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Review

Effects of microplastics on soil microorganisms and microbial functions in nutrients and carbon cycling – A review

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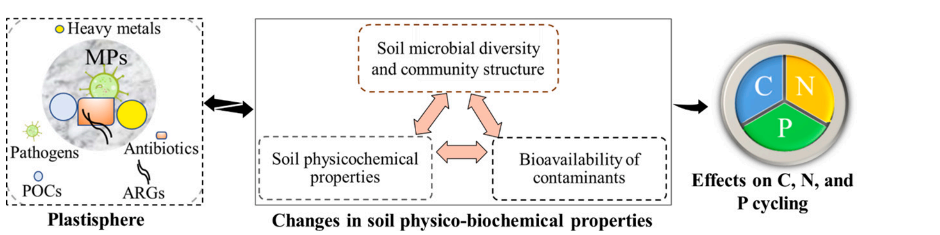
HIGHLIGHTS

- MPs increased relative abundance of plastic degrading bacteria in soil.
- MPs at ≤1 % increased abundance of N_2-fixing and P-solubilizing bacteria in soil.
- MPs decreased abundance of soil nitrifiers and ammonia oxidation in soil.
- MPs altered availability of emerging contaminants to soil microorganisms.
- Global data adequacy is key to estimate MP effects on soil microorganisms.

GRAPHICAL ABSTRACT



Abbreviations: ABC, ATP- binding cassette; AMF, arbuscular mycorrhizal fungi; AOA, ammonia-oxidizing archaea; AOB, ammonia-oxidizing bacteria; AP, available phosphorus; ARGs, antibiotic-resistance genes; ATP, adenosine triphosphate; BD, bulk density; C, carbon; CEC, cation exchange capacity; Cd, cadmium; CH_4, methane; CIP, ciprofloxacin; CO_2, carbon dioxide; Cu, copper; DOC, dissolved organic carbon; EPS, extracellular polymeric substances; GHGI, greenhouse gas intensity; GWP, global warming potential; LDPE, low density polyethylene; MBC, microbial biomass carbon; MP, microplastic; N, nitrogen; NH_4^+, ammonium; N_2O, nitrous oxide; OM, organic matter; OTC, oxytetracycline; P, phosphorus; PA, polyamide; PAHs, polycyclic aromatic hydrocarbons; PAN, polyacrylonitrile; Pb, lead; PBAT, polybutylene adipate terephthalate; PBS, polybutylene succinate; PE, polyethylene; PES, polyester; PET, polyethylene terephthalate; PFAS, poly- and per-fluoroalkyl substances; PHB, polyhydroxy butyrate; PLA, polylactic acid; POCs, persistent organic contaminants; PP, polypropylene; PS, polystyrene; PSB, phosphate solubilizing bacteria; PTFE, polytetrafluorethylene; PUF, polyurethane foam; PVC, polyvinyl chloride; ROS, reactive oxygen species; SOM, soil organic matter; UV, ultraviolet radiation; WHC, water holding capacity.

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ABSTRACT

The harmful effects of microplastics (MPs) pollution in the soil ecosystem have drawn global attention in recent years. This paper critically reviews the effects of MPs on soil microbial diversity and functions in relation to nutrients and carbon cycling. Reports suggested that both plastisphere (MP-microbe consortium) and MP-contaminated soils had distinct and lower microbial diversity than that of non-contaminated soils. Alteration in soil physicochemical properties and microbial interactions within the plastisphere facilitated the enrichment of plastic-degrading microorganisms, including those involved in carbon (C) and nutrient cycling. MPs conferred a significant increase in the relative abundance of soil nitrogen (N)-fixing and phosphorus (P)-solubilizing bacteria, while decreased the abundance of soil nitrifiers and ammonia oxidisers. Depending on soil types, MPs increased bioavailable N and P contents and nitrous oxide emission in some instances. Furthermore, MPs regulated soil microbial functional activities owing to the combined toxicity of organic and inorganic contaminants derived from MPs and contaminants frequently encountered in the soil environment. However, a thorough understanding of the interactions among soil microorganisms, MPs and other contaminants still needs to develop. Since currently available reports are mostly based on short-term laboratory experiments, field investigations are needed to assess the long-term impact of MPs (at environmentally relevant concentration) on soil microorganisms and their functions under different soil types and agro-climatic conditions.

1. Introduction

Versatility, stability, durability, and low production cost made plastics the most promising material for packaging, building, manufacturing and agricultural industry production (Europe and Plastics- the Facts, 2022; Wang et al., 2021; Yang et al., 2021). The world's annual plastic production in 2021 increased by 4 % and reached an annual production of ~3.91×10^8 tons, 90 % of which was discharged as waste directly or indirectly into the soil (Europe and Plastics- the Facts, 2022; Zhou et al., 2020). China's share in global plastic production continued to grow and reached 32 % of world plastic production in 2021, while Europe plastic manufacturing declined and contributed to 15 % (57.2 million tons) of the global market (Europe and Plastics- the Facts, 2022). It is noteworthy, however, that due to low recycling rate (35 %) (Europe and Plastics- the Facts, 2022), plastic waste can accumulate in soils for a long period (Yang et al., 2022). Limited and inappropriate recovery, prolonged exposure to ultraviolet radiations (UV), hydrolysis, mechanical wear and microbial degradation result in the formation of smaller (<5 mm) plastic particles, termed as microplastics (MPs), in the soil (Duan et al., 2021; Khalid et al., 2020; Meng et al., 2022).

The MPs are manufactured for 3D printing, adhesives, cosmetics, personal care products, paints, and electronics, and can directly enter into the soil ecosystem through sewage systems, irrigation water, and municipal solid waste landfills (Fajardo et al., 2022; Lehner et al., 2019). Additionally, MPs produced by progressive fragmentation of large plastics under suitable environmental conditions are the major secondary sources of soil MPs (Wang et al., 2021; Yang et al., 2022; Bradney et al., 2019). Soil amendments such as sewage sludge, organic fertilizers, biosolids, and irrigational water, along with plastic mulching practices increased the vulnerability of fertile agricultural soils to hazardous MP pollutants (Fajardo et al., 2022; Lehner et al., 2019). According to Nizzetto et al. (2016), the annual input of MPs (in the year 2016) into European and North American farmlands was 63,000–430,000 tons and 44,000–300,000 tons, respectively. In China, a total of around 100 trillion MP particles might have entered the soil through agricultural films (Huang et al., 2020), with concentrations ranging from 7000 to 43,000 plastic particles kg^{-1} soil. It is estimated that annually 35 billion to 2.2 trillion MP particles accumulate through compost application in the cropped soils of Germany (Rong et al., 2021; Weithmann et al., 2018). A recent meta-analysis revealed that the global MP concentration in surface soil (up to 5 cm depth) was around 4.4×10^{11} particles km^{-2}, with an average concentration of 500 ± 266.7 mg kg^{-1} soil (Wei et al., 2022). The global plastic input to terrestrial ecosystems is estimated to be 4-23 times higher than to the ocean (Chen et al., 2020a; Horton et al., 2017), and is expected to increase further in the near future.

Soil microorganisms are the major living pools of the soil ecosystem. They regulate various ecosystem functions including biogeochemical elemental cycles, organic matter (OM) decomposition, toxin removal, plant growth promotion, and maintenance of ecological equilibrium and soil health. Soil microorganisms are widely used as bioindicators of soil quality (Zhou et al., 2020; Qi et al., 2020a; Wang et al., 2020a). The MPs can trigger substantial changes in physicochemical characteristics and biochemistry of the soil (Supplementary Information, Table S1). Accumulation of MPs in the soil profile has been shown to significantly affect soil structure, porosity, bulk density (BD), water holding capacity (WHC), pH, cation exchange capacity (CEC), dissolved organic carbon (DOC) content, and nutrient availability (Meng et al., 2022; Horton et al., 2017; de Souza Machado et al., 2018). Moreover, MPs provide an ideal niche for soil microorganisms for colonization (e.g., plastic-degrading microbes, including Proteobacteria and Ascomycota) and biofilm formation (Zhang et al., 2023). The MP-contaminated soils thus host a distinct microbial community structure with a lower microbial diversity (richness and evenness) than uncontaminated soils (Rillig et al., 2023). Consequently, the changes in microbial diversity (e.g., genetic diversity, functional diversity, microbial abundance, and activity) and soil physicochemical properties can significantly affect the microbially mediated biogeochemical elemental cycling and nutrient turnover. Fig. 1 illustrates the effect of MPs on soil properties, soil microbial community structure and their functions.

The soil biogeochemical cycle entails the transformation and mobility of essential chemical elements between organisms and the external environment (Rogers et al., 2020). Soil microorganisms, such as autotrophic and heterotrophic bacteria and fungi, N_2-fixing bacteria, nitrifiers, denitrifiers and P-solubilizers are the key players in the transformation and processing of carbon (C), nitrogen (N) and phosphorus (P) in the terrestrial ecosystem. In recent studies, MPs have been found to significantly alter the diversity and typical functional roles of the above-mentioned microorganisms and their associated enzymes (e.g., urease, phosphatase, β-glucosidase, and sucrase), and thus either increased or decreased soil gaseous emissions, i.e., nitrous oxide (N_2O), carbon dioxide (CO_2) and methane (CH_4) (Wang et al., 2021; Guo et al., 2020; Ren et al., 2020). The factors that decide the level of effects (positive, negative, or neutral) on soil microorganisms are the MP dose, type, composition, and associated contaminants, soil types and physicochemical properties, exposure period, soil management practices and agroclimatic conditions. Owing to their high surface area, hydrophobic nature, and diverse surface functional groups, MPs can act as a potential carrier of persistent organic contaminants (POCs), heavy metals and other emerging contaminants (Bradney et al., 2019; Atugoda et al., 2021; Boughattas et al., 2022), and influence the behaviour, mobility, bioavailability, and toxicity (additive or antagonistic effect) of the MP-bound contaminants to soil microorganisms (Cao et al., 2021; An et al., 2023).

Although the effects of MPs on terrestrial ecosystems have been extensively studied, most of these studies were focused to understand MPs distribution, sources, and ecotoxicological effects in soil (Guo et al., 2020; Bläsing and Amelung, 2018; Sajjad et al., 2022). In the last few years, a few review articles (Table S2) have also been published with an emphasis on MPs-influenced alterations in soil properties and soil microbial communities and their functions. However, only a limited number of reviews (Kumar et al., 2022a; Shen et al., 2023; Shen et al., 2021; Wang et al., 2022a) have primarily discussed the MPs-influenced changes in soil nutrient dynamics and elemental cycling. Not much stress has been given to understand how MPs could influence soil microbial diversity (i.e., genetic diversity, functional diversity, microbial abundance, and activity) in relation to biogeochemical elemental cycling in soils. A small number of reviews (Wang et al., 2022b; Huang et al., 2022) previously focused on the interaction of MP and organic/inorganic contaminants, their bioavailability, and toxicity, but still, there is a lack of understanding of the combined toxicity of MPs and other emerging contaminants on soil microorganisms responsible for biogeochemical elemental cycling. With this background, the current review focuses on the effect of MPs on (1) soil microbial diversity and community structure, and MP-microbe interactions, (2) soil biogeochemical cycles and greenhouse gas emissions, and (3) combined toxicity of MPs and other emerging contaminants to soil microorganisms and effects on their functional roles.

2. MP-microbe interactions and biofilm formation

Soil is a habitat for microorganisms and provides nutrients for microbial survival. MPs serve as mediators to colonize and transport bacteria, fungi, and other microorganisms from one phase to another (e.g., solid or solution) within the soil. Microorganisms, including bacteria and fungi, attach to the surface of MPs in the soil through a matrix of extracellular polymeric substances (EPS) (composed of proteins, lipids, polysaccharides, and nucleic acids) produced by the microorganisms to form a 'biofilm' (Sooriyakumar, 2022; Zettler et al., 2013). The EPS act as a shield against UV and toxic compounds and provide a suitable environment for microbial colonization and growth (Rillig et al., 2023; Wang et al., 2022b). In addition, biofilms facilitate the exchange of metabolites, genetic materials, and signalling molecules between different microbial cells, which in turn facilitate the selective enrichment of specific microbial species (Flemming et al., 2016). The biofilm production by microorganisms depends on the MP substrate (polymer composition, size, shape, surface properties, and degree of weathering), location, and synergistic relationships between colonizing microorganisms and environmental conditions (i.e., soil pH, nutrients, and temperature) that are conducive to EPS production (Rillig et al., 2023; Wang et al., 2022b; Sun et al., 2022a). Microbial community characteristics such as the cell size, population, and biomass as well as C sources in the soil are important for biofilm production on MPs (Zhao et al., 2021a). The attachment of microorganisms to MP surfaces produces a synergistic consortium of microorganisms, known as the 'Plastisphere' (Kirstein et al., 2019). Plastisphere describes the composition and diversity of microorganisms that are associated with plastics/MPs in aquatic and terrestrial ecosystems. However, unlike aquatic plastisphere, soil plastisphere is much less mobile, and therefore, the soil environment plays an important role in regulating plastisphere microbial diversity and ecological functions (Rillig et al., 2023). The soil plastisphere harbours a distinct microbial consortium with a lower microbial diversity than the surrounding bulk soil (Huang et al., 2019). For instance, the application of low-density polyethylene (LDPE) and polystyrene (PS) MPs significantly decreased soil bacterial diversity (Shannon index), but the relative abundance of Actinobacteria on LDPE (230 % higher) and Proteobacteria on PS (115 % higher) MPs were significantly higher than MP unamended soil (Huang et al., 2019; Zhu et al., 2022a). Similarly, Ascomycota was found as a dominant fungus in soil plastisphere than in the surrounding soil (Gkoutselis et al., 2021; Rüthi et al., 2023). The soil plastisphere could act as an environmental filter and facilitate the enrichment of plastic-degrading microorganisms, and thus lower the microbial diversity and richness. The soil plastisphere is also reported to increase the proportion of pathogenic bacteria and antibiotic-resistance genes (ARGs) on MP surfaces and in MP-contaminated soils (Zhu et al., 2022a; Ding et al., 2021). Fig. 2. illustrates the development and

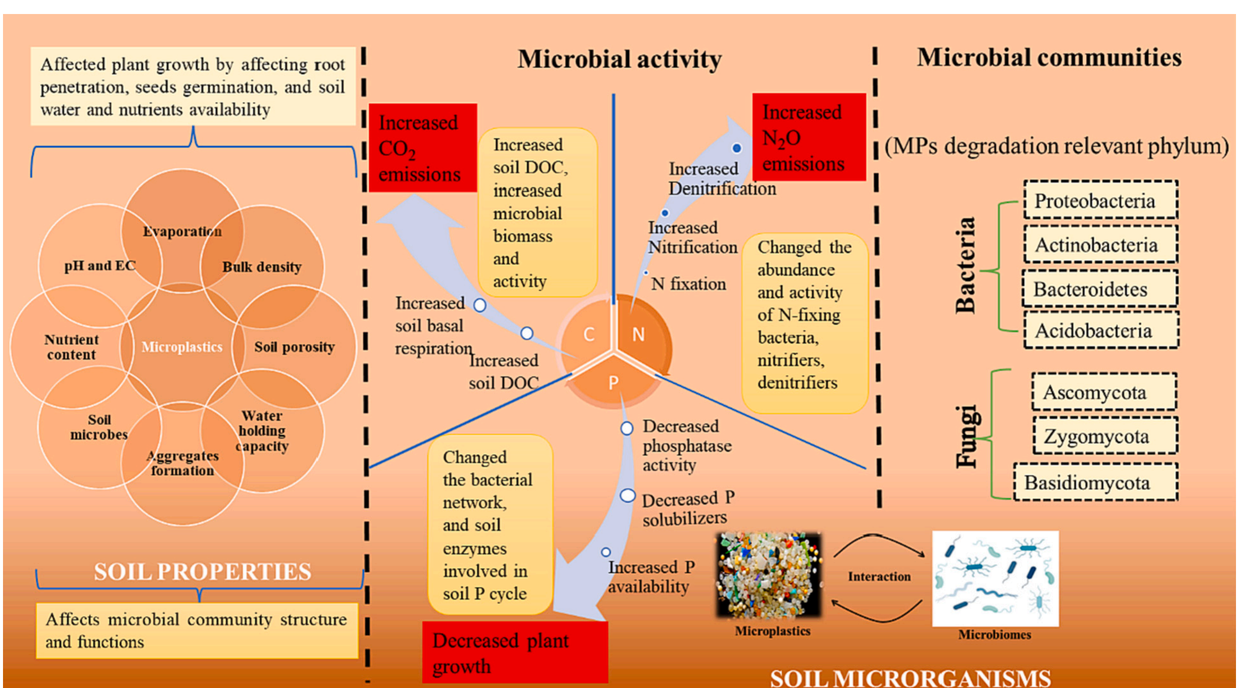

Fig. 1. Schematic representation of MPs in the soil and their possible effects on soil properties, soil microbial communities, and biogeochemical cycles. Arrows represent directional interactions and changes in the normal functioning of the ecosystem.
(Adapted with modification from Zhang et al. (2021)).

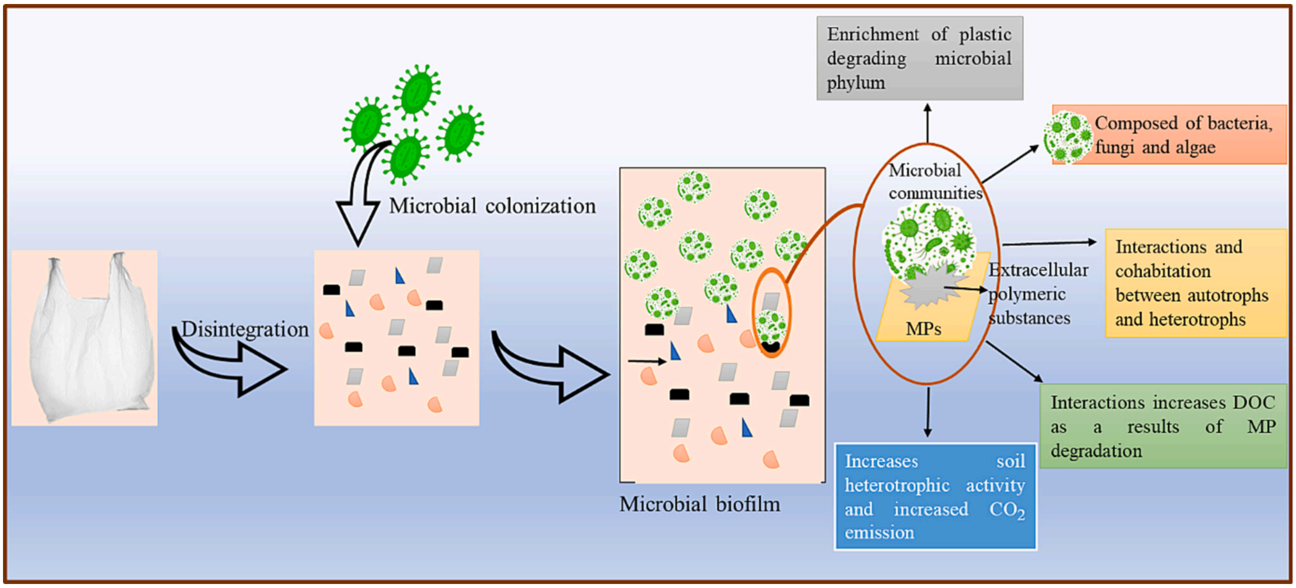

Fig. 2. Development and colonization of microorganisms on MP surface and their impacts on microbial diversity and soil properties.
(Adapted with modification from Wang et al. (2021)).

colonization of microorganisms on MP surfaces and their impacts on microbial diversity and soil properties. A detailed discussion on MP-induced changes in soil microbial diversity and community structure has been given in Section 3.

3. Effect of MPs on soil microbial diversity and community structure

Soil bacteria are sensitive to environmental changes induced by contaminants, including MPs (Bardgett and Van Der Putten, 2014). The solid hydrophobic surfaces of MPs affect the attachment of specific bacteria, and those bacteria that can use MP-associated chemical compounds as a nutritional source dominate community structure in the plastisphere (De Tender et al., 2015; Harrison et al., 2011).

3.1. *Microbial diversity*

The MPs can affect soil microbial diversity positively (Feng et al., 2022a; Gao et al., 2021), negatively (Fei et al., 2020; Sun et al., 2022b; Hou et al., 2021), or insignificantly (Rong et al., 2021; Huang et al., 2019; Zhu et al., 2022b), depending on MP type, size, concentration, polymer composition, surface characteristics, soil properties, microbial composition, and exposure time (Zhou et al., 2020; Fei et al., 2020; Sun et al., 2022b; Chen et al., 2021). For instance, at 5 % (w/w), larger polyethylene (PE) (150 μm) MPs in clay soil lowered bacterial and fungal community richness and diversity; however, smaller MPs (13 μm) enriched bacterial and fungal populations (Ren et al., 2020). Fei et al. (2020) reported that adding 5 % polyvinyl chloride (PVC) and 1 % and 5 % PE in acidic loamy soil decreased soil alpha diversity; however, 1 % PVC had no effect on soil bacterial diversity. LDPE at 7 % (*w*/w) significantly decreased soil bacterial diversity throughout the experimental period; however, 2 % (w/w) LDPE initially enriched the bacterial diversity with no further change upon additional incubation (Rong et al., 2021), which could be ascribed to low MP doses and short incubation period. It should be noted that a recent metanalysis by Liu et al. (2023) based on 92 published articles (involving both biodegradable and non-degradable MPs), found that MPs at varying concentrations significantly decreased the soil microbial diversity (Shannon index) and community structure, with the more pronounced effect of MPs (biodegradable) on soil bacteria but a non-significant effect to soil fungi. It is noted, however, that at a low concentration ($\leq$1 %), MPs offered no significant effect on soil bacterial diversity and community composition over a short incubation period (30-60 days) (Yan et al., 2021; Qin et al., 2023). Also, under long-term exposure (one year), polyamide (PA), PS, polyethylene terephthalate (PET), and PVC at 2 % (w/w) did not alter soil microbial diversity and richness, but microbial community structure altered significantly (Zhang et al., 2023). In addition to bacteria, MPs in soil can cause substantial changes in soil fungal community structure and diversity (Hou et al., 2021). A few fungal genera such as *Aspergillus*, *Fusarium*, and *Penicillium* are reported to utilize complex C sources derived from MPs (Accinelli et al., 2020; Muñoz et al., 2015), showing their high relative abundance and diversity in MP-polluted soils. For instance, the relative abundance of arbuscular mycorrhizal fungi (AMF) hyphae, arbuscules, and coils significantly increased in the plant rhizosphere in polyester (PES)-amended soils (de Souza Machado et al., 2019). The MPs influenced changes in soil biophysical properties (e.g., soil structure, BD, porosity, water dynamics, and symbiotic bacteria), and plant biomass and root status could influence AMF diversity and functions (Gao et al., 2021; Hou et al., 2021).

3.2. *Microbial community composition*

The group Actinobacteria is widely described as a hydrocarbon degrader in soil (Isaac et al., 2015; Woźniak-Karczewska et al., 2019), and is known for the degradation of synthetic polymers (Gao et al., 2021; Zhu et al., 2022b; Abraham et al., 2017). Similarly, members of the phyla Proteobacteria and Bacteroidetes are characterized by an ability to degrade complex OM (Rong et al., 2021; Yi et al., 2021). Previous studies have found that MPs could facilitate the enrichment of plastic-degrading species, such as Actinobacteria, Bacteroidetes, and Proteobacteria in both MP surface (i.e., biofilms) and MP-amended soils (Sun et al., 2022b; Hou et al., 2021; Li et al., 2022a; Qiu et al., 2023). Zhang et al. (2019) named active MP-colonizing bacteria, such as Chloroflexi, Acidobacteria, Bacteroidetes, and Gemmatimonadetes, “Keystone Species”, and MPs serving as “*special microbial accumulators*”. Ren et al. (2020) reported that the application of large PE MPs (150 μm) increased the relative abundance of Actinobacteria from 31 to 36 % in clay soils over 30 days of incubation. In the phylum Actinobacteria, pathogenic genera (e.g., *Nocardia*, *Aeromicrobium*, and *Amycolaptosis*) have the potential to adapt and survive in highly MP-polluted soils (Rong et al., 2021; Zhu et al., 2022b; Yi et al., 2021). For instance, in a long-term (one-year) pot experiment, an application of PVC and PE at 2 % (w/

w) significantly increased the relative abundance of *Nocardia* in silty loam soils. Similarly, an application of membranous PE and fibrous polypropylene (PP) in loamy sandy soil significantly increased the relative abundance of *Aeromicrobium* and *Nocardia* over 29 days of exposure (Yi et al., 2021). More interestingly, Huang et al. (2019) observed a significant increase in the relative abundance of opportunistic pathogenic *Nocardia* on PE fragments, from 0.77 % to 33.32 % after 90 days of incubation. Nevertheless, PVC (having 24-30 % phthalates) at 0.5 % significantly enriched the human pathogenic fungi, i.e., *Exophiala*, *Cladophialophora*, *Fonsecaea*, *Capronia*, and *Rhinocladiella* in sandy loam soils of Jiangxi Province, China (Zhu et al., 2022b). It should be noted, however, that MPs-induced changes in the soil microbial diversity and community structure are not resolved yet and need future research to identify the toxicity causing culprits, i.e., MPs itself or plasticizers or MPs-bound organic or inorganic contaminants.

3.3. Mechanism for MP toxicity to soil microorganisms

The MPs can render toxicity to soil microorganisms directly by causing biotoxicity or indirectly by changing the microhabitats and nutrient availability (Fig. 3). The oxidative stress mediated by reactive oxygen species (ROS) and/or the toxic effect of leached MP additives (e.g., heavy metals, plasticizers, antioxidants, flame retardants, and photostabilizers) can cause direct biotoxicity to soil microorganisms (Chen et al., 2021; Wei et al., 2019). The MP-influenced changes in soil physicochemical and microbiological properties (soil BD, porosity, pH, nutrient cycling and availability, biofilm formation, and OM decomposition) can also indirectly regulate soil microbial diversity (Fig. 3) (Wei et al., 2022; Huang et al., 2019). The increase in the soil macropores (plastipores) could alter the heterogenous distribution of water, air, and nutrients, and thus increase the relative abundance of copiotrophic bacteria (bacteria found in nutrient rich environments, e.g., Proteobacteria and Actinobacteria) and their functions (e.g., increased CO_2 emissions) (Negassa et al., 2015). Among different soil physicochemical properties, pH is the most important attribute that plays a critical role in microbial membrane-bound proton pump and protein stability, and as a result, a small change in soil pH can impose physiological constraints on exposed microorganisms (Kang et al., 2021). Palansooriya et al. (2022) observed a strong correlation between soil pH (decreased from 5.63 to 5.2) and microbial diversity ($r^2 = 0.93$ between pH and Chao1 index)

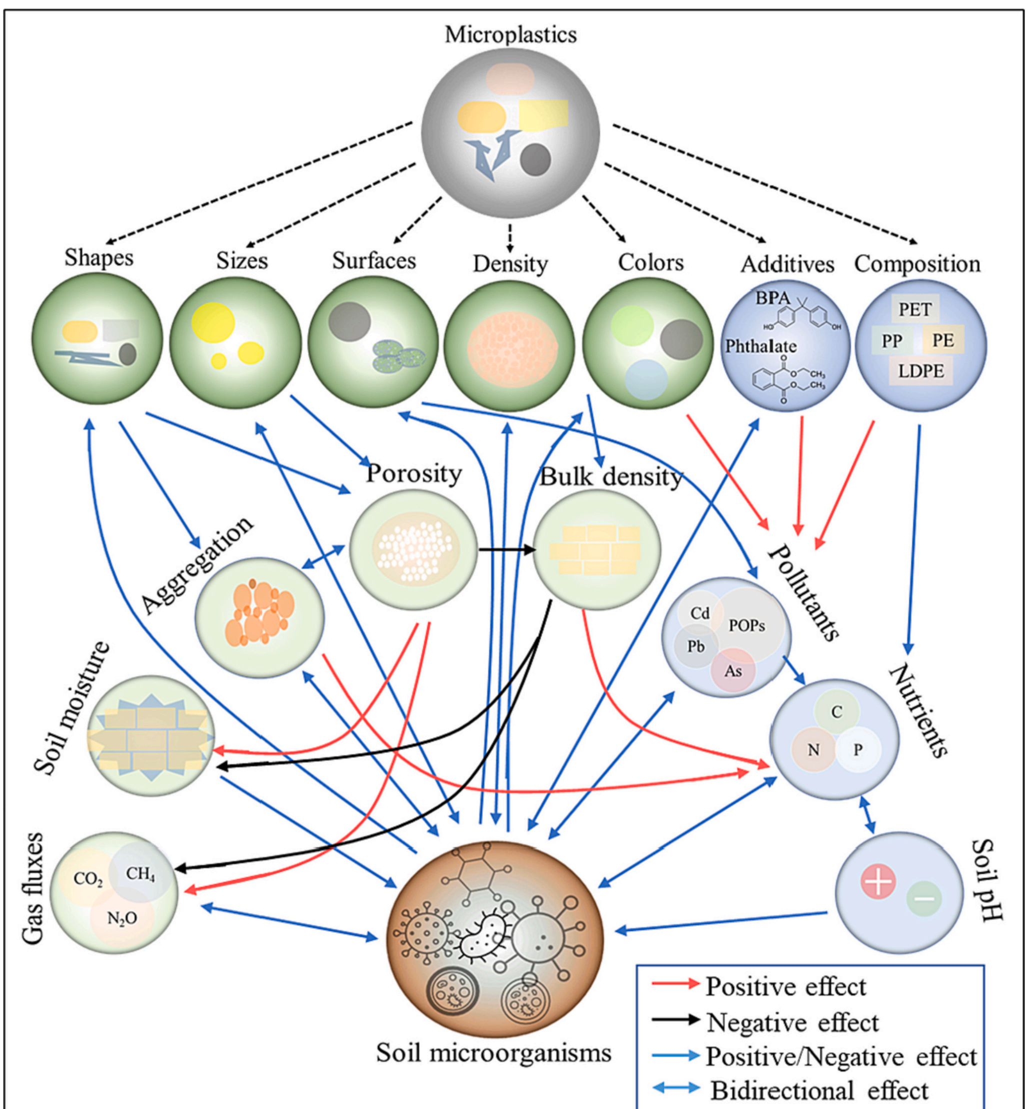

Fig. 3. Plausible pathways for interactions of MPs with microorganisms in relation to soil properties. Dark green and light green bubbles represent physical attributes of MP and soil, respectively, while dark blue and light blue bubbles represent chemical attributes of MP and soil, respectively. Grey and brown bubbles represent MP and soil microorganisms, respectively.
(Modified with permission from Zhang et al. (2021)).

after 100 days of LDPE application (at 3, 5 and 7 % w/w rates). The change in soil pH also significantly increased the relative abundance of Firmicutes (r^2 = -0.99) but decreased the abundance of Verrucomicrobia (r^2 = 0.93). The change in soil pH could cause direct toxicity to soil microorganisms by inhibiting their enzyme activities and cell metabolism, or indirectly by limiting the nutrient availability (i.e., by affecting the microbially mediated nutrient cycling and nutrient adsorption to soil colloids) and increased ionic toxicity (e.g., heavy metals) (Zhalnina et al., 2015). In addition, the adsorption of nutrients by MPs and increased soil microbial N demand (due to deposition of recalcitrant C) could create imbalance in the nutrients (ammonium $(NH_4^+ - N)$, nitrate $(NO_3^- - N)$) availability in soil and thus altering the microbial community structure and their associated functions (Zhang et al., 2023).

4. Effects of MPs on microbial-mediated soil biogeochemical cycles

Soil microorganisms play a pivotal role in the formation and degradation of soil organic matter (SOM); however, biological processes involving microorganisms, such as gaseous emissions, and nutrient cycling and availability can be significantly affected by physico-biochemical disturbances (Han et al., 2022a; Xiang et al., 2022). The effects of MPs on soil microbial activity and soil biogeochemical cycles are shown in Table 1.

4.1. C cycle

MP pollution in the terrestrial system can interfere with soil C turnover (Wang et al., 2021; Shen et al., 2023; Wang et al., 2022a). It can significantly change soil DOC, soil basal respiration, microbial biomass carbon (MBC), and soil CO_2 and CH_4 emissions (Wan et al., 2023; Yang et al., 2018; Zhang et al., 2022).

4.1.1. Dissolved organic carbon

Soil DOC represents one of the largest reduced C pools on earth. It serves as a sensitive indicator of changes in soil quality (nutrient availability, structure, moisture, and SOM degradation) and is a crucial component of soil biogeochemical cycling (Bolan et al., 2011; Liu et al., 2017). In a long-term (one-year) study, PA, PS, PET, and PVC application at 2 % (w/w) significantly increased the DOC content of silty loam soils (Zhang et al., 2023). However, Meng et al. (2022) and Ren et al. (2020) found that the addition of LDPE (at 0.5-2 % w/w) and PE (at 5 % w/w) did not significantly affect soil DOC, though smaller PE (13 μm) particles changed the DOC composition by accelerating the formation of aromatic fractions in fertilized soil. The weathering/leaching of MPs

Table 1
Different types of MPs and their effects on soil microbial activity, enzyme activity and elemental cycles.

MP type and size	Concentration of MPs	Soil type	Exposure period	Effect on soil microbial/enzymatic activity	Effect on soil biogeochemical cycles	References
PE, PAN and hydrochar	0.5 % w/w	–	5 months	Hydrochar-PE mixture increased the expression of genes (*mcrA*) involved in methane production PP-hydrochar mixture significantly increased N_2O reductase genes (*nosZ*) involved in soil N_2O emissions	Hydrochar-PE mixture increased soil CH_4 emissions by 83.5 % Hydrochar-PP mixture increased soil N_2O emissions by 3- and 4-folds relative to control and hydrochar amended soils, respectively	(Han et al., 2022b)
PE, PS, PA, PLA, PBS, and PHB (39-80 μm)	0.2 and 2 % (w/w)	Sandy loam soil	120 days	Soil urease, phosphatase, and catalase activities increased under 2 % PLA, PBS, and PHB, but at 0.2 % concentration all the MPs decreased soil phosphatase activity	All the MPs greatly changed the relative abunace N_2-fixing bacteria (*Nocardia*), nitrifiers (*Nitrospirae*), denitrifiers (Gemmatimonadetes), and P-solubalizers (*Streptomyces* and *Sphingomonas*)	(Feng et al., 2022a)
PE, PAN and hydrochar	0.5 % w/w	–	5 months	MPs-hydrochar significantly increased nitrogen-fixation genes (*nif*D, *nif*H, and *nif*K), and PAN-hydrochar significantly increased nitrate-reduction genes (*nir*B, *nir*D, *nrf*A, and *nrf*H)	MPs reduced cumulative NH_3 volatilization	(Feng et al., 2022b)
PET (200 μm) and biochar	0.5 % (w/w)	Udalfs soil	4 months	PET-biochar mixture significantly lowered methanogenesis functional genes (*mcrA*) and N_2O reductase gene (*nosZ*)	The PET and PET-biochar reduced cumulative CH_4 emissions by 53 and 61 %, respectively MPs-biochar mixture increased soil cumulative N_2O by 38 % relative to biochar treatment	(Han et al., 2022a)
PA, PE, PP, PET, PES, PS, PU (Films; 1.55 mm, fibres; 1.26 mm, foams and fragments; 1.28 mm)	0.4 % (w/w)	Sandy soil	31 days	MPs increased Acid phosphatase and decreased β-glucosidase activities	Soil respiration slightly increased under PE foams, but other MPs showed no effect on it	(Zhao et al., 2021b)
PVC (678 μm) LDPE (300 μm)	1 and 5 % (w/w)	–	29 days	Significantly increased soil nitrate reductase activity	Altered the relative abundance RA of N_2-fixer (*Bradyrhizobium*), nitrifiers, and denitrifying bacteria (*Nitrospira*)	(Huang et al., 2023)
LDPE (37.5 μm)	5, 10, 15 g m^{-2}	Loamy sand soil	287 days	LDPE addition significantly increased the soil α-glucosidase, soil β-glucosidase, and Leucine amino peptidase (LAP) activity	–	(Lin et al., 2020)
PLA (20-50 μm)	2 % (w/w)	–	70 days	PLA addition significantly reduced soil urease, β-glucosidase, and catalase activity compared with straw amended soils after 30 days of incubation	MPs addition increased soil ammonia oxidation	(Chen et al., 2020b)
PE	0.5, 1.0, 2.0, 4.0, and 8.0 % (w/w)	Clay	6 months	–	Decreased relative abundance of N_2-fixing and denitrification gene copy numbers	(Zhou et al., 2023)

*PA: Polyamide; PAN: Polyacrylonitrile; PBS: Polybutylene succinate, PE: Polyethylene; PET: Polyethylene terephthalate; PHB: Polyhydroxybutyrate; PLA: Polylactic acid; LDPE: Low density polyethylene; PP: Polypropylene; PS: Polystyrene; PUF: Polyurethane foam; PVC: Polyvinyl chlorine.

(Galgani and Loiselle, 2021; Romera-Castillo et al., 2018), MPs-nutrients interaction (Galgani and Loiselle, 2021), enhanced MPs-microbe interaction (Huang et al., 2019), and positive priming effect of MPs on SOM degradation (Rillig and Lehmann, 2020) are the major factors contributing to the increased soil DOC upon MPs application to the soil. An increase in the relative abundance of Bacteroides (C-solubilizing bacteria) and Chloroflexi (photosynthesis bacteria) in MP-polluted soils can have an impact on soil C-cycling.

4.1.2. Soil CO_2 emission

The MP-influenced changes in soil DOC and the positive/negative priming effect of MPs on SOM degradation could impact soil basal respiration rates and gaseous C emissions (Rillig and Lehmann, 2020). PE MPs (<150 μm) at 5 % w/w significantly increased soil CO_2 emission by 24-28.67 % compared with control soils after 30 days of exposure (Gao et al., 2021). The authors observed a significant positive correlation between soil CO_2 emission and relative abundance of *Mycobacterium*, *Aeromicrobium*, *Amycolatopsis*, *Nocardioides*, and *Mortierella* species. However, it is noteworthy that at environmentally relevant concentrations (≤1 %), Zhang et al. (2022), Xiao et al. (2022), and Yu et al. (2022) observed no significant changes in soil CO_2 emissions when LDPE (0.01 and 0.1 % w/w), PE (0.1-1.0 % w/w), and PE (1 % w/w) MPs were applied. In contrast, at 1 % w/w, LDPE MPs increased CO_2 emissions by 15 and 17 %, showing a dose-dependent response (Zhang et al., 2022). The increased microbial biomass and microbial activity in response to the metabolic stress caused by MP addition are the primary reasons for increased soil CO_2 emissions (Gao et al., 2021; Zhang et al., 2022). Yang et al. (2018) and Rillig and Lehmann (2020) suggested that increased microbial respiration rate with MP addition may be due to increased soil porosity and air circulation.

It is noteworthy that a few studies also assessed soil bacterial functional genes that encode for soil C degradation to unveil the mechanism involved in MPs-influenced changes in soil organic carbon (SOC) degradation and CO_2 emission (Zhang et al., 2022; Guo et al., 2021; Qian et al., 2018). In contrast to increased soil CO_2 emission under 1 % (w/w) aged LDPE application, a substantial decrease in the relative abundance of bacterial functional genes encoding starch (*sga*), hemicellulose (*abfA*, *manB*, and *xylA*), and cellulose (*cex*) hydrolysis in silt loam soils of Gansu Province, China, was observed after 30 days of MP exposure (Zhang et al., 2022). The author predicted that under MP exposure, fungi might be a prominent player in degrading SOC and accelerated CO_2 emission (Zhang et al., 2022), which calls for future studies accounting for fungi functional genes and CO_2 emission under different MPs exposure. Similarly, PA (75 μm) MPs at 1 % (w/w) decreased soil C metabolism-related genes *mnp*, *chiA*, *accA*, *pccA*, *mcrA*, *pmoA*, and *mmoX*, but at 0.3 % (w/w), PA MPs promoted these gene abundances after 20 days of treatment (Sun et al., 2023). A similar decrease in soil C-fixation gene (*cbb*L gene) and C-hydrolases such as chitinase (coded as *chi*-A) and β-glucosidase (coded as β-*glu*) by >50 % in the soils contaminated with plastic mulched residues was observed (Qian et al., 2018). Similarly, in a long-term laboratory experiment, an increased level of α-glucosidase (by 85 %), β-glucosidase (by 36-55 %) and leucine amino peptidase (83-116 %) activity was observed under LDPE application after 287 days of exposure (Lin et al., 2020). In contrast, depending on soil properties, PE MPs at 1 % (w/w) showed no significant changes in soil CO_2 emissions, but genes encoding for hemicellulose (*abfA*, *xylA*, and *manB*), starch (*sga*), and lignin (*mnp*) decomposition increased significantly after 28 days of microcosm experiment (Yu et al., 2022). The variability in the findings might be due to MP types and composition or soil properties. It should be noted, however, these short-term (<30 days) microcosm studies were conducted in a small glass bottle (Zhang et al., 2022; Yu et al., 2022; Sun et al., 2023) which may not mimic natural field conditions under long-term MP exposure. For instance, in a long-term pot experiment (154 days), Guo et al. (2021) observed no significant changes in the bacterial gene (encodes for C-degradation) numbers when 0.1-1.0 % w/w PES MPs were applied. Therefore, the variability in experimental conditions, soil properties (texture, SOC, and pH), exposure period, MP types and their composition makes it difficult to draw a precise conclusion about the response of soil C-turnover and CO_2 emission under MP pollution.

4.1.3. Soil CH_4 emission

Soil MP pollution is also reported to have a significant effect on soil CH_4 emissions, increasing the global warming potential (GWP) and greenhouse gas intensity (GHGI) (Han et al., 2022b; Ren et al., 2021). The co-occurrence of PE-hydrochar mixture (PE at 0.5 % w/w and hydrochar at 1 % w/w) significantly increased the methanogens gene (*mcrA*) number, and increased soil CH_4 emissions and GHGI by 83.5 and 36.5 %, respectively, compared to hydrochar alone over 104 days of exposure (Han et al., 2022b). However, no significant changes in CH_4 emissions, GWP, and GHGI occurred in the soils amended with a PP-hydrochar mixture (PP at 0.5 % w/w and hydrochar at 1 % w/w) (Han et al., 2022b). The PE MPs potentially changed the impact of hydrochar on soil methanogens and methanotrophs, leading to an increased abundance of genes (*mcrA*) involved in the conversion of inorganic and organic C into CH_4 (Han et al., 2022b). In contrast to these findings, under a long-term (104 days) microcosm study, PET, PET-biochar mixture (PET 0.5 % w/w and biochar 1 % w/w) mitigated soil CH_4 emissions by 53 % and 61 %, and significantly decreased GWP and GHGI values relative to unamended control soil (Han et al., 2022a). The increased soil redox potential (Eh) and decreased methanogenesis functional genes (*mcrA*) are the prime reasons for CH_4 oxidation in MPs amended soils (Han et al., 2022a). However, these studies did not reveal the MPs-influenced changes in the relative abundance of methanogens and methanotrophs to unveil the mechanisms for such variations in gene abundance and gaseous emission. Future studies covering low MP concentrations and varying soil conditions are needed to assess the implications of MPs on CH_4 emissions.

4.2. N cycle

Nitrogen (N) is an essential element for the functions of organisms in the terrestrial ecosystem, and its redox cycles are fundamental to energy metabolism and material transformation. Previous studies have reported that MPs in terrestrial ecosystems can affect the transformation of soil N and its biogeochemical cycling (Wang et al., 2022a; Zeb et al., 2022).

4.2.1. Biological N_2-fixation

Biological N-fixation is the enzyme-catalysed reduction of N_2 to NH_3, $NH_4^+ - N$, or organic nitrogen (Raymond et al., 2004). Most of the N_2-fixing bacteria belong to phyla: Proteobacteria, Actinobacteria, Bacteroidetes, and Firmicutes (Abadi et al., 2021), and their relative abundance and distribution are significantly affected by soil MPs pollution. The addition of MPs significantly increased the relative abundance of N_2-fixing bacteria belonging to the family Burkholderiaceae and Xanthobacteriaceae (Phylum: Proteobacteria) (Fei et al., 2020; Zhu et al., 2022b; Yi et al., 2021; Riveros et al., 2022). MPs in soils could create an anaerobic atmosphere on the inner surface of the MPs (Huang et al., 2021; Li et al., 2020), facilitating the proliferation of anaerobic N_2-fixing bacteria in MP-amended soils (Riveros et al., 2022). Similarly, an increase in the relative abundance of N_2-fixing bacteria *Bradyrhizobium* (class α-Proteobacteria) in red acidic soil, clay soil, sandy loam soil, and the gut of Springtail (*Folsomia candida*) upon the addition of PVC, PET, and polylactic acid (PLA) at 0.3 % and 1 % (w/w), PVC at 0.5 %, and PE (500 μm) at 0.5 % and 1 % (w/w), respectively, was reported by Sun et al. (2022b), Yan et al. (2021), Zhu et al. (2022b), and Judy et al. (2019). As a result, an enrichment of N_2-fixing genes (*nifD*, *nifK*, and *nifH*) in sandy loam soils was observed under 0.5 % PVC (composed of 24-30 % phthalates) application after 30-60 days of treatment (Zhu et al., 2022b). A similar increase in *nifH* gene abundance and N_2-fixing *Clostridium* and *Anaeromyxobacter* were observed under 0.3 % PA MP application (Sun et al., 2023). Interestingly, Rong et al. (2021) observed an increased expression of *nif*H genes in both 2 and 7 % LDPE treatments, suggesting that MPs might have increased the abundance of LDPE resistance N_2-fixing bacteria. In contrast to the preceding findings, a significant decrease in relative abundance of N_2-fixing bacteria, such as *Microvirga* (N_2-fixing root nodule bacteria), *Cupriaridus*, *Bacillus* sp. (free-living N_2-fixing bacteria), *Anaeromyxobacter*, *Geobacter*, and *Desulfobacca*, occurred when PVC (0.3, 1, and 5 % w/w), PET (0.3 and 1 % w/w), PLA (0.3 and 1 % w/w), and LDPE (1, 5, and 7 % w/w) MPs were added (Rong et al., 2021; Sun et al., 2022b; Yan et al., 2021; Huang et al., 2023). In another study, Bryant et al. (2016) investigated nitrogen fixation on plastic surfaces and found an enrichment of nitrogenase genes *nifH*, *nifD*, and *nifK* on the surface of MPs. Therefore, it is evident that the MPs can facilitate the proliferation of N_2-fixing bacteria but resistivity/sensitivity of microorganisms, MPs type and concentration, soil types, soil microbial composition, and plasticizer composition are the major determining factors.

4.2.2. Nitrification and denitrification

Nitrification and denitrification are the two critical pathways for the release of reactive N from the soil system. Previous studies have reported that MPs in soil can strongly affect microbial-mediated soil nitrification and denitrification processes (Huang et al., 2021; Li et al., 2020; Huang et al., 2023). The effect of MPs on soil nitrification and denitrification is associated with changes in substrate availability (NH_4^+ and NO_3^-) (Gao et al., 2021; Liu et al., 2017), increased soil porosity (Chen et al., 2020a), the additional anaerobic atmosphere created on the inner surface of the MPs (Huang et al., 2021; Li et al., 2020), and MPs or plasticizers-induced toxicity to soil nitrifiers and denitrifiers (Zhu et al., 2022b). Therefore, MP type, size, concentration, polymer composition, and soil conditions determine whether MP promotes or inhibits soil nitrification and denitrification processes leading to increased or decreased soil N availability and N_2O emissions (Zhu et al., 2022b; Li et al., 2020; Wang et al., 2016).

Nitrification is a process in which ammonia is converted to nitrite and then to nitrate under aerobic conditions (Bernhard, 2010). Ammonia oxidation is an integral part of soil nitrification, involving two stage oxidations, (i) NH_3 or NH_4^+ oxidation into hydroxylamine (NH_2OH), followed by (ii) oxidation of hydroxylamine (NH_2OH) to nitrite (NO_2^-) under aerobic conditions (Zhu et al., 2013). The first stage ammonia oxidation (NH_3/NH_4^+ to NH_2OH) is mainly catalysed by ammonia monooxygenase enzyme (coded by *amoA* gene) produced by ammonia-oxidizing bacteria (AOB) and ammonia-oxidizing archaea (AOA), and second stage transformation (NH_2OH to NO_2^-) is driven by hydroxylamine reductase (encoded by *hao* gene) produced by AOB (Rong et al., 2021; Shen et al., 2021). Ammonia monooxygenase enzyme is a commonly used biomarker to study soil nitrification, and its protein product is responsible for the rate-determining first step of nitrification (Rong et al., 2021; Zheng et al., 2016). Previous studies have reported positive and negative effects of MPs on soil microorganisms carrying AOB *amoA* genes involved in soil NH_4^+ oxidation (Rong et al., 2021; Sun et al., 2022b). Rong et al. (2021) reported an increased abundance of AOB *amoA* genes under 7 % (w/w) LDPE (150-250 μm) application over an incubation period of 90 days; however, LDPE at both 2 % and 7 % (w/w) decreased AOA *amoA* genes abundance substantially after 15 days of LDPE application. The increased nitrification potential of AOB in response to external environmental changes demonstrated a higher tolerance of AOB to soil MP pollution. However, at lower concentrations (≤1 %), Sun et al. (2022b) observed that PVC, PET, and PLA at 0.3 % and 1 % (w/w) significantly decreased *amoA* gene abundances by >50 % after 20 days of exposure. Similar findings were also reported by Zhu et al. (2022b) and Sun et al. (2023) under PVC (0.5 %) and PA (0.3 % and 1 % w/w) application. The researchers reported that a decreased *amoA* gene abundance and soil NO_3^- content was strongly corroborated with decreased *Nitrospira* abundance (Rong et al., 2021; Zhu et al., 2022b; Sun et al., 2023). Differences in the above findings could be attributed to variations in soil properties, incubation period, and native soil microbial composition. In addition to this, MP types and their polymeric compositions are also major determining factors for changing soil N transformation (Sun et al., 2022b; Seeley et al., 2020). For instance, Seeley et al. (2020) reported that polyurethane foam (PUF) and PLA at 0.5 % (w/w) increased the relative abundance of AOB *amoA* genes, but at similar levels, PVC decreased the abundance of AOB *amoA* genes relative to unamended marsh sediments. The results corroborated with high soil NO_3^- and NO_2^- contents and low soil NH_4^+ content in PUF- and PLA-amended soils, whereas high soil $NH_4^+$and low NO_3^- and NO_2^-contents in PVC-amended soils, after 16 days of incubation (Seeley et al., 2020).

Denitrification is the microbial-mediated process that converts nitrate into N_2 gas under anaerobic conditions (Bernhard, 2010). Nitrate reductase, nitrite reductase (coded by the *nirS* or *nirK* gene), and nitrous oxide reductase (coded by the *nosZ* gene) are the key functional enzymes involved in soil denitrification (Han et al., 2022a; Li and Liu, 2022; Liu et al., 2020). Nitrate reductase is involved in the reduction of NO_3^- to NO_2^-, while nitrite reductase reduces NO_2^- into nitric oxide (NO) and nitrogen dioxide (NO_2) (Liu et al., 2020). Meanwhile, nitrous oxide reductase catalyses the reduction of N_2O to dinitrogen (N_2). Denitrifiers carrying *nirS* genes are typically considered complete denitrifiers involved in the complete conversion of NO_3^- to N_2, whereas *nirK*-associated denitrifiers are likely to be incomplete denitrifiers that produce N_2O as an end product (Seeley et al., 2020; Helen et al., 2016; Saggar et al., 2013). Compared with controls, *nirS* gene abundances decreased by 38.46 % following the addition of 18 % LDPE MPs, but *nirK* and *nosZ* gene numbers were not affected (Gao et al., 2021). The effect of MPs on AOB decreased substrate availability (NO_3^-) for soil denitrification, causing a decreased *nirS* gene abundance and soil N_2O emissions in LDPE-amended soils (Gao et al., 2021). PET, PVC, and PLA MPs at 0.3 % and 1 % (w/w) dosing significantly decreased *nirS* and *nirK* gene abundances after 20 days of exposure (Sun et al., 2022b). In contrast, Sun et al. (2023) observed a stimulatory effect on *nirS* and *nirK* when 0.3 % (w/w) PA was applied, but at 1 % (w/w) PA MPs had no significant effect after 20 days of exposure. Alterations in the relative abundance of nitrifiers (*Nitrospira*) and denitrifiers (*Pseudomonas*, *Bryobacter*, *Geothrix*) were strongly linked with *nirS* and *nirK* abundance. Application of PE MPs (at 1 % w/w) resulted in a significant stimulatory effect on the *nirS* gene and a corresponding increase in soil N_2O emission in paddy soils of southern China after 28 days of exposure (Yu et al., 2022). The above stimulatory effect was closely related to the pH and inorganic N content of the soil. LDPE (150-250 μm) MPs addition at 2 and 7 % (w/w) significantly stimulated the abundance of *nirK* genes throughout an incubation period of 90 days, but *nirS* genes were initially stimulated then diminished over longer experimental periods (Rong et al., 2021). The authors suggested that the promotion of *nirK* genes abundance on MP addition could be related to an increased abundance of soil denitrifying bacteria, such as *Pseudomonas*, *Stenotrophomonas*, *Brachybacterium*, and *Achromobacter* (Rong et al., 2021). Seeley et al. (2020) observed the highest abundance of *nirS* genes under PUF and PLA treatments suggesting higher denitrification activity, whereas PVC application significantly decreased *nirS* gene abundance and lowered denitrification activity in sediments. The inhibitory effects of PUF and PLA on the soil ammonification process (AOB *amoA* genes) increased the substrate availability (NO_3^- and NO_2^-) for soil denitrifying bacteria, resulting in increased soil denitrification activity (*nirS* genes) in PUF- and PLA-amended soils (Seeley et al., 2020). Based on previous studies, it could be predicted that bacteria containing copper nitrite reductase (*nirS*) would be very sensitive to even small MP pollution, and *nirK* denitrifiers would play a prominent role in the denitrification process in highly polluted soils. Moreover, MPs in soils could facilitate the proliferation of soil denitrifying bacteria that carry *nirK* genes, which could result in an incomplete soil denitrification process and greater soil N_2O emissions. A meta-analysis by Su et al. (Su et al., 2023) based on 60 published studies found that MP exposure in soil could significantly increase the denitrification rate (17.8 %) by altering the denitrifiers genes (increased *nir* copy numbers by 18.4 % and decreased *nos* copy number by 11.0 %) and nitrate reductase activity (by 4.8 %). As a result, soil nitrite concentration increased by 38.8 % and soil NO_3^- concentration decreased by 22.4 %; thus, resulting in an increased N_2O emission by 140.6 % (Su et al., 2023). It should be noted, however, that the observations of Su et al. (2023) were mostly from short-term microcosm experiments (average exposure period 21 days), which need to be investigated under long-term mesocosm conditions.

4.3. P cycle

Soil P cycle is a complex nutrient movement involving many physical, chemical, and biological processes that regulate soil available phosphorus (AP) and plant growth. To date, only a few studies reported the varying effects of MPs on soil P content and its availability (Yan et al., 2021; Li and Liu, 2022; Dong et al., 2020). For instance, Liu et al. (2017) and Yan et al. (2021) observed an increased level of soil AP upon MP exposure. The authors reported that the increased soil AP could be attributed to increased soil phosphatase activity and P-solubilizing bacteria that could lead to increased microbe-mediated solubilization of inorganic P and mineralization of soil organic P (Yan et al., 2021; Liu et al., 2019; Qi et al., 2020b). In contrast to these findings, Dong et al. (2020) and Li and Liu (2022) reported decreased levels of soil AP upon MPs exposure. The smaller size, larger surface area, and charged surface functional groups of MPs might influence the adsorption-desorption of inorganic P, thereby causing decreased P bioavailability (Li and Liu, 2022). Also, the inhibitory effects of MPs on soil enzymes can regulate the mineralization and solubilization of P, reflecting decreased soil AP (Zettler et al., 2013).

Phosphorus solubilizing microbes especially phosphate solubilizing bacteria (PSB) play a key role in the conversion of inorganic P to soluble phosphate (PO_4^{3-}) ions (Wan et al., 2020). Fei et al. (2020) reported a significant increase in the relative abundance of PSB Burkholderiaceae (phthalate degrading bacteria) after the application of 5 % PVC (18 μm) and 1 % and 5 % PE (678 μm) MPs in acid loamy soils, resulting in greater acid phosphatase activity in MPs amended soils. Similarly, an enrichment of Burkholderiaceae was observed under 0.5 % phthalate (24-30 %) plasticized PVC application after 60 days of exposure (Zhu et al., 2022b). Similarly, Yan et al. (2021) found that AP increased by adding 0.1 and 1 % di (2-ethylhexyl) phthalate plasticized PVC MPs in acidic soils, but at 1 % unplasticized PVC decreased AP content in fertile paddy soils over 35 days of incubation. The changes in AP by the addition of 0.1 and 1 % PVC MPs were likely due to variations in the relative abundance of PSB and their solubilizing capacity (Zhu et al., 2022b; Yan et al., 2021). The MP-influenced changes in soil WHC and moisture content might positively affect soil phosphatase activity, whereas decreased microaggregate stability due to MP pollution could decrease the phosphatase activity and AP. AMFs are the group of plant symbionts that greatly regulate the P solubilization and availability (Wang, 2017). MP pollution greatly altered the community structure, diversity, and colonization ability of AMF (Fang et al., 2021; Lehmann et al., 2020; Wang et al., 2022d); thereby, affecting soil P status and availability. A metanalysis by Wan et al. (2023) reported that depending on polymer type, MPs at low concentrations (< 0.5 % w/w) increased the soil fungi and enzymes activity involved in soil P-cycling, but at an elevated concentration (1.0–3.0 % w/w) they render toxicity, causing decrement in the levels of soil AP and total P. So far, only a few reports have highlighted the effects of MPs on soil P dynamics. Further studies involving advanced molecular techniques are needed to understand and address possible future effects of MPs on soil ecosystems and crop productivity.

5. Combined effect of MPs and their associated contaminants on soil microorganisms

The hydrophobic nature and high surface area of MPs could facilitate the adsorption of various inorganic and organic contaminants from the surrounding environment (Wang et al., 2019). Most researchers have focused on the toxicity of MPs alone to soil microorganisms, and there are few studies on the combined effects of MPs and associated contaminants on soil microorganisms.

5.1. MPs and inorganic contaminants

Heavy metals are frequently used as additives to improve the properties of plastics. Due to mechanical and biological processes, these additives enter terrestrial ecosystems over time (Cao et al., 2021). Therefore, heavy metals are frequently detected as inorganic pollutants in plastic-polluted areas. Owing to small size, strong hydrophobicity, and large surface area, MPs can adsorb toxic inorganic contaminants such as heavy metals through complexation, electrostatic interaction, hydrogen bonding, and surface complexation (Bradney et al., 2019; Huang et al., 2022), and can cause synergistic or antagonistic effect to exposed aquatic and terrestrial organisms (Cao et al., 2021; Li et al., 2022b; Liu et al., 2021; Liu et al., 2022). However, the capacity of soil and MPs to adsorb heavy metals would greatly regulate heavy metal bioavailability in the soil (An et al., 2023). Feng et al. (2022a) observed a significant increase in Pb(II) availability under 2 % PE, PS, PA, PLA, polybutylene succinate (PBS), and polyhydroxy butyrate (PHB) amended soils, while at 0.2 % (*w*/w), Pb(II) availability was decreased significantly due to concentration-dependent changes in soil properties (pH, CEC, and DOC). Li et al. (2023) and Wang et al. (2023) observed an increased bioavailability of cadmium (Cd) when PE (0.5-1.0 % w/w), PP (1 % w/w), polybutylene adipate terephthalate (PBAT, 1.0 % w/w), and PLA (1.0 % w/w) was added due to increase in soil pH. In contrast, Yang et al. (2022) reported that PVC MPs (0.1-10 μm) at 2, 7, and 10 % (*w*/w) significantly decreased available methyl mercury $(CH_3\text{-}Hg)^+$ in red and alkali paddy soils of Hunan Province and Inner Mongolia, China. The authors suggested that MPs influenced changes in soil dissolved organic matter, sulfate reduction, and abundance of mercury methylators such as Proteobacteria and Firmicutes are the possible factors for reduced bioavailability of $(CH_3\text{-}Hg)^+$ in the paddy soils (Yang et al., 2022). Therefore, MPs can affect the distribution, fate, transformation, bioavailability, and toxicity of heavy metals to exposed soil micro- and meso-fauna (Cao et al., 2021; Wang et al., 2020b; Yu et al., 2020; Meng et al., 2023).

The combined exposure of PES microfibres (0.2 % w/w)- Cd (II) (5 mg kg^{-1}) mixture did not change soil bacterial alpha-diversity (Shannon, Simpson, and Chao1 index), but enhanced the growth of PES-degrading bacteria such as Proteobacteria, Cyanobacteria, Acidobacteria, Bacteroidetes (Zeb et al., 2022). The application of PES increased the relative abundance of bacterial genera *Woeseia*, *Devosia*, and *Hydrogenophoga* (Proteobacteria) (Zeb et al., 2022), which are known to decrease Cd(II) bioavailability (by altering the soil pH), and regulated the genes involved in C metabolism, adenosine triphosphate (ATP)-binding cassette transporters (ABC transporters) and oxidative phosphorylation in the plant rhizosphere (Ding et al., 2019). Moreover, the combined exposure of PES-Cd mixture significantly altered the bacterial genera *Sphingomonas* (N_2-fixing bacteria) and *Ferrogenebacter* (involved in C mineralization), thereby decreasing the soil C and N-mineralization and bioavailability of Cd to lettuce (*Lactuca sativa*) (Zeb et al., 2022). Similarly, the combined application of PS, polytetrafluoroethylene (PTFE) (0.1-10 μm and 10-100 μm), and arsenic (As), i.e., As (III) and As(V) (1.4, 24.7, 86.3 mg kg^{-1}) significantly increased the relative abundance of Proteobacteria and Bacteroidetes, while PS and PTEF alone decreased their abundance, after 7 weeks of exposure (Dong et al., 2021). Changes in soil pH, SOC, and resistivity against arsenic contamination changed the native bacterial community structure in the

MP-As contaminated soil. Moreover, soil urease, acid phosphatase, dehydrogenase, and peroxidase activity decreased significantly under combined PS, PTFE, and As exposure, resulting in a significant decrease in soil available N and P (Dong et al., 2021). The combined application also reduced the As bioavailability by hydrogen (H)-bonding with exposed oxygen (O)-containing functional groups of MPs and increased As adsorption with SOM due to π-complex formation between MPs and SOM (Dong et al., 2021). Li et al. (2024) observed an increased relative abundance of Chloroflexi, Actinobacteria, Acidobacteria, Ascomycota and Basidiomycota after 60 days of PE MPs application (0.5-1.0 % w/w) in Cd (8.96 mg kg^{-1} soil) and lead (Pb) (260.15 mg kg^{-1} soil) contaminated soils. In addition, the increase in soil pH (8.05 to 8.16) decreased the gene abundance involved in soil methane oxidation (Mox) P-solubilization (gcd) and thiosulfate reduction (*soxB*, *soxY*, *soxZ*, and *soxC*), but increased the gene abundance responsible for ammonia oxidation (*gdhA*) and sulfur reduction (*cysI*) (Li et al., 2024). An application of PE microbeads and PE microbeads-copper (Cu(II)) mixture significantly affected SOM degradation, and decreased soil respiration by 28 and 37 % compared to unamended control soils after 14 days of exposure (Wijesekara et al., 2018). Also, the PE microbeads alone decreased soil dehydrogenase activity by 36 %, while the PE-Cu(II) mixture decreased soil dehydrogenase activity by 58 %, indicating a substantial effect on soil microbial growth and activity (Wijesekara et al., 2018). The PE-Cu (II) mixture could have damaged the microbial cells and their nucleic acids and limited their nutrient and energy accessibility, thus decreasing soil microbial and soil dehydrogenase activity (Wijesekara et al., 2018).

Heavy metals and MPs in combination also affected the community structure and functions of plant AMF directly or indirectly (altering soil properties). Wang et al. (2020b) studied the combined influence of PE, PLA (1 and 10 %), and Cd(II) (5 mg kg^{-1}soil) on the AMF community. The PE (10 % w/w)-Cd mixture significantly increased AMF Glomeraceae, while PLA (10 %)-Cd increased AMF Archaeosporaceae. In addition, Cd and MPs mutually affected AMF genera such as *Ambispora*, implying potential threats to root symbiosis and plant performance (Wang et al., 2020b). The AMF showed a tolerance to Cd(II) toxicity, but MP-influenced changes in soil pH and MPs-Cd(II) combined toxicity significantly altered the AMF diversity under MPs-Cd(II) exposure (Wang et al., 2020b). Thus, the interaction between MPs and heavy metals could result in synergistic or antagonistic effects on soil microorganisms; however, MP type, polymer composition, surface functional groups, heavy metal type, soil pH, and resistivity/sensitivity of concerned microorganisms are the major determinants (Table 2). Future studies involving a wide range of MPs and heavy metals under different ecological conditions are needed to further understand their interactions and toxicity.

5.2. MPs and organic contaminants

With the development of printing, textile, pesticide, and pharmaceutical industries, more and more organic contaminants such as poly- and perfluoroalkyl substances (PFAS), polycyclic aromatic hydrocarbons (PAHs), pesticides, and antibiotics are released into the soil

Table 2
Combined effect of MPs and emerging contaminats on soil microorganisms and their functions.

MP type and concentration	Dose of MPs	Contaminants and concentration	Soil pH	Exposure period	Effect on soil microbial diversity	Effect on microbial function	Reference
PE	0.5, 1.0, and 2.0 % (w/w)	Cd (12 mg kg^{-1})	6.75	14 days	PE did not change bacterial diversity indices (Chao 1, Shannon, and Simpson indexes)	Suppressed β-glucosidase and *N*-acetyl-gucosaminidase activity Decreased gene abundance of amoA gene	(Lan et al., 2023)
PE (0.5 and 1.0 μm)	0.5 and 1.0 % (w/w)	Cd (8.96 mg kg^{-1}) Pb (260.15 mg kg^{-1})	8.05	60 days	Increased the RA of Chloroflexi, Actinobacteria, Acidobacteria, Ascomycota, and Basidiomycota	Significantly decreased the gene abundance involved in soil methane oxidation (Mox) P-solubilization (*gcd*) and thiosulfate reduction (*soxB*, *soxY*, *soxZ*, and *soxC*) Increased the gene abundance responsible for ammonia oxidation (*gdhA*) and sulfur reduction (*cysI*)	(Li et al., 2024)
PE (75 μm) and PLA (75 μm)	2 and 20 % (w/w)	Cd (1.03 mg kg^{-1})	5.2	60 days	PE MPs (at 20 % w/w) increased RA of Chloroflexi, Acidobacteria, and Plantomycetota but decreased the RA of Gemmatimonadota PLA (at 20 % w/w) significantly increased the RA (98.5 %) of Firmicutes	Enriched the functional gens involved in nitrate reduction and nitrate/nitrite respiration	(Li et al., 2023)
PE (100-150 μm)	1 % (w/w)	Ciprofloxacin (10 mg kg^{-1})	8.3	35 days	Synergistically decreased diversity indices (Chao 1 and Shannon indexes)	PE addition significantly decreased ciprofloxacin degradation efficiency of the soil	(Wang et al., 2020c)
LDPE (1 mm)	5 % (w/w)	Tetracycline (10 mg kg^{-1})	7.5	35 days	PE and tetracycline synergistically increased RA of *Aeromicrobium*, *Rhodococcus*, *Mycobacterium*, and *Intrasporangium*	No significant effect on soil urease and phosphatase activity	(Ya et al., 2023)
PE	0.2 % w/w	Oxytetracycline (5.0-150 mg kg^{-1})	–	42 days	Increased RA of Bacteroidetes and Patescibacteria, but decreased RA of Gemmatimonadetes compared to only PE and oxytetracycline application	No significant effect on soil sucrase, dehydrogenase, and urease activity	(Guo et al., 2022)
PS (0.1-100 μm) and PTFE (0.1-100 μm)	0.25-5.0 % (w/w)	As (III & IV) (1.4, 24.7, and 86.3 mg kg^{-1})	5.59	–	MPs and As together decreased the RA of Proteobacteria but increased the abundance of Chloroflexi and Acidobacteria	Suppressed soil urease, acid phosphatase, dehydrogenase, and peroxidase activity	(Dong et al., 2021)
PE and PLA	0.1-10 % (w/w)	Cd (5 mg kg^{-1})	6.1	30 days	MPs did not change the AMF diversity but altered the community structure	–	(Wang et al., 2020b)

*AMF: Arbuscular mycorrhizal fungi; PE: Polyethylene; LDPE: Low density polyethylene; PLA: Polylactic acid; PS: Polystyrene; PTFE: Polytetrafluoroethylene; RA: Relative abundance.

environment (Xiang et al., 2022; Qian et al., 2017). MPs serve both as a source and sink for organic contaminants (Bradney et al., 2019; Wang et al., 2022d). Several organic contaminants such as PFAS, bisphenols, and phthalate are added to plastics as additives during the manufacture to improve the performance, functionality, and aging properties of the basic plastic polymer (Kumar et al., 2022b). MPs are mostly hydrophobic and can adsorb many organic contaminants through hydrophobic interaction, electrostatic interaction, H-bonding, halogen-bonding, and π-π interaction (Chang et al., 2022; Dissanayake et al., 2022); thereby, influencing their long-range transport, bioavailability, and toxicity (Fajardo et al., 2022; Boughattas et al., 2022; Li et al., 2018). MPs- organic contaminants interaction may pose either a synergistic or an antagonistic effect on soil microbial diversity (Qiu et al., 2022), affecting their ecological functions, including organic contaminants degradation (Chang et al., 2022).

In a microcosm experiment, the addition of PE and ciprofloxacin (CIP) decreased soil microbial diversity, increased the abundance of *Achromobacteria* and *Serratia* (phylum; Proteobacteria), and decreased the overall CIP degradation efficiency of the soil (Wang et al., 2020c). Similarly, a combined application of LDPE (at 5 % w/w) and tetracycline (10 mg kg^{-1}) significantly decreased the soil microbial diversity and tetracycline degradation (by 1 mg kg^{-1} after 35 days of exposure), and thus resulted in an increased relative abundance of ARGs (by 500 ppm compared to only tetracycline application) after 35 days of exposure (Ya et al., 2023). Fajardo et al. (2022) reported that application of PE MPs and antibiotic mixture (15 μM of ibuprofen, sertraline, amoxicillin, and simazine) at 0.1 % w/w significantly increased the relative abundance of Actinobacteria, Verrucomicrobia, and Acidobacteria, and greatly influenced the functions related to xenobiotic degradation (benzene degradation) and carbohydrate and amino acid metabolism after 15 days of exposure (Fajardo et al., 2022). In contrast to these findings, PE MPs at 0.2 % (w/w) with oxytetracycline (OTC) diminished the effects of OTC on bacterial community richness (Sobs and Chao1 index) but significantly decreased community diversity (Guo et al., 2022). The OTC + PE MPs significantly increased the relative abundance of bacteria belonging to Bacteroidetes and Patescibacteria, whereas Gemmatimonadetes abundance decreased significantly (Guo et al., 2022). However, OTC + PE MPs application did not change soil urease, dehydrogenase, and sucrase activity after 42 days of MP exposure (Guo et al., 2022). Studies related to the combined toxicity of MPs and organic contaminants are very limited and seek long-term mesocosm studies covering a wide range of organic contaminants and MPs under relevant concentration.

Owing to the considerable capacity to adsorb antibiotics and simultaneously promote microbial colonization, MP surfaces could serve as a carrier of ARGs (Lu et al., 2020; Sathicq et al., 2021), which is a huge concern recently and warrants investigations to understand the role of MPs in the dissipation of ARGs in the soil environment. The MPs in soil could increase the ARGs abundance by (1) increasing the residence time of antibiotics due to adsorption on the MP surface, which affects the migration and biotransformation of the antibiotic, inducing the emergence of ARGs by gene mutation, and (2) enrichment of antimicrobial resistance bacteria, stimulating ARG emergence and horizontal ARG transfer. Combatting the adverse implications of the above interactions is an upcoming big challenge for the global scientific community (Ma et al., 2020).

6. Conclusions and future research directions

The current issue of plastic pollution in the soil ecosystem will continue to grow due to the rise in plastic production and lack of proper waste management system. The MP type, size, concentration, polymer composition, surface properties, and exposure period have an impact on soil microbial attributes, but a more extensive global database is needed to predict which MP attribute impacts the soil microbial properties more than the other attribute at environmentally relevant concentration. The importance of MP-microbe interactions and their impacts on the soil ecosystem and biogeochemical cycles have gained wide attention recently, and an understanding of mechanistic interactions between soil microorganisms and MPs/plasticizers is currently lacking. Following are some of the research challenges that need to be addressed to minimise the adverse effects of MP pollution on soil quality and maintain soil microbial diversity and functions:

- Future studies should focus on assessing the MPs-influenced changes in microbial diversity and functions under environmentally relevant MP concentrations.
- Although biodegradable plastics could be a feasible option for the future, research is needed to assess the effects of bioplastic's hazardous additives on terrestrial ecosystems and nutrient cycling.
- Limited understanding of MP-microbial interactions, biofilm formation, microbial-microbial interactions, and antimicrobial resistance development in MP-polluted soil necessitates future investigations using advanced microscopic, spectroscopic, and omics techniques.
- Some studies suggested that alteration in soil microorganisms and their functions is mainly because of plasticizers released from MPs. Future studies are needed to understand the fate of MPs, the release of plasticizers, and their toxicity by keeping plasticizers as a control.
- Additional research is needed to understand the occurrence and behaviour of heavy metals, emerging contaminants, and ARGs on MPs and their combined toxicity to soil microorganisms.
- Most available studies are based on weeks or months of laboratory simulation data, reflecting only preliminary transitory responses. Therefore, it is essential to establish field experiments with adequate replications and appropriate controls to assess the long-term impacts of MPs on soil microorganisms and their functions.

CRediT authorship contribution statement

Vijay Kumar Aralappanavar: Writing – original draft, Visualization, Formal analysis. **Raj Mukhopadhyay:** Writing – original draft, Formal analysis. **Yongxiang Yu:** Writing – review & editing. **Jingnan Liu:** Writing – original draft. **Amit Bhatnagar:** Writing – review & editing, Conceptualization. **Sarva Mangala Praveena:** Writing – review & editing. **Yang Li:** Writing – review & editing. **Mike Paller:** Writing – review & editing. **Tanveer M. Adyel:** Writing – review & editing. **Jörg Rinklebe:** Writing – review & editing. **Nanthi S. Bolan:** Writing – review & editing. **Binoy Sarkar:** Writing – review & editing, Writing – original draft, Validation, Supervision, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.scitotenv.2024.171435.

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