that appropriate mulching designs can enhance both rhizosphere microbial function and crop productivity.

7.3 Integrated nutrient management strategies for rapeseed productivity

Integrated nutrient management that combines mineral fertilizers with organic inputs and biofertilizers offers a route to optimize rhizosphere functioning and rapeseed yield. In winter oilseed rape, a comprehensive review showed that productivity and N-use efficiency are highly sensitive to N rate, fertilizer type, timing, and preceding crops, with N-efficient cultivars and optimized N application schedules capable of reducing fertilizer N inputs by up to 50% while maintaining yield (Rathke et al., 2006). Complementary work in rapeseed-mustard systems found that recommended mineral fertilization combined with farmyard manure, Azotobacter and phosphate-solubilizing bacteria (PSB) significantly increased plant height, branching, biomass, seed and biological yields, oil content, and economic returns, indicating strong synergy between organic and microbial inputs in supporting nutrient availability and plant performance.

More recent trials integrating PGPR and organic amendments with reduced mineral N further highlight benefits for rapeseed productivity and resource efficiency. In water-limited environments, combining PGPR inoculation and vermicompost with reduced chemical fertilizers increased grain yield, oil content and biodiesel production, improving nutrient uptake while enabling a 67% reduction in chemical fertilizer use (Nasrollahzadeh et al., 2023). In pot experiments with oilseed rape, mixed organic-chemical fertilization treatments rich in organic inputs (25% chemical, 75% organic) produced the highest aboveground biomass and enhanced bacterial abundance, diversity and ecological network complexity in rhizosphere soils, though they also increased potential plant pathogenicity, underscoring that integrated nutrient strategies must balance productivity gains with careful monitoring of rhizosphere microbial risks (Wang et al., 2024).

8 Challenges and Future Perspectives

Root-microbe signaling in rapeseed rhizospheres is increasingly recognized as central to nutrient acquisition, stress tolerance, and rhizosphere engineering, yet key molecular mechanisms remain poorly resolved. Reviews of plant-microbe interactions emphasize that root exudates composed of organic acids, amino acids, sugars, and secondary metabolites act as biochemical cues that recruit beneficial microbes and modulate plant health, but most mechanistic insights derive from model species rather than Brassica napus. Chemotaxis, attachment, immune evasion, and biofilm formation have been identified as critical steps in rhizosphere colonization, but the fine-scale regulation of these processes by rapeseed genotypes and growth stages is largely unknown.

Even for plant growth-promoting rhizobacteria (PGPR), current understanding of signal specificity and downstream plant responses is incomplete. Work on root exudate-driven chemotaxis shows that representative chemoeffectors and corresponding bacterial chemoreceptors are beginning to be identified, yet how these chemotactic responses integrate with rapeseed immune signaling, hormonal pathways, and stress physiology is unresolved. More broadly, root signals are recognized as orchestrating complex inter-organismal communications in the rhizosphere, but the precise metabolites and pathways coordinating recruitment, cooperation, and competition among microbial guilds around rapeseed roots remain a major research gap.

Multi-omics approaches offer powerful tools to move from descriptive rapeseed microbiome surveys toward mechanistic, functional understanding, but integrative frameworks are still emerging. Conceptual overviews of rhizosphere multi-omics highlight how metagenomics, metatranscriptomics, metaproteomics, and metametabolomics can jointly capture microbiome composition, gene activity, and signaling networks at the root-soil interface, yet emphasize that rhizosphere-specific datasets and tailored software pipelines remain limited. Reviews of soil-plant-microbial profiling similarly argue that integrating DNA-based, transcriptomic, metabolomic, ionomic, and phenomic data is essential for predicting rhizosphere processes and translating microbiome insights into crop improvement, but standardized workflows and cross-scale causal inference are still lacking.

Proof-of-concept multi-omics studies in other crops demonstrate the potential relevance for rapeseed. A meta-analysis across eight legumes used combined community profiling, functional gene analysis, and network-based co-expression to identify developmental-stage-specific marker bacteria linked to plant growth phenotypes and metabolic pathways such as secondary metabolite biosynthesis and carbon fixation. Broader metagenomic work in rhizosphere systems underscores that high-resolution functional profiling can reveal key microbial players in nutrient cycling and plant health, but also highlights persistent challenges in data integration, interpretation, and connecting functional signatures to field performance and management interventions.

Climate change-driven stresses such as drought, heat, and altered precipitation patterns are expected to be perceived most acutely at the rapeseed root-soil interface, yet belowground adaptation strategies are only beginning to be articulated. A bottom-up synthesis argues that combined abiotic stresses reshape root traits, rhizodeposition, and rhizosphere microbiota, and that plastic responses in root architecture and microbe recruitment may be among the most promising targets for adaptation and mitigation in agroecosystems. Complementary reviews detail how plant-microbe interactions contribute to resilience under climate stress via antioxidant regulation, phytohormone modulation, and root exudation-driven recruitment of beneficial microbes, but note that the specific consequences of climate extremes for rhizosphere community assembly remain underexplored.

For *Brassica napus* specifically, drought has been identified as a major constraint on germination, growth, and yield, with current management relying largely on agronomic and breeding strategies rather than explicit rhizosphere manipulation. Recent analyses of rapeseed yield and growth duration across China show that both climate variables and adaptive crop management (e.g., cultivar choice, planting dates) significantly influence productivity under changing conditions, suggesting that refined management can partially offset climatic impacts. Future work integrating these system-scale insights with rhizosphere-level manipulation-through microbiome engineering, optimized exudate profiles, and root trait selection-will be crucial for developing climate-resilient rapeseed systems.

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