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Soil microorganisms as bioindicators of agroecosystem condition: a review of their ecological and trophic groups, functional roles, and the impact of anthropogenic factors

Alla Levishko, Iryna Gumeniuk*, Olena Sherstoboeva

Institute of Agroecology and Environmental Management of NAAS, Kyiv, Ukraine

* Corresponding author E.mail: gumenyuk.ir@gmail.com

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Abstract
Soil is the foundation of agroecosystems. It is a physical surface where plants can grow. But it is also a living resource that provides services to the environment and helps to keep the Earth's natural cycles working. The soil microbiome is a highly diverse community of organisms that include bacteria (70–90% of the total mass), as well as fungi, archaea, protozoa, and algae. These organisms work together to break down organic matter, recycle nutrients, and fight off diseases to keep the soil healthy. Ecological-trophic groups show what soil is like, based on how it is made, what nutrients are available, how much air is in it, and how much humans have disturbed it. Their ratio and activity are a direct response to these conditions. It is impossible to assess the state of soil agroecosystems without a deep understanding of the role of the main ecological groups of microorganisms. The number, activity, and ratio of different types of microorganisms can be used to indicate changes in soil processes. The aim of this review is to summarise the role and impact of factors on ecological-trophic groups as bioindicators of the condition of soil agroecosystems.

Keywords*: bioindicators, soil microorganisms, ecological-trophic groups, soil agroecosystems, anthropogenic impact, soil microorganisms, fertilisers*

Introduction

Soil is the fundamental basis of agroecosystems, functioning not only as a physical substrate for plant growth, but also as a dynamic, complex bioresource system that provides ecosystem services and supports global biogeochemical cycles (Köberl *et al.*, 2020). Soil health, shaped by the interaction of biotic and abiotic processes, directly correlates with crop productivity, product quality and the resilience of agrocenoses, and also plays a decisive role in climate regulation through carbon sequestration and greenhouse gas emission moderation (Iqbal *et al.*, 2025). Soil microorganisms are an integral part of this health, mediating its functions and ecosystem services as sensitive, dynamic bioindicators that respond to environmental changes more quickly than traditional physicochemical parameters. Assessment of microbiological characteristics reveals aspects of biodiversity, the presence of phytopathogens and key bioregulatory mechanisms, reflecting the dynamics of processes in the soil, its resistance to anthropogenic pressure and regeneration potential, which surpasses static chemical methods (Bhaduri *et al.*, 2022; Poroshenko, 2020; Wang *et al.*, 2024). The soil microbiome is a highly diverse community comprising bacteria (70–90% of biomass), fungi, archaea, protozoa, and algae that provide decomposition of organic residues, nutrient cycling, and pathogen suppression to maintain fertility and phytosanitary status (Yu *et al.*, 2024). The assessment of microbial associations goes beyond taxonomic identification, emphasising functional relationships, where empirical data demonstrate a differentiated response of the microbiome structure to abiotic influences, such as pH or organic matter content, with variable sensitivity to agrochemicals (Malal *et al.*, 2025). In particular, the microbiome of vineyard soils shows greater stability under the action of herbicides compa-

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red to orchard soils, which highlights the limitations of focusing on dominant groups and the importance of their interactions and adaptability. Thus, the role of ecological-trophic groups of soil microorganisms in assessing the state of agroecosystems is key and multifaceted, as they serve as an integral indicator of soil health and its response to anthropogenic influences (tillage, use of fertilisers or pesticides, etc.). The transition from a general understanding of the microbiome to an analysis of its ecological and trophic structure allows for a deeper understanding of the mechanisms of these processes, which is the basis for further consideration of the classification and functional role of these groups. The aim of the review is to summarise the functional role and influence of factors on ecological-trophic groups as bioindicators of the agroecosystem conditions.

Classification of ecological-trophic groups: trophism and ecological role

Ecological-trophic groups are a classification of soil microbiota based on the way they obtain energy and carbon and their functional role in the soil ecosystem, especially in the context of biogeochemical cycles (Fierer *et al*., 2007; Ho *et al*., 2017). These functional markers of soil reflect its chemical composition, nutrient availability, aeration level, and degree of anthropogenic stress, as their ratio and activity are a direct response to these conditions (Bhaduri *et al*., 2022). Microorganisms are divided into several key categories based on their trophism. The most numerous group is chemoheterotrophs, or saprophytes, which obtain energy and carbon by oxidising organic substances, performing the main work of decomposing organic matter, and mineralising nutrients (Fierer *et al*., 2007; Patyka and Volkogon, 2024). In contrast, chemolithoautotrophs use energy obtained from the oxidation of inorganic compounds (e.g., ammonium, nitrites, or sulphur) and obtain carbon from CO_2. These microorganisms are very important for the process of nitrification (Starke R. *et al*., 2021). Separate categories also include oligotrophs, which are able to exist at very low nutrient concentrations, and their dominance can be an indicator of soil poverty, and coprotrophs, which respond quickly to an excess of readily available organic matter (Malik *et al*., 2020; Baimagambetova *et al*., 2024). From an ecological (functional) point of view, these groups are closely related to biogeochemical cycles (Yao *et al*., 2017). In the nitrogen cycle, ammonifiers (proteolytics) play a key role, decomposing proteins to NH_4, determining the intensity of nitrogen mineralisation; nitrifiers, which convert ammonium to nitrates, making nitrogen available to plants but prone to leaching; and denitrifiers, whose activity leads to the loss of nitrogen into the atmosphere in the gaseous form of N_2O and N_2 and serves as an indicator of poor aeration or waterlogging of the soil (Demyanyuk *et al*., 2018; Bhaduri *et al*., 2022). Nitrogen fixers, which fix atmospheric nitrogen and convert it into biologically available compounds, are vital for natural fertility (Demyanyuk *et al*., 2018; Chaika *et al*., 2017). Micromycetes play an indispensable role in the carbon cycle, specialising in the decomposition of the most resistant organic compounds, such as lignin and cellulose, contributing to the formation of humus (Fierer *et al*., 2007; Patyka and Volkohon, 2024). Alongside them are cellulolytic and amylolytic bacteria, which are responsible for the decomposition of fresh plant residues (Chaika *et al*., 2017; Baimagambetova *et al*., 2024). Actinomycetes are also involved in the decomposition of resistant organic matter and often act as antagonists to phytopathogens, which is a sign of good sanitary conditions. In contrast, an increase in the proportion of phytopathogens is a direct indicator of biological contamination and a disturbance in the phytosanitary balance (Bhaduri *et al*., 2022). Thus, monitoring the ratios between these ecological-trophic groups, for example, the ratio of fungi to bacteria (F/B ratio) or coprophages to oligotrophs, allows us to obtain a comprehensive functional portrait of the soil, which is indispensable for assessing its health and sustainability. This classification not only systematises microbial processes, but also serves as a basis for understanding how these groups respond to external influences, which leads to an analysis of their role as bioindicators (Ho *et al*., 2017).

Ecological-trophic groups as bioindicators of the state of agroecosystems

Assessing the condition of soil agroecosystems is impossible without a deep understanding of the role of the main ecological and trophic groups of microorganisms, whose abundance, activity, and ratio are sensitive bioindicators of soil process dynamics (Patyka and Volkogon, 2024; Bhaduri *et al*., 2022; Demyanyuk *et al*., 2018). These groups play a decisive role in key biogeochemical cycles, regulating the availability of nutrients for plants and determining the phytosanitary condition of the soil. The key functional groups used for soil diagnosis are ammonifiers, which are responsible for the primary stage of organic nitrogen mineralisation

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as their high activity is a direct indicator of intensive nitrogen turnover and, accordingly, is important for ensuring the initial nitrogen nutrition of plants (Pesakovic *et al.*, 2003). In parallel with this, oligotrophs and nitrogen fixers are critically important for soil enrichment with nitrogen, as they are capable of fixing atmospheric nitrogen N_2, converting it into forms accessible to plants, thereby increasing the natural fertility of the soil. and a decrease in their numbers, especially in the case of excessive application of mineral fertilisers or chemical pollution, may indicate a disturbance in the natural balance of the nitrogen cycle (Demyanyuk *et al.*, 2018). Micromycetes, which specialise in the decomposition of complex and resistant polymers such as cellulose and lignin, make a significant contribution to the decomposition of organic matter, which is a key stage in the formation of humus. However, this group also includes phytopathogenic species, whose increase in number is an alarming sign of a disturbance in the microbial balance in the agroecosystem, which increases the risk of disease in cultivated plants (Symochko *et al.*, 2021). Actinomycetes also play an active role in the decomposition of resistant organic substances and humus formation. In addition, they are known for their antagonistic action against some pathogens, which makes them important for maintaining the phytosanitary stability of the soil (Symochko *et al.*, 2021). To assess the intensity of decomposition of specific substrates, groups such as amylolytic bacteria, which are responsible for the decomposition of starch, are used, as their activity reflects the rate of utilisation of readily available soil carbohydrates (Baimagambetova *et al.*, 2024). Finally, the ratio between different trophic groups is an indicator of the overall nutrient saturation of the soil. In particular, oligotrophs, which are microorganisms capable of surviving and functioning actively even at very low nutrient concentrations, so their dominance in the microbial complex is often an indicator of soil poverty or degradation, while an increase in the number of coprophiles (which, on the contrary, require a high concentration of readily available organic matter) indicates a fresh influx of organic residues (Baimagambetova *et al.*, 2024). The role of ecological-trophic groups of soil microorganisms in assessing the state of agroecosystems is key and multifaceted, as they function as sensitive bioindicators of soil process dynamics, and the study of these functional groups allows for an in-depth assessment of soil condition in four main areas, which exceeds the capabilities of purely chemical analysis (Patyka and Volkogon, 2024; Bhaduri *et al.*, 2022). Firstly, microorganisms directly reflect the biological activity and potential fertility of the soil, where the intensity of organic matter mineralisation is a direct indicator of the rate of nutrient turnover, since the high activity of such decomposers as ammonifiers, amylolytics and other heterotrophs indicates rapid and efficient decomposition of plant residues, which is a sign of healthy and fertile soil, and at the same time, the soil's nitrogen fixation potential, which correlates with the number of nitrogen-fixing microorganisms (both free and symbiotic), allows us to assess the natural supply of available nitrogen in the soil (Pesakovic *et al.*, 2003; Demyanyuk *et al.*, 2018).

Secondly, the microbial complex is an extremely sensitive indicator of soil resistance to anthropogenic impact (stress), since changes in the quantitative and qualitative composition of ecological-trophic groups serve as an early indicator of chemical contamination with heavy metals or pesticides, for example, a decrease in the total microbial population or the dominance of stress-resistant oligotrophs may signal toxic effects, as confirmed by studies that reveal correlations between the number of microorganisms and the content of acid-soluble forms of lead and other pollutants, In addition, analysis of the microbiota allows us to assess the positive effects of biological products (e.g., *Trichoderma*), since the use of such agents contributes to a targeted change in the development of certain ecological-trophic groups, increasing the overall biological activity of the soil and at the same time suppressing unwanted phytopathogens, such as fungi of the genus *Fusarium* (Bhaduri *et al.*, 2022; Symochko *et al.*, 2021).

Thirdly, microbiological analysis is critical for assessing the phytosanitary status of an agroecosystem, where the ratio between pathogens and their antagonists is a key marker, and an increase in the number of phytopathogenic microfungi is a direct indicator of increased biological pollution of agroecosystems, which is the result of intense anthropogenic pressure and the selection of more aggressive strains, and accordingly increases the risk of diseases in cultivated plants (Symochko *et al.*, 2021). Finally, analysis of the microbial complex provides unique opportunities for assessing the effecttiveness of specific agricultural technologies, as it allows for an objective assessment of how different soil cultivation systems, crop rotations, cover crops, or the application of different types of fertilisers affect the biological condition of the soil, its stability, and its ability to self-regenerate. Thus, ecological-trophic groups are an integral tool for verifying and optimising sustainnable farming practices, and this multifacted nature of

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bioindicators becomes particularly relevant when analysing specific agrotechnical influences, such as tillage and fertilisation, which directly modulate the structure of the microbiome (Patyka and Volkogon, 2024; Demyanyuk *et al.*, 2018).

The article by Australian scientists examines the role of trophic interactions between bacteria in formation the structure and diversity of soil protist communities in natural ecosystems in Australia, highlighting the dominant bottom-up control of bacteria over protists as a key factor in microbial assembly, where the authors analysed DNA from 216 soil samples using 16S rRNA sequencing for bacteria and 18S rRNA for protists, revealing strong correlations between bacterial diversity and functional groups of protists (consumers, parasites, phototrophs), with the highest connections in co-occurrence network, and the conclusions emphasise that these interactions enhance the multifunctionality of the ecosystem, contributing to organic decomposition and biogeochemical cycles, with bacteria predominating over the top-down influence of invertebrates, which is important for maintaining soil fertility (Nguyen *et al.*, 2023).

Research into the interactions of ecological-trophic groups (ammonifiers, nitrifiers, cellulolytics, oligotrophs) in the microbiocenoses of chernozem (black soil), dark grey and sod-podzolic soils of agroecosystems shows that these groups serve as bioindicators of soil condition under the influence of fertilisers and hydrothermal factors, where the total biomass of microorganisms and the ratio of groups (e.g., mineralisation-immobilisation) are key criteria for diagnosing ecological status, and microorganisms that produce exopolysaccharides, which have a strong connection with all trophic groups of microorganisms, as they are their structural components, have been found to be the main block-forming factor, due to their strong influence on the total microbial mass content in the soil (Demyanyuk *et al.*, 2018). For agroecosystem soils with a dark grey soil type, the characteristic of the total biomass content of microorganisms is the basis for the block constructing gremium, which confirms the state of the microbiocenosis and the processes occurring in it under the influence of the studied biotic and abiotic factors, while the microbiocenosis of sod-podzolic soil, unlike other studied soil types, clearly responded to fertiliser application and depended on the action of hydrothermal factors, where the contrast in the hydrothermal regime range caused chaotic interaction between the main characteristics in the microbiocenosis of sod-podzolic soil, with the emergence of direct and indirect links between them (Demyanyuk *et al.*, 2018). Regardless of changes in hydrothermal factors, the interactions between the characteristics of the total microbial mass content, eutrophic microorganisms that use mineral and organic forms of nitrogen, and exopolysaccharide producers were stable, and it has been proven that the assessment of the ecological state of the soil and the impact of applicable agricultural mea-sures on it should be carried out based on indicators of the total content of microbial biomass in the soil and the correlation between the number of microorganisms that form the gremium graph (Demyanyuk *et al.*, 2018).

A study of the impact of mineral (N 30–90 kg/ha) and organic fertilisers on ammonifiers as a trophic group in acidic soils under oats shows that a decrease in the number of ammonifiers is a bioindicator of suppression, while protease activity increases, reflecting the adaptation of the microbiocenosis in agroecosystems (Pesakovic *et al.*, 2003). A review of the interactions of ecological-trophic groups of microorganisms in the soil of agroecosystems as indicators of biosafety emphasises that soil microbiological activity affects plants, and changes in groups (e.g., saprophytes vs. symbionts) signal degradation due to anthropogenic impact (Symochko *et al.*, 2021). The use of ecological-trophic groups of microorganisms as bioindicators of the state of arid pastures has been substantiated, where it has been established that the microbial composition reflects the ratio of organic synthesis and decomposition processes, as well as the effectiveness of biostimulants. it has been experimentally proven that arid soils are characterised by low levels of nitrogen fixers and overall enzymatic activity (catalase), however, high urease activity is preserved, and the authors propose a strategy for the biologisation of agriculture through the use of organomicrobial complexes, which allows to increase yields and restore the ecological stability of agrocenoses (Baimagambetova *et al.*, 2024). Generally, Table 1 summarises the functional role and indicator potential of the main ecological-trophic groups of soil microorganisms, demonstrating their integral value for monitoring agroecosystems. In general, these groups provide a dynamic assessment of biogeochemical processes, surpassing static chemical methods due to their sensitivity to change.

The influence of agrotechnical factors on the structure and function of ecological-trophic groups

Transformation of the microbiome under the influence of tillage. The transformation of the struc-

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Table 1. *Key ecological-trophic groups as bioindicators: functions and indicator values*

Group	Functional role	Indicator value (examples)	Key quotes
Ammonifiers (proteolytics)	Mineralisation of organic nitrogen (NH_3/NH_4)	Intensity of nitrogen turnover; reduction – suppression (N 30–90 kg/ha)	Pesakovic et al., 2003; Demyanyuk et al., 2018
Nitrogen fixers (oligonitrophiles)	Fixation of N_2 into available forms	Natural fertility; dominance of oligotrophs – degradation	Demyanyuk et al., 2018; Baimagambetova et al., 2024
Micromycetes (fungi)	Cellulose/lignin decomposition, humus formation	Phytosanitary balance; growth of pathogens – risk of disease	Symochko et al., 2021
Actinomycetes	Decomposition of resistant organic matter, antagonism to pathogens	Stress resistance; correlation with exopolysaccharides	Simochko et al., 2021; Demyanyuk et al., 2018
Amylolytic bacteria	Decomposition of starch (readily available carbohydrates)	Decomposition rate; correlation with coprophages	Baimagambetova et al., 2024
Oligotrophs/ coprotrophs	Adaptation to low/high organic matter	Nutrient saturation; oligotrophs – soil poverty	Baimagambetova et al., 2024

ture and functionality of the microbiome under the influence of tillage is one of the key aspects of agricultural technology, where ecological-trophic groups play the role of early indicators of change. Traditional tillage is a critical agrotechnical technique aimed at improving aeration, weed control and crop residue destruction. However, intensive mechanical action is accompanied by a number of negative effects: increased erosion, degradation of fungal hyphae and carbon loss. Sustainable alternatives, such as no-till and conservation tillage, help preserve soil physical structure and moisture. Studies show that abandoning ploughing usually leads to an increase in microbial biomass and enzyme activity, although this effect correlates with the physical and chemical properties of the soil. In particular, intensive methods significantly reduce the carbon and nitrogen content in microbial biomass compared to surface or chisel tillage (Hsiao *et al*., 2025). Analysis of the metabolic coefficient (qCO_2) indicates higher microbial respiration rates in untilled systems, but this effect may be levelled out within 10 years, indicating the adaptive ability of the microbiome to restore equilibrium. Enzymes involved in the cycling of elements (β-glucosidase, urease, phosphatase) are most sensitive in the upper layer (0–10 cm), where their activity is suppressed by intensive mechanical intervention. Changes in microbial communities under the influence of tillage are largely mediated by the transformation of the soil microclimate. Conservation methods ensure a stable cool and moist surface regime, while ploughing increases the temperature, accelerating microbial mineralisation of residues. Long-term monitoring (over 30 years) confirms that abandoning ploughing contributes to an increase in the number of: arbuscular mycorrhizal fungi (AMF) – by 17%; actinomycetes – by 6%; Gram-positive bacteria – by 5%. At the same time, the number of saprophytic fungi decreases by approximately 14%. No-till farming also stimulates the activity of carbon, nitrogen and phosphorus cycle enzymes (β-glucosaminidase and phosphodiesterase) by 26–42%. Reduced tillage contributes to the optimisation of functional bioregulation of the soil through the redistribution of taxa: a decrease in the number of amoA genes and an increase in the proportion of *Alphaproteobacteria* and *Actinobacteria*. These groups play a key role in the degradation of xenobiotics and the regulation of greenhouse gas emissions. Thus, a balanced selection of cultivation methods in crop rotations is the foundation for the formation of a healthy microbiome, which reduces the dependence of agrocenoses on synthetic fertilisers and pesticides. These changes in microbial communities naturally lead to an analysis of the impact of fertilisation systems, where the availability of nutrients becomes the next key factor in modulating ecological-trophic groups (De Andrade Barbosa *et al*., 2019; Yang, 2021). Studies of soil samples from traditional and organic farming areas in the Kyiv region show that organic farming systems increase the overall number of microorganisms in most ecological-trophic groups (ammonifiers, cellulose degraders), with the exception of oligotrophic and phosphate-solubilising bacteria, which dominate in conventional systems as indicators of available phosphorus deficiency. Quantitative analysis using differential diagnostic media and serial dilutions revealed that conventional tillage promotes the selection of phosphate-transforming bacteria capable of mobilising hard-to-access phosphorus compounds, while organic tillage promotes cellulose degraders that decompose plant residues. Such studies indicate the adaptation of trophic groups to local stress conditions, such as phosphorus deficiency or mechanical disturbance. These changes highlight the role of ecological-trophic groups as early bioindicators: the growth of phosphate solubilisers in

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traditional systems signal the degradation of P resources, while the dominance of cellulose degraders in organic systems signals an intensification of the C cycle, which correlates with increased resistance of agroecosystems to anthropogenic factors. Thus, monitoring trophic groups during cultivation not only diagnoses the state of agroecosystems, but also guides agrotechnical measures to preserve biodiversity and soil fertility (Gumeniuk *et al.*, 2022).

Modulation of the microbiome by fertilisation systems. The transformation of the functional potential of the microbiome under the influence of fertilisation systems is a continuation of agrotechnical influences, where ecological-trophic groups respond to changes in the availability of macronutrients, affecting the cycling of nutrients. The availability of nutrients is a determining factor in the productivity of agrocenoses. Global consumption of mineral fertilisers is growing steadily and, according to FAO (2012) forecasts, will reach 200 million tonnes annually by 2050. However, prolonged intensive use of fertilisers radically changes the biological properties, ecological functions and overall quality of the soil. Macroelements (N, P, K) applied to stimulate crop yields enter into complex interactions with soil biota, causing significant changes in its structure. In particular, in 30 of the 38 Black-Box ecosystem projects studied, significant changes in the composition of microbial communities, including arbuscular mycorrhizal fungi (AMF), were recorded as a result of mineral loading (Yang, 2021).

Nitrogen fertilisers: stimulation and suppression of microbial processes. Current standards for mineral nitrogen application in agroecosystems often exceed planetary limits for its cyclical processing, causing irreversible damage to the environment. Although under natural conditions, nitrogen deficiency limits primary production and its moderate supply can stimulate microbial growth, in agriculture, excessive doses lead to degradation processes.

Key mechanisms of nitrogen excess impact:

1. Physicochemical changes: Systematic application of nitrogen fertilisers increases the osmotic potential of the soil solution, increases the concen-tration of free NH_3 and causes acidification of the environment. This directly restructures microbial associations.
2. Reduction of biomass: It has been proven that prolonged nitrogen loading leads to a sustained decrease in total microbial biomass.
3. Transformation of trophic networks: High doses of nitrogen stimulate the development of root hydrocarbon microorganisms, while limiting the growth of groups originating directly from root tissues due to changes in the metabolism of the plant itself.
4. Changes in functional groups of denitrifiers and nitrifiers: Long-term experiments have shown that elevated nitrogen levels alter the ratio between different classes of proteobacteria: the abundance of denitrifiers of the class α-Proteobacteria decreases, while the proportion of γ-Proteobacteria increases. In addition, the composition of communities dominated by the nirS and nirK genes is transformed.

Studies of alpine ecosystems and agrocenoses confirm that the accumulation of NO_3 in the soil sharply accelerates the rate of nitrification, while suppressing the biodiversity of bacteria and fungi. The inertia of these changes is particularly worrying: even 9 years after the cessation of nitrogen application (at a dose of 60 kg N/ha), the nitrification rate remained 108% higher than the control. This indicates that certain microbiological parameters of the soil lose their ability to return to their original state after prolonged anthropogenic influence (Yang, 2021). These effects of nitrogen fertilisers logically extend to the analysis of phosphorus and potassium fertilisers, where similar mechanisms modulate other cycles.

Phosphorus and potassium fertilisers: cycle and rhizosphere modulation. Mineral phosphorus fertilisers are a critically important component of plant nutrition, as phosphorus is involved in the formation of cell membranes, nucleic acids and the development of reproductive organs. The assimilation of phosphorus by agrocenoses occurs through three main channels: direct absorption by plants, biochemical modification of the rhizosphere, and indirectly through the activity of soil microorganisms. All these pathways undergo significant transformations under the influence of mineral phosphorus compounds. Chinese researchers showed that prolonged use of phosphorus fertilisers (NPK combinations) increases the total content of PLFA of bacterial and anaerobic origin (e.g., markers of Gram-negative bacteria and methanogens), correlating with the intensity of the phosphorus cycle ($r > 0.6$; $p < 0.05$). This leads to a profound restructuring of microbial communities: an increase in copiotrophs and anaerobes, reflecting adaptation to increased phosphorus availability, with enhanced mineralisation processes (Zhong *et al.*, 2010).

Impact on the functional specialisation of the microbiome:

1. Adaptation to deficiency: Under conditions of low

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soil phosphorus availability, the microbial community activates mechanisms for dissolving (solubilising) hard-to-reach compounds. Such soils are dominated by bacteria of the genera *Burkholderiales* and *Massilia* spp., capable of producing exopolysaccharide phosphatase. In addition, the synthesis of acid and alkaline phosphatases, which are responsible for the mineralisation of organophosphorus compounds, is enhanced.

2. Energy metabolism and carbon cycle: High phosphorus application rates stimulate the growth of microorganisms that intensively consume carbon from root exudates. This leads to changes in carbon use efficiency, transformation of the microbial biomass pool, and acceleration of microbial turnover, which ultimately affects the total organic carbon content in the soil (Samaddar *et al.*, 2019). Thus, phosphorus loading radically changes the activity of the functional groups of microorganisms responsible for phosphorus transformation, which indirectly affects the balance of other nutrients. The rational combination of mineral phosphorus and the stimulation of biological solubilisation processes is the fundamental basis for the development of strategies for sustainable soil fertility management (Levishko and Mamenko, 2025).

Potassium is an indispensable element for plant vegetation, as it regulates the functioning of stomata, osmotic potential and the synthesis of stress proteins, which directly transforms the chemical properties of the rhizosphere. According to 29 years of monitoring data, the systematic application of potash fertilisers leads to a decrease in pH and available nitrogen content, while increasing the concentration of mobile potassium in the soil profile. Such changes in the environment contribute to an increase in the number and species richness of bacterial communities, but are accompanied by a decrease in the MacIntosh dominance index, indicating a change in population heterogeneity. In addition, the transformation of the potassium regime adjusts the metabolic ability of bacteria to utilise various sources of carbon. In soils with potassium deficiency, its application activates the functional genes responsible for the carbon, nitrogen and phosphorus (C, N, P) cycles and changes the ratio of microorganisms involved in ammonification and denitrification processes. However, the overall effect of mineral nutrition on the microbiota remains dependent on the type of fertiliser, dosage and accompanying agronomic measures (Chen, *et al.*, 2020). These fertilisation processes are closely linked to other stresses, such as salinisation, which exacerbates the imbalance of microbial groups, moving on to the analysis of anthropogenic pollution factors, where ecological-trophic groups serve as sensitive indicators of degradation.

Salinisation as a factor in the transformation of microbial communities. Soil salinisation is one of the key anthropogenic factors affecting biodiversity and the organisation of microbial and fungal communities, transforming ecological-trophic groups into sensitive bioindicators of agroecosystem degradation (Rasheela et al., 2025; Shaaban, 2024). In the Gurbantunggut Desert (China), analysis of the impact of salinity on the structure of the microbiome showed the dominance of the taxa *Proteobacteria, Bacteroidetes, Actinobacteria* and *Halobacteria* taxa in saline niches, which serve as potential indicators of tolerance to high salinity, as their prevalence correlates with electrical conductivity (EC) and signals the adaptation of trophic groups to stress (Rasheela *et al.*, 2025). After the recultivation of saline-alkaline soils with organic fertilisers, six bacterial types with increased abundance were observed to dominate, emphasising the role of saprophytic and heterotrophic groups as markers of recovery, although overall microbial diversity decreases proportionally to EC growth, with fungal communities showing higher resistance than bacterial communities (Rasheela *et al.*, 2025; Shaaban, 2024). Adaptive bacteria, such as halophiles, which demonstrate resistance to osmotic stress, predominate in saline soils, while nutrient availability significantly modulates the structure of plant associations and microbial biomass in epileptic and endoleptic horizons, depending on their content (Rasheela *et al.*, 2025). A phytoremediation model based on the cultivation of salt-tolerant legumes in coastal salt marsh ecosystems promotes nutrient accumulation and radically transforms diazotrophic, bacterial and mycological communities, enriching the taxonomic composition at different depths of the profile, where symbiotic nitrogen fixers (e.g., *Rhizobia*) are key indicators of N-cycle improvement (Schmitz *et al.*, 2022). Research on the response of the microbiome to nutrient availability through mulching on the Leso Plateau (China) confirms these trends, emphasising the role of organic additives in restoring the functional stability of soils, where organic fertilisers enhance the resistance of ecological-trophic groups, improving nitrogen and carbon cycling under salt stress (Malal *et al.*, 2025; He *et al.*, 2025). Secondary anthropogenic salinisation (from irrigation) in the saline soils of Ningxia (China) reduces bacterial diversity (Shannon/Chao1 indices) more than fungal diversity, changing the dominant types (*Proteobacteria* 11.75–24.88%, *Ascomycota* 47.93–80.11%), simplifies bacterial-fungal interaction networks, enhancing

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cooperation but reducing ecosystem stability and multifunctionality, where network complexity is a key predictor of ecosystem positivity and microbial d-iversity. Overall, anthropogenic salinisation (poor irrigation, climate change) threatens 50% of arable land, simplifying bacterial communities with the dominance of halophilic taxa (*Halomonas, Bacillus*), but with a loss of functional diversity (nitrogen fixation/denitrification), limiting the fertility of saline agricultural soils (Schmitz *et al.*, 2022; Li *et al.*, 2021). High salinity (0.22–19.98 dS/m from anthropogenic irrigation) reduces bacterial diversity, alters composition (decline of *Actinobacteria/Chloroflexi*, increase in *Proteobacteria/Bacteroidetes*) and destabilises networks where deterministic processes (variable selection) dominate the assembly and nitrogen cycle functions (ammonification, nitrification) are suppressed, with gene verification (nifH, amoA) (Li *et al.*, 2021). A study of the effect of organic and mineral fertilisers on ecological-trophic groups (symbiotic nitrogen-fixing bacteria, heterotrophic saprophytes) under salt stress shows that organic fertilisers (vermicompost) enhance the resistance of the microbiome, by increasing bacterial richness, stimulating salt-tolerant taxa and mitigating the negative impact on functionality, while mineral fertilisers suppress diversity and impair multifunctionality (Malal *et al.*, 2025). Short-term salt stress causes significant changes in the functional activity of microbial communities, with initial structural stability, but without full recovery within 70 days of incubation, leading to reduced diversity, network complexity and degradation of multifunctionality, where vermicompost acts as a strategic tool to minimise the effects, while inorganic fertilisers exacerbate the risks (Malal *et al.*, 2025). Thus, salinisation transforms trophic groups, making halophiles and saprophytes dominant indicators, and organic additives the key to recovery, highlighting the need for monitoring for sustainable agroecosystem management (Rasheela *et al.*, 2025; Shaaban, 2024).

Extreme ecosystem pollution: changes in microbial communities and bioremediation

In the context of modern agroecosystems, extreme pollution, such as toxic emissions or mechanical damage, poses a serious threat to soil stability, disrupting the balance of biotic processes and threatening global food security. These impacts are particularly sensitive at the level of microbial communities, where the transformation of taxa and functions serves as an early signal of degradation, opening a window for scientific analysis of their adaptability. For example, a comprehensive ana-lysis of edaphic sites that have been intensively affected by mortar shell detonations (particularly in the Sumy region of Ukraine) confirms a profound structural and functional transformation of soil ecosystems. Ecological-trophic groups of microorganisms serve as sensitive bioindicators of anthropogenic stress, such as secondary salinisation. The intensive influx of heavy metal compounds creates stable anthropogenic stress, which, due to its vector of influence on the microbiota, leads to a radical restructuring of the bacteriome. Selective pressure from pollutants causes a sharp reduction in the relative abundance *of Actinobacteria* and *Proteobacteria*, while representatives of *the Firmicutes* type occupy a dominant position as resistant saprophytes and heterotrophs (Maslovska *et al.*, 2025). During microbiological monitoring, a group of Ukrainian scientists led by Maslovska identified a group of bacterial isolates capable of maintaining metabolic activity at high concentrations of Cu, Fe, Mn, Co, Cd, and Cr, which significantly exceed background levels. Among them, the strains *Bacillus sp.* IMV B-8154 and *Streptomyces sp.* IMV Ac-5058, identified as promising PGPBs for bioremediation, are of the greatest scientific and practical value. In particular, the strain *Bacillus sp.* IMV B-8154 strain is characterised by extreme adaptability: it is thermostable and halotolerant (with the ability to develop at NaCl concentrations of up to 10%), and also has a pronounced PGP potential, which includes nitrogen fixation, siderophore and auxin synthesis. This makes it a key indicator of the restoration of trophic chains. Thus, although technogenic pressure reduces overall biological diversity, the formation of stable microbial consortia is observed, which paves the way for the biological recultivation of territories. It has been experimentally proven that the isolated metal-resistant PGPB strains are capable of stimulating the development of soft wheat (*Triticum aestivum*) even on toxic substrates from blast zones. The combination of high resistance to heavy metals, salt tolerance and the ability to stimulate plant growth makes these microorganisms an optimal basis for the development of new biotechnologies for the restoration of saline-metallogenic soils in regions affected by military operations (Maslovska *et al.*, 2025). However, the successful implementation of such biotechnologies is impossible without a comprehensive analysis of how military action has affected the soil microbiota and the development of an appropriate bioremediation strategy. As a result of the full-scale invasion, significant areas of Ukrainian agroecosystems have suffered substantial mechanical destruction and chemical poisoning with toxic substances. This has led

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an urgent need to establish diagnostic indicators of soil bioactivity and implement effective bioremediation methods to revitalise these areas. Ecological and functional groups (nitrogen fixers, phosphate mobilisers, streptomycetes) are key indicators of damage here. To assess the state of microbiocenoses, a group of Ukrainian scientists led by Biliavska used the method of sowing soil suspensions on agarised nutrient media, followed by analysis of the main ecological and functional groups. Additionally calculated indices of mineralisation, immobilisation, oligotrophy and pedotrophy allowed the direction of microbial processes to be characterised. Based on these data, a five-level gradation of microbiota damage was developed, ranging from critical to weak (Biliavska *et al.*, 2024). The monitoring results showed extreme suppression of microflora in the epicentres of explosions. Compared to the control areas, there was a sharp reduction in the number of prokaryotes responsible for the transformation of nitrogen, phosphorus and organic matter. In particular, in craters from aerial bombs, the number of nitrogen fixers and streptomycetes was only 7 and 8% of the control, respectively, and the number of oligotrophs, amylolytics and phosphate mobilisers varied between 19.2 and 26%. Even deeper degradation was recorded at the sites of anti-tank shell explosions, where the number of key groups decreased to 1.5–10% of the normative indicators. This limits the circulation of N, P and organic matter, serving as a critical indicator of degradation. In order to restore biological activity, a bioaugmentation method was used by introducing microbial biomass based on the strains *Dietzia maris* IMV B-7350, *Rhodococcus erythropolis* IMV B-7351, *Bacillus subtilis* IMV B-7349, *Pseudomonas aureofaciens* IMV B-7558 and *Streptomyces violaceus* IMV Ac-5027. These strains are capable of degrading toxicants and increasing the adaptive potential of agrocenoses. A follow-up analysis six months later confirmed the high effectiveness of these measures: in bomb craters, the number of phosphate mobilisers and nitrogen fixers exceeded the undamaged control indicators by 1.5–3.8 times, and the number of streptomycetes increased 12 times compared to the initial state. A similar positive trend was observed in craters from unexploded ordnance, where the number of nitrogen fixers increased 20.5 times, which made it possible to change the status of the studied soils to slightly toxic or non-toxic. In general, the practical value of this study lies in the creation of an algorithm for land revitalisation, which involves the integration of microbiological monitoring into the state environmental monitoring system and the further development of a comprehensive phytomicrobial bioremediation with correction of the humus state of soils in production conditions (Biliavska *et al.*, 2024). The prospects for the implementation of bioremediation algorithms are significantly expanded when comparing Ukrainian experience with global trends in military waste degradation. Microbiota transformations in military action zones highlight the need for comprehensive strategies that integrate omic technologies (metagenomics, transcriptomics, proteomics) to identify and stimulate adaptive groups. Scientists from Ecuador presented the results of a bibliometric analysis of publications on microbial degradation of ammunition waste (2013–2023) and the patent base over the last two decades. The study forms an integrated approach to the use of microorganisms in damaged areas, highlighting the latest developments in the field of decomposition of explosives such as TNT, hexogen and octogen. Current trends show a shift from general biodegradation studies to in-depth analysis using non-traditional microorganisms, along with integrated soil remediation methods (introduction of beneficial microorganisms, phytoremediation). Over the past twenty years, there has been a steady increase in interest, transforming fundamental knowledge into practical patented technologies (Corredor *et al.*, 2024).

Microbial degradation is a key tool for managing areas contaminated with explosives. Studying the metagenomic and proteomic profiles of microbial communities allows for more accurate predictions of remediation effectiveness. Environmental contamination with explosives has been documented since World War I, leading to the formation of toxic and mutagenic products that require the remediation of not only soil but also groundwater. At military training grounds and in combat zones, persistent contamination with hexogen, octogen and TNT has been recorded, which suppresses microbial activity through combined effects with other pollutants, causing changes in the gene pool and metabolism of microorganisms. Microbiome transformations promote the proliferation of adaptive organisms (through enzyme reconfiguration, modified protein synthesis, and new metabolic pathways for nitrogen), but the energy costs of nitramine degradation create a bottleneck. Microbiome stability depends on metabolite interactions, competition for resources, and factors such as leaching; the presence of nitroaromatic compounds requires the stimulation of amino and nitroreductases, as many microorganisms die from mutagenic effects or membrane destruction. 16S rDNA sequencing data confirm the changes: in soils with TNT, the

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proportion *of Proteobacteria* increases to 90% (compared to 47% in clean soils), *Acidobacteria* decreases, and atypical genera (*Achromobacter*, *Phaeospirillum*, *Thiobacillus*, *Microbacterium*) appear. Contamination with high-energy nitrogen compounds leads to exponential growth of *Pseudomonas*, *Arthrobacter*, *Geobacter* and *Archaea* groups (up to 15% compared to <1% in the background), which disrupts the balance, impairs nutrient cycling and is exacerbated by the destruction of the structure from detonations. These processes are often accompanied by the release of heavy metals, increasing toxicity (Corredor *et al*., 2024; Moliszewska *et al*., 2025). Complete soil restoration is extremely difficult, but biologically mediated remediation, particularly targeted microbial bioremediation, remains the most promising approach for cleaning up xenobiotics and high-energy compounds. Further research should focus on the complex metagenomic profiles of soil microbiomes to combine ecological richness with the principles of sustainable land use. The integration of patented microbiological proces-ses into the military sphere offers low-cost solutions for minimising the environmental damage caused by military operations, ammunition production or training, which is critical for affected regions and ecosystem restoration. Given the significant impact of military activities, continued investment in remediation is a prerequisite for safe land use. The effectiveness of bioremediation measures depends on the nature of the technogenic substrate, which requires analysis of the impact of military activities on soil contamination with heavy metals and the state of microbiocenoses. Military activities have a destructive impact due to the massive contamination of metal-containing debris from shells, rockets and ammunition, leading to the release of heavy metals and the creation of pockets of toxic impact.

The study by Moliszewska *et al.* aimed to measure heavy metal levels in areas affected by artillery shelling and analyse their effect on soil microorganisms, with a particular focus on the evolution of metal-resistant populations. X-ray fluorescence spectrometry was used for the chemical analysis of soil samples and rocket debris, while the classical Koch and Hangay approaches were used for microbiological aspects. It was found that iron concentration was dominant (81991.3 ± 132.8 ppm), while for Ni, Cu and Cr, the values ranged from 4.6 to 407.5 ppm; cobalt was absent. The number of aerobic chemoorganotrophic bacteria ranged from 1.8×10^6 to 3.7×10^6 CFU/g, while the population of chromium-resistant forms was approximately ten times smaller; anaerobic forms accounted for 1.4×10^6 – 2.6×10^6 CFU/g. Three months after the initial fixation, a noticeable increase in the number of all types of microorganisms, including metal-tolerant ones, was observed, indicating the adaptation processes of the microbial community. The data obtained prove that soil microbial associations have a high reserve for self-regeneration and neutralisation of heavy metals in technogenically transformed soils. These adaptation mechanisms are not unique to military zones, but rather reflect general patterns of selection of resistant microbial groups in technogenic environments. Similar processes are observed by Finnish scientists in technogenic zones, such as railway transport areas contaminated with petroleum hydro-carbons and metals. Simulated diesel/petrol contamination at a former railway site (Finland) led to an increase in bacteria (10–1000 times), a decrease in diversity (Shannon index) and a shift towards degraders (*Proteobacteria*, *Firmicutes*, *Betaproteobacteria*). Biostimulation treatment consisted of adding nitrogen in the form of urea and enhanced growth (16S rRNA +15 times), added *Actinobacteria*, accelerated the degradation of petroleum hydrocarbons (reducing leakage by 19–34%), while natural attenuation is slower, and oxidation mobilises contaminants (Simpanen *et al*., 2016). Similar transformations of the microbiota caused by combined pollution with metals and organic compounds are also observed in local studies of technogenic areas in Ukraine. A study of technogenic load along the Chop–Uzhhorod–Sambir highway revealed a significant transformation of soil microbiota caused by the accumulation of heavy metals. In areas adjacent to the railway, an increase in the number of ammonifiers, enterobacteria and spore-forming forms was recorded against the background of suppression of nitrogen fixers, micromycetes and amylolytic microflora. Lead (0.72–1.72 MPC) was identified as the key destructive factor, whose strong correlation with ecological-trophic groups allows the latter to be used as bioindicators of pollution. Natural self-purification processes, accompanied by the appearance of pigment bacteria, are activated only outside the immediate influence of railways (Bobryk *et al*., 2016). Thus, accumulated experience from various man-made areas, including military and transport, emphasises the universality of these processes, which can be adapted for broader environmental restoration. Contamination from military activities, like other anthropogenic stresses, transforms the microbiota, forming stable consortia as a basis for bioremediation with the integration of omic technologies for monitoring and restoring agroecosystems.

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Conclusions

Consequently, ecological-trophic groups of microorganisms serve as a fundamental basis for assessing the state of soil ecosystems, reflecting biogeochemical processes and responding to anthropogenic influences as sensitive bioindicators. Agrotechnical factors such as tillage and fertilisation significantly transform the structure of the microbiome, stimulating or suppressing key groups, which highlights the need to transition to sustainable practices to preserve fertility. Salinisation and anthropogenic pollution, including military actions, simplify microbial communities, dominated by resistant taxa, but open the way to bioremediation through adaptive consortia. Research, from local monitoring in Ukraine to global surveys, demonstrates the effective-eness of bioaugmentation and -omic technologies in restoring balance, turning degradation into opportunities for revitalisation. Ultimately, integrating microbiological monitoring into agronomic strategies is key to sustainable land use, minimising risks and enhancing the resilience of agroecosystems.

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