

Managing soil contamination risks: Microbiome and agricultural practices: a review

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Abstract. Microbial diversity and function are central components of soil quality and overall soil health. When ecological conditions shift—whether because of farming practices or contamination—soil microbial communities can undergo structural and functional changes that ultimately alter soil fertility and ecosystem performance. To effectively assess how anthropogenic agricultural stressors affect soil functions, we need tools that provide valuable information to various soil stakeholders (farmers, industry, authorities, and citizens) to address these stressors through environmental risk assessment. Some measures should also be implemented to reduce the risk of ongoing contamination from common agricultural practices, such as the distribution of fertiliser products, particularly those of livestock origin. This review presents potential methods for assessing soil contamination using soil microbiome analysis, highlighting their challenges. Moreover, methods to reduce the load of emerging soil contaminants (antibiotics, microplastics) and organic fertilising products based on microbial processes are also described.

Keywords: soil, microbiome, risk assessment, indicators, contaminants, soil health

1. INTRODUCTION

Soils have long been considered capable of absorbing and degrading organic pollutants without incurring major adverse effects; however, this view is overly simplistic. Many contaminants can persist and accumulate in soils, and their retention and degradation are finite processes controlled by soil properties, pollutant chemistry, bioavailability, and microbial activity (Correia *et al.*, 2025). In recent decades, this perception has been further revised in light of well-documented cases of soil contamination from industrial activities, intensive agriculture, and waste mismanagement, leading to the recognition that soil is a fragile, non-renewable resource whose formation occurs over geological timescales and whose functions are increasingly compromised by anthropogenic pressures and climate-driven changes (FAO and ITPS, 2015; Telo da Gama, 2023; FAO, UNEP, 2021; Chen *et al.*, 2025).

Intensive agriculture and the diffuse presence of organic pollutants from diverse sources (industrial, urban, agricultural) are among the main drivers disrupting large-scale

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soil biodiversity and complex food webs (EEA, 2017). Environmental pollution from substances such as organic compounds, agricultural chemicals, pharmaceuticals, and hazardous chemicals present in urban and industrial waste, including litter and plastics, is a major source of soil contamination and a global issue (Shetty *et al.*, 2023). Because of their negative impacts, several ecosystem services provided or regulated by soil are being compromised (Pereira *et al.*, 2018), thereby affecting animals, the environment, and human health (Jones *et al.*, 2013). The ecosystem services provided by soil are closely linked to the multitude of organisms (bacteria, fungi, archaea, protists, algae, nematodes, and meso- and macrofauna) that inhabit it. Among these, microorganisms are collectively referred to as the microbiome, which includes their genes and genomes as well as their functional potential (Giovannetti *et al.*, 2022; Berg *et al.*, 2020). The soil microbiome drives key processes (*e.g.* nutrient cycling, organic matter degradation, bioremediation) that are essential for soil ecosystem functioning (Hartman and Six, 2023). Microbial diversity and activity therefore represent an important component of soil quality and contribute significantly to soil health. However, changing ecological conditions—for example, alterations in the physical or chemical characteristics of soil resulting from agricultural practices or pollution events—can modify microbial community structure and function (Meena, 2023), thereby affecting soil health, fertility, and quality.

To properly evaluate the impact of anthropogenic stressors, particularly those of agricultural origin, on soil functions, it is necessary to develop appropriate indicators and tools that provide useful information to diverse soil stakeholders (farmers, industry, authorities, and citizens) and support environmental risk assessment. In addition, measures should be considered to mitigate the risk of chronic contamination arising from common agricultural practices. This review presents possible approaches for soil microbiome-based assessments, highlighting their challenges and outlining potential methods to reduce the risk of soil contamination associated with the application of organic fertilising products.

2. SOURCES OF CONTAMINATION AND THE REGULATORY FRAMEWORK

Organic pollutants, such as synthetic chemicals, pharmaceuticals, and microplastics, are entering the environment with increasing frequency, typically at trace levels. Although the presence of these contaminants in aquatic systems is well documented, their long-term effects on soil biodiversity and ecosystem services remain poorly understood (Osman *et al.*, 2023; Tariq *et al.*, 2024; Pérez-Méndez *et al.*, 2025; Meng *et al.*, 2025). While substantial information exists on the threats they pose to humans and aquatic ecosystems, their impacts on soils (*e.g.*, biodiversity, ecosystem services, and indirect effects on humans) and on aboveground organisms remain insufficiently understood

and evaluated. Moreover, although many of these substances are monitored in surface waters, this is not yet the case for soils, as there is currently no EU-wide legal framework for soil monitoring.

Soil pesticide loads have been steadily declining since 2016 (Silva *et al.*, 2019), partly due to the implementation of Directive 2009/128 on the sustainable use of pesticides, the review of authorised active substances, and Regulation (EC) No 1107/2009 governing their marketing. Nevertheless, between 2011 and 2022, the EU still used more than 350,000 tonnes of pesticides (Schneider *et al.*, 2023; <https://ec.europa.eu/eurostat/statistics>), some of which are known to exert pronounced effects on soil microbiomes (Walder *et al.*, 2022; Ni *et al.*, 2025). Per- and polyfluoroalkyl substances (PFAS) have raised particular concern for their risks to human health. This large group of thousands of highly stable and persistent synthetic organic compounds is widely used across society and in many industrial sectors (Walder *et al.*, 2022). Ongoing production and use have led to PFAS contamination of drinking water, rivers, and wastewater, and to their accumulation in soils and living organisms, with serious consequences for human health, including reduced antibody responses to vaccines (Schneider *et al.*, 2023; Walder *et al.*, 2022). In the EU, around 100 000 sites are believed to be potential PFAS emitters, and the annual health-related costs associated with PFAS exposure are estimated at €52–84 billion, due to the high proportion of citizens expected to exceed the tolerable weekly intake (Walder *et al.*, 2022). To limit these impacts, after a protracted period of voluntary and mandatory restrictions (Reinikainen *et al.*, 2024), two legal acts entered into force in early 2023 to reduce PFAS exposure through food and drinking water (Commission Regulation (EU) 2022/2388 and Directive (EU) 2020/2184, respectively). Furthermore, in January 2023, several EU Member State authorities submitted a proposal to ECHA to reduce PFAS emissions into the environment.

According to Eurostat's Environmental Data Centre on Waste, the EU generated 2.23 billion tonnes of solid waste in 2022, 5.3% of which was classified as hazardous, including plastics (https://ec.europa.eu/eurostat/statistics-explained/index.php?title=Waste_statistics). Plastics are extensively used in agricultural production (*e.g.*, mulching films and protective covers) and represent an important source of plastic inputs to soils. In the European Union, agricultural plastics are estimated to generate 0.4–0.6 million tonnes of non-packaging plastic waste annually, according to Eurostat assessments and sector analyses. This widespread use is consistent with global estimates indicating that agricultural value chains consume millions of tonnes of plastic each year, with a large fraction remaining poorly collected and often accumulating in soils or being improperly disposed of (FAO, 2021). However, plastics and microplastics can also enter soils through multiple pathways, including sewage sludge, compost and other organic amendments,

irrigation with reclaimed water or wastewater, atmospheric deposition, and urban and industrial sources. The breakdown of plastic residues generates microplastics (particles < 5 mm) and nanoplastics (1–100 nm), which pose increasing risks to ecosystem integrity and food safety (Blasing and Amelung, 2018).

Growing evidence indicates that microplastics alter soil microbial communities and foster the persistence of antibiotic resistance genes (ARGs) (Li *et al.*, 2024a, b). For example, microplastics have been shown to inhibit the dissipation of ARGs in soil (Sun *et al.*, 2018), and ARG abundance has been linked to microplastic size and weathering state (Lu *et al.*, 2020; Li *et al.*, 2025). Microplastics can also act as carriers for other pollutants (He *et al.*, 2022; Athulya *et al.*, 2024), such as persistent organic contaminants (Rodrigues *et al.*, 2019), heavy metals (Gao *et al.*, 2021), and antibiotics (Li *et al.*, 2018; 2025).

Several countries have introduced threshold values for microplastic content in organic fertilisers, but these differ between jurisdictions and rarely target the same size fractions. As a result, animal-derived fertilisers can be a significant source of microplastic contamination in soils. Reported microplastic concentrations in farmyard manure and similar amendments range from 0 to 3 780 particles kg⁻¹ soil (Wu *et al.*, 2021), reflecting variation in livestock diets and on-farm plastic use. Microplastic abundance in soils also increases with long-term application of mineral fertilisers (Cusworth *et al.*, 2024) and from tyre wear from agricultural machinery, wind transport, runoff, and atmospheric deposition (Allen *et al.*, 2002).

The effects of microplastic pollution on agricultural productivity remain poorly understood, largely due to the scarcity of long-term field trials and the use of unrealistically high microplastic concentrations in many experimental studies. Since microplastic levels in agricultural soils are expected to keep rising due to both agricultural and non-agricultural inputs, it is crucial to clarify their impacts on agroecosystems. The long-term consequences of plastic use in agricultural soils are difficult to reverse (Santás-Miguel, 2025). Most documented interactions between microplastics and soil fauna, vegetation, microbes, and crop yields are negative, indicating a growing threat to agricultural productivity and food security as microplastics accumulate over time. With no rapid, large-scale solutions currently available to address microplastic pollution, it is increasingly important to reassess our dependence on plastics in agriculture and other sectors (Cusworth *et al.*, 2024).

Antibiotics have long been widely used in the livestock sector as growth promoters, therapeutics, and prophylactics. They have also been applied as plant protection products: a recent study showed that antibiotics such as gentamicin, kasugamycin, oxolinic acid, oxytetracycline, streptomycin, validamycin, and zhongshengmycin have been used in 39 countries, mostly outside the EU (Verhaegen *et al.*, 2024). Streptomycin, in particular, has been used since the 1950s

to control various bacterial plant diseases, notably fire blight caused by *Erwinia amylovora*, and its widespread use has been associated with the selection and dissemination of resistance determinants. Notably, similar streptomycin resistance genes and mobile genetic elements have been identified in both plant-associated bacteria and human pathogens. However, direct transfer between these groups has not been unequivocally demonstrated (Verhaegen *et al.*, 2023).

There is growing concern that vectors carrying streptomycin resistance genes may spread beyond plant-pathogenic bacteria to other species, including important human pathogens such as *Salmonella enterica* and *Klebsiella pneumoniae*, with potential implications for soil microbial communities as well (Miller *et al.*, 2022; Verhaegen *et al.*, 2023).

High levels of several classes of antibiotics have been detected in various animal manures (*e.g.*, Martínez-Carballo *et al.*, 2007; Rasschaert *et al.*, 2020), and their application to fields has been linked to changes in soil microbiomes and enhanced dissemination of ARGs (Gillings, 2013). Despite a marked decline in the use and sales of veterinary antibiotics across the EU, total sales in 2022 in the EU and associated countries (31 in total) still amounted to around 4 500 t (EMA, 2023). In addition to antibiotic-resistant bacteria and ARGs, organic fertilisers may contain antibiotic residues and other co-selecting agents, such as copper, zinc, and veterinary pharmaceuticals, which together may facilitate ARG selection and transfer in soils (Fang *et al.*, 2014).

This is critical because antibiotic residues in soil typically show highly variable persistence and bioavailability rather than consistent accumulation to toxic concentrations, as their fate is strongly influenced by antibiotic properties, soil characteristics, sorption processes, and microbial activity (Brandt *et al.*, 2015; Cycoń *et al.*, 2019). In contrast, heavy metals impose a long-term selective pressure on soil microbiomes, driving co-selection for antibiotic resistance (Murray *et al.*, 2024; Song *et al.*, 2020). Furthermore, mobile genetic elements, which have also been detected in animal manure, have emerged as major contributors to the environmental spread of clinically important ARGs (Li *et al.*, 2024a, b).

Taken together, this overview underlines the need for standardised tools for environmental risk assessment that can significantly improve toxicity evaluations of these contaminants for terrestrial biodiversity and related soil ecosystem services, thereby helping to close current gaps in environmental regulation. Likewise, identifying and implementing effective options to remove or reduce these contaminants from agricultural inputs could help minimise contamination risks.

3. METHODS TO EVALUATE THE IMPACT OF CONTAMINANTS ON THE SOIL MICROBIOME

Determining contaminant concentrations in soils remains challenging because of soil heterogeneity and the complex physical and chemical interactions between contaminants and soil components. Approaches based on soil microbial communities provide complementary insights into the biological effects and ecological impacts of contaminant exposure, complementing chemical analyses. In this context, the soil microbiome has emerged as a highly sensitive and early indicator of environmental stress, often responding more rapidly than the soil's physicochemical properties (Ma *et al.*, 2022). Consequently, advances in omics technologies have led to the increasing use of microbiome-based approaches for environmental health assessment (Debode *et al.*, 2024). Chemical determinations and omics-based analyses should therefore be regarded as complementary tools for evaluating both the presence of contaminants and their functional consequences in soil systems.

Advances in next-generation sequencing (NGS) technologies have transformed environmental microbiology by enabling high-resolution analysis of microbial communities and their temporal dynamics (Satam *et al.*, 2023). Metabarcoding and shotgun metagenomics are the two main methodological approaches used in environmental microbiology studies. Metabarcoding uses the sequencing of taxonomically informative genetic fragments to identify the taxa present within a sample. Typically, to characterise bacterial taxa, the 16S rRNA gene is amplified by PCR and sequenced. In contrast, in fungi, the internal transcribed spacers (ITS) of the 18S-26S ribosomal DNA region are used as targets. Thus, the obtained sequences are aligned with those in curated reference databases to determine taxonomic classification. Three databases for bacterial sequence annotation are commonly used for this purpose: Greengenes, SILVA, and the Ribosomal Database Project (RDP). For fungi, the Unite database is the most commonly used.

When using shotgun metagenomics, all DNA present in the sample is extracted, fragmented, and sequenced, thus allowing the microbial biodiversity in soil (archaea, bacteria, eukaryotes, and viruses) to be characterised. Unlike metabarcoding methods, metagenomic shotgun sequencing allows the characterisation of the taxonomic and functional diversity of the soil sample microbiome. Although consolidated methodologies are available, the different steps from sampling to sample conservation to bioinformatic analysis are subject to biases that can lead to incorrect observations (Nearing *et al.*, 2021). For this reason, the standardisation of methodologies is necessary to implement risk analysis procedures with these technologies effectively (Debode *et al.*, 2024; Nearing *et al.*, 2021).

4. CHALLENGES IN THE MICROBIOME-BASED ASSESSMENT OF SOIL QUALITY

Characterising microbial community composition, diversity, and functional roles requires a series of methodological steps (Stefani *et al.*, 2015). Early culture-dependent approaches provided initial insights, but culture-independent methods, including plate profiling, now offer a far more comprehensive view of microbial assemblages and their ecological interactions (Davis *et al.*, 2005; Eichorst *et al.*, 2007; Cerqueira *et al.*, 2008; Schmidt and Eickhorst, 2014). These techniques have enabled the detailed characterisation of soil microbial communities in space and time and the assessment of their functional and trophic interactions (Philippot *et al.*, 2012; Cristescu, 2014). Numerous methods have been developed to inventory microbial species composition and to elucidate the dynamics and processes underlying biodiversity in bulk and rhizospheric soils (Philippot *et al.*, 2012; Cristescu, 2014), but their application in broad monitoring programmes remains challenging.

Despite rapid advances in NGS technologies, the integration of environmental microbiome data into risk assessment protocols remains limited by substantial knowledge gaps. Environmental microbiomes are highly dynamic and respond to perturbations, including contamination, over time. At the same time, soil microbial communities show heterogeneous distributions and complex spatial structure (Maron, 2011). In this context, identifying taxonomic markers that reliably reflect soil health is far from straightforward.

One increasingly popular approach in microbial ecology is to identify a core microbiome, defined as “any set of microbial taxa, as well as the associated genomic or functional attributes characteristic of a specific host or environment” (Neu *et al.*, 2021). Conceptually, the core microbiome represents the stable fraction of the community across niches, geographical locations, and time. Deviations from this baseline are expected to signal risk conditions associated with environmental stressors. However, there is still no consensus on how to designate a core microbiome in practice. Two main strategies are used: one based on taxonomic community composition and another based on functional profiles (Sharon *et al.*, 2022).

Taxonomy-based approaches rely on taxa detected by 16S rRNA gene sequencing and metagenomics. Methods based on taxon occurrence, abundance, or combined occurrence-abundance criteria have been proposed (Neu *et al.*, 2021), but they often identify different sets of core taxa (Custer *et al.*, 2023). In contrast, function-based approaches define the core microbiome as a stable functional core represented by functional-genetic categories. Here, variation in taxonomic composition is treated as secondary, under the assumption that multiple species can occupy the same niche and perform equivalent functions (Sharon *et al.*, 2022).

Computational tools such as PiCRUST, PiCRUST2, and Tax4Fun have been developed to infer functional profiles from metabarcoding data. Their usefulness in environmental applications, however, remains debated (Escalas, 2019). Their predictive power is constrained by reference genome databases that poorly represent soil microbiomes (Choi *et al.*, 2017) and are biased toward microorganisms relevant to human health (Sun *et al.*, 2020).

Shotgun metagenomics offers a more robust alternative, enabling simultaneous reconstruction of both the taxonomic composition and the functional contributions of individual taxa (Durazzi *et al.*, 2021). Detection of allelic variants of functional genes can indicate functional redundancy, a feature linked to ecological resilience and stability (Biggs *et al.*, 2020). Establishing standardised methods for defining the core microbiome is therefore essential for the development of microbiomebased environmental risk assessment protocols.

4.1. Biodiversity indices

Biodiversity indices derived from NGS data are widely used to characterise ecosystem status and to evaluate contaminant impacts on soil quality. Three main categories of indices, operating at different spatial scales, are commonly distinguished (Debode *et al.*, 2024; Lo, 2010):

- Alpha diversity indices, which measure species diversity within a local community.
- Beta diversity indices, which quantify differences in species composition between communities or ecosystems.
- Gamma diversity indices, which estimate overall diversity at broader scales, such as landscapes or biomes.

Environmental microbiology studies primarily employ alpha and beta diversity metrics. In the context of risk assessment, beta diversity measures effectively capture variation in species composition across samples. Conversely, applying alpha diversity metrics poses greater challenges. For instance, while dysbiosis in the human microbiota is typically associated with reduced alpha diversity (Debode *et al.*, 2024), the relationship between alpha diversity and ecosystem health is more complex in environmental contexts. Pesticides, for instance, can either stimulate or inhibit microbial growth (Lo, 2010). Thus, within environmental risk assessment, the assumption that higher biodiversity always signals better environmental health is not necessarily valid. However, alpha diversity metrics are relative values that depend strictly on the underlying methodology; consequently, they do not represent absolute biological truths, preventing direct comparisons across methods or scales (Shade, 2017). These indices are useful tools within a single comparative experimental design. However, they do not allow establishing an absolute threshold value (a normative cutoff) to be included in an assay. Different alpha diversity indices weight components of biodiversity—such as species richness, the relative abundance of rare versus dominant taxa, evenness, and phylogenetic related-

ness—differently. Consequently, the choice of index requires careful and explicit justification (Roswell *et al.*, 2021). Moreover, in our view, the inherently relative nature of alpha diversity makes it unsuitable for defining quantitative risk thresholds for environmental harm, which restricts its usefulness in environmental risk assessment (ERA).

5. A CASE STUDY OF TERRITORIAL ASSESSMENT OF ENVIRONMENTAL CONTAMINANTS

This case study presents a territorial monitoring approach to assess the occurrence of environmental contaminants in agricultural soils and organic amendments and their potential implications for soil quality. The assessment focuses on selected chemical contaminants, including heavy metals and polycyclic aromatic hydrocarbons (PAHs), analysed in soil and digestate matrices through standard physicochemical methods, and interpreted in relation to agricultural management practices and potential impacts on soil biological components.

The study is framed within intensively managed agroecosystems, where high external inputs and livestock-derived fertilisers may increase the risk of contaminant accumulation. This pressure has progressively degraded agroecosystems, with a severe acceleration in the last century, leading to reductions in soil fertility and in agricultural and natural biodiversity (Tilman *et al.*, 2002).

In this context, adopting sustainable soil management practices can help protect and restore ecosystem services generated by the rural system. Among these practices, the following can be considered particularly effective:

- The use of organic matrices (such as livestock effluents, digestates, *etc.*) to supply crops and soil biological components with nutritional elements and improve the physical characteristics of the soil.
- The application of conservative soil management practices to minimise disturbance to the soil ecosystem.
- The maintenance of a permanent vegetal cover on the soil through cover crops and crop residues.

This approach is even more crucial in areas characterised by a high livestock density, where integrated management strategies use all available organic matrices, in particular livestock effluents, which require efficient use in terms of quantity, timing, and distribution methods to limit environmental risks due to contamination (*e.g.*, with nitrate, phosphorus, heavy metals, and antibiotics). This is the case in the Lombardy Region in Italy, where agriculture plays a key role in the regional and national economy and is primarily characterised by heavy use of external inputs, modest crop diversification, and a high animal-based fertiliser load, resulting in a high risk of soil contamination.

In response to these challenges, regional authorities have since 2011 established a network of farms for environmental monitoring, focusing on assessing soil quality using selected physicochemical parameters. Continuous and structured monitoring within this network has been

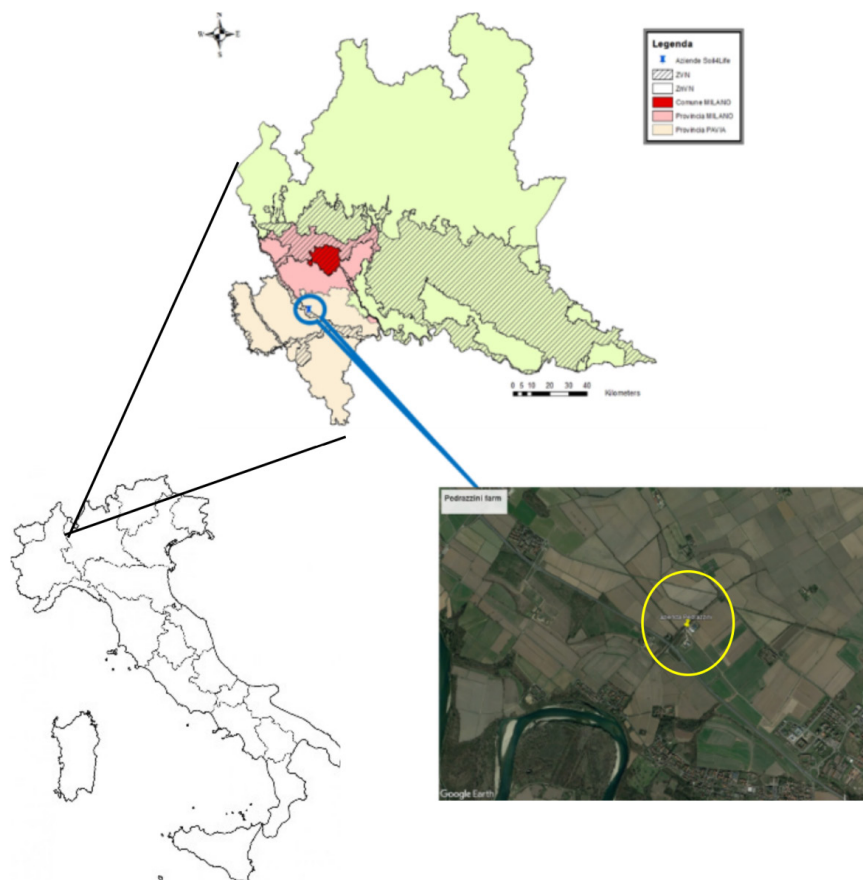


Fig. 1. Location of the study area.

Table 1. Physical-chemical characterisation of the farm soil: average values in the upper horizons

Year	Texture (%)			pH (H ₂ O)	TOC (g kg ⁻¹)	CEC (meq 100 g ⁻¹)	TKN (g kg ⁻¹)	N-NO ₃ (mg kg kg ⁻¹)	P ₂ O ₅ (mg kg kg ⁻¹)
	Sand	Silt	Clay						
2011	63	30	7	ND	8.67	ND	ND	ND	ND
2019	-	-	-	6.1	8.13	17.6	ND	ND	ND
2020	-	-	-	5.8	11.57	31.2	ND	ND	ND
2022	-	-	-	ND	11.72	ND	1.19	3.0	77.5
2023	67	21	12	6.9	11.60	20.0	1.42	12.5	86.0

ND – not determined.

conducted since 2019. Here, we present a representative case study of a farm located in the province of Pavia (southern Lombardy), illustrating typical agricultural management of the Lombard Plain, including cereal-based cropping systems (maize, barley, and rice), minimum tillage, and flood irrigation (Fig. 1).

Land use and agricultural management practices are the main factors that determine the monitoring strategy for evaluating the potential risk associated with anthropogenic activities. The monitoring plan defined the environmental matrices to be monitored (soil and digestates), the related physical-chemical parameters to be analysed (texture, pH, electrical conductivity (EC), total organic carbon (TOC), cation exchange capacity (CEC), CaCO₃, total Kjeldahl

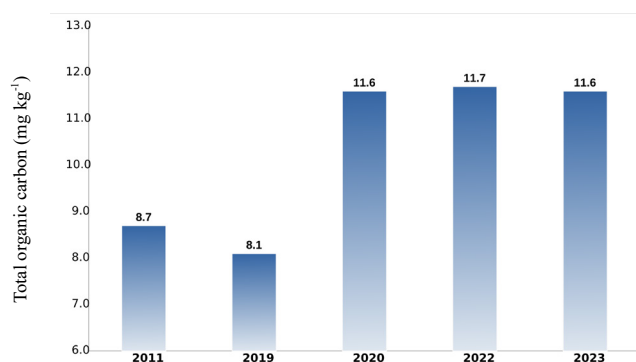
Nitrogen (TKN), N-NO₃, and P₂O₅), and the content of major contaminants (heavy metals and polycyclic aromatic hydrocarbons (PAHs)).

The soil was a sandy-sandy loam with a high skeleton content, subacid pH, a high CEC (>20), and a medium-low organic matter content (Table 1).

Organic fertilisation was performed using a zootechnical biodigestate (a mix of vegetable biomass and poultry manure processed by anaerobic digestion) characterised by high nutrient content (Table 2), distributed at pre-sowing (a solid fraction applied with a manure spreader) and during crop growth (a liquid fraction applied with low-pressure tankers).

Table 2. Chemical analyses of biodigestate samples

Digestate code	Year	Residue at 105°C	pH	Total N (%)	Total P	N-NH ₄	N-NO ₃
					(mg kg ⁻¹)		
PAPSR-PEDR_DL_2	2022	8.44	7.70	0.63	13 200	2 960	< 1
PAPSR-PEDR_DL_1	2023	13.41	7.92	0.62	16 100	3 410	< 1

**Fig. 2.** Average total organic carbon (TOC) content in the upper soil horizon of the farm soils.

The distribution of the biodigestate (first applied in 2018) contributed to an increase in the organic matter content observed in subsequent years (Fig. 2). The analysis of contaminant content in the same soil consistently yielded values below the limits set by the relevant Italian legislation (Legislative Decree 152/2006) (Tables 3 and 4). Specific PAH content was detected in only a few samples.

The results of this case study, which align with data collected from similar contexts in the region, indicate that the use of the biodigestate had a low impact on the risk of soil contamination with organic compounds. Such results suggest that the distribution of microbially processed animal-derived fertilisers can serve as a useful indicator for reducing the risk of soil contamination (see also below).

6. MEASURES TO REDUCE THE CONTAMINATION RISK AND LOAD IN SOIL

Microorganisms are critical to the breakdown of environmental contaminants (Sharma, 2021). To develop effective bioremediation strategies to degrade specific pollutants (Domeignoz-Horta *et al.*, 2021) and potentially create new bioremediation technologies, it is vital to isolate and cha-

racterise the mechanisms and metabolic pathways of fungi and bacteria that degrade these pollutants in soil (Barone *et al.*, 2024). While various studies have shown the potential of microorganisms for bioremediation purposes (Table 5), the factors that influence the effectiveness of bioremediation or contaminant degradation remain to be understood. The chemical composition of pollutants, the environmental conditions conducive to their degradation, the accessibility of microorganisms, and the microbial adaptability to varying conditions and metabolic versatility all affect biodegradation efficiency (Negri *et al.*, 2004). Furthermore, analysing the genetic potential of microbial communities in polluted environments helps reveal their metabolic capabilities. This information can subsequently inform the design of tailored bioremediation strategies (Bala *et al.*, 2022). Therefore, genomic and proteomic investigations can explore the genetic and enzymatic mechanisms underlying biodegradation, thereby promoting the development and implementation of bioremediation approaches across diverse environmental settings. These advanced techniques have already provided valuable insights into the genetic and enzymatic mechanisms associated with biodegradation (Chakraborty and Das, 2016), offering a holistic view of microbial communities and allowing researchers to unravel the complex metabolic pathways and enzymatic processes involved in the breakdown of contaminants (Zhang and Bennett, 2005; Sakshi and Haritash, 2020; Narayanan *et al.*, 2023). In addition, the ability of microorganisms to degrade specific pollutants, as well as their ecological roles and interactions within microbial consortia, shall be assessed. By elucidating the intricate web of microbial interactions, researchers can better understand how different microorganisms collaborate to enhance biodegradation processes.

Table 3. Average content of heavy metals in the farm soils after the biodigestate application

Year	As	Cd	Cr_tot	Hg	Ni	Pb	Cu	Zn
	(mg kg ⁻¹ d.w.)							
2019	5.28	0.160	19.21	0.148	13.64	26.1	13.09	41.6
2020	5.49	0.145	19.43	0.139	13.59	28.4	13.81	41.7
2023	5.50	0.095	18.55	N.D.	14.35	22.5	16.55	46.0
Legal limits	20	2	150	1	120	100	120	150

Table 4. Content of specific PAHs in the farm soils after the biodigestate application

Field	n.	Year	Benzo(a)_anthracene	Benzo(a)_pyrene	Benzo(b)_fluoranthene	Chrysene	Pyrene
(mg kg ⁻¹) d.w.							
A	1	2019	<0.01	<0.01	<0.01	<0.01	<0.01
	2		<0.01	<0.01	<0.01	<0.01	<0.01
	3		<0.01	<0.01	<0.01	<0.01	<0.01
B	1	2019	<0.01	<0.01	<0.01	<0.01	<0.01
	2		<0.01	<0.01	<0.01	<0.01	<0.01
	3		<0.01	<0.01	<0.01	<0.01	<0.01
C	1	2019	<0.01	<0.01	<0.01	<0.01	<0.01
	2		<0.01	<0.01	<0.01	<0.01	<0.01
	3		<0.01	<0.01	<0.01	<0.01	<0.01
A	1	2020	<0.01	<0.01	<0.01	<0.01	<0.01
	2		<0.01	<0.01	<0.01	<0.01	<0.01
	3		<0.01	<0.01	<0.01	<0.01	<0.01
B	1	2020	0.021	0.011	0.014	0.021	0.021
	2		<0.01	<0.01	<0.01	<0.01	<0.01
	3		0.014	<0.01	0.011	0.012	0.012
C	1	2020	<0.01	<0.01	<0.01	<0.01	<0.01
	2		<0.01	<0.01	<0.01	<0.01	<0.01
	3		<0.01	<0.01	<0.01	<0.01	<0.01
Legal limits			0.5	0.1	0.5	5	5

However, reducing the risk of introducing contaminants into agricultural soils can also be pursued by microbial-based processes applied to inputs that are potential contributors to soil contamination, *i.e.*, organic fertilising products, as described hereafter.

6.1. Antibiotics

Antibiotic concentrations can be reduced through processes such as biodegradation, transformation, and sorption. They can be pursued by exploiting fungal capacities to metabolise various compounds as carbon sources, and by exploiting non-specific enzymatic systems, including extracellular lignin-modifying enzymes (particularly laccase and various peroxidases) and intracellular enzymes (*e.g.*, the cytochrome P450 system) (Ghariani *et al.*, 2024). This oxidative potential could degrade micropollutants, which are typically resistant to natural breakdown processes, particularly in soil contamination (Table 6). However, the structure and physicochemical properties of antibiotics are key factors that determine the possible metabolic pathways for their degradation during biological treatment. For example, the tendency to adsorb onto particles can reduce their bioavailability (Wu *et al.*, 2009; Ingerslev *et al.*, 2001) and biodegradation rate, which can range from near-complete biodegradation (*e.g.*, macrolides) to very limited apparent removal (*e.g.*, fluoroquinolones), where sorption

to solid matrices plays a major role, reflecting differences in sorption behaviour and environmental conditions. In this regard, the characteristics of the specific animal manure (*i.e.*, C/N, total organic carbon content, moisture) or the modification of the physico-chemical conditions of the manure through the incorporation of bulking agents, to increase air circulation, modify pH, *etc.*, which promote the microbial activity, can modify the biodegradation rate, playing a significant role in the removal of antibiotics (Storteboom *et al.*, 2007). For example, the addition of sawdust, rice husk or spent mushroom growing substrate promoted the reduction in extractable antibiotic concentrations (by 14.9–33.4% in the case of swine manure, lower with chicken manure, where fluoroquinolones, a highly refractory group of antibiotics, are dominant), and decreased ARGs during the manure composting process (Zhang *et al.*, 2019a). Similarly, bamboo charcoal added during pig manure composting favoured a strong reduction in ciprofloxacin concentrations (up to 99%), likely reflecting a combination of biodegradation and sorption processes, and allowed decreases in the concentrations of norfloxacin and chlorotetracycline to levels below instrumental detection limits. Composting chicken manure with the addition of various inorganic compounds (zeolite, superphosphate, and ferrous sulphate together) altered the bacterial community and

Table 5. List of the principal genera of bacteria, microalgae and fungi showing bioremediation capacity

Genus	Reference
Bacteria	
<i>Alcaligenes</i>	Durán <i>et al.</i> (2019)
<i>Bacillus</i>	Wang <i>et al.</i> (2020)
<i>Enterobacter</i>	Ramasamy <i>et al.</i> (2017)
<i>Flavobacterium</i>	Chaudhary <i>et al.</i> (2019)
<i>Pseudomonas</i>	Pacwa-Płociniczak <i>et al.</i> (2014)
<i>Alcanivorax</i>	Yakimov <i>et al.</i> (2007)
<i>Thalassolituus</i>	Mahjoubi <i>et al.</i> (2017)
<i>Cycloclasticus</i>	Kasai <i>et al.</i> (2002)
<i>Oleispira</i>	Yakimov <i>et al.</i> (2003)
<i>Marinobacter</i>	Chernikova <i>et al.</i> (2020)
Microalgae/Cyanobacteria	
<i>Spirulina</i>	El-Sheekh and Hamouda (2014)
<i>Chlorella</i>	Kalhor <i>et al.</i> (2017)
<i>Spirogyra</i>	Nweze <i>et al.</i> (2009)
<i>Scenedesmus</i>	El-Sheekh <i>et al.</i> (2013)
<i>Oscillatoria</i>	Chavan <i>et al.</i> (2008)
<i>Chlorococcum</i>	Semple <i>et al.</i> (1999)
<i>Synechocystis</i>	Patel <i>et al.</i> (2015)
<i>Nannochloropsis</i>	Chernikova <i>et al.</i> (2020)
<i>Selenastrum</i>	Chan <i>et al.</i> (2006)
Fungi	
<i>Aspergillus</i>	Al-Hawash <i>et al.</i> (2019)
<i>Curvularia</i>	Balaji <i>et al.</i> (2014)
<i>Drechslera</i>	Obuekwe <i>et al.</i> (2005)
<i>Lasioidiplodia</i>	Wang <i>et al.</i> (2014)
<i>Mucor</i>	Su <i>et al.</i> (2006)
<i>Penicillium</i>	Govarthanan <i>et al.</i> (2017)
<i>Rhizopus</i>	Hasan (2014)
<i>Trichoderma</i>	Zafra <i>et al.</i> (2015)
<i>Cryptococcus</i>	Krallish <i>et al.</i> (2006)

ARGs: *Firmicutes*, the most important potential host bacteria for ARGs, were strongly reduced in the community after the addition of zeolite (Peng *et al.*, 2018).

In this context, it is important to distinguish between different processes contributing to the observed decrease in antibiotic concentrations (Fig. 3). Reported reductions may reflect true biodegradation or transformation. However, they may also result from other mechanisms, such as irreversible sorption to organic matter, reduced extractability, dilution during treatment, or partitioning between solid and liquid phases. For this reason, the term “removal” is used here to indicate the overall decrease in the extractable fraction, unless otherwise specified.

The method for processing the manure can also affect the efficacy of antibiotic degradation, as temperature and oxygen availability vary, thereby influencing microbial

activity. Generally, the biodegradation capacity of the manure management process is high during composting, lower during anaerobic digestion, and the lowest during manure storage and after application to the soil (Massé *et al.*, 2014). An optimised composting process (30 days for composting, reaching at least a temperature of 50°C, with the matrix water content of 50% and pH 9.0) reduced the level of antibiotics by about 30-78%, depending on the compound, and decreased the presence of ARGs and mobile genetic elements in the compost by 45 and 27%, respectively, and their relative abundance by about 35% (Lu and Lu, 2019).

Composting reduced antibiotic degradation from 47.3 to 98.8%, depending on the type of manure (*i.e.*, cattle, swine, poultry, and mixed manures) (Gaballah *et al.*, 2021). Biodegradation occurs mainly during the thermophilic phase, even at high initial concentrations (Zhang *et al.*, 2019b; Selvam *et al.*, 2013; Wang *et al.*, 2016). However, the intensity of the process can affect its outcome. Manures subjected to high-intensity processing (*i.e.*, with the addition of bulking agents, watering, and turning) promoted and sped up the biodegradation of antibiotic compounds belonging to various classes (chlortetracycline, tylosin, and monensin) more than low-intensity management (Storteboom *et al.*, 2007). Considering also that the persistence of several compounds (*i.e.*, erythromycin, roxithromycin, salinomycin, tetracycline, doxycycline, clindamycin, and clarithromycin) under anaerobic conditions was longer than under aerobic conditions (Schlüsener *et al.*, 2006), the degradation by aerobic microorganisms, fostered by aeration of the matrix obtained with turning, can be the major pathway to eliminate these compounds. This is supported by data about the metabolisation of oxytetracycline, which varied from 55-75% after anaerobic digestion to 85-99% after composting (Massé *et al.*, 2014), or of enrofloxacin (up to 74 %), ciprofloxacin, and doxycycline (90%) after composting poultry manure (Esperón *et al.*, 2020), chicken and broiler manures (Yang *et al.*, 2018; Slana *et al.*, 2017). These high removal rates after composting likely result from a combination of biodegradation, increased aerobic microbial activity, and sorption processes, which together decrease extractable antibiotic concentrations. Indeed, the half-life of chlortetracycline increased in the order composting > manure storage > soil (Massé *et al.*, 2014), while manure storage did not affect the biodegradation of tetracyclines and sulfadiazine (Chen *et al.*, 2012).

Although the effect of temperature on antibiotic removal is variable, it can be an important factor in their degradation. The observed seasonal variation in the degradation rates of tetracyclines and sulphonamides, higher in summer than in winter, aligns with the common increase in microbial activity during warm seasons (Liu *et al.*, 2018). Compounds of the tetracycline group (except doxycycline) and the sulphonamide group degrade easily at

Table 6. List of fungal species able to degrade antibiotics

Species name	Antibiotic contamination	Mechanism	Reference
<i>Aspergillus flavus</i>	Amoxicillin	Biodegradation	Mohammadi <i>et al.</i> (2021a, b)
<i>Aspergillus terreus</i> FZC3	Gentamicin	Biosorption and biodegradation	Liu <i>et al.</i> (2016)
<i>Cunninghamella elegans</i>	Flumequine	Biotransformation	WHO (2019)
<i>Ganoderma lucidum</i>	20 different antibiotics	Biodegradation	Salandez <i>et al.</i> (2022)
<i>Gloeophyllum striatum</i>	Ciprofloxacin, Enrofloxacin	Biodegradation and metabolite identification	WHO (2019)
<i>Irpex lacteus</i> sb, <i>Trametes versicolor</i>	Ciprofloxacin, Norfloxacin, Ofloxacin	Biodegradation	Čvančarová <i>et al.</i> (2015)
<i>Mucor ramannianus</i>	Enrofloxacin	Biotransformation	Picariello <i>et al.</i> (2022)
<i>Penicillium commune</i>	Oxytetracycline	Biodegradation	Ahumada-Rudolph <i>et al.</i> (2021)
<i>Epicoccum nigrum</i>			
<i>Trichoderma harzianum</i>			
<i>Aspergillus terreus</i>			
<i>Beauveria bassiana</i>			
<i>Penicillium oxalicum</i> RJJ-2	Erythromycin	Biodegradation	Ren <i>et al.</i> (2021)
<i>Penicillium restrictum</i>	Sulfamethoxazole, Erythromycin, Tetracycline	Biodegradation	Fakhri <i>et al.</i> (2021)
<i>Pestalotiopsis guepini</i>	Ciprofloxacin Norfloxacin	Biotransformation	Pan and Chu (2017)
<i>Pleurotus ostreatus</i>	Sulfonamides Tetracyclines	Biodegradation	Camacho-Arévalo <i>et al.</i> (2021)
<i>Pleurotus ostreatus</i>	Ciprofloxacin	Biodegradation	Sidhu <i>et al.</i> (2019)
<i>Pycnoporus sanguineus</i> , <i>Phanerochaete chrysosporium</i>	Ciprofloxacin	Biodegradation	Gao <i>et al.</i> (2018)
<i>Trametes polyzona</i>	Amoxicillin	Biodegradation	Lueangjaroenkit <i>et al.</i> (2019)
<i>Trametes versicolor</i>	Azithromycin	Bio-oxidation	Del Álamo <i>et al.</i> (2022)
<i>Trametes versicolor</i>	Azithromycin	Biodegradation	Tormo-Budowski <i>et al.</i> (2021)
<i>Trametes versicolor</i>	Cefalexin, Ciprofloxacin, Etracycline	Biodegradation	Badia-Fabregat <i>et al.</i> (2016)
<i>Trametes versicolor</i>	Ofloxacin	Biodegradation	Gao <i>et al.</i> (2018)
<i>Trametes versicolor</i>	Erythromycin, Ciprofloxacin, Azithromycin, Cefalexine	Biodegradation	Cruz-Morató <i>et al.</i> (2013)
<i>Trametes versicolor</i>	Norfloxacin Ciprofloxacin	Biodegradation	Patel <i>et al.</i> (2020)
<i>Trichoderma harzianum</i>	Clarithromycin	Biodegradation	Buchicchio <i>et al.</i> (2016)
<i>Trichoderma viride</i>	Ciprofloxacin Norfloxacin	Identification of degraded products	Picariello <i>et al.</i> (2022)

high temperatures. At the same time, fluoroquinolones have variable behaviour, and macrolides generally degrade at normal temperatures (Gaballah *et al.*, 2021).

The concentration and class of the antibiotic, as well as the bioreactor operating conditions, including the feedstock and inoculum type, affect the potential rate of antibiotic degradation, also in anaerobic digestion. Antibiotics found in pig and cattle farm manure were still detected in derived digestates, though at lower levels (Widyasari-Mehta *et al.*, 2016; Spielmeyer *et al.*, 2014, 2015). However, no biodegradation was observed for sulfadiazine and sulfamethizole after anaerobic digestion of pig manure, while erythromycin was clearly removed (up to 99% under thermophilic conditions) (Feng *et al.*, 2017). This could be accounted

for by anaerobic biotransformation and by irreversible sorption to the biodigestate. Sorption was considered the major removal pathway, indicating that apparent removal did not necessarily correspond to actual degradation (Wallace *et al.*, 2018).

Nevertheless, the mesophilic phase may be the best temperature regime for antibiotic biodegradation during anaerobic digestion. Mesophilic and thermophilic anaerobic digestion achieved higher chlortetracycline removal than psychrophilic operations, whereas only the thermophilic process enabled effective degradation of monensin (Massé *et al.*, 2014). However, the dilution factor must be taken into account when estimating the degradation potential, as biogas plants are also fed with other matrices that

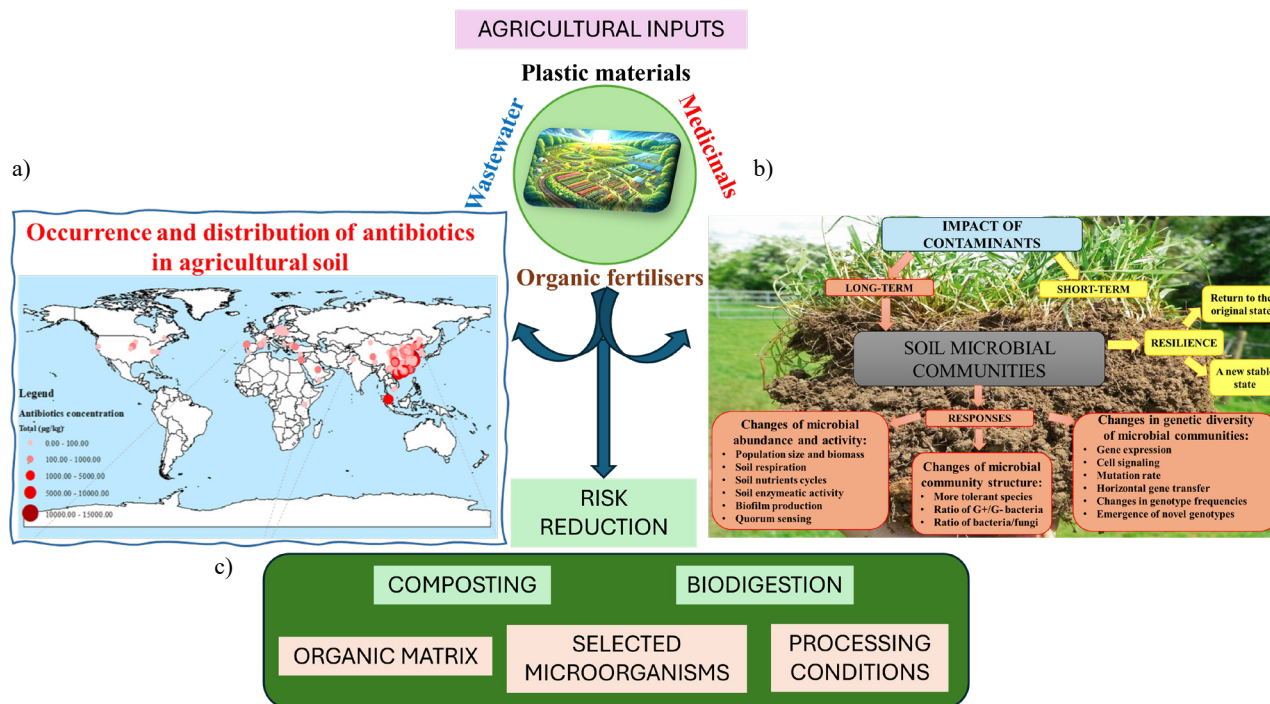


Fig. 3. Impact of various sources of contaminants on agriculture and the environment: a) distribution and occurrence of antibiotics in agricultural soils (source: Fang *et al.* 2023); b) effect of different types of contaminant accumulation on the soil microbiome; c) composting and biodigestion as possible methods to reduce the risk of contaminant accumulation in soil and factors affecting their efficacy.

do not contain antibiotics (e.g., maize silage) and because of the mass balance between the time the manure enters the digesters and the time of transfer of the biodigestate out.

As in the composting process, the origin of the matrix can affect residue detection: antibiotic residues were absent or present at lower levels when cattle manure was digested than when pig slurry was digested (Spielmeyer *et al.*, 2014). The removal efficiency of antibiotics during anaerobic digestion ranged from 17.8 to 100% for cattle manure and from 0 to 98% for swine manure, with an average of about 73% in both cases (Gaballah *et al.*, 2021). Integrating anaerobic digestion with proper manure handling and storage could improve antibiotic reduction (Gurmessa *et al.*, 2020). Introducing a sedimentation post-treatment of biogas slurry enabled separation of the solid fraction, which was composted and stored more effectively. It increased the removal of various antibiotics, particularly in summer (Jin *et al.*, 2016).

Promising methods tested for the degradation of antibiotics in animal-derived fertilising products include phytoremediation *via* artificially constructed wetlands, chemical oxidation, and electrochemical enhancement of microbial activity. Constructed wetlands are artificial systems that simulate natural wetlands and employ microbial biodegradation, rhizoremediation, and chemical degradation to remove antibiotics from wastewater (Nguyen *et al.*, 2019; McCorquodale-Bauer *et al.*, 2023). The various

constructed wetland systems can exhibit diverse efficiency in antibiotic removal: on average, the integrated wetland system has a removal capacity of about 72%, while surface-flow, vertical-flow, and horizontal-flow systems can achieve about 85, 95-98, and 95-98%, respectively (Gaballah *et al.*, 2021). Nevertheless, their removal capacity also varies by antibiotic group, generally in the following order: sulphonamides < fluoroquinolones < tetracyclines and macrolides, with average removal rates ranging from 77 to 92%, respectively. The differences in performance among these systems are due to the plant species used, the substrate and its aeration, and the wastewater characteristics. *Canna indica*, *Juncus effusus*, *Phragmites australis*, and *Thypha* sp. are the most frequent species utilised for phytoremediation, which are characterised by a long root system, suitable to promote rhizobacterial development (Gaballah *et al.*, 2020) and antibiotic accumulation in their tissues (Rosa *et al.*, 2019; Chung *et al.*, 2017). Substrates with small pore sizes (e.g., made of clay-rich or zeolite) performed better than other substrates (Liu *et al.*, 2019; Chen *et al.*, 2016). Chemical oxidation is another pathway that can reduce antibiotic contamination, eventually exploiting substances (e.g., polyphenols) obtained from the recycling of agri-food waste as catalysts. Ozonation or application of hydrogen peroxide, alone or in combination with a salt to increase desorption, allowed the removal of more than 90% of oxy-tetracyclines from cow manure (Uslu and Balcioglu, 2009).

Enhanced degradation of sulfamethazine within a short time was achieved in microbial electrochemical reactors, a system that improves microbial metabolism (Quejigo *et al.*, 2019). However, optimisation of these techniques is necessary before they can be adopted in practice.

6.2. Microplastics

Organic fertilisers may contribute to microplastic contamination in ecosystems (Nizzetto *et al.*, 2016; Athulya *et al.*, 2024). Even though the source and accumulation pathways of microplastics in agricultural soils due to fertilising practices are still limited (Corradini *et al.*, 2019; El Hayany *et al.*, 2022; Weithmann *et al.*, 2018; Yang *et al.*, 2021), no major impacts on the soil bio-physico-chemical properties were observed after long-term (22-year) application of a high amount of compost (Colombini *et al.*, 2022). The composting phases can significantly reduce, but never fully eliminate, microplastics from agri-food waste. Fertiliser samples from composting and anaerobic digestion plants contained different amounts of plastic particles, depending on substrate pretreatment (particularly sieving and sifting), waste type (*e.g.*, household versus commercial waste), or processing method (Weithmann *et al.*, 2018).

In this context, it is important to distinguish among the processes that affect the observed changes in microplastic abundance. Reductions may reflect physical removal, fragmentation into smaller particles, or changes in detectability, rather than true biodegradation of the polymer matrix. Changes in microplastic abundance and characteristics have been reported to be influenced by composting conditions (*e.g.*, temperature, enzymatic activity, and microbial communities) (Ali *et al.*, 2021; Gui *et al.*, 2021), although these effects do not necessarily indicate complete polymer degradation. Hyperthermophilic composting technology has been reported to enhance the reduction and transformation of microplastics in sewage sludge (Chen *et al.*, 2020), although some of this effect may be attributable to fragmentation and particle-size redistribution. The addition of biochar in the composting matrix significantly promoted the enrichment of microbial genera (*e.g.*, *Bacillus*, *Thermobacillus*, *Luteimonas*, *Chryseolinea*, and fungal genera such as *Aspergillus* and *Mycothermus*) that may be involved in microplastic transformation or degradation processes; however, their specific role in polymer breakdown requires further confirmation (Sun *et al.*, 2022).

Nevertheless, the knowledge gap regarding the contribution of organic fertilising products to soil contamination by microplastics and the efficacy of different processing methods requires further investigation, particularly to distinguish between physical removal, fragmentation, and true biodegradation of polymeric materials.

7. CONCLUSIONS

Maintaining and restoring soil health is a major, long-term endeavour that requires efforts from all sectors of society. The EU has embarked on a mission for soil (A Soil Deal for Europe), which is in line with several EU strategic documents and considered critical also for the successful implementation of all other missions launched in recent years: Climate adaptation mission, Cancer mission, Ocean mission, and Cities mission (EU Com, 2020). The link between soil and these other missions may not be obvious. Yet soils are not only the foundation of food systems, contributing to several ecosystem services, but also represent cultural heritage and support economic activity. Analysis of the soil microbiome can provide valuable insights into soil quality and its response to contamination. When integrated with chemical and physical assessments, it can support the evaluation of soil health and guide the development of strategies to reduce contamination risks associated with agricultural practices, thereby promoting more sustainable agriculture.

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8. REFERENCES

- Ahumada-Rudolph, R., Novoa, V., Becerra, J., Cespedes, C., Cabrera-Pardo, J.R., 2021. Mycoremediation of oxytetracycline by marine fungi mycelium isolated from salmon farming areas in the south of Chile. *Food Chem. Toxicol.* 152, 112198.
- Al-Hawash, A.B., Zhang, X., Ma, F., 2019. Removal and biodegradation of different petroleum hydrocarbons using the filamentous fungus *Aspergillus* sp. RFC-1. *Microbiologyopen* 8, e00619. <https://doi.org/10.1002/mbo3.619>
- Ali, S.S., Elsamahy, T., Al-Tohamy, R., Zhu, D.C., Mahmoud, Y., Koutra, E., *et al.*, 2021. Plastic wastes biodegradation: mechanisms, challenges and prospects. *Sci. Total Environ.* 780, 146590. <https://doi.org/10.1016/j.scitotenv.2021.146590>
- Allen, S., Allen, D., Karbalaee, S., Maselli, V., Walker, T.R., 2022. Micro(nano)plastics sources, fate, and effects: What we know after ten years of research. *J. Hazardous Mat. Advances* 6, 100057. <https://doi.org/10.1016/j.hazadv.2022.100057>
- Athulya, P.A., Waychal, Y., Rodriguez-Seijo, A., Devalla, S., Doss, C.G.P., Chandrasekaran, N., 2024. Microplastic interactions in the agroecosystems: Methodological advances and limitations in quantifying microplastics from agricultural soil. *Environ. Geochem. Health.* 46, 85.
- Badia-Fabregat, M., Lucas, D., Pereira, M.A., Alves, M.A., Pennanen, T., Fritze, H., *et al.*, 2016. Continuous fungal treatment of non-sterile veterinary hospital effluent: pharmaceuticals removal and microbial community assessment. *Appl. Microbiol. Biotechnol.* 100, 2401-2415.

- Bala, S., Garg, D., Thirumalesh, B.V., Sharma, M., Sridhar, K., Inbaraj, B.S., *et al.*, 2022. Recent strategies for bioremediation of emerging pollutants: A Review for a Green and Sustainable Environment. *Toxics* 10, 484. <https://doi.org/10.3390/toxics10080484>
- Balaji, V., Arulazhagan, P., Ebenezer, P., 2014. Enzymatic bioremediation of polyaromatic hydrocarbons by fungal consortia enriched from petroleum-contaminated soil and oil seeds. *J. Environ. Biol.* 35, 521–529. <https://doi.org/10.13140/2.1.1528.3846>
- Barone, G.D., Rodríguez-Seijo, A., Parati, M., Johnston, B., Erdem, E., Cernava, T., *et al.*, 2024. Harnessing photosynthetic microorganisms for enhanced bioremediation of microplastics: A comprehensive review. *Environ. Sci. Ecotechnol.* 20, 100407.
- Berg, G., Rybakova, D., Fischer, D., Cernava, T., Champomier Vergès, M.-C., *et al.*, 2020. Microbiome definition re-visited: old concepts and new challenges. *Microbiome* 8, 103. <https://doi.org/10.1186/s40168-020-00875-0>
- Biggs, C.R., Yeager, L.A., Bolser, D.G., Bonsell, C., Dichiera, A.M., Hou, Z., *et al.*, 2020. Does functional redundancy affect ecological stability and resilience? A review and meta-analysis. *Ecosphere* 11, e03184. <https://doi.org/10.1002/ecs2.3184>
- Blasing, M., Amelung, W., 2018. Plastics in soil: analytical methods and possible sources. *Sci. Total Environ.* 612, 422–435. <https://doi.org/10.1016/j.scitotenv.2017.08.086>
- Brandt, K.K., Amézquita, A., Backhaus, T., Boxall, A., Coors, A., Heberer, T., *et al.*, 2015. Ecotoxicological assessment of antibiotics: A call for improved consideration of microorganisms. *Environ. Int.* 85, 189–205. <https://doi.org/10.1016/j.envint.2015.09.013>
- Buchicchio, A., Bianco, G., Sofo, A., Masi, S., Caniani, D., 2016. Biodegradation of carbamazepine and clarithromycin by *Trichoderma harzianum* and *Pleurotus ostreatus* investigated by liquid chromatography - high-resolution tandem mass spectrometry (FTICR MS-IRMPD). *Sci. Total Environ.* 557–558, 733–739. <https://doi.org/10.1016/j.scitotenv.2016.03.119>
- Camacho-Arèvalo, R., Eymar, E., Gimez, A., Mayans, B., Antan-Herrero, R., Garcia-Delgado, C., 2021. Spent mushroom substrates as biofilter to reduce antibiotics (tetracyclines and sulfonamides) from wastewaters to be used in hydroponic cultures. In: III Int. Symp. Soilless Culture and Hydroponics: Innovation and Advanced Technology for Circular Horticulture 1321, 63–70.
- Cerqueira, L., Azevedo, N.F., Almeida, C., Jardim, T., Keevil, C.W., Vieira, M.J., 2008. DNA mimics for the rapid identification of microorganisms by fluorescence in situ hybridization (FISH). *Int. J. Mol. Sci.* 9, 1944–1960. <https://doi.org/10.3390/ijms9101944>
- Chakraborty, J., Das, S., 2016. Molecular perspectives and recent advances in microbial remediation of persistent organic pollutants. *Environ. Sci. Pollut. Res.* 23, 16883–16903. <https://doi.org/10.1007/s11356-016-6887-7>
- Chan, S., Luan, T., Wong, M., Tam, N., 2006. Removal and biodegradation of polycyclic aromatic hydrocarbons by *Selenastrum capricornutum*. *Environ. Toxicol. Chem.* 25, 1772–1779. <https://doi.org/10.1897/05-354R.1>
- Chaudhary, D.K., Kim, D.U., Kim, D., Kim, J., 2019. *Flavobacterium petrolei* sp. nov. a novel psychrophilic, diesel-degrading bacterium isolated from oil-contaminated Arctic. *Soil. Sci. Rep.* 9, 4134. <https://doi.org/10.1038/s41598-019-40667-7>
- Chavan, A., Mukherji, S., 2008. Treatment of hydrocarbon-rich wastewater using oil degrading bacteria and phototrophic microorganisms in rotating biological contactor: Effect of N:P ratio. *J. Hazard. Mater.* 154, 63–72. <https://doi.org/10.1016/j.jhazmat.2007.09.106>
- Chen, H., Gao, B., Li, Y., 2025. Soil pollution and remediation: emerging challenges and innovations. *Frontiers in Environ. Sci.* 13, 1606054. <https://doi.org/10.3389/fenvs.2025.1606054>
- Chen, J., Ying, G., Wei, X., Liu, Y., Liu, S., Hu, L., *et al.*, 2016. Removal of antibiotics and antibiotic resistance genes from domestic sewage by constructed wetlands: Effect of flow configuration and plant species. *Sci. Total Environ.* 571, 974–982. <https://doi.org/10.1016/j.scitotenv.2016.07.085>
- Chen, Y., Zhang, H., Luo, Y., Song, J., 2012. Occurrence and assessment of veterinary antibiotics in swine manures: A case study in east China. *Chin. Sci. Bull.* 57, 606–614. <https://doi.org/10.1007/s11434-011-4830-3>
- Chen, Z., Zhao, W.Q., Xing, R.Z., Xie, S.G., Yang, X.G., Gui, P., *et al.*, 2020. Enhanced in situ biodegradation of microplastics in sewage sludge using hyperthermophilic composting technology. *J. Hazard. Mater.* 384, 121271. <https://doi.org/10.1016/j.jhazmat.2019.121271>
- Chernikova, T.N., Bargiela, R., Toshchakov, S.V., Shivaraman, V., Lunev, E.A., Yakimov, M.M., *et al.*, 2020. Hydrocarbon-degrading bacteria *alcanivorax* and *marinobacter* associated with microalgae *Pavlova lutheri* and *Nannochloropsis oculata*. *Front. Microbiol.* 11, 572931. <https://doi.org/10.3389/fmicb.2020.572931>
- Choi, J., Yang, F., Stepanauskas, R., Cardenas, E., Garoutte, A., Williams, R., *et al.*, 2017. Strategies to improve reference databases for soil microbiomes. *ISME J.* 11, 829–834. <https://doi.org/10.1038/ismej.2016.168>
- Chung, H.S., Lee, Y., Rahman, M.M., Abd El-Aty, A.M., Lee, H.S., Kabir, *et al.*, 2017. Uptake of the veterinary antibiotics chlortetracycline, enrofloxacin, and sulphathiazole from soil by radish. *Sci. Total Environ.* 605–606, 322–331. <https://doi.org/10.1016/j.scitotenv.2017.06.231>
- Colombini, G., Rumpel, C., Houot, S., Biron, P., Dignac, M.F., 2022. A long-term field experiment confirms the necessity of improving biowaste sorting to decrease coarse microplastic inputs in compost amended soils. *Environ. Pollution* 315, 120369. <https://doi.org/10.1016/j.envpol.2022.120369>
- Corradini, F., Meza, P., Eguiluz, R., Casado, F., Huerta-Lwanga, E., Geissen, V., 2019. Evidence of microplastic accumulation in agricultural soils from sewage sludge disposal. *Sci. Total Environ.* 671, 411–420. <https://doi.org/10.1016/j.scitotenv.2019.03.368>
- Correia, A.A.S., Rasteiro, M.G., 2025. A review of persistent soil contaminants: assessment and remediation strategies. *Environments* 12, 229. <https://doi.org/10.3390/environments12070229>
- Cristescu, M.E., 2014. From barcoding single individuals to meta-barcoding biological communities: towards an integrative approach to the study of global biodiversity. *Trends Ecol. Evol.* 29, 566–571. <https://doi.org/10.1016/j.tree.2014.08.001>
- Cruz-Morató, C., Ferrando-Climent, L., Rodríguez-Mozaz, S., Barceló, D., Marco-Urrea, E., Vicent, T., *et al.*, 2013.

- Degradation of pharmaceuticals in non-sterile urban wastewater by *Trametes versicolor* in a fluidized bed bioreactor. *Water Res.* 47, 5200-5210.
- Custer, G.F., Gans, M., van Diepen, L.T.A., Dini-Andreote, F., Buerkle, C.A., 2023. Comparative analysis of core microbiome assignments: Implications for Ecological Synthesis. *mSystems* 8, e01066-22. <https://doi.org/10.1128/mSystems.01066-22>
- Cusworth, S.J., Davies, W.J., McAinsh, M.R., Gregory, A.S., Storkey, J., Stevens, C.J., 2024. Agricultural fertilisers contribute substantially to microplastic concentrations in UK soils. *Commun Earth Environ.* 5, 7. <https://doi.org/10.1038/s43247-023-01172-y>
- Čvančarová, M., Moeder, M., Filipová, A., Cajthaml, T., 2015. Biotransformation of fluoroquinolone antibiotics by ligninolytic fungi-metabolites, enzymes, and residual antibacterial activity. *Chemosphere* 136, 311-320.
- Cycoń, M., Mroziński, A., Piotrowska-Seget, Z., 2019. Antibiotics in the soil environment-degradation and their impact on microbial activity and diversity. *Frontiers Microbiology* 10, 338.
- Davis, K.E.R., Joseph, S.J., Janssen, P.H., 2005. Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria. *Appl. Environ. Microbiol.* 71, 826-834. <https://doi.org/10.1128/AEM.71.2.826-834.2005>
- Debode, F., Caulier, S., Demeter, S., Dubois, B., Gelhay, V., Hulin, J., *et al.*, 2024. Roadmap for the integration of environmental microbiomes in risk assessments under EFSA's remit. *EFSA Supporting Publications* 21, 8602E. <https://doi.org/10.2903/sp.efsa.2024.EN-8602>
- Del Álamo, A.C., Pariente, M.I., Molina, R., Martínez, F., 2022. Advanced bio-oxidation of fungal mixed cultures immobilized on rotating biological contactors for the removal of pharmaceutical micropollutants in a real hospital wastewater. *J. Hazard Mater.* 425, 128002.
- Domeignoz-Horta, L.A., Shinfuku, M., Junier, P., Poirier, S., Verrecchia, E., Sebag, D., *et al.*, 2021. Direct evidence for the role of microbial community composition in the formation of soil organic matter composition and persistence. *ISME Commun.* 1, 64. <https://doi.org/10.1038/s43705-021-00071-7>
- Durán, R.E., Méndez, V., Rodríguez-castro, L., Barra-sanhueza, B., Salvà-serra, F., Moore, E.R.B., *et al.* 2019. Genomic and physiological traits of the marine bacterium *Alcaligenes aquatilis* QD168 isolated from Quintero Bay, Central Chile, reveal a robust adaptive response to environmental stressors. *Front. Microbiol.* 10, 528. <https://doi.org/10.3389/fmicb.2019.00528>
- Durazzi, F., Sala, C., Castellani, G., Manfreda, G., Remondini, D., De Cesare, A., 2021. Comparison between 16S rRNA and shotgun sequencing data for the taxonomic characterisation of the gut microbiota. *Sci. Rep.* 11, 3030. <https://doi.org/10.1038/s41598-021-82726-y>
- Eichorst, S.A., Breznák, J.A., Schmidt, T.M., 2007. Isolation and characterization of soil bacteria that define *Terriglobus* gen. nov. in the phylum Acidobacteria. *Appl. Environ. Microbiol.* 73, 2708-2717. <https://doi.org/10.1128/AEM.02140-2146>
- El Hayany, B., Rumpel, C., Hafidi, M., El Fels, L., 2022. Occurrence, analysis of microplastics in sewage sludge and their fate during composting: a literature review. *J. Environ. Manag.* 317, 115364. <https://doi.org/10.1016/j.jenvman.2022.115364>
- El-Sheekh, M.M., Hamouda, R.A., 2014. Biodegradation of crude oil by some cyanobacteria under heterotrophic conditions. *Desalin. Water Treat.* 52, 1448-1454. <https://doi.org/10.1080/019443994.2013.794008>
- El-Sheekh, M.M., Hamouda, R.A., Nizam, A.A., 2013. Biodegradation of crude oil by *Scenedesmus obliquus* and *Chlorella vulgaris* growing under heterotrophic conditions. *Int. Biodeterior. Biodegrad.* 82, 67-72. <https://doi.org/10.1016/j.ibiod.2012.12.015>
- Escalas, A., Hale, L., Voordeckers, J.W., Yang, Y., Firestone, M.K., Alvarez-Cohen, L., *et al.*, 2019. Microbial functional diversity: From concepts to applications. *Ecology Evolution* 9, 12000-12016. <https://doi.org/10.1002/ece3.5670>
- Esperón, F., Alberó, B., Ugarte-Ruiz, M., Domínguez, L., Carballo, M., Tadeo, J.L., *et al.*, 2020. Assessing the benefits of composting poultry manure in reducing antimicrobial residues, pathogenic bacteria, and antimicrobial resistance genes: a field-scale study. *Environ. Sci. Pollution Res.* 27, 27738-27749. <https://doi.org/10.1007/s11356-020-09097-1>
- European Commission, 2006. Thematic Strategy for Soil Protection. COM (2006) 231.
- European Commission, 2020. European Missions: A Soil Deal for Europe - Implementation Plan. URL https://research-and-innovation.ec.europa.eu/document/download/1517488c-767a-4f47-94a0-bd22197d18fa_en?filename=soil_mission_implementation_plan_final.pdf.
- European Environment Agency, 2017. Landscapes in transition. An account of 25 years of land cover change in Europe. EEA Report No. 10/2017, Copenhagen.
- European Medicines Agency, 2023. Sales of veterinary antimicrobial agents in 31 European countries in 2022. European Medicines Agency. URL https://www.ema.europa.eu/en/documents/report/sales-veterinary-antimicrobial-agents-31-european-countries-2022-trends-2010-2022-thirteenth-esvac-report_en.pdf.
- Fakhri, H., Shahi, A., Ovez, S., Aydin, S., 2021. Bioaugmentation with immobilized endophytic *Penicillium restrictum* to improve quorum quenching activity for biofouling control in an aerobic hollow-fiber membrane bioreactor treating antibiotic-containing wastewater. *Ecotoxicol. Environ. Saf.* 210, 111831.
- Fang, H., Han, Y., Yin, Y., Pan, X., Yu, Y., 2014. Variations in dissipation rate, microbial function and antibiotic resistance due to repeated introductions of manure containing sulfadiazine and chlortetracycline to soil. *Chemosphere* 96, 51-56. <https://doi.org/10.1016/j.chemosphere.2013.07.016>
- Fang, L., Chen, C., Li, S., Ye, P., Shi, Y., Sharma, G., *et al.*, 2023. A comprehensive and global evaluation of residual antibiotics in agricultural soils: Accumulation, potential ecological risks, and attenuation strategies. *Ecotoxicology Environ. Safety* 262, 115175. <https://doi.org/10.1016/j.ecoenv.2023.115175>
- FAO, 2021. Assessment of agricultural plastics and their sustainability: A call for action. Food and Agriculture Organization of the United Nations, Rome.
- FAO, ITPS, 2015. Status of the World's Soil Resources (SWSR) – Technical Summary. Food and Agriculture Organization of the United Nations and Intergovernmental Technical Panel on Soils, Rome, Italy.
- FAO, UNEP, 2021. Global Assessment of Soil Pollution: Report. FAO, Rome. <https://doi.org/10.4060/cb4894en>

- Feng, L., Escolà Casas, M., Mørck Ottosen, L.D., Bjarne Møller, H., Bester, K., 2017. Removal of antibiotics during the anaerobic digestion of pig manure. *Sc. of The Total Environ.* 603-604, 219-225. <https://doi.org/10.1016/j.scitotenv.2017.05.280>
- Gaballah, M.S., Abdelwahab, O., Barakat, K.M., Aboagye, D., 2020. A novel horizontal subsurface flow constructed wetland planted with *Typha angustifolia* for treatment of polluted water. *Environ. Sci. Pollut. Res.* 27, 28449-28462. <https://doi.org/10.1007/s11356-020-08669-5>
- Gaballah, M.S., Guo, J., Sun, H., Aboagye, D., Sobhi, M., Muhmood, A., Dong, R., 2021. A review targeting veterinary antibiotics removal from livestock manure management systems and future outlook. *Bioresource Technology* 333, 125069. <https://doi.org/10.1016/j.biortech.2021.125069>
- Gao, N., Liu, C.X., Xu, Q.M., Cheng, J.S., Yuan, Y.J., 2018. Simultaneous removal of ciprofloxacin, norfloxacin, sulfamethoxazole by co-producing oxidative enzymes system of *Phanerochaete chrysosporium* and *Pycnoporus sanguineus*. *Chemosphere* 195, 146-155.
- Gao, X., Hassan, I., Peng, Y.T., Huo, S.L., Ling, L., 2021. Behaviors and influencing factors of the heavy metals adsorption onto microplastics: a review. *J. Clean. Prod.* 319, 128777. <https://doi.org/10.1016/j.jclepro.2021.128777>
- Ghariani, B., Alessa, A.H., Ben Atitallah, I., Louati, I., Alsaigh, A.A., Mechichi, T., Zouari-Mechichi, H., 2024. Fungal bioremediation of the β -Lactam antibiotic ampicillin under laccase-induced conditions. *Antibiotics (Basel)*, 13, 407. <https://doi.org/10.3390/antibiotics13050407>
- Gillings, M.R., 2013. Evolutionary consequences of antibiotic use for the resistome, mobilome and microbial pangenome. *Front. Microbiol.* 4, 4.
- Giovannetti, M., Salvioli di Fossalunga, A., Stringlis, I.A., Proietti, S., Fiorilli, V., 2023. Unearthing soil-plant-microbiota crosstalk: Looking back to move forward. *Front. Plant Sci.* 13. <https://doi.org/10.3389/fpls.2022.1082752>
- Govarthanan, M., Fuzisawa, S., Hosogai, T., Chang, Y.C., 2017. Biodegradation of aliphatic and aromatic hydrocarbons using the filamentous fungus *Penicillium* sp. CHY-2 and characterization of its manganese peroxidase activity. *RSC Adv.* 7, 20716-20723. <https://doi.org/10.1039/C6RA28687A>
- Gui, J.X., Sun, Y., Wang, J.L., Chen, X., Zhang, S.C., Wu, D.L., 2021. Microplastics in composting of rural domestic waste: abundance, characteristics, and release from the surface of macroplastics. *Environ. Pollut.* 274, 116553. <https://doi.org/10.1016/j.envpol.2021.116553>
- Gurmesa, B., Pedretti, E.F., Cocco, S., Corti, G., 2020. Manure anaerobic digestion effects and the role of pre- and post-treatments on veterinary antibiotics and antibiotic resistance genes removal efficiency. *Sci. Total Environ.* 137532. <https://doi.org/10.1016/j.scitotenv.2020.137532>
- Hartmann, M., Six, J., 2023. Soil structure and microbiome functions in agro-ecosystems. *Nat. Rev. Earth Environ.* 4, 4-18. <https://doi.org/10.1038/s43017-022-00366-w>
- Hasan, I.F., 2014. Biodegradation of Kerosene by *Aspergillus niger* and *Rhizopus stolonifer*. *J. Appl. Environ. Microbiol.* 2, 31-36. <https://doi.org/10.12691/jaem-2-1-7>
- He, S., Wei, Y., Yang, C., He, Z., 2022. Interactions of microplastics and soil pollutants in soil-plant systems. *Environ. Pollut.* 315, 120357. <https://doi.org/10.1016/j.envpol.2022.120357>
- Ingerslev, F., Halling-Sorensen, B., . Biodegradability of metronidazole, olaquinox, and tylosin and formation of tylosin degradation products in aerobic soil-manure slurries. *Ecotoxicol. Environ. Safety* 48, 311-320. <https://doi.org/10.1006/eesa.2000.2026>
- Jin, H.M., Huang, H.Y., Guan, Y.X., Xu, C.Y., Chang, Z.Z., Quian, Y.T., 2016. Characteristics of degradation tetracyclines and sulfonamides during wastewater treating processes in an intensive swine farm. *J. Ecol. Nat. Environ.* 32, 978-985.
- Jones, B.A., Grace, D., Kock, R., Alonso, S., Rushton, J., Said, M.Y., *et al.*, 2013. Zoonosis emergence linked to agricultural intensification and environmental change. *Proc. Natl. Acad. Sci. USA* 110, 8399-8404.
- Kalhor, A.X., Movafeghi, A., Mohammadi-Nassab, A.D., Abedi, E., Bahrami, A., 2017. Potential of the green alga *Chlorella vulgaris* for biodegradation of crude oil hydrocarbons. *Mar. Pollut. Bull.* 123, 286-290. <https://doi.org/10.1016/j.marpolbul.2017.08.045>
- Kasai, Y., Kishira, H., Harayama, S., 2002. Bacteria belonging to the genus *Cyclocasticus* play a primary role in the degradation of aromatic hydrocarbons released in a marine environment. *Appl. Environ. Microbiol.* 68, 5625-5633. <https://doi.org/10.1128/AEM.68.11.5625-5633.2002>
- Krallish, I., Gonta, S., Savenkova, L., Bergauer, P., Margesin, R., 2006. Phenol degradation by immobilized cold-adapted yeast strains of *Cryptococcus terreus* and *Rhodotorula creatinivora*. *Extremophiles* 10, 441-449. <https://doi.org/10.1007/s00792-006-0517-0>
- Li, J., Zhang, K., Zhang, H., 2018. Adsorption of antibiotics on microplastics. *Environ. Pollut.* 237, 460-467. <https://doi.org/10.1016/j.envpol.2018.02.050>
- Li, X., Bickel, S., Wicaksono, W.A., Lin, X., Berg, G., Zhu, Y., 2025. Unraveling antibiotic resistance dynamics at the soil-plant interface under climate change for One Health. *One Health Adv.* 3, 16. <https://doi.org/10.1186/s44280-025-00081-3>
- Li, Y., Li, R., Hou, J., Sun, X., Wang, Y., Li, L., *et al.*, 2024a. Mobile genetic elements influence the dissemination of clinically important antibiotic resistance genes (ARGs) in the environment. *Environ. Res.* 243, 117801. <https://doi.org/10.1016/j.envres.2023.117801>
- Li, Y., Shi, X., Zeng, M., Qin, P., Fu, M., Luo, S., *et al.*, 2024b. Effect of polyethylene microplastics on antibiotic resistance genes: A comparison based on different soil types and plant types. *J. Hazardous Materials* 472, 134581. <https://doi.org/10.1016/j.jhazmat.2024.134581>
- Liu, H., Pu, C., Yu, X., Sun, Y., Chen, J., 2018. Removal of tetracyclines, sulfonamides, and quinolones by industrial-scale composting and anaerobic digestion processes. *Environ. Sci. Pollut. Res.* 25, 35835-35844. <https://doi.org/10.1007/s11356-018-1487-3>
- Liu, L., Liu, Y.-H., Liu, C.-X., Huang, X., 2016. Accumulation of antibiotics and tet resistance genes from swine wastewater in wetland soils. *Environ. Eng. Manag. J.* 15, 2137-2145. <https://doi.org/10.30638/eemj.2016.231>
- Liu, X., Guo, X., Liu, Y., Lu, S., Xi, B., Zhang, J., *et al.*, 2019. A review on removing antibiotics and antibiotic resistance genes from wastewater by constructed wetlands: Performance and microbial. *Environ. Pollut.* 254, 112996. <https://doi.org/10.1016/j.envpol.2019.112996>
- Lo, C.-C., 2010. Effect of pesticides on soil microbial community. *J. Environ. Sci. Health, Part B* 45, 348-359. <https://doi.org/10.1080/03601231003799804>

- Lu, X.M., Lu, P.Z., 2019. Synergistic effects of key parameters on the fate of antibiotic resistance genes during swine manure composting. *Environ. Pollution* 252, 1277-1287. <https://doi.org/10.1016/j.envpol.2019.06.073>
- Lu, X.M., Lu, P.Z., Liu, X.P., 2020. Fate and abundance of antibiotic resistance genes on microplastics in facility vegetable soil. *Sci. Tot. Environ.* 709, 136276. <https://doi.org/10.1016/j.scitotenv.2019.136276>
- Lueangaroenkit, P., Teerapatsakul, C., Sakka, K., Sakka, M., Kimura, T., Kunitake, E., *et al.*, 2019. Two manganese peroxidases and a laccase of *Trametes polyzona* KU-RNW027 with novel properties for dye and pharmaceutical product degradation in a redox mediator-free system. *Mycobiology* 47, 217-229.
- Ma, F., Wang, C., Zhang, Y., Chen, J., Xie, R., Sun, Z., 2022. Development of microbial indicators in ecological systems. *Int. J. Environ. Res. Public Health* 19, 13888.
- Mahjoubi, M., Cappello, S., Souissi, Y., Jaouani, A., Cherif, A., 2017. Microbial bioremediation of petroleum hydrocarbon contaminated marine environments. In: *Recent Insights in Petroleum Science and Engineering*. IntechOpen, 326-350. <https://doi.org/10.5772/intechopen>
- Maron, P.-A., Mougél, C., Ranjard, L., 2011. Soil microbial diversity: Methodological strategy, spatial overview and functional interest. *Comptes Rendus Biologies* 334, 403-411. <https://doi.org/10.1016/j.crv.2010.12.003>
- Martínez-Carballo, E., González-Barreiro, C., Scharf, S., Gans, O., 2007. Environmental monitoring study of selected veterinary antibiotics in animal manure and soils in Austria. *Environ. Pollut.* 148, 570-579. <https://doi.org/10.1016/j.envpol.2006.11.035>
- Massé, D.I., Cata Saady, N.M., Gilbert, Y., 2014. Potential of biological processes to eliminate antibiotics in livestock manure: An Overview. *Animals* 4, 146-163. <https://doi.org/10.3390/ani4020146>
- McCorquodale-Bauer, K., Grosshans, R., Zvomuya, F., Cicek, N., 2023. Critical review of phytoremediation for the removal of antibiotics and antibiotic resistance genes in wastewater. *Sci. Total Environ.* 870, 161876. <https://doi.org/10.1016/j.scitotenv.2023.161876>
- Meena, M., Yadav, G., Sonigra, P., Nagda, A., Mehta, T., Swapnil, P., *et al.*, 2023. Multifarious responses of forest soil microbial community toward climate change. *Microb. Ecol.* 86, 49-74. <https://doi.org/10.1007/s00248-022-02051-3>
- Meng, S., Zhang, Z., 2025. Effects of microplastics on soil environment and land plant growth: a review. *Environ. Monit. Assess.* 197, 861. <https://doi.org/10.1007/s10661-025-14316-8>
- Miller, S.A., Ferreira, J.P., Lejeune, J.T., 2022. Antimicrobial use and resistance in plant agriculture: a one health perspective. *Agriculture* 12, 1-27. <https://doi.org/10.3390/agriculture12020289>
- Mohammadi, M., Gheibi, M., Fathollahi-Fard, A.M., Eftekhari, M., Kian, Z., Tian, G., 2021. A hybrid computational intelligence approach for bioremediation of amoxicillin based on fungus activities from soil resources and aflatoxin B1 controls. *J. Environ. Manag.* 299, 113594.
- Murray, L.M., Hayes, A., Snape, J., Kasprzyk-Hordern, B., Gaze, W.H., Murray, A.K., 2024. Co-selection for antibiotic resistance by environmental contaminants. *npj Antimicrobials Resistance* 2, 9. <https://doi.org/10.1038/s44259-024-00026-7>
- Narayanan, M., Ali, S.S., El-Sheekh, M., 2023. A comprehensive review on the potential of microbial enzymes in multipollutant bioremediation: Mechanisms, challenges, and future prospects. *J. Environ. Manag.* 334, 117532. <https://doi.org/10.1016/j.jenvman.2023.117532>
- Nearing, J.T., Comeau, A.M., Langille, M.G.I., 2021. Identifying biases and their potential solutions in human microbiome studies. *Microbiome* 9, 113. <https://doi.org/10.1186/s40168-021-01059-0>
- Negri, M., Manfredini, A., Saponaro, S., Sorlini, C., Bonomo, L., Valle, A., *et al.*, 2004. Solid phase treatment of an aged soil contaminated by polycyclic aromatic hydrocarbons. *J. Environ. Sci. Health, Part A* 39, 1-17. <https://doi.org/10.1081/ESE-120027365>
- Neu, A.T., Allen, E.E., Roy, K., 2021. Defining and quantifying the core microbiome: Challenges and prospects. *Proc. National Academy of Sciences* 118, e2104429118. <https://doi.org/10.1073/pnas.2104429118>
- Nguyen, H.T.T., Chao, H.R., Chen, K.C., 2019. Treatment of organic matter and tetracycline in water by using constructed wetlands and photocatalysis. *Appl. Sci.* 9, 1-16. <https://doi.org/10.3390/app9132680>
- Ni, B., Xiao, L., Lin, D., Zhang, T., Zhang, Q., Liu, Y., *et al.*, 2025. Increasing pesticide diversity impairs soil microbial functions. *Proc. Natl. Acad. Sci. U.S.A.* 122, e2419917122. <https://doi.org/10.1073/pnas.2419917122>
- Nizzetto, L., Futter, M., Langaas, S., 2016. Are agricultural soils dumps for microplastics of urban origin? *Environ. Sci. Technol.* 50, 10777-10779. <https://doi.org/10.1021/acs.est.6b04140>
- Nweze, N., Aniebonam, C., 2009. Bioremediation of petroleum products impacted freshwater using locally available algae. *Bio-Research* 7, 484-490. <https://doi.org/10.4314/br.v7i1.45477>
- Obuekwe, C., Badrudeen, A.M., Al-Saleh, E., Mulder, J.L., 2005. Growth and hydrocarbon degradation by three desert fungi under conditions of simultaneous temperature and salt stress. *Int. Biodeter. Biodegrad.* 56, 197-205. <https://doi.org/10.1016/j.ibiod.2005.05.005>
- Osman, A.I., Hosny, M., Eltaweil, A.S., Omar, S., Elgarahy, A.M., Farghali, M., *et al.*, 2023. Microplastic sources, formation, toxicity and remediation: a review. *Environ. Chem. Lett.* 21, 2129-2169. <https://doi.org/10.1007/s10311-023-01593-3>
- Pacwa-Płociniczak, M., Plaza, G.A., Poliwoda, A., Piotrowska-Seget, Z., 2014. Characterization of hydrocarbon-degrading and biosurfactant-producing *Pseudomonas* sp. P-1 strain as a potential tool for bioremediation of petroleum-contaminated soil. *Environ. Sci. Pollut. Res.* 21, 9385-9395. <https://doi.org/10.1007/s11356-014-2872-1>
- Pan, M., Chu, L.M., 2017. Fate of antibiotics in soil and their uptake by edible crops. *Sci. Total Environ.* 599, 500-512. <https://doi.org/10.1016/j.scitotenv.2017.04.214>
- Patel, H., Calip, G.S., DiDomenico, R.J., Schumock, G.T., Suda, K.J., Lee, T.A., 2020. Prevalence of cardiac risk factors in patients prescribed azithromycin before and after the 2012 FDA warning on the risk of potentially fatal heart rhythms. *Pharmacotherapy* 40, 107-115.
- Patel, J.G., Kumar, J.I.N., Kumar, R.N., Khan, S.R., 2015. Enhancement of pyrene degradation efficacy of

- Synechocystis* sp. by construction of an artificial microalgal-bacterial consortium. *Cogent Chem.* 1, 1064193. <https://doi.org/10.1080/23312009.2015.1064193>
- Peng, S., Li, H.J., Song, D., Lin, X.G., Wang, Y.M., 2018. Influence of zeolite and superphosphate as additives on antibiotic resistance genes and bacterial communities during factory-scale chicken manure composting. *Bioresour. Technol.* 263, 393-401. <https://doi.org/10.1016/j.biortech.2018.04.107>
- Pereira, P., Bogunovic, I., Muñoz-Rojas, M., Brevik, E.C., 2018. Soil ecosystem services, sustainability, valuation and management. *Current Opinion in Environ. Sci. Health* 5, 7-13. <https://doi.org/10.1016/j.coesh.2017.12.003>
- Pérez-Méndez, M.A., Fraga-Cruz, G.S., Domínguez-García, S., Pérez-Méndez, M.L., Bocanegra-Díaz, C.I., Nápoles-Rivera, F., 2025. Microplastic pollution in soil and water and the potential effects on human health: A Review. *Processes* 13, 502. <https://doi.org/10.3390/pr13020502>
- Philippot, L., Ritz, K., Pandard, P., Hallin, S., Martin-Laurent, F., 2012. Standardisation of methods in soil microbiology: progress and challenges. *FEMS Microbiol. Ecol.* 82, 1-10. <https://doi.org/10.1111/j.1574-6941.2012.01436.x>
- Picariello, E., Baldantoni, D., De Nicola, F., 2022. Investigating natural attenuation of PAHs by soil microbial communities: insights by a machine learning approach. *Restor. Ecol.* Article e13655.
- Quejigo, J.R., Tejedor-Sanz, S., Schroll, R., Esteve-Núñez, A., 2019. Electrodes boost microbial metabolism to mineralise antibiotics in manure. *Bioelectrochemistry* 128, 283-290. <https://doi.org/10.1016/j.bioelechem.2019.04.008>
- Ramasamy, S., Arumugam, A., Chandran, P., 2017. Optimization of *Enterobacter cloacae* (KU923381) for diesel oil degradation using response surface methodology (RSM). *J. Microbiol.* 55, 104-111. <https://doi.org/10.1007/s12275-017-6265-2>
- Rasschaert, G., Elst, D.V., Colson, L., Herman, L., Ferreira, H.C.C., Dewulf, J., *et al.*, 2020. Antibiotic residues and antibiotic-resistant bacteria in pig slurry used to fertilise agricultural fields. *Antibiotics* 9, 34. <https://doi.org/10.3390/antibiotics9010034>
- Reinikainen, J., Bouhouille, E., Sorvari, J., 2024. Inconsistencies in the EU regulatory risk assessment of PFAS call for readjustment. *Environ. Int.* 186, 108614. <https://doi.org/10.1016/j.envint.2024.108614>
- Ren, J., Wang, Z., Deng, L., Niu, D., Huhetaoli, Li, Z., *et al.*, 2021. Degradation of erythromycin by a novel fungus, *Penicillium oxalicum* RJJ-2, and the degradation pathway. *Waste Biomass Valorization* 12, 4513-4523. <https://doi.org/10.1007/s12649-021-01343-y>
- Rodrigues, J.P., Duarte, A.C., Santos-Echeandia, J., Rocha-Santos, T., 2019. Significance of interactions between microplastics and POPs in the marine environment: a critical overview. *Trac. Trends Anal. Chem.* 111, 252-260. <https://doi.org/10.1016/j.trac.2018.11.0>
- Rosa, J., Leston, S., Crespo, D., Freitas, A., Sofia, A., Pouca, V., *et al.*, 2019. Uptake of enrofloxacin from seawater to the macroalgae *Ulva* and its use in IMTA systems. *Aquaculture* 516, 734609. <https://doi.org/10.1016/j.aquaculture.2019.734609>
- Roswell, M., Dushoff, J., Winfree, R., 2021. A conceptual guide to measuring species diversity. *Oikos* 130, 321-338. <https://doi.org/10.1111/oik.07202>
- Sakshi, Haritash, A.K., 2020. A comprehensive review of metabolic and genomic aspects of PAH-degradation. *Arch. Microbiol.* 202, 2033-2058. <https://doi.org/10.1007/s00203-020-01929-5>
- Salandez, V., Emami, S., Taha, A.Y., La Saponara, V., 2022. Use of *Ganoderma lucidum* grown on agricultural waste to remove antibiotics from water. *bioRxiv*. <https://doi.org/10.1101/2022.08.07.503092>
- Santás-Miguel, V., Rodríguez-López, L., Arias-Estévez, M., Rodríguez-Seijo, A., 2025. Microplastics as carriers of antibiotic resistance genes in agricultural soils: A call for research. *Pedosphere* 35(1), 12-16. <https://doi.org/10.1016/j.pedsph.2024.08.001>
- Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., *et al.*, 2023. Next-generation sequencing technology: Current Trends and Advancements. *Biology* 12, 997. <https://doi.org/10.3390/biology12070997>
- Schlüsener, M., von Arb, M., Bester, K., 2006. Elimination of macrolides, tiamulin, and salinomycin during manure storage. *Arch. Environ. Contam. Toxicol.* 51, 21-28. <https://doi.org/10.1007/s00244-004-0240-8>
- Schmidt, H., Eickhorst, T., 2014. Detection and quantification of native microbial populations on soil-grown rice roots by catalyzed reporter deposition-fluorescence in situ hybridization. *FEMS Microbiol. Ecol.* 87, 390-402. <https://doi.org/10.1111/1574-6941.12232>
- Schneider, K., Barreiro-Hurle, J., Rodriguez-Cerezo, E., 2023. Pesticide reduction amidst food and feed security concerns in Europe. *Nat. Food* 4, 746-750. <https://doi.org/10.1038/s43016-023-00834-6>
- Selvam, A., Zhao, Z., Li, Y., Chen, Y., Leung, K.-S., Wong, J.W., 2013. Degradation of tetracycline and sulfadiazine during continuous thermophilic composting of pig manure and sawdust. *Environ. Technol.* 34, 2433-2441. <https://doi.org/10.1080/09593330.2013.772644>
- Semple, K.T., Cain, R.B., Schmidt, S., 1999. Biodegradation of aromatic compounds by microalgae. *FEMS Microbiol. Lett.* 170, 291-300. <https://doi.org/10.1111/j.1574-6968.1999.tb13386.x>
- Shade, A., 2017. Diversity is the question, not the answer. *The ISME J.* 11, 1-6. <https://doi.org/10.1038/ismej.2016.118>
- Sharma, P., 2021. Efficiency of bacteria and bacterial assisted phytoremediation of heavy metals: an update. *Bioresour. Technol.* 328, 124835. <https://doi.org/10.1016/j.biortech.2021.124835>
- Sharon, I., Martín Quijada, N., Pasolli, E., Fabbri, M., Vitali, F., Agamennone, V., *et al.*, 2022. The core human microbiome: Does it exist and how can we find it? A Critical Review of the Concept. *Nutrients* 14, 2872. <https://doi.org/10.3390/nu14142872>
- Shetty, S.S., Sonkusare, S., Naik, P.B., Kumari, N.S., Madhyastha, H., 2023. Environmental pollutants and their effects on human health. *Heliyon* 9, e19496. <https://doi.org/10.1016/j.heliyon.2023.e19496>
- Sidhu, H., D'Angelo, E., O'Connor, G., 2019. Retention-release of *Ciprofloxacin* and *Azithromycin* in biosolids and biosolids-amended soils. *Sci. Total Environ.* 650, 173-183.
- Silva, V., Mol, H.G.J., Zomer, P., Tienstra, M., Ritsema, C.J., Geissen, V., 2019. Pesticide residues in European agricultural soils – A hidden reality unfolded. *Sci. Total Environ.* 653, 1532-1545. <https://doi.org/10.1016/J.SCITOTENV.2018.10.441>

- Slana, M., Zigon, D., Sollner-Dolenc, M., 2017. Enrofloxacin degradation in broiler chicken manure under field conditions and its residuals effects to the environment. *Environ. Sci. Pollut. Res.* 24, 13722-13731. <https://doi.org/10.1007/s11356-017-8722-1>
- Song, T., Zhu, C., Xue, S., Li, B., Ye, J., Geng, B., *et al.*, 2020. Comparative effects of different antibiotics on antibiotic resistance during swine manure composting. *Bioresour. Technology* 315, 123820. <https://doi.org/10.1016/j.biortech.2020.123820>
- Spielmeyer, A., Ahlborn, J., Hamscher, G., 2014. Simultaneous determination of 14 sulfonamides and tetracyclines in biogas plants by liquid-liquid extraction and liquid chromatography tandem mass spectrometry. *Anal. Bioanal. Chem.* 406, 2513-2524. <https://doi.org/10.1007/s00216-014-7649-3>
- Spielmeyer, A., Breier, B., Großmeier, K., Hamscher, G., 2015. Elimination patterns of worldwide used sulfonamides and tetracyclines during anaerobic fermentation. *Bioresour. Technol.* 193, 307-314. <https://doi.org/10.1016/j.biortech.2015.06.081>
- Stefani, F.O.P., Bell, T.H., Marchand, C., de la Providencia, I.E., El Yassimi, A., St-Arnaud, M., *et al.*, 2015. Culture-dependent and -independent methods capture different microbial community fractions in hydrocarbon-contaminated soils. *PLoS ONE* 10, e0128272. <https://doi.org/10.1371/journal.pone.0128272>
- Storteboom, H.N., Kim, S.C., Doesken, K.C., Carlson, K.H., Davis, J.G., Pruden, A., 2007. Response of antibiotics and resistance genes to high-intensity and low-intensity manure management. *J. Environ. Qual.* 36, 1695-1703. <https://doi.org/10.2134/jeq2007.0006>
- Su, D., Li, P., Frank, S., Xiong, X., 2006. Biodegradation of benzo[a]pyrene in soil by *Mucor* sp. SF06 and *Bacillus* sp. SB02 co-immobilized on vermiculite. *J. Environ. Sci.* 18, 1204-1209. [https://doi.org/10.1016/S1001-0742\(06\)60063-6](https://doi.org/10.1016/S1001-0742(06)60063-6)
- Sun, M., Ye, M., Jiao, W., Feng, Y., Yu, P., Liu, M., *et al.*, 2018. Changes in tetracycline partitioning and bacteria/phage-mediated ARGs in microplastic-contaminated greenhouse soil facilitated by sophorolipid. *J. Hazardous Materials* 345, 131-139. <https://doi.org/10.1016/j.jhazmat.2017.11.036>
- Sun, S., Jones, R.B., Fodor, A.A., 2020. Inference-based accuracy of metagenome prediction tools varies across sample types and functional categories. *Microbiome* 8, 46. <https://doi.org/10.1186/s40168-020-00815-y>
- Sun, Y., Shaheen, S.M., Ali, E.F., Abdelrahman, H., Sarkar, B., Song, H., *et al.*, 2022. Enhancing microplastics biodegradation during composting using livestock manure biochar. *Environ. Pollution* 306, 119339. <https://doi.org/10.1016/j.envpol.2022.119339>
- Tariq, M., Iqbal, B., Khan, I., Khan, A.R., Jho, E.H., Salam, A., *et al.*, 2024. Microplastic contamination in the agricultural soil-mitigation strategies, heavy metals contamination, and impact on human health: a review. *Plant Cell Rep.* 43, 65. <https://doi.org/10.1007/s00299-024-03162-6>
- Telo da Gama, J., 2023. The role of soils in sustainability, climate change, and ecosystem services. *Ecologies* 4, 552-567. <https://doi.org/10.3390/ecologies4030036>
- Tilman, D., Cassman, K.G., Matson, P.A., Naylor, R., Polasky, S., 2002. Agricultural sustainability and intensive production practices. *Nature* 418, 671-677.
- Tormo-Budowski, R., Cambrónero-Heinrichs, J.C., Durán, J.E., Masis-Mora, M., Ramírez-Morales, D., Quirós-Fournier, J.P., *et al.*, 2021. Removal of pharmaceuticals and ecotoxicological changes in wastewater using *Trametes versicolor*: a comparison of fungal stirred tank and trickle-bed bioreactors. *Chem. Eng. J.* 410, 128210.
- Uslu, M.Ö., Balcioglu, I.A., 2009. Comparison of the ozonation and Fenton process performances for the treatment of antibiotic containing manure. *Sci. Total Environ.* 407, 3450-3458. <https://doi.org/10.1016/j.scitotenv.2009.01.045>
- Verhaegen, M., Bergot, T., Liebana, E., Stancanelli, G., Streissl, F., Mingeot-Leclercq, M.-P., *et al.*, 2023. On the use of antibiotics to control plant pathogenic bacteria: a genetic and genomic perspective. *Front. Microbiol.* 14, 1221478. <https://doi.org/10.3389/fmicb.2023.1221478>
- Verhaegen, M., Mahillon, J., Caulier, S., Mingeot-Leclercq, M.-P., Bragard, C., 2024. Data collection on antibiotics for control of plant pathogenic bacteria. EFSA supporting publication 2024:EN-8522. 195 <https://doi.org/10.2903/sp.efsa.2024.EN-8522>
- Walder, F., Schmid, M.W., Riedo, J., Valzano-Held, A.Y., Banerjee, S., Büchi, L., *et al.*, 2022. Soil microbiome signatures are associated with pesticide residues in arable landscapes. *Soil Biol. Biochem.* 174, 108830. <https://doi.org/10.1016/j.soilbio.2022.108830>
- Wallace, J.S., Garner, E., Pruden, A., Aga, D.S., 2018. Occurrence and transformation of veterinary antibiotics and antibiotic resistance genes in dairy manure treated by advanced anaerobic digestion and conventional treatment methods. *Environ. Pollut.* 236, 764-772. <https://doi.org/10.1016/j.envpol.2018.02.024>
- Wang, C., Liu, H., Li, J., Sun, H., 2014. Degradation of PAHs in soil by *Lasioidiplodia theobromae* and enhanced benzo[a]pyrene degradation by the addition of Tween-80. *Environ. Sci. Pollut. Res.* 21, 10614-10625. <https://doi.org/10.1007/s11356-014-3050-1>
- Wang, D., Lin, J., Lin, J., Wang, W., Li, S., 2020. Biodegradation of petroleum hydrocarbons by *Bacillus subtilis* BL-27, a strain with weak hydrophobicity. *Molecules* 24, 3021. <https://doi.org/10.3390/molecules24173021>
- Wang, L., Chen, G., Owens, G., Zhanga, J., 2016. Enhanced antibiotic removal by the addition of bamboo charcoal during pig manure composting. *RCS Advances* 6, 27575-27583. <https://doi.org/10.1039/C5RA27493A>
- Weithmann, N., Möller, J.N., Löder, M.G.J., Piehl, S., Laforsch, C., Freitag, R., 2018. Organic fertiliser as a vehicle for the entry of microplastic into the environment. *Sci. Adv.* 4(4):eaap8060. <https://doi.org/10.1126/sciadv.aap8060>
- WHO, 2019. Antimicrobial resistance [WWW Document]. URL <https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance> (accessed 7.16.24).
- Widyasari-Mehta, A., Hartung, S., Kreuzig, R., 2016. From the application of antibiotics to antibiotic residues in liquid manures and digestates: A screening study in one European center of conventional pig husbandry. *J. Environ. Manag.* 177, 129-137. <https://doi.org/10.1016/j.jenvman.2016.04.012>
- Wu, C., Spongberg, A.L., Witter, J.D., 2009. Sorption and biodegradation of selected antibiotics in biosolids. *J. Environ. Sci. Health A44*, 454-461. <https://doi.org/10.1080/10934520902719779>

- Wu, R.T., Cai, Y.F., Chen, Y.X., Yang, Y.W., Xing, S.C., Liao, X.D., 2021. Occurrence of microplastic in livestock and poultry manure in South China. *Environ. Pollut.* 277, 116790. <https://doi.org/10.1016/j.envpol.2021.116790>
- Yakimov, M., Giuliano, L., Gentile, G., Crisafi, E., Chernikova, T., Abraham, W., *et al.*, 2003. *Oleispira antarctica* gen. nov. sp. nov. a novel hydrocarbonoclastic marine bacterium isolated from Antarctic coastal sea water. *Int. J. Syst. Evol. Microbiol.* 53, 779-785. <https://doi.org/10.1099/ijs.0.02366-0>
- Yakimov, M.M., Timmis, K.N., Golyshin, P.N., 2007. Obligate oil-degrading marine bacteria. *Curr. Opin. Biotechnol.* 18, 257-266. <https://doi.org/10.1016/j.copbio.2007.04.006>
- Yang, B., Meng, L., Xue, N., 2018. Removal of five fluoroquinolone antibiotics during broiler manure composting. *Environ. Technol.* 39, 373-381. <https://doi.org/10.1080/09593330.2017.1301568>
- Yang, J., Li, R., Zhou, Q., Li, L., Li, Y., Tu, C., *et al.*, 2021. Abundance and morphology of microplastics in an agricultural soil following long-term repeated application of pig manure. *Environ. Pollut.* 272, 116028. <https://doi.org/10.1016/j.envpol.2020.116028>
- Zafra, G., Moreno-Montaña, A., Absalón, Á.E., Cortés-Espinosa, D.V., 2015. Degradation of polycyclic aromatic hydrocarbons in soil by a tolerant strain of *Trichoderma asperellum*. *Environ. Sci. Pollut. Res.* 22, 1034-1042. <https://doi.org/10.1007/s11356-014-3357-y>
- Zhang, C., Bennett, G.N., 2005. Biodegradation of xenobiotics by anaerobic bacteria. *Appl. Microbiol. Biotechnol.* 67, 600-618. <https://doi.org/10.1007/s00253-004-1864-3>
- Zhang, J., Lin, H., Ma, J.W., Sun, W.C., Yang, Y.Y., Zhang, X., 2019a. Compost-bulking agents reduce the reservoir of antibiotics and antibiotic resistance genes in manures by modifying bacterial microbiota. *Sci. Total Environ.* 649, 396-404. <https://doi.org/10.1016/j.scitotenv.2018.08.212>
- Zhang, M., He, L.Y., Liu, Y.S., Zhao, J.L., Liu, W.R., Zhang, J.N., *et al.*, 2019b. Fate of veterinary antibiotics during animal manure composting. *Sci. Total Environ.* 650, 1363-1370. <https://doi.org/10.1016/j.scitotenv.2018.09.147>