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Plant- and soil-derived polyphenols shape soil microbiomes and crop outcomes: a systematic review and meta-analysis

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Background: Polyphenols from root exudates and polyphenol-rich organic inputs may shape soil microbiomes, enzyme activities, and crop nutrient outcomes, with relevance to regenerative agriculture.

Objectives: To quantify the effects of plant- and soil-derived polyphenols/polyphenol-rich soil inputs on i) soil microbial alpha-diversity and enzyme activity and ii) crop yield and nutrient quality and to summarise mechanistic pathways and evidence certainty.

Methods: Following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 statement, we searched PubMed, Web of Science, Scopus, Embase, and CAB Abstracts (1990–March 2025) plus grey literature. Fifteen controlled studies (163 observations) met the Population, Intervention, Comparator, Outcomes, and Study design (PICOS) eligibility. Random-effects meta-analysis pooled standardised mean differences (SMDs; Hedges' *g*) for continuous outcomes. To ensure reproducibility and statistical independence, we prespecified decision rules for selecting endpoints/time points and aggregated multiple within-study outcomes into study-level composites within each domain. We explored moderators [polyphenol source class, purified vs. complex inputs, environment (field vs. controlled), soil pH, soil organic carbon (SOC), duration, and dose, where reported] via subgroup analyses and mixed-effects meta-regression. We assessed certainty using the Grading of Recommendations, Assessment, Development and Evaluation (GRADE) approach.

Results: Polyphenol inputs increased soil microbial alpha-diversity (pooled across Shannon/Simpson indices) [SMD = +0.58, 95% confidence interval (CI) 0.32–0.83; high certainty] and soil enzyme activity (SMD = +0.49, 95% CI 0.24–0.73; moderate certainty). Crop yield increased modestly (+6.8%, 95% CI 2.7–10.9; moderate certainty), while micronutrients iron (Fe) and zinc (Zn) improved

modestly (low–moderate certainty) due to limited reporting and imprecision. Yield and nutrient-quality outcomes were secondary endpoints in most included studies and were available in a smaller, uneven subset, limiting generalisability. Heterogeneity was moderate ($I^2 \approx 50\%$) and was partly consistent with differences between purified compounds vs. complex organic amendments and field vs. controlled environments.

Conclusion and future directions: Plant- and soil-derived polyphenol inputs meaningfully enhance soil microbial diversity and enzyme activity and may deliver smaller, context-dependent gains in yield and crop micronutrient quality; future multi-season field trials with standardised polyphenol chemistry/dose reporting and functional multi-omics are needed to clarify persistence, dose–response relationships, and causal mechanisms.

KEYWORDS

enzyme activity, grade, meta-analysis, nutrient cycling, polyphenols, PRISMA 2020, rhizosphere, soil microbiome

Introduction

Soil microbiomes underpin nutrient cycling, organic-matter turnover, and plant–soil feedbacks that collectively shape crop productivity and food nutrient quality. Plants release polyphenols such as flavonoids, phenolic acids, tannins, and lignin-derived compounds into soils via root exudation, residue inputs, and litter decomposition, where these compounds influence microbial community assembly and function (1–5). In this manuscript, “polyphenols” refers specifically to plant- and soil-derived polyphenols acting within the soil/rhizosphere (agroecosystem context), not human dietary polyphenols. Because polyphenols can act as redox mediators and metal chelators, they may alter microbial metabolism, stabilise enzymes, and affect nutrient availability (6, 7). Polyphenols may also favour microbes capable of phenolic metabolism while suppressing opportunistic pathogens, thereby reshaping rhizosphere function and plant nutrition (2–4). However, the literature spans contrasting intervention modes (purified compounds vs. complex organic amendments), environments (field vs. greenhouse/microcosm), and crop functional groups, which likely contribute to heterogeneity and complicate generalisation. Scattered evidence is found in systems, chemistries, and methods between purified compounds and composted pomaces, making it difficult to generalise (8, 9).

Knowledge gap: Existing syntheses rarely quantify pooled effects on microbial diversity, enzyme activity, and crop outcomes while explicitly testing whether intervention complexity (purified vs. complex), environment, and soil properties explain heterogeneity and while grading certainty across outcomes.

We therefore asked the following:

1. What is the influence of polyphenol inputs on soil microbial alpha-diversity and enzyme activity?

2. Do polyphenol inputs improve crop yield and nutrient quality, and how robust is the evidence?
3. Which intervention types and edaphic conditions modulate effects and explain heterogeneity?

Figure 1 summarises the hypothesised pathways linking polyphenol inputs to soil and crop outcomes. Context modifiers include polyphenol chemistry, purified vs. complex inputs, dose, soil pH, SOC, environment (field/controlled), and exposure duration.

Methods

Ethics, protocol, and reporting

We adhered to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 statement and followed the Cochrane Handbook guidance. Certainty of evidence was assessed using the Grading of Recommendations, Assessment, Development and Evaluation (GRADE) approach. There were no animal or human subjects.

Eligibility criteria (PICOS)

Eligibility was defined using the Population, Intervention, Comparator, Outcomes, and Study design (PICOS):

Population: Agricultural or managed soils (crop/cover-crop systems), rhizosphere, and bulk soil.

Intervention: Plant-derived polyphenols or polyphenol-rich soil inputs (flavonoids, phenolic acids/coumarins, lignins, and tannins; polyphenol-rich composts/pomaces; residue-derived phenolics; and

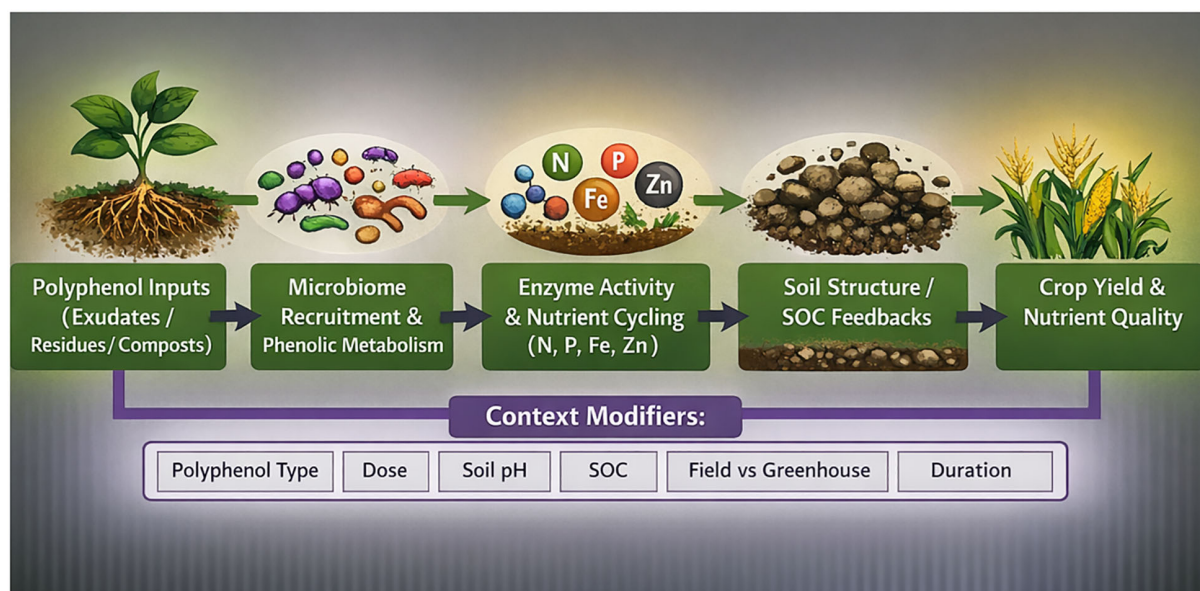


FIGURE 1

Conceptual model linking plant-/soil-derived polyphenols to soil microbiome function and crop outcomes. Polyphenols enter soils via root exudates and polyphenol-rich organic inputs. Proposed pathways include microbial recruitment/phenolic metabolism, enzyme stabilisation and nutrient cycling via redox/chelation processes, and interactions with soil organic matter affecting aggregation and N mineralisation. Key modifiers: polyphenol chemistry, purified vs. complex inputs, dose, soil pH, soil organic carbon, environment (field vs. controlled), and exposure duration.

root exudate-driven interventions). We classified inputs as purified compounds vs. complex organic amendments *a priori*.

Comparator: No-polyphenol control or non-polyphenolic control; where genetics were used (e.g., exudation mutants), the comparator was the relevant wild type/deficient control.

Outcomes: Primary microbial diversity (Shannon/Simpson), microbial biomass, enzyme activities (dehydrogenase, urease, and 2-glucosidase). Secondary yield: plant nutrient levels (protein, Fe, and Zn) and antioxidant capacity.

Design: Controlled field/greenhouse studies and controlled observational investigations in peer-reviewed journals. Exclusions: reviews, lack of controls, non-soil/plant systems, and studies that do not provide extractable statistics.

1,710 were screened, 1,634 were excluded, 76 full texts were assessed, and 15 were included (Figure 2).

Data extraction

We extracted bibliographic information, design, soils/crops, purified vs. complex input classification, intervention chemistry/dose/duration, comparators, and quantitative results [means $\pm$ standard deviation (SD) or standard error (SE), sample size (n), and p-values (p)]. We digitised graphical data using WebPlotDigitizer v4.7.

Risk of bias and quality

We applied the Cochrane Risk of Bias 2 tool (RoB2) in experimental trials and the Newcastle–Ottawa Scale in observational studies. Overall, there were nine low-risk studies (60%), four moderate-risk studies (27%), and two high-risk studies (13%). We excluded high-risk studies from sensitivity analyses.

Statistical analysis

Effect size was computed as the standardised mean difference (SMD; Hedges' g) for continuous outcomes (positive values favoured polyphenol inputs). Random-effects models were estimated using restricted maximum likelihood (REML); 95% confidence intervals (CIs), between-study variance (τ^2 ; tau-

Information sources and search strategy

Databases included PubMed, Web of Science, Scopus, Embase, and CAB Abstracts (1990–March 2025). Grey literature included Google Scholar, institutional repositories, and AGRIS. The language was restricted to English. Deduplication was performed in EndNote X20. Full Boolean strings are in [Appendix A](#).

Study selection

Two reviewers independently screened titles/abstracts and full texts, with a third reviewer resolving conflicts. PRISMA flow identified 2,052 records, of which 342 duplicates were removed,

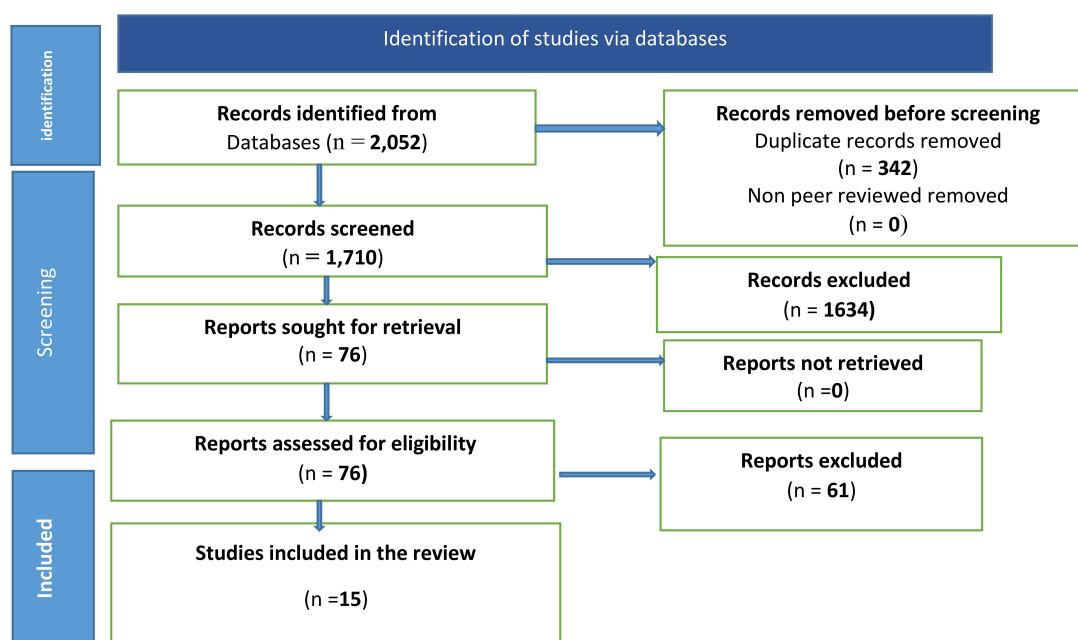


FIGURE 2

PRISMA 2020 flow diagram of study selection. Counts shown for identification, deduplication, screening, full-text eligibility, and included studies. PRISMA, Preferred Reporting Items for Systematic Reviews and Meta-Analyses.

squared), and heterogeneity using the I^2 (I-squared) statistic were reported. Moderator effects were evaluated using subgroup analyses and mixed-effects meta-regression, reporting the moderator test statistic (QM), model explanatory power (R^2), and residual heterogeneity; positive values favoured polyphenol inputs.

Handling multiple outcomes per study

Microbial diversity

If both Shannon and Simpson were reported, Shannon was prioritised; if both were central outcomes, effect sizes were averaged within study using inverse-variance weighting to generate one diversity effect per study.

Enzyme activity

Multiple enzymes reported within a study were aggregated into a within-study composite (inverse-variance weighted) to yield one enzyme effect per study.

Multiple time points

The final reported time point was used in primary analyses; the longest-duration time point was tested in sensitivity analyses, when available.

These steps maintained statistical independence in pooled models.

Moderator and diagnostic analyses

Prespecified moderators were polyphenol class, purified vs. complex, environment (field vs. greenhouse/microcosm), soil pH, soil organic carbon (SOC), dose (when consistently reported), and

duration. Moderator effects were evaluated using subgroup analyses and mixed-effects meta-regression (REML), reporting QM statistics, model R^2 , and residual heterogeneity (τ^2 and I^2 res). Influence and outlier diagnostics included leave-one-out analyses and Cook's distance. Publication bias was assessed using funnel plots and Egger's test; trim-and-fill analysis was exploratory.

Certainty of evidence

We used GRADE (high to very low), considering risk of bias, inconsistency, indirectness, imprecision, and publication bias (Table 1).

Results

Study selection

A total of 2,052 records were found; 342 of them were duplicate entries; therefore, 1,710 titles/abstracts were filtered. A total of 76 articles were evaluated, of which 15 articles were included (Figure 2). Figure 2 shows the PRISMA 2020 flow diagram of study selection. The figure represents the identification of records, the elimination of duplicates, screening, eligibility, and inclusions at the end, with a count at each stage.

Study characteristics

The 15 studies involved temperate, tropical, and Mediterranean systems with wheat, maize, rice, soybean, tomato, cowpea, lettuce,

TABLE 1 Summary of findings (GRADE): outcomes, direction, certainty, and rationale. Summary of findings and certainty of evidence (GRADE).

Outcome	No. of studies	Direction of effect	Pooled effect (95% CI)	Certainty (GRADE)	Reasons for downgrade
Soil microbial diversity	13	↑	SMD = +0.58 (0.32, 0.83)	High	Minor inconsistency
Soil enzyme activity	12	↑	SMD = +0.49 (0.24, 0.73)	Moderate	Moderate heterogeneity
Crop yield	10	↑	+6.8% (2.7%, 10.9%)	Moderate	Imprecision
Nutrient quality (Fe, Zn)	7	↑	+5.6% (1.9%, 9.4%)	Low–moderate	Limited reporting

Certainty ratings follow the GRADE approach.

SMD, standardised mean difference; CI, confidence interval; GRADE, Grading of Recommendations, Assessment, Development and Evaluation.

and cover-crop systems; the soils were of sandy loam, clay, and lateritic (5, 10, 11). Arid/semi-arid and high-latitude systems were sparse, limiting transferability across all climates. Flavonoid-rich residues, lignin/tannin amendments, phenolic acids/coumarins, and polyphenol-rich composts/pomaces were used as interventions (n = 5, n = 4, n = 3, and n = 3, respectively).

Across studies, interventions varied substantially in complexity (purified compounds vs. complex organic matrices), which plausibly contributes to heterogeneity (2, 8, 12).

Table 2 provides a summary of the included studies, including the design, crop/soil, intervention, comparator, outcomes, and main findings. All the records included experimental design, agronomic

TABLE 2 Characteristics of included studies (n = 15).

Author (year)	Design	Crop/soil type	Intervention (polyphenol source)	Comparator	Outcomes measured	Main findings
Han et al. (5)	Field	Wheat/loam	Crop-derived phenolics	No amendment	Microbial diversity, enzyme activity	↑ Shannon +0.5 SMD; ↑ dehydrogenase activity
Li et al. (13)	Greenhouse	Rice/clay	Root exudate polyphenols	Sterile control	Microbial composition, N uptake	↑ N uptake 18%; beneficial taxa enriched
Yang et al. (14)	Field	Tomato/sandy loam	Polyphenol-rich compost	Conventional compost	Diversity, yield	↑ Diversity 22%; ↑ yield 8%
Clocchiatti et al. (12)	Microcosm	Barley/loam	Phenolic exudates	Control	Saprotrophic fungi	↑ Fungal abundance; ↑ β-glucosidase
Iijima et al. (11)	Field	Soybean/loam	Flavonoid–saponin mix	Untreated	Nodulation, enzyme activity	↑ Urease 35%; ↑ nodulation
Liu & Murray (15)	Greenhouse	Cowpea/laterite	Flavonoid supplementation	None	Rhizobia specificity	Improved nodule formation
Hawkes et al. (16)	Field	Mixed species/forest soil	Condensed tannins	No tannins	C/N mineralisation	↓ N immobilisation; ↑ turnover
Kerins et al. (17)	Microcosm	Soil aggregates	Tannins	Organic matter only	Structure, C/N	↑ Aggregate stability; ↑ soil C
Nierop et al. (6)	Lab	Forest soil	Catechols	Control	Protein–phenol complexation	↓ N mineralisation; ↑ immobilised N
Hättenschwiler & Vitousek (18)	Field	Forest floor	Polyphenol mix	None	Decomposition, N flux	Regulated decomposition
Kraus et al. (8)	Field	Temperate soil	Tannin extracts	Control	Nutrient dynamics	↑ Soil C; ↓ N losses
Adamczyk et al. (9)	Greenhouse	Pea/loam	Modified phenolics	No input	Microbial activity	Differential enzyme responses
Harbort et al. (2)	Field	Arabidopsis	Coumarins	Wild type	Microbiome, Fe nutrition	↑ Fe uptake; selective recruitment
Voges et al. (4)	Greenhouse	Arabidopsis	Coumarins	Mutant deficient	Microbiome structure	↑ Beneficial taxa
Seitz et al. (10)	Field	Cover crops	Root exudates	No cover crop	Microbial trajectory	↑ Diversity 0.4 SMD; ↑ enzyme activity

↑, significant increase relative to control; ↓, decrease relative to control. SMD, standardised mean difference; CI, confidence interval.

environment, polyphenol source, control treatment, quantified outcomes, and main results. Arrows indicate direction and meaning ($p < 0.05$).

Risk of bias

There were nine low-risk studies, four moderate-risk studies, and two high-risk studies. The omission of high-risk studies altered the pooled SMDs by less than 0.05 and I^2 by 54 to 46, which implies robustness.

Soil microbial alpha-diversity

In 13 studies, polyphenol inputs enhanced microbial alpha-diversity: SMD = +0.58 (95% CI 0.32–0.83, $p < 0.001$), with moderate heterogeneity ($I^2 = 54\%$). Heterogeneity is consistent with context dependence: effects tended to be larger under field conditions than controlled environments, and complex inputs often produced stronger responses than purified compounds (where directly comparable), consistent with co-delivered substrates and soil structural feedbacks under field settings (3–5, 10).

The forest plot of the effects of microbial diversity is shown in Figure 3. The SMDs (Hedges' g) of the studies, with a 95% confidence interval and a pooled random-effects estimate, showed the precision of the inverse-variance.

Soil enzyme activity

Twelve studies reported dehydrogenase, beta-glucosidase, and/or urease. The combined effect was SMD = +0.49 (95% CI 0.24–0.73, $p < 0.001$), $I^2 = 47\%$. Meta-regression suggested that dose and SOC moderated responses ($R^2 = 0.38$, $p = 0.02$). This pattern

supports but does not prove greater stimulation where carbon availability and binding surfaces may support enzyme stabilisation and microbial metabolism (7, 9).

The enzyme activity forest plot shown in Figure 4, with pooled Hedges' g for dehydrogenase, β -glucosidase, and urease activities with 95% CIs. The study focused on the production and quality of nutrients in crops.

Crop yield and nutrient quality

Agronomic traits were reported in 10 studies, typically as secondary endpoints. Yield rose by +6.8% (95% CI 2.7%–10.9%, $p < 0.01$). Nutrient outcomes {micronutrients [iron (Fe) and zinc (Zn)]; $n = 7$ studies} improved modestly [+5.6% (1.9%–9.4%)], and protein/antioxidant outcomes were inconsistently reported. Because nutrient-quality data came from a smaller and uneven subset, and because polyphenol quantification was not standardised, these agronomic/nutritional conclusions should be interpreted cautiously. Crop functional groups may partially explain heterogeneity: legume systems sometimes showed larger responses, plausibly aligning with flavonoid-mediated symbiosis signalling, but direct evidence remains limited across the included dataset (11, 15).

Figure 5 displays a forest plot of yield and nutritional data. The figure displays the change in percentage and SMDs on yield and plant nutrient measures, along with pooled estimates based on random effects and 95% confidence intervals.

The results were subject to sensitivity and publication bias

Funnel plots were symmetrical; $p = 0.21$ by Egger's test. Trim-and-fill less adjusted the pooled estimates (−0.03). There was a shift of SMDs of 0.04 via leave-one-out analyses.

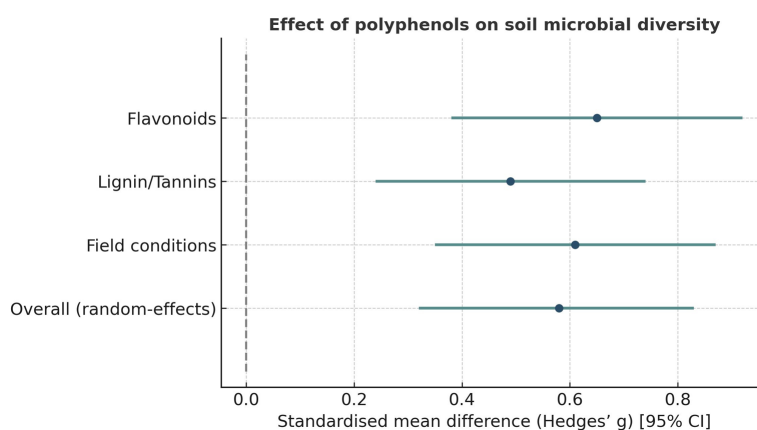


FIGURE 3

Forest plot: effects of polyphenol inputs on soil microbial alpha-diversity. Effect size is Hedges' g (SMD) with 95% CI. Alpha-diversity indices include Shannon and/or Simpson; within-study aggregation rules are described in Methods. Positive values favour polyphenol inputs.

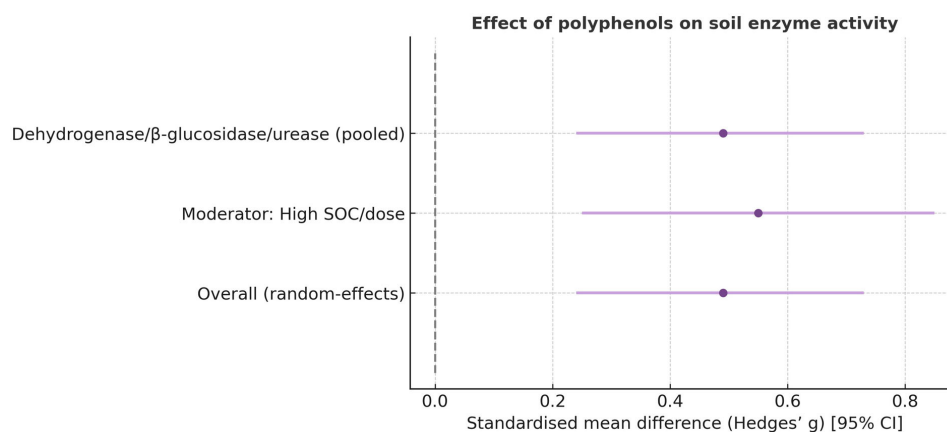


FIGURE 4

Forest plot: effects of polyphenol inputs on soil enzyme activity. Effect size is Hedges' *g* (SMD) with 95% CI. Enzyme activity includes dehydrogenase, beta-glucosidase, and/or urease; multiple enzymes within a study were aggregated as described in Methods. Positive values favour polyphenol inputs.

Certainty of evidence (GRADE)

Table 1 shows the summary of findings (GRADE). Microbial diversity indicated high (minor inconsistency); enzyme activity, moderate (heterogeneity); yield, moderate (imprecision); and quality of nutrient, low-moderate (limited reporting).

Table 3 shows the risk-of-bias domain-level judgements for included studies. Experimental studies were assessed using RoB2 domains (randomisation process, deviations from intended interventions, missing outcome data, measurement of outcomes, and selection of reported results). Observational studies were assessed using the Newcastle–Ottawa Scale domains (selection, comparability, and outcome). Ratings are shown per study and summarised as low risk/some concerns/high risk.

Discussion

Principal findings

This review provides quantitative evidence that polyphenol-rich inputs improve soil biological functioning and agronomic performance, with moderate effect sizes for microbial diversity and enzyme activity and small-to-moderate downstream increases in yield and crop micronutrients. Effects were the strongest for lignin/tannin and flavonoid sources and under field conditions, emphasising context-dependent efficacy (8, 10).

Critical interpretation of heterogeneity

Heterogeneity likely reflects real contrasts in intervention mode and context. Purified compounds isolate chemical effects but may not reproduce field-relevant matrices, whereas complex organic amendments can co-deliver carbon substrates, minerals, and microbial inocula that interact with polyphenols. Field settings

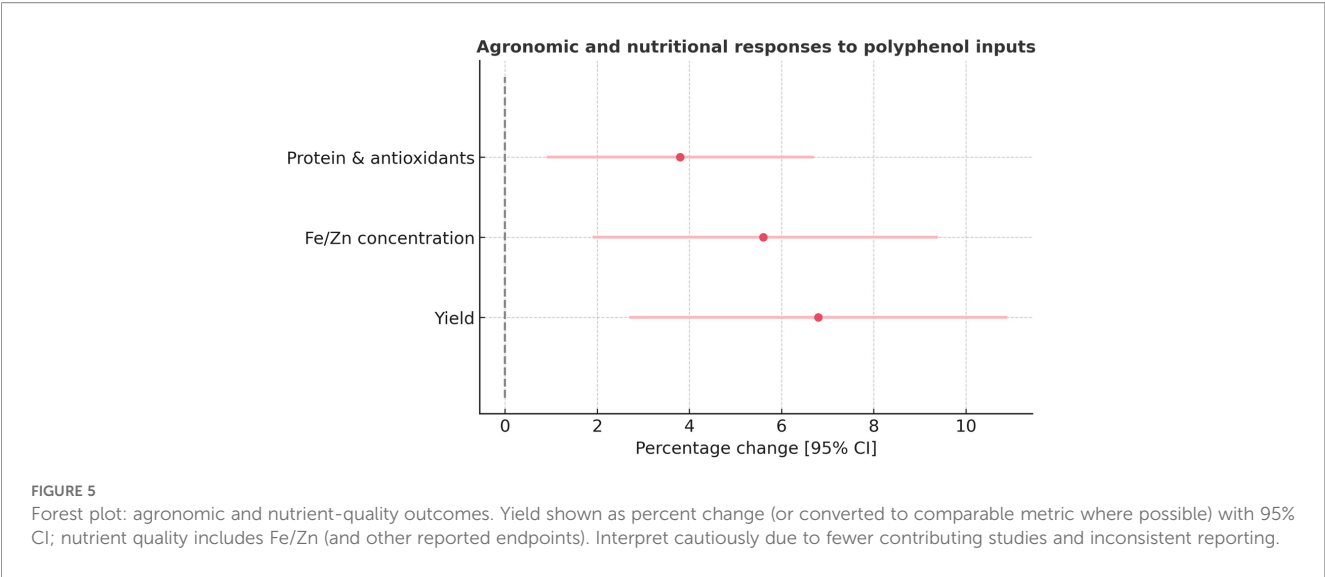
integrate plant feedbacks, soil structure, and hydrology, which may amplify or buffer responses relative to controlled environments. Differences among crop functional groups (e.g., legumes vs. cereals) may further modulate outcomes through distinct exudation profiles and microbial symbioses (8, 10).

Mechanistic interpretation

Polyphenols behave as multifunctional redox mediators and metal chelators, shaping microbial metabolism and stabilising enzymes. Flavonoids and coumarins recruit beneficial taxa (e.g., *Rhizobium* and *Pseudomonas*) and enhance Fe acquisition via chelation/complexation pathways (2, 3). Tannins and lignin derivatives interact with proteins and organic matter, forming complexes that regulate N mineralisation, influence aggregate stability, and modulate carbon-to-nitrogen ratio (C/N) turnover (6, 16, 17). Collectively, these eco-chemical pathways underpin observed improvements in enzymatic activity, nutrient cycling, and plant nutrition (5, 9). However, mechanistic inference remains constrained because relatively few studies simultaneously quantified polyphenol chemistry and measured functional microbial pathways using multi-omics, so mechanisms should be viewed as plausible pathways rather than confirmed causal chains.

Implications for sustainable management

Results support integrating polyphenol-rich amendments (e.g., grape pomace, tea composts, and legume residues) into regenerative practices to bolster soil organic carbon, microbial efficiency, and micronutrient bioavailability, potentially reducing reliance on synthetic fertilisers (19, 20). Field conditions yielded larger responses than microcosms, underscoring the role of soil structure, hydrology, and root feedbacks. Benefits were most evident in neutral to slightly acidic soils with moderate SOC.



Routine monitoring of total polyphenol content in composts can help balance stimulation against transient N immobilisation (7). Given the limited and uneven evidence base for nutrient-quality endpoints, practice recommendations should prioritise soil-function gains, while treating yield/nutrient improvements as promising but context-dependent.

Methodological notes

We adopted random-effects models and reported I^2 , τ^2 , and bias diagnostics, aligning with best practice. While Hedges’ g supports cross-metric synthesis, future analyses may use log response ratio (lnRR) for agronomic interpretability and robust-variance/

TABLE 3 Risk of bias domain-level judgements. Experimental/intervention studies (RoB2). Judgement options: Low risk/some concerns/high risk.

Study ID	RoB2 D1	RoB2 D2	RoB2 D3	RoB2 D4	RoB2 D5	Overall
Han et al. (5)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Li et al. (13)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Yang et al. (14)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Clocchiatti et al. (12)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Iijima et al. (11)	Some concerns	Low risk	Low risk	Low risk	Some concerns	Some concerns
Liu & Murray (15)	Some concerns	Low risk	Low risk	Low risk	Some concerns	Some concerns
Hawkes et al. (16)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Kerins et al. (17)	Some concerns	Low risk	Low risk	Low risk	Some concerns	Some concerns
Nierop et al. (6)	Some concerns	Low risk	Low risk	Low risk	Some concerns	Some concerns
Hättenschwiler & Vitousek (18)	High risk	Some concerns	Low risk	Some concerns	High risk	High risk
Kraus et al. (8)	High risk	Some concerns	Low risk	Some concerns	High risk	High risk
Adamczyk et al. (9)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Harbort et al. (2)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Voges et al. (4)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk
Seitz et al. (10)	Low risk	Low risk	Low risk	Low risk	Low risk	Low risk

RoB2 domain key:

- D1: bias arising from the randomisation process,
- D2: bias due to deviations from intended interventions,
- D3: bias due to missing outcome data,
- D4: bias in the measurement of the outcome,
- D5: bias in the selection of the reported result.

Overall judgement rule (recommended footnote): overall is low risk only if all domains are low, and high risk if ≥1 domain is high (or multiple critical concerns); otherwise, some concerns.

multilevel models where multiple correlated outcomes are reported (dmetar/metafor capabilities).

Limitations and research needs

Several limitations affect inference strength and explain GRADE downgrades for some outcomes. First, many studies were short in duration (often <90 days), limiting conclusions about persistence, seasonal dynamics, and carry-over effects. Second, multi-season field trials were rare, restricting understanding of whether microbiome and enzyme changes translate into durable yield and nutrient gains across variable climate and management conditions. Third, the evidence base showed geographic concentration in temperate and tropical regions, with limited representation of arid, semi-arid, and high-latitude systems; this may constrain generalisability across soil types and climates.

Mechanistically, relatively few studies used metabolomics, functional gene profiling, or transcriptomics to directly connect polyphenol chemistry to microbial pathways, and outcome reporting for crop nutrient quality (e.g., Fe/Zn) was inconsistent. These gaps contributed to imprecision (wide confidence intervals and fewer contributing studies) and indirectness for some crop-quality endpoints.

Accordingly, GRADE certainty was high for microbial diversity (consistent direction and moderate heterogeneity), moderate for enzyme activity and yield (heterogeneity and/or imprecision), and low-moderate for nutrient quality outcomes (limited reporting, imprecision, and indirect mechanistic linkage). Future work should prioritise multi-season, field-scale studies with standardised reporting of polyphenol dose/chemistry, baseline soil properties, and multi-omics endpoints to clarify dose-response relationships, persistence, and causal microbial functions (13, 21–29).

Synthesis

Polyphenols constitute a biochemically grounded lever for ecological intensification: they mediate rhizosphere signalling, reorganise microbial networks, stabilise enzymes, and improve nutrient density. Targeted management that marries polyphenol chemistry with soil context can unlock durable gains in soil health and climate resilience (30, 31).

Conclusions and practical recommendations

Polyphenol-rich inputs are associated with moderate improvements in soil microbial diversity and enzyme activity, with smaller and less certain gains in yield and nutrient quality. We recommend the following:

1. Select inputs by chemistry and complexity: Flavonoid- and lignin/tannin-rich inputs and complex organic amendments show more consistent effects.

2. Match to site conditions: Effects are often stronger in field settings and where SOC is moderate.
3. Monitor polyphenol content and N dynamics (especially for tannin-rich inputs) to manage transient N immobilisation risks.
4. Integrate with legumes/cover crops where appropriate, while recognising that crop-group evidence remains uneven.
5. Design for persistence: Prioritise multi-season outcomes and standardised polyphenol quantification.

Major findings

- Polyphenol-rich residues and root exudates significantly enhance soil microbial diversity and enzymatic activity.
- Meta-analysis indicates a pooled SMD of +0.58 for microbial diversity and +6.8% increase in crop yield.
- Lignin- and flavonoid-derived polyphenols exhibit the strongest biostimulant effects.
- Mechanisms include redox modulation, metal chelation, and selective microbial recruitment.
- Polyphenols offer a bio-based lever for regenerative and climate-resilient agriculture.

Data availability statement

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found below: <https://doi.org/10.5281/zenodo.17593808>.

Author contributions

UP-C: Writing – original draft, Conceptualization, Validation, Writing – review & editing, Visualization, Methodology, Supervision. OC: Writing – review & editing, Writing – original draft, Visualization, Methodology, Validation. AU: Writing – review & editing, Methodology, Validation, Supervision, Writing – original draft, Visualization. MB: Validation, Writing – review & editing, Methodology, Visualization, Writing – original draft. UJN: Writing – original draft, Writing – review & editing, Methodology, Visualization, Validation. UN: Validation, Methodology, Writing – review & editing, Supervision, Visualization, Writing – original draft. RE-N: Supervision, Writing – review & editing, Writing – original draft, Visualization, Validation. OB: Visualization, Writing – review & editing, Validation, Writing – original draft, Methodology. UE: Writing – original draft, Supervision, Writing – review & editing, Methodology, Visualization, Validation. MM: Methodology, Supervision, Validation, Writing – review & editing, Writing – original draft, Visualization. AM: Validation, Methodology, Writing – review & editing, Writing – original draft, Visualization.

FR: Writing – original draft, Visualization, Methodology, Validation, Writing – review & editing.

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Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declared that generative AI was not used in the creation of this manuscript.

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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fsoil.2026.1753138/full#supplementary-material>

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