



REVIEW ARTICLE

Multi-omics approaches to assess the impact of emerging contaminants in soil ecosystems

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Abstract

Emerging contaminants (ECs), such as pharmaceuticals, microplastics (MPs), per- and polyfluoroalkyl substances (PFAS), polycyclic aromatic hydrocarbons (PAH), endocrine-disrupting compounds (EDC) and heavy metals, are progressively affecting soil ecosystems through multiple inputs such as wastewater irrigation, biosolid amendment, agricultural runoff and atmospheric deposition. Despite their widespread occurrence, ECs are rarely incorporated into regular soil monitoring frameworks and remain mainly unregulated. Their persistent accumulation disrupts fundamental soil physicochemical characteristics, microbial community composition, soil-plant interactions, ultimately threatening ecosystem functions. Conventional ecotoxicological techniques lack the mechanistic precision necessary to capture the systemic, multi-scale changes that ECs cause throughout biological hierarchies. Multi-omics approaches, integrating metagenomics, metatranscriptomics, metaproteomics and metabolomics, have enabled comprehensive, system-level insights into EC-induced perturbations at the genetic, transcriptional, protein and metabolic levels. This review synthesises recent advances in the application of multi-omics to unravel the impacts of ECs on soil microbial communities, with a particular focus on changes in taxonomic structure, functional gene expression, enzymatic activities and metabolic pathways. Despite the transformative potential of multi-omics for ecological risk assessment and bioremediation, challenges such as data integration and dimensionality, standardisation and interpretation persist. Furthermore, substantial variability in analytical workflows and dependence on non-soil reference databases restrict inter-study comparability and practical application. Continued advancements will hinge on standardised methodologies, open-access soil databases, artificial intelligence (AI) driven data integration and long-term field investigations to enhance the reproducibility and ecological relevance. Integrating multi-omics with geospatial modelling and decision-support systems provides a pathway for translating molecular insights into actionable strategies for sustainable soil management and ecosystem restoration in the face of ECs.

Keywords: bioremediation; ecological risk assessment; metagenomics; microbiome; soil contamination.

Introduction

Soil ecosystems, the backbone of terrestrial life, are increasingly threatened by the proliferation of emerging contaminants (ECs), a heterogeneous group of synthetic and naturally occurring compounds. These contaminants have recently been detected in the environment and remain largely unregulated (1). They include pharmaceuticals, personal care products, industrial chemicals, pesticides, microplastics (MPs) and nanomaterials, which primarily originate from anthropogenic activities. They are introduced into terrestrial systems through wastewater irrigation, agricultural runoff, biosolid application and atmospheric deposition (2). Although typically present at low concentrations, ECs exert persistent and cumulative impacts on soil health, microbial diversity and key ecosystem services (3).

The continuous input of ECs into soil environments leads to their accumulation and persistence, significantly increasing ecotoxicological risks for soil biota and organisms across higher trophic levels (4). Beyond direct chemical toxicity, ECs significantly alter soil microbial communities, which are key regulators of nutrient cycling, organic matter turnover and soil structure, resulting in functional and compositional shifts that undermine soil fertility and ecosystem resilience (5). The extent of soil contamination by ECs is widespread, with pesticide residues detectable in 83 % of agricultural topsoils across the European Union (6). Similarly, per- and polyfluoroalkyl substances (PFAS) have been detected in global soils at concentrations exceeding 160 ng/kg, with 31 % of groundwater samples surpassing safe thresholds (7) and have even been reported in remote areas like Antarctica (8).

Many ECs exhibit pronounced recalcitrance, as evidenced by the persistence of organochlorine pesticides such as dieldrin and endrin, persisting in soils for decades, with endrin half-lives exceeding 14 years under certain conditions (9). Furthermore, pharmaceutical residues such as antibiotics, hormones and triclosan are commonly found in biosolid-amended and wastewater-irrigated soils at concentrations ranging from 0.10–200 µg/kg, where they contribute to the development of antimicrobial resistance and disrupt microbial-mediated nutrient cycling (10). Pharmaceutical mixtures such as sulfamethoxazole and tetracycline at concentrations exceeding ≥ 100 mg/L under controlled experimental conditions have been shown to reduce microbial functional diversity and shift communities toward Gram-negative and fungal dominance (11). Similarly, microplastic contamination elevates the abundance of actinobacteria and proteobacteria while reducing acidobacteria and basidiomycota, thereby disrupting key ecological functions (3). In wastewater-irrigated soils, persistent ECs like carbamazepine and fluconazole accumulate in plant tissues, indicating both microbial and food chain exposure risks (12).

Emerging contaminants are rarely included in terrestrial monitoring programs, which mostly track legacy or approved pollutants, compounding the problems they pose. These limitations hinder their early detection and risk mitigation, thereby requiring integrated and innovative assessment tools capable of capturing the subtle and systemic impacts of ECs in soil environments (13). Recent advancements in analytical chemistry and high-throughput omics technologies have revolutionised the detection and characterisation of ECs across molecular to community levels. Multi-omics approaches, including genomics, transcriptomics, proteomics and metabolomics, provide a holistic framework to elucidate the biological responses to EC exposure, capturing complex interactions that single-omics studies often overlook (14). These platforms enable the identification of stress-responsive genes, proteins and metabolites, offering mechanistic insights into toxicity and adaptive mechanisms (15). Although widely applied in biomedical research, the adoption of multi-omics in soil ecotoxicology remains limited, emphasising the need for a more comprehensive structure that aligns with the one health framework linking soil health, ecosystem resilience and human wellbeing (16).

Despite increasing recognition of ECs in terrestrial environments, most existing reviews have focused on aquatic systems, isolated contaminant classes, or single-omics analyses, providing limited understanding of the combined ecological and molecular effects on soil ecosystems. The current review synthesises recent advances in multi-omics approaches for assessing ECs in soil ecosystems, examining how integrated genomic, transcriptomic, proteomic and metabolomic analyses can improve the understanding of contaminant fate, microbial community responses and ecosystem-level consequences. By combining multi-omics evidence across contaminant classes, this review shows how systems-level approaches reveal molecular biomarkers, stress mechanisms and early signs of ecological damage beyond conventional methodologies and it highlights the need for standardised multi-omics approaches to support sustainable soil and food security.

Materials and Methods

A systematic literature review was performed based on PRISMA 2020 guidelines to identify studies reporting about ECs and use of multi-omics approaches in the soil ecosystems. The relevant literature from January 2015 to March 2026 was retrieved from the Scopus, Web of Science, PubMed, ScienceDirect and Google Scholar databases with combinations of the keywords associated with ECs, soil ecosystem, soil microbiome, multi-omics, metagenomics, metaproteomics, metabolomics, ecotoxicology, soil health and bioremediation. Studies were included if they were peer-reviewed research or review articles written in English that addressed soil ecosystems or plant-soil-microbe interactions, focused on ECs and used one or more omics tools to evaluate the ecology, source tracking or bioremediation of contaminated soil. Only conference abstracts, editorials, book chapters, duplicate records and exclusively aquatics-oriented studies were excluded. All retrieved records were filtered by titles, abstracts and full-text evaluation based on the predefined inclusion and exclusion criteria and the process of selection of the study was documented by the PRISMA 2020 flow diagram (Fig. 1). Information on contaminant classes, ecosystem characteristics, omics platforms, microbial responses, functional pathways, ecological impacts and remediation outcomes was extracted and synthesised into thematic sections to provide an overview of current advances, challenges and prospects of multi-omics applications for assessing ECs in soil ecosystems.

Sources and types of emerging contaminants in soils

Pharmaceuticals and personal care products

Pharmaceuticals and personal care products (PPCPs) encompass a wide array of bioactive compounds used in human and veterinary medicine, cosmetics, livestock farming, aquaculture and industrial applications (17, 18). Pharmaceuticals and personal care products enter soil ecosystems through multiple pathways, including the application of manure from medicated livestock and irrigation with contaminated wastewater, biosolid amendments (19), landfill leachates and atmospheric deposition (20). Their widespread use and incomplete removal by conventional wastewater treatment systems have led to their frequent detection in terrestrial environments. Pharmaceutical residue levels in agricultural soils can range greatly, from 0.02 to more than 1700 ng/g, depending on the type and source of the substance. According to previous studies, lincomycin and sulfamethoxazole concentrations were recorded as 1757 ng/g and 425 ng/g respectively (21). Among 59 antibiotics reported in agricultural soils worldwide, tetracyclines (72.2 %) and sulfonamides (69.2 %) were the most frequently detected classes (22).

Antibiotics alter soil microbial processes even at low concentrations. Sulfamethoxazole, sulfadiazine and trimethoprim reduce soil respiration, whereas oxytetracycline (30 mg/kg) and sulfadiazine (100 mg/kg) inhibit nitrification. Conversely, ciprofloxacin and norfloxacin have been reported to stimulate nitrification at low concentrations (1 mg/kg soil). Soil enzymes were highly sensitive, showing 35–80 % inhibition, including a 41.3 % reduction in alkaline phosphatase at 10 mg/kg oxytetracycline and up to 80.8 % inhibition at > 30 mg/kg (23). Moreover, studies have shown that plants take up certain PPCPs; for example, lettuce and carrots irrigated with treated wastewater accumulated carbamazepine and sulfamethoxazole in edible tissues, raising concerns about food safety (19). The residues pose potential risks to

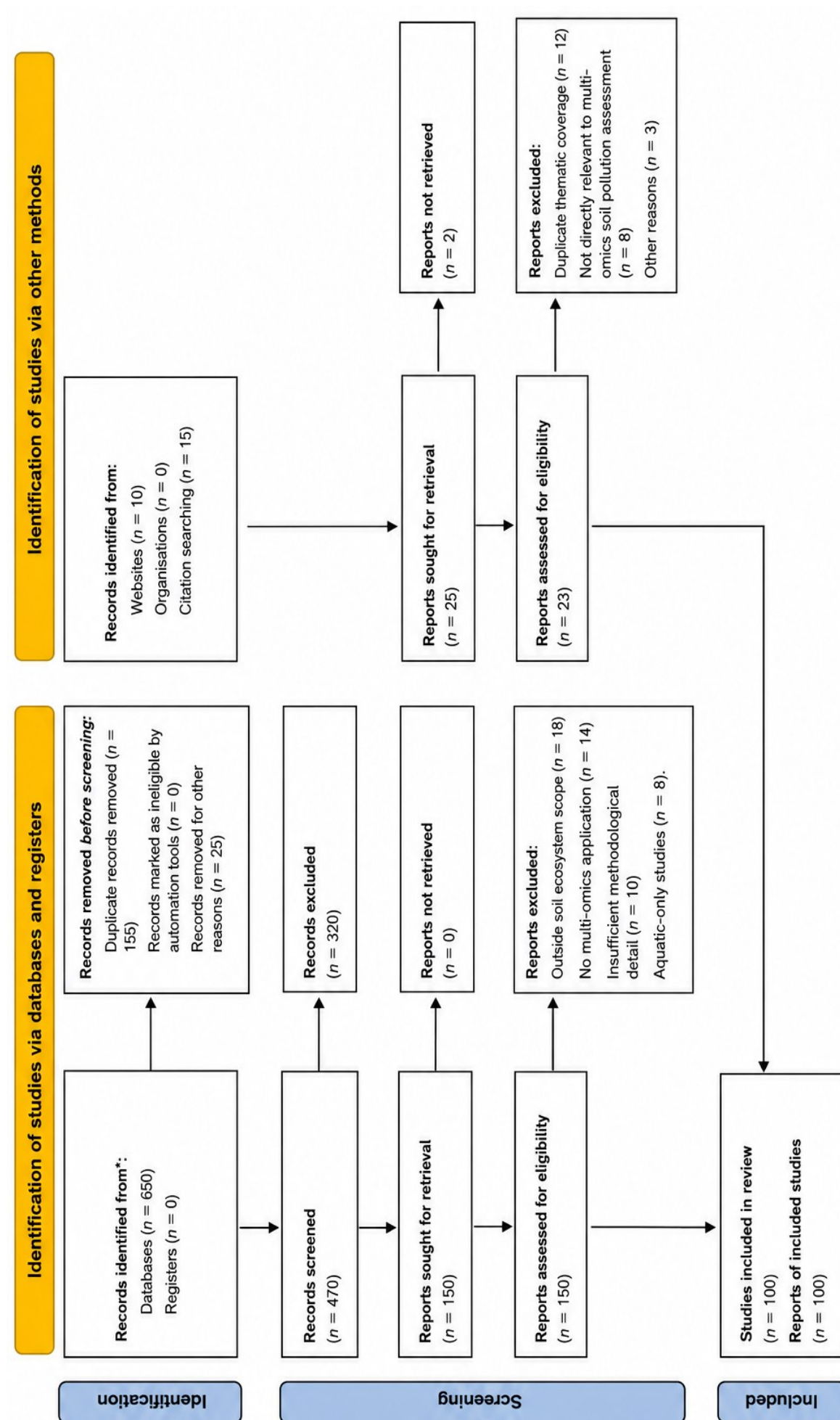


Fig. 1. PRISMA 2020 flow diagram depicting the systematic search strategy and study selection process adopted.

aquatic ecosystems, soil microbial communities and crop safety. The diversity of EC entry routes from biosolid application and irrigation to atmospheric deposition is illustrated in Fig. 2, which summarises the dominant sources, environmental pathways and biological impact zones across the soil ecosystem.

Microplastics and engineered nanomaterials

Microplastics, defined as plastic particles smaller than 5 mm (24), are increasingly prevalent in terrestrial ecosystems due to the degradation of synthetic polymers such as polyethylene (PE), polypropylene (PP), polystyrene (PS), polyvinyl chloride (PVC), nylon and polylactic acid (PLA). Sources include the breakdown of agricultural plastic films, packaging waste and microbeads in personal care products and irrigation with treated municipal wastewater (25). Recent studies have documented MP concentrations ranging from 100 to over 67000 particles per kg of soil, with evidence of uptake in plants and soil fauna (26).

Engineered nanomaterials (ENMs), typically defined as particles < 100nm, represent another class of emerging soil contaminants. Common ENMs include silver (Ag), titanium dioxide (TiO₂), zinc oxide (ZnO) and carbon (C) nanotubes, which enter soils through biosolid application, agrochemical formulations and industrial runoff (27). Due to their high surface area and reactivity, ENMs can interfere with microbial respiration, enzymatic functions and plant-microbe interactions even at low concentrations (< 1mg/kg) (28). Both MPs and ENMs exhibit high environmental persistence and can adsorb other pollutants, elevating their ecotoxicological impact.

Hormones and endocrine-disrupting compounds

Endocrine-disrupting compounds (EDCs) are exogenous substances that interfere with the hormonal systems of organisms, leading to adverse developmental, reproductive, neurological and immune effects. Both natural and synthetic hormones, such as estrogens, androgens and progestins, are increasingly detected in terrestrial systems due to expanding industrial activity and intensified

agriculture (29). Key sources include human excretion (via sewage and biosolids), veterinary pharmaceuticals in livestock manure and land-applied wastewater sludge (30). It is estimated that approximately 30000 kg of natural and 700 kg of synthetic estrogens are released annually from human sources, with an additional 83000kg contributed by livestock waste entering aquatic environments and agricultural soils through wastewater discharge and manure application globally (31).

Notable EDCs include steroidal estrogens (e.g., estrone, 17 β -estradiol), pesticides like DDT, industrial compounds such as polychlorinated biphenyls (PCBs) and persistent pollutants like PFAS and polybrominated diphenyl ethers (PBDEs). Although PFAS and PBDEs are broader contaminant classes, numerous compounds within these groups have displayed endocrine-disrupting properties, disrupting hormone production, transport and receptor signalling pathways. These compounds are capable of exerting adverse effects at low concentrations (ng/L– μ g/kg) and studies have shown that soil-applied biosolids containing estrogens and EDCs can reduce microbial activity, inhibit enzyme function and alter plant hormone signalling pathways (32). Exposure to EDC has been associated with adverse reproductive, developmental, endocrine, metabolic, cardiovascular, hepatic, urinary and immunological effects in both humans and animals, highlighting their widespread physiological consequences across multiple organ systems (33).

Industrial chemicals

Per- and polyfluoroalkyl substances are a diverse group of synthetic fluorinated compounds that have been used in industrial processes and consumer products for decades. They are characterised by strong C-F bonds and functional groups such as perfluoroalkyl and perfluorocarboxylic acids, which confer exceptional resistance to thermal, chemical and microbial degradation (33). Compounds such as perfluorooctanoic acid (PFOA) and perfluorooctane (PFOS) are particularly concerning as their concentrations have been documented in agricultural soils ranging from 0.2–70 μ g/kg,

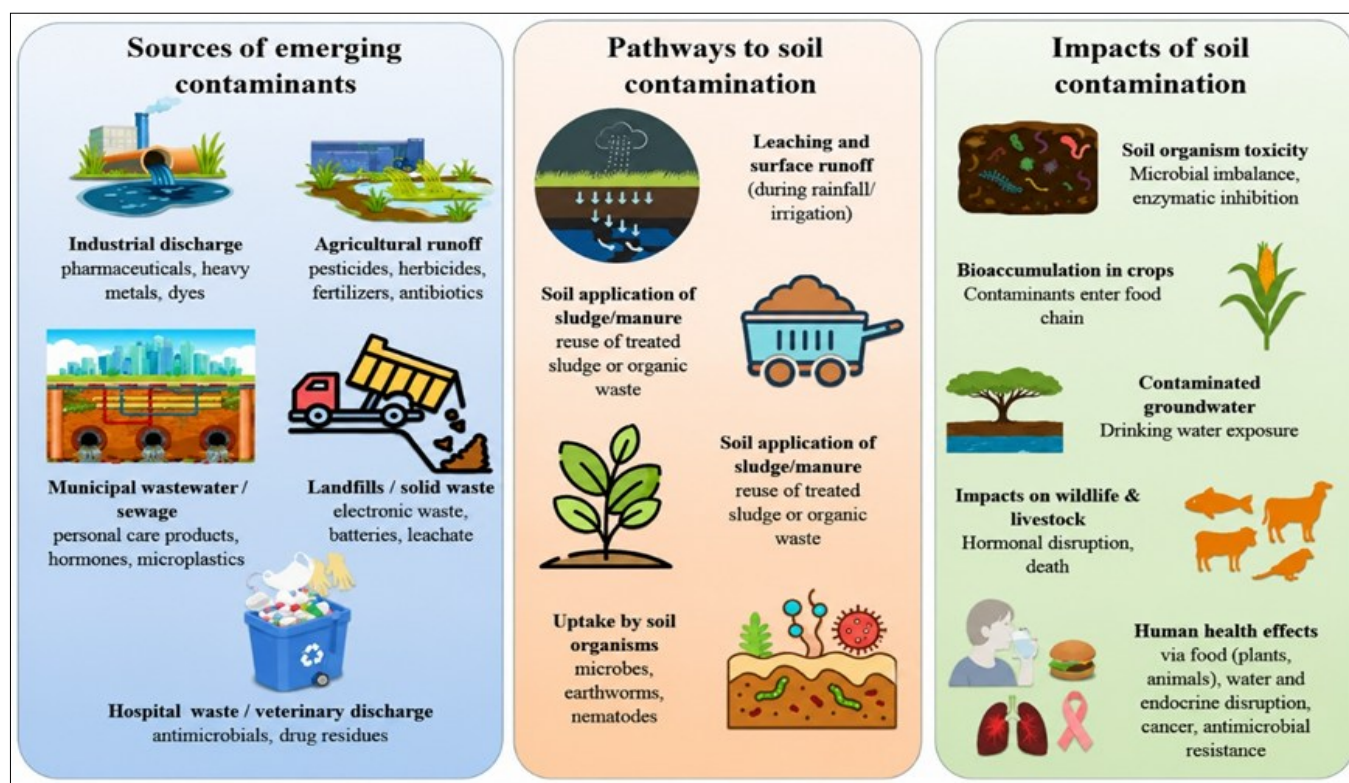


Fig. 2. Emerging contaminants in soil: Sources, pathways and impacts.

particularly in areas irrigated with treated wastewater or amended with contaminated biosolids (34). After approximately 35 years of cumulative use, soil concentrations reached 2.5–8.6 ng/g for total PFAS at 30 cm depth and up to 433 ng/g¹ in long-term plots due to the one-time application of biosolids in agricultural areas. Polyfluoroalkyl substances exposure has also been linked to endocrine disruption, immunotoxicity, developmental abnormalities and reproductive dysfunctions in both humans and wildlife (7).

Polycyclic aromatic hydrocarbons

Polycyclic aromatic hydrocarbons (PAHs) are a class of persistent organic pollutants generated from both natural sources, such as fossil fuel deposits and anthropogenic activities involving incomplete combustion of coal, petroleum, biomass and organic waste (35). Due to their hydrophobicity, low volatility and strong affinity for organic matter, PAHs tend to accumulate in soil matrices and act as long-term reservoirs of toxicity, with concentrations at contaminated sites ranging from 10 to over 10000 µg/kg, depending on proximity to industrial areas (36). Polycyclic aromatic hydrocarbons concentrations vary widely across soil environments, with urban soils containing 1.2–524 µg/g, industrial soils 19–855 µg/kg and agricultural soils 600–2800 mg/kg in surface layers (37). These levels often exceed guidelines in polluted areas, with PAHs such as benzo[a]pyrene predominating in toxicity risk assessments (38).

Heavy metals and metalloids (as emerging concerns)

Heavy metals and metalloids such as cadmium (Cd), arsenic (As), lead (Pb), mercury (Hg), chromium (Cr), copper (Cu), Zinc (Zn) and nickel (Ni) are persistent and re-emerging as soil contaminants due to their persistence, bioaccumulation and toxicity to ecosystems and humans (39). They originate from geogenic inputs, including weathering of parent rocks, volcanic emissions and natural geochemical processes and anthropogenic inputs such as mining, smelting, industrial waste disposal, fossil fuel combustion and agrochemicals (40). After entering the soil, heavy metals disrupt microbial communities by inhibiting enzymatic activities (e.g., dehydrogenase, urease) and suppressing microbial biomass. Such exposure often decreases sensitive taxa such as acidobacteria and nitrospira while increasing the abundance of metal-tolerant groups,

including proteobacteria and firmicutes (41). In plants, metals such as Cd, Pb and As are phytotoxic, causing chlorosis, stunted growth and yield reduction (15–20 %) with Cd accumulation in tubers like potatoes being a key food safety concern (42). These metals bioaccumulate across trophic levels, posing chronic human health risks, including neurological and developmental disorders, through dietary exposure (43). Despite regulatory efforts, legacy contamination from decades of industrial emissions continues to threaten food security and soil ecosystem resilience globally (44).

Impact of emerging contaminants on the soil ecosystem

Effects on soil physicochemical properties, fertility and bioaccumulation

The emerging pollutants alter fundamental physicochemical properties, with adverse effects cascading from soil structure through to biota and food chains (Fig. 3). Microplastic contamination in agricultural lands decreased water-stable aggregates by 20 % and impaired structural stability. It also reduced bulk density but increased porosity by 7–15 % (3). Engineered nanomaterials further modify soil pH, CEC, redox potential and hydraulic conductivity. Heavy metal contamination by Pb, Ni and Cr compounded these effects by enzymatic inhibition and declining bacterial populations by 10–82 % (45). Long-term phosphorus (P) fertiliser use elevated soil Cd, forming Cd-P precipitates that hamper plant nutrient uptake and lead to phosphatase inhibition by 20–50 % (46).

Antibiotic residues, such as tetracyclines and sulfonamides, disrupted the nitrogen (N) cycle and increased N₂O emissions. The uptake of pharmaceuticals in soil fauna has also been confirmed with *Eisenia foetida* accumulating diclofenac and fluoxetine with bioconcentration factors of 7.0–69.6 and 14.1–20.4 respectively and ofloxacin concentrations at 265 ng/g (47). Endocrine-disrupting compounds (EDCs) from sewage sludge and pesticide inputs disrupt plant hormonal balance, reducing germination, root growth and chlorophyll content, thus threatening crop productivity and ecological stability through persistent and complex interactions (48). However, knowledge gaps persist for contaminants such as tramadol, with limited information on crop uptake pathways and multi-omics responses, highlighting the need for further research on

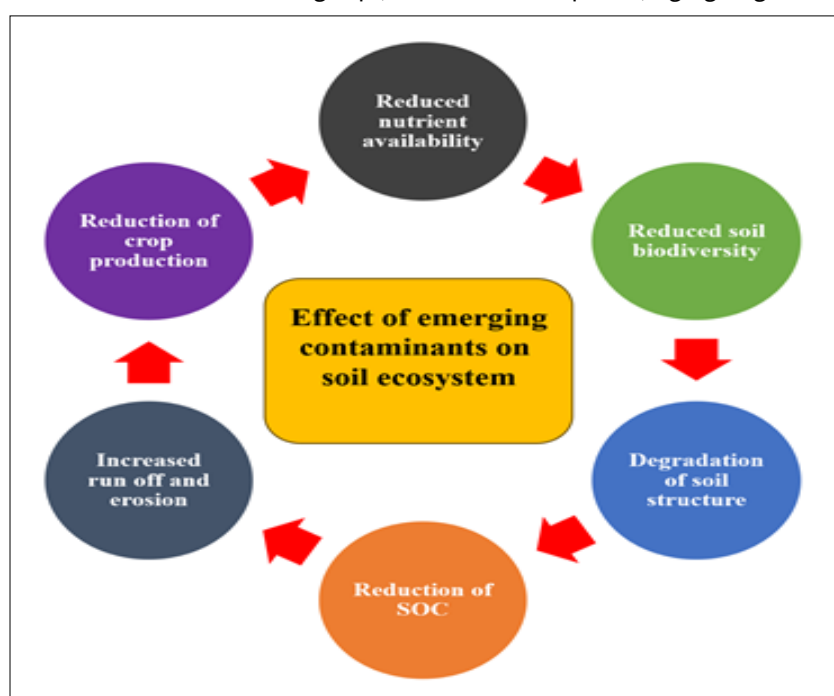


Fig. 3. Impact of emerging contaminants on the soil ecosystem (SOC: Soil organic carbon).

their bioaccumulation and molecular impacts in soil-plant systems.

Soil microbial disruptions

a. Alteration of microbial diversity : Exposure to ECs reduces soil microbial richness and evenness, with reported reductions of 20–60 % in alpha-diversity across contaminant classes (49). Polycyclic aromatic hydrocarbons contaminated soils showed 20–40 % reductions in Shannon diversity, increased β -diversity and upregulation of PAH-degrading genes (*PAH-RHD α*) (50). The increase in β -diversity indicates greater spatial heterogeneity in microbial communities, creating uneven ecological niches and selective pressure across the soil environment. Further, co-contamination by PFAS and heavy metals suppressed Chao1 diversity by 25–50 % and significantly reduced fungal diversity. Antibiotics such as sulfamethoxazole and tetracycline can reduce bacterial diversity by 15–40 % within 30 days of exposure (51), depleting sensitive *Acidobacteria* and *Verrucomicrobia* phyla, while enriching resistant groups like *Betaproteobacteria* (52). The resilience of microbes to ECs varies depending on the chemical nature of the contaminant, exposure duration and pre-existing soil microbial diversity (53). However, recovery patterns remain compound specific. For example, soil biota recovers compositionally within 90 days after oxytetracycline exposure, whereas PFAS-contaminated soils retain altered microbial structure after 12 months. Fungal communities respond to PFAS within 4 months, while bacterial shifts emerge only after approximately 1 year, underscoring divergent sensitivity timescales across microbial kingdoms. Soils with higher baseline diversity recover more effectively, consistent with the ecological insurance hypothesis (54).

b. Changes in community composition : Soil contamination by ECs enriches tolerant, opportunistic taxa while depleting sensitive functional groups. Across pharmaceutical and PPCP contaminated soils, Proteobacteria increased by 28–50 %, with *Pseudomonas*, *Bacillus*, *Sphingomonas*, *Sphingobium* and *Arthrobacter* becoming dominant (55). Microplastics and nanomaterials further promote colonisation by opportunistic microbes and fungi such as *Aspergillus* and *Fusarium*, creating new ecological niches and enhancing greenhouse gas emissions (56). Co-occurring contaminants amplify these impacts by accelerating community turnover and impairing nutrient cycling. These compositional shifts are closely associated with increased antibiotic resistance genes (ARGs) and reduced plant growth-promoting functions (57). Overall, long-term exposure to ECs induced shifts that reduced microbial network complexity by 30–40 % (58). These disruptions lead to compromised soil fertility, reduced organic matter decomposition and loss of ecosystem services.

Impairment of ecological functions

Emerging contaminants markedly impair key soil ecological functions by disrupting nutrient cycling, enzyme activities and organic matter decomposition. Nitrogen cycling processes are reduced by 15–40 %, with altered expression of functional genes and increased N₂O emissions under contaminant stress (59). Phosphorus cycling is similarly affected, with 20–50 % declines in phosphatase activity due to heavy metals and PFAS-induced P precipitation and inhibition (60). Carbon mineralisation decreases by 10–35 %, particularly in soils containing MPs and nanomaterials that suppress dehydrogenase activity (61). Similarly, significant inhibition of N fixing genera such as *Rhizobium* and *Bradyrhizobium* has been reported due to contaminant exposure, increasing reliance on external agrochemical inputs (51). Advanced analyses, such as nuclear magnetic resonance (NMR) spectroscopy, revealed selective

inhibition of lignin and suberin (62), affecting humus formation and soil structural integrity. These cumulative effects could lower overall soil fertility by 15–38 %, reinforcing reliance on chemical inputs and reducing long-term soil resilience (63). These effects are further magnified by long-term wastewater irrigation: soils treated with reclaimed water for many years accumulate EDCs, as well as pharmaceuticals (64); these soils also exhibit a reduction in antibiotic-resistance gene profiles and changes in their resistome composition (65) and antibiotic-resistance residues persist for years after irrigation ends, even in metal co-contaminated soils (66), reflecting the persistence of these compound classes and their impact on soil microbial activity and diversity (67, 68). A comprehensive overview of how major ECs behave in wastewater-irrigated soils, detailing their environmental pathways, crop absorption rates and molecular data to illustrate their full impact on the ecosystem is depicted in Table 1.

Multi-omics approaches to assess the impacts of emerging contaminants

Traditional ecotoxicological assays, which measure discrete endpoints like microbe abundance or enzyme activity, offer little mechanistic insight into how ECs cause these cascade ecological disruptions. Multi-omics methods encompassing metagenomics, metatranscriptomics, metaproteomics and metabolomics overcome this constraint by simultaneously capturing genomic potential, active gene expression, functional protein profiles and biochemical intermediates (Fig. 4). Together, these platforms provide a systems-level framework for evaluating stress responses and adaptive mechanisms that cannot be fully resolved using a single omics approach.

Metagenomics

Metagenomics characterises soil microbial communities by DNA sequencing, capturing both taxonomic profiles and functional gene dynamics. Unlike traditional genomics, which targets individual isolates, metagenomics analyses DNA extracted directly from environmental samples, allowing for a comprehensive assessment of microbial diversity, metabolic pathways and resistance genes (69). Common sequencing platforms used for soil metagenomic studies include the Illumina NovaSeq platform for high-throughput short-read sequencing, the PacBio single-molecule real-time sequencing platform for better genome assembly and the Oxford Nanopore sequencing platform for long-read real-time analysis. Typical workflows involve DNA extraction, high-throughput amplicon or shotgun sequencing, quality filtering, taxonomic/functional annotation using databases like SILVA or KEGG and downstream statistical analyses including phylogenetic and network modelling.

Metagenomic studies have revealed significant shifts in microbial composition and community restructuring under EC exposure (70). Functional gene profiling frequently identifies the proliferation of ARGs, including *β -lactamase*, *tetR* and *macB*, often co-located with mobile genetic elements like class 1 integrons, Tn3 transposons and IncP plasmids, indicating horizontal gene transfer in EC-impacted systems (71). This approach enables the identification of genetic determinants associated with contaminant degradation. For instance, *atzA/trzN* genes in *Streptomyces nigr* LM01 mediated atrazine conversion to hydroxyatrazine or cyanuric acid (72), while the *CarE* carboxyesterase gene in *Rhodococcus erythropolis* D310-1 catalyses the de-esterification of chlorimuron ethyl (73). Metagenomics has also uncovered enrichment of genes linked to biofilm formation, pollutant degradation (e.g.,

Table 1. Environmental fate, plant uptake and omics-based insights of emerging contaminants in wastewater-irrigated soils

Contaminant	Compound	Observed concentration in soil/irrigation water	Crop uptake	Soil fate	Multi-omics insights	Key modulating factors	Ref
Pharmaceuticals	Carbamazepine	Soil: 3.6–7.1 ng/g; Irrigation water: 784.8 ± 1378.6 ng/L	Parsley: up to 2470 ng/g FW; Wheat shoots: up to 44 % translocation; detectable in tomato	Moderately persistent; high mobility in water; low sorption to soil organic matter	Metatranscriptomics links exposure to activation of plant xenobiotic stress pathways and aquaporin-mediated uptake genes	Irrigation water concentration; plant species and root physiology; soil organic matter content	(12)
	Tramadol	Irrigation water: 500-100000 ng/L; Soil K _d : 0.9–5.5 L/kg	Not reported	Sorption increases with clay content; hysteresis observed across all soil types; cation exchange dominant below pKa	Not yet reported	Clay content (7.4 % → K _d ~ 0.9; 41.9 % → K _d ~ 5.5 L/kg); pH relative to pKa; effluent matrix composition	(23)
	Diclofenac	Surface/groundwater: up to 8000 ng/L; Soil (reclaimed water irrigation): <1–140 ng/g	Tomato fruit: up to 11630 ng/kg DW	Low leaching and volatilisation; accumulates preferentially in upper soil layers	Preliminary evidence suggests EC-induced shifts in microbial metabolic gene expression; formal omics characterisation lacking	Soil texture; organic matter content; irrigation frequency; plant species	(17, 18)
Physical contaminants	Microplastics (MPs)	Mulched soils: 571 items/kg; non-mulched: 263 items/kg; intensive agriculture (SW China): 7100–42960 items/kg; semi-arid soils: ~1100 items/kg	Increased shoot and root biomass by ~46-48 %; reduced photosynthesis; induced oxidative stress in root tissues	Enrichment in soil macropores and cracks; vertical migration to deeper layers via preferential flow; 72 % associated with soil aggregates; redistribution via wind erosion and irrigation	Metagenomics: altered microbial community composition and diversity; enrichment of Patescibacteria; reduced water-stable aggregates (~20 %) compromising of microbial microhabitat integrity	Polymer type, size and shape (fibres vs. fragments vs. films); mulching and irrigation practices; soil texture; particle size distribution	(25, 26)
Persistent synthetic pollutants	PFAS (PFOA, PFOS)	Soil: 0.01–100 ng/g; Irrigation effluent: 70–1300 ng/L; Groundwater: <0.03–8300 ng/L	Wheat grain: 1-40 ng/g DW; maize: variable by compound class	PFOA: high mobility; estimated groundwater breakthrough in ~10 years; PFOS: low mobility; breakthrough estimated at ~50 years	Metagenomics and transcriptomics: altered root transporter gene expression; upregulation of oxidative stress and xenobiotic detoxification pathways; fungal community disruption within 4 months; bacterial shifts after ~1 year	Chain length and functional group chemistry; soil organic carbon; cation concentration; pH; plant species	(7)

Antibiotics	Tetracycline	Irrigation water: 120–800 ng/L; Soil: up to 50 ng/g	Up to 90 ng/g in leafy vegetables (DW)	Strong adsorption to topsoil via cation bridging; highly persistent; limited leaching	Metagenomics: enrichment of tetA, tetM ARGs; shifts toward Bacteroidetes and γ-Proteobacteria; altered nitrification gene abundance	Irrigation water source (fishpond > domestic effluent); soil organic matter content; pH	(47, 67)
	Sulfamethazine	Irrigation water: 80–500 ng/L; Soil: up to 50 ng/g	Variable; generally lower than tetracyclines	Moderate persistence; more mobile than tetracyclines; partial photodegradation at surface	Metagenomics: enrichment of sul1 and sul2 sulfonamide resistance genes; altered Proteobacteria:Firmicutes ratios	Soil texture; irrigation source; redox conditions	(47, 67)
	Sulfamethoxazole	Effluent: ~300 ng/L; Soil: < 20 ng/g	Not significant in edible tissues	Leaches to subsurface; partially degraded via photolysis and microbial co-metabolism	Metatranscriptomics and metagenomics: reduced nitrifying bacterial activity (amoA downregulation); decreased community diversity	Irrigation timing; soil organic matter; depth of application	(21)
	Trimethoprim	Detected after prolonged irrigation: ~60 ng/L	Trace amounts in edible parts	Moderate degradation; some accumulation in clay layers	Changes in microbial resistance gene profiles	Irrigation duration, clay content	(68)
	Ofloxacin	Effluent: ~150 ng/L; Soil: 10–30 ng/g	Spinach: 5.6 ng/g DW (BCF ≈ 0.02)	Strong sorption to organic matter and clay via cation exchange; surface accumulation; limited leaching	Metagenomics: alters antibiotic resistance gene dynamics; enriches fluoroquinolone resistance genes (qnrS, qnxAB) in reclaimed water-irrigated soils	Soil organic carbon content; redox status	(66)
Antibiotic resistance markers	Oxolinic acid / Nalidixic acid	Soil surface: 5–20 ng/g (4 years post-irrigation)	Not detected in crops	Strong surface adsorption; limited vertical migration; persistent under low-turnover conditions	Omics characterisation not yet been reported	Proximity to irrigation outlet; soil depth; legacy irrigation history	(66)
	ARGs (sul1, tetA, qnrS)	Abundant in irrigated soils; effluent >> freshwater irrigation	Not directly quantifiable	Persist in soil for months to years post-irrigation cessation; transferable via mobile genetic elements	Metagenomics: ARG enrichment highest in fishpond-irrigated soils; co-located with class 1 integrons and IncP plasmids; mobile genetic element mobilisation confirmed	Soil clay content and moisture; irrigation history; co-occurring heavy metals	(64)
	Bisphenol A (BPA)	Soil: up to 52 ng/g	ND-0.8 ng/g FW	Low to moderate mobility; sorption to organic matter; degradable under aerobic conditions	Transcriptomics and proteomics: endocrine disruption biomarkers expressed; altered steroid hormone receptor gene activity	Soil redox status, organic matter content and aerobic degradation capacity	(65)
Endocrine-disrupting compounds	Estrone (E1)	Surface runoff: < 50 ng/L	Not detected in crops	Rapidly degradable in aerobic surface soil; sorbs to OM; persists under anaerobic conditions	Transcriptomics: disruption of steroidogenesis and xenoestrogen response pathways in soil biota; maize root metabolic transformation confirmed	Soil aeration; organic matter content; temperature	(30)
	Phthalates (DEHP)	Soil: 100–1000 ng/g	ND-2.4 ng/g DW	High affinity for soil organic carbon; slow biodegradation; accumulates in OM-rich horizons	Metabolomics: altered lipid metabolism pathways; disruption of fatty acid β-oxidation and mitochondrial function identified via acylcarnitine profiling	Soil organic carbon content; temperature; microbial community composition	(52)
	Nonylphenol	Soil: up to 200 ng/g	ND-1.3 ng/g DW	Strongly adsorbed to organic matter; recalcitrant; low leaching potential	Proteomics and enzyme assays: disruption of microbial extracellular enzyme activity (dehydrogenase, phosphatase)	Organic matter content, pH and soil microbial diversity	(65)

FW: fresh weight; ND: not detected; OM: organic matter; K_{oc}: soil-water distribution coefficient; pK_a: acid dissociation constant; BCF: bioconcentration factor; MPs: microplastics; PFAS: per- and polyfluoroalkyl substances; PFOA: perfluorooctanoic acid; PFOS: perfluorooctanesulfonic acid; ARGs: antibiotic resistance genes (*sul1*, *sul2*: sulfonamide resistance genes; *tetA*, *tetM*: tetracycline resistance genes; *qnrS*, *qnxAB*: fluoroquinolone resistance genes; *amoA*: ammonia monooxygenase gene; BPA: bisphenol A; DEHP: di(2-ethylhexyl) phthalate; E1: estrone; IncP: incompatibility group P (plasmid family).

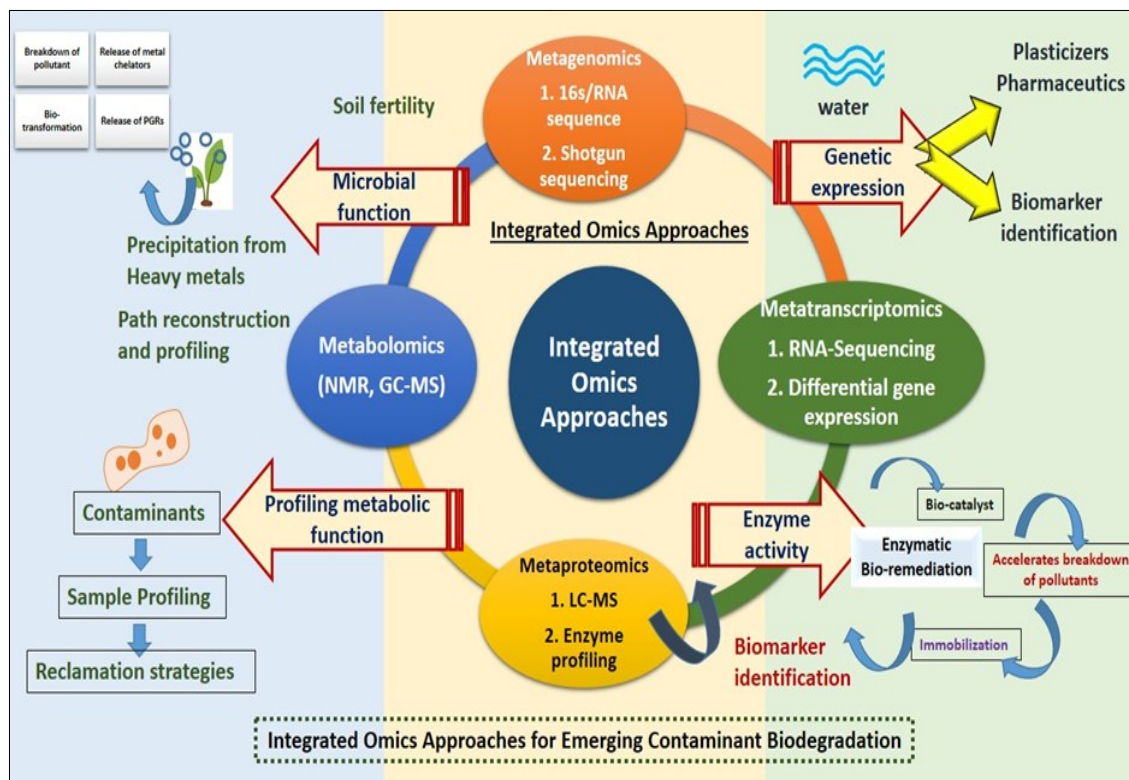


Fig. 4. Integrated multi-omics workflow for assessing emerging contaminant impacts on soil microbiomes. (NMR: nuclear magnetic resonance; GC-MS: gas chromatography-mass spectrometry; LC-MS: liquid chromatography-mass spectrometry; RNA: ribonucleic acid)

monooxygenases, dioxygenases) and stress adaptation in soils. These functional genomic insights inform predictive microbial ecology, with trait-based genomic models of microbial resilience and ecosystem function under contaminant stress (74).

Metatranscriptomics

Metatranscriptomics enables the analysis of total RNA, primarily messenger RNA (mRNA), extracted from environmental samples, allowing researchers to assess which microbial genes are actively expressed under specific environmental conditions (5). Metatranscriptomics uses community-wide mRNA sequencing to identify which genes are actively transcribed under environmental conditions, whereas metagenomics captures a community's genetic potential (75).

In contaminated soils, active expression of xenobiotic degradation pathways such as cytochrome P450s, glutathione S-transferases and flavin-containing monooxygenases has been observed, as well as upregulation of multidrug efflux pumps and mobile genetic element-associated transcripts that promote resistance proliferation (76). Under antibiotic and EC stress, important nutrient-cycling genes, such as *nifH* (nitrogen fixation) and *amoA* (ammonia oxidation), are differently expressed, suggesting alteration of microbial-mediated soil nutrient fluxes (36). In soils exposed to antibiotics and PAHs, enhanced detoxification, amino acid metabolism and stress tolerance pathways have been found by differential expression analysis utilising methods like DESeq2 and edgeR (77). At the organism level, *Arthrobacter* sp. QD15-4 expresses genes for dimethyl phthalate (DMP) cleavage via pathways linked to energy metabolism and ABC transporters, whereas upregulation of cytochrome P450 and glutathione S-transferase in *Folsomia candida* exposed to dibutyl phthalate demonstrates conserved oxidative stress mitigation mechanisms in soil fauna (78). Metatranscriptomics provides the mechanistic resolution required to connect EC exposure to soil process degradation by recording active metabolic

states rather than genetic potential, bridging community dynamics and ecosystem function.

Metaproteomics

Metaproteomics enables the comprehensive identification and quantification of proteins actively expressed by microbial communities, providing direct insights into functional responses to ECs. This technique captures the real-time proteomic profile, reflecting enzymatic pathways involved in contaminant degradation, stress adaptation and metabolic function under specific environmental pressures (79).

Meta proteomics reveals shifts in actively expressed proteins under EC stress, including the upregulation of stress-response enzymes (e.g., superoxide dismutase and catalase) and the downregulation of key nutrient-cycling proteins such as nitrogenase and phosphatases in soils contaminated with heavy metals and PFAS (80). Metagenome-assembled genomes (MAGs) supplement studies by linking proteins to microbial species and their functional potential, even if they are mostly derived from metagenomic analyses. For instance, in pesticide-contaminated paddy soils, MAGs of *Pseudomonas* and *Rhodococcus* enriched with biphenyl-degradation genes have made it easier to understand matching degradation proteins found using metaproteomic studies (81). This technique has been pivotal in characterising contaminant-induced shifts in protein expression, revealing direct detection of methane monooxygenase (MMO) proteins in unenriched groundwater samples (80). In pharmaceutical-exposed wastewater bioreactors, cytochrome P450s, flavin-containing monooxygenases and hydrolases were strongly upregulated, indicating active detoxification and transformation (82). In oil-contaminated marine sediments, alkane hydroxylases and aromatic ring-hydroxylating dioxygenases were found to be predominantly expressed by *Alcanivorax* and *Cycloclasticus* spp., emphasising their role in natural attenuation (83).

In agricultural soils, metaproteomics has revealed novel hydrolases and reductases from *Bradyrhizobium* and *Sphingomonas* to mediate neonicotinoid insecticide degradation and phthalate esterases were identified in municipal wastewater treatment systems (52). Recent methodological innovations, such as optimised protein extraction from sediments and biofilms and high-resolution mass spectrometry (HRMS) for low-abundance proteins have significantly improved the resolution and applicability of metaproteomic studies (84).

Metabolomics

Metabolomics comprehensively profiles low molecular weight metabolites (50–1500 Da) within a biological system, reflecting the actual physiological state and real-time biochemical activity influenced by genetic and environmental factors (85). Advanced analytical platforms such as NMR and HRMS enable both untargeted and targeted metabolomics to detect hundreds of metabolites in complex environmental matrices (86). Metabolomics has identified pollutant-induced shifts in lipid, nucleotide and energy metabolism. Microbes can transform pollutants such as pharmaceuticals and PAHs into less toxic or energetically useful forms, although they may also generate harmful intermediates (87). Metabolic network modelling has further predicted microbial breakdown of ECs, linking specific metabolic routes to detoxification (88). In *Eisenia fetida* exposed to phenanthrene, metabolic alterations correlated with soil organic C levels, demonstrating pollutant bioavailability and biotransformation (89).

Integrative omics and system-level understanding

Individual omics platforms each illuminate a distinct biological stratum, but their integration unlocks a systems-level understanding of how ECs restructure soil microbiome function that no single platform can provide (90). Each omics layer contributes to understanding the microbial responses to environmental contaminants by bridging multiple biological layers. This enables researchers to identify functional genes, expression patterns, protein activities and metabolic shifts, enabling a holistic interpretation of microbial adaptations to contaminant-induced stress. Genomics and metagenomics identify genes involved in degradation and resistance, while transcriptomics pinpoints those that are actively expressed under stress. Proteomics provides insights into functional proteins, including enzymes associated with detoxification and redox balance and metabolomics uncovers biochemical transformations and pathway intermediates (91). For herbicide contaminants, transcriptomic profiling has revealed that genes in the shikimate pathway are upregulated by glyphosate exposure, which is reversed by the addition of aromatic amino acids, due to which a definitive molecular mechanism has been identified for a particular class of contaminants (92). Notable applications of omics-based observations across biological pathways and contaminant classes, demonstrating the range of mechanistic insights that various platforms bring to an integrated knowledge of EC impacts

are represented in Table 2. Critically, these layers are not always consistent; in microbial systems, mRNA-protein correlations usually account for only 16–36 % of the variation in protein abundance and the existence of a gene does not ensure catalytic activity or active expression (93). Therefore, multi-omics integration overcomes regulatory disconnects that might otherwise complicate mechanistic interpretation, rather than being merely additive.

These integrated analyses reveal condition-specific network disruptions, where metabolic gene co-expression links contaminant stress to collapsed C and N cycling, while resilient taxa such as *Thermaceae* and *Paenibacillaceae* act as key stabilisers under soil moisture and electrical conductivity perturbations (94). Coupled metatranscriptomic and metabolomic data show strong upregulation of xenobiotic degradation pathways (e.g., naphthalene and biphenyl) in crop rhizospheres, alongside the identification of reactive oxygen species (ROS) signalling hubs that coordinate community-level response (95). Network-based multi-omics further demonstrate convergence of signalling induced by heavy metals (Ca²⁺, MAPK and hormone pathways) on antioxidant defence systems, often accompanied by depletion of plant growth-promoting bacteria (96). Collectively, these integrative frameworks enable prediction of microbiome resilience, identification of keystone taxa and detection of metabolic bottlenecks, thereby guiding targeted and systems-informed bioremediation strategies. In the rhizosphere of alfalfa, integration of transcriptomics, 16S rRNA profiling and metabolomics revealed dominant microbial genera (*Pseudomonas*, *Rhodococcus*, *Brevundimonas*) and stress-related metabolites (pantothenic acid, malic acid) that contributed to petroleum hydrocarbon degradation (97). Temporal and spatial omics analyses have further illuminated microbial plasticity and niche differentiation. High temporal resolution is particularly pertinent because microbial responses to EC exposure are highly dynamic, with early molecular changes frequently preceding quantifiable changes in community structure and ecosystem function. Capturing these temporal alterations allows the discovery of brief stress reactions, adaptive mechanisms and recovery trajectories that would otherwise go undiscovered. Genomic adaptations often precede transcriptomic and proteomic shifts, reflecting early reprogramming in response to ECs (98). Single-cell multi-omics studies have revealed intra-population heterogeneity, identifying rare but ecologically significant microbial subgroups with specialised resistance or degradative capabilities (99).

Beyond soil microbial communities, integrative omics has been increasingly applied to plant-microbe-soil systems to unravel contaminant degradation pathways and adaptive responses under stress. Studies have shown that incorporating transcriptomics and metabolomics increases the identification of functional microbial guilds engaged in pollutant degradation, nutrient cycling and plant growth promotion in polluted soils (95). Computational multi-omics frameworks have been developed to identify biomarkers and molecular pathways within microbiome-host systems. Omics also

Table 2. Omics-based observations on microbial responses to contaminants

Contaminant	Observed change	Omics approach	Affected pathway	Ecological implication	Reference
Antibiotics	Loss of diversity	Metagenomics	Sulfur metabolism	Nutrient imbalance	(65)
Glyphosate	Gene expression shift	Transcriptomics	Shikimate pathway	Plant-microbe interaction change	(92)
Triclosan	Downregulated proteins	Proteomics	Oxidative stress enzymes	Reduced microbial resilience	(10)
Polybrominated diphenyl ethers (PBDEs)	Altered metabolite profiles	Metabolomics	Amino acid biosynthesis	Affects microbial growth	(32)

offers new avenues in human health risk assessments, particularly for endocrine-disrupting chemicals (EDCs) (65, 66, 68). Studies have shown that genomics, epigenomics, transcriptomics and metabolomics can collectively elucidate the health impacts of prenatal EDC exposure, linking it to altered gene expression, microbiome shifts and disease risk (5, 100). Furthermore emphasised that environmental omics aids in identifying unknown environmental targets, mapping toxicity pathways and supporting risk assessment frameworks and environmental policy (92, 100).

Challenges and future perspectives

Although multi-omics technologies provide revolutionary insights, their widespread use in soil ecotoxicology is constrained by interrelated technical, analytical and ecological challenges that must be addressed to realise their potential for ecological risk assessment and treatment.

A fundamental constraint is soil matrix complexity and extraction bias. Co-extraction of humic substances with nucleic acids introduces community profiling biases, especially in organic-rich or clay soils. Soil metabolomics still struggles in this regard, limiting quantitative interpretation under EC stress and requiring standardised protocols for extraction. Integrating metagenomics, metatranscriptomics, metaproteomics and metabolomics requires robust statistical and network tools capable of handling multi-scale, high-dimensional datasets. Most published EC studies are single-omics, short-term or single-contaminant in design, making it difficult to infer causal mechanisms for realistic mixtures in field soils. Spatial heterogeneity further compounds these analytical difficulties. Omics profiling of bulk soil masks hotspots of toxicity and resilience operating at microaggregate and rhizosphere scales, where contaminant concentrations and microbial activity differ markedly from bulk measurements. The detection of contamination hotspots and microbial functional niches may be enhanced by combining multi-omics with spatially resolved techniques, such as laser microdissection, imaging mass spectrometry, geostatistics and GIS-based mapping. Another key challenge is the absence of uniform soil-specific bioinformatics pipelines. Most existing analytical approaches are based on data sets from clinical or aquatic microbial ecosystems that do not reflect the high diversity and functional complexity of soil microbial ecosystems. More species-specific reference databases and computational pipelines need to be compiled and built to enhance the accuracy and ecological relevance of multi-omics interpretations.

Looking forward, systems-level modelling represents the most promising trajectory for translating multi-omics data into predictive and actionable outcomes. Integrated network models combining gene, protein and metabolite data are emerging to identify key hubs controlling contaminant degradation and nutrient cycling under contaminant exposure. Coupling multi-omics with ecosystem and transport models (e.g., for PFAS or pesticide mixture in soil-water-plant continua) is proposed to predict long-term impacts on soil fertility and to optimise bioremediation strategies. Targeted application in bioremediation and soil health monitoring represents another promising research direction. Omics-guided selection and design of pollutant-degrading microbial consortia and nano-/bio-based soil represents a major applied opportunity, moving the field from descriptive community profiling to actionable

indicators of soil health and resilience that integrate seamlessly with functional assays. Furthermore, integrating multi-omics with digital soil mapping, geospatial modelling, artificial intelligence and decision-support systems can accelerate ecological risk assessment and enable precision bioremediation strategies.

This review is also subject to certain limitations. Many of the studies included were very different in the experimental designs, concentrations of contaminants, soil types and analytical methods used, making direct quantitative comparisons difficult. In addition, most evidence is derived from controlled laboratory experiments, with relatively few long-term field studies available for validation. The rapidly evolving nature of omics technologies may have also resulted in the underrepresentation of recently developed analytical tools and workflows.

Conclusion

This review examines the transformative potential of integrated multi-omics, including metagenomics, metatranscriptomics, metaproteomics and metabolomics, as a systematic framework for evaluating the impact of emerging contaminants (ECs) such as pharmaceuticals, PFAS, microplastics (MPs) and heavy metals on soil ecosystems. These contaminants steadily accumulate in agricultural soils through wastewater irrigation and biosolid amendment, altering critical microbial communities, nutrient cycling and soil fertility. While standard ecotoxicological methods lack the resolution to capture complex biological reactions, multi-omics integration represents a paradigm shift in soil ecotoxicology, offering unprecedented mechanistic insights into how ECs disrupt soil ecosystems at multiple biological scales. This method is vital for a one health perspective, as it ties soil integrity and ecosystem resilience to human health and global food security, particularly addressing the bioaccumulation through food chain. Nevertheless, significant barriers remain before multi-omics can be routinely implemented in soil ecotoxicology. The absence of standardised protocols remains a critical bottleneck limiting the fields capacity to translate multi-omics findings into actionable soil health indicators and bioremediation protocols. To advance the field, future progress must depend on the establishment of standardised international frameworks, long-term field validation studies, interoperable soil databases and AI-assisted data integration platforms that can convert multi-omics discoveries into scalable solutions for sustainable soil ecosystem management.

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Authors' contributions

SKK contributed to the conceptualisation of the study and preparation of the manuscript. EM was responsible for manuscript review and supervision. SS, JP, TM, SAP and SKB contributed to manuscript review and visualisation. All authors read and approved the final version of the manuscript.

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