

Trends in Global Soil Research and a Microbiome-Based Framework for Soil Health Assessment

Njomza Gashi ^{1,2} , Maja Mikolás ¹ , Péter Dávid ¹ , Péter Fauszt ¹ , Ferenc Gál ¹, László Stündl ³ , Judit Remenyik ¹  and Melinda Paholcsek ^{1,*}

- ¹ Center for Complex Systems and Microbiome Innovations, Faculty of Agricultural and Food Sciences and Environmental Management, University of Debrecen, 4032 Debrecen, Hungary; njomza.gashi@agr.unideb.hu (N.G.); mikolas.maja@agr.unideb.hu (M.M.); david.peter@agr.unideb.hu (P.D.); fauszt.peter@agr.unideb.hu (P.F.); drgalferencgabor@gmail.com (F.G.); remenyik@agr.unideb.hu (J.R.)
- ² Department of Food Technology with Biotechnology, Faculty of Agriculture and Veterinary, University of Prishtina, 10 000 Prishtina, Kosovo
- ³ Institute of Food Technology, Faculty of Agricultural and Food Sciences and Environmental Management, University of Debrecen, 4032 Debrecen, Hungary; stundl@agr.unideb.hu
- * Correspondence: paholcsek.melinda@agr.unideb.hu

Abstract

Soil health is fundamental for food security, climate regulation, and ecosystem resilience, yet global research and development efforts remain uneven and fragmented. To provide a more integrated perspective, this study examines global soil health research and development trends between 1990 and 2025 while proposing a microbiome-based framework for soil health assessment. Using a PRISMA-based methodology, we combined data from international development projects, scientific publications, patent data, and microbiome-related initiatives to evaluate temporal, thematic, and regional patterns in soil research. The results reveal a sustained increase in global soil-related research, with nutrient management and soil degradation remaining dominant topics, while soil microbiome research and carbon sequestration have emerged as the fastest-growing areas, particularly since 2015. However, significant regional disparities persist, with research concentrated in Asia, Europe, and North America. To address the lack of a coherent microbiome-based soil health assessment system, we propose a structured microbial indicator framework based on twelve functional microbial groups, evaluated through culturable abundance, functional gene abundance, and relative abundance. Additionally, we introduce a unified, database-driven microbiome reference framework that interprets soils relative to known types and conditions. Overall, this study highlights the global transition toward biologically driven and system-oriented soil research and provides a conceptual foundation for more standardized, scalable, and ecologically meaningful soil health assessment.

Keywords: soil health; soil microbiome; soil health assessment; microbial indicators; microbiome-based framework; soil degradation



Academic Editor: Robert P. Larkin

Received: 27 April 2026

Revised: 5 June 2026

Accepted: 10 June 2026

Published: 12 June 2026

Copyright: © 2026 by the authors.

Licensee MDPI, Basel, Switzerland.

This article is an open access article distributed under the terms and conditions of the [Creative Commons Attribution \(CC BY\)](https://creativecommons.org/licenses/by/4.0/) license.

1. Introduction

Soil is far more than the physical substrate beneath our feet; it is a living and highly dynamic system that underpins ecosystem functioning, food production, and human well-being. It supports a wide range of essential processes, including plant growth, water regulation, nutrient transformations, and the maintenance of an immense and largely hidden biological diversity [1]. In fact, soils are estimated to host nearly 59% of all life on

Earth, making them the most biologically diverse habitat on the planet [2]. Even at very small scales, this complexity becomes evident, a single gram of soil may contain thousands of species and millions of microorganisms, interacting through intricate networks that drive nutrient cycling, plant productivity, and carbon dynamics. Consistent with this, the FAO highlights that soils support approximately 95% of global food production and form the foundation of resilient agrifood systems [3].

Despite this central role, soil is increasingly under pressure. Current estimates suggest that around 75% of global soils are already degraded, with projections indicating that up to 90% could be affected by 2050 if current trends persist [4,5]. Much of this degradation is linked to intensified agricultural practices. For instance, the widespread use of fertilizers, often characterized by excessive nitrogen inputs relative to phosphorus and potassium, has disrupted nutrient balances and altered ecosystem functioning. Excess nitrogen contributes to eutrophication and water contamination, while inefficient phosphorus use accelerates the depletion of finite reserves and creates accessibility challenges, particularly in low-income regions. At the same time, insufficient potassium availability can limit plant water-use efficiency, reducing resilience to drought and threatening long-term productivity [6]. Tillage practices further influence soil structure and function, although their effects are not always linear. Variations in tillage intensity can alter aggregate stability, pore structure, gas exchange, and the turnover of organic matter. Both excessive disturbance and soil compaction, often associated with heavy machinery, can degrade soil structure, reduce infiltration capacity, and disrupt hydraulic processes, ultimately impairing soil functionality [7].

These pressures do not act in isolation. Climate change is increasingly interacting with land management practices, amplifying their impacts. Rising temperatures, shifting precipitation patterns, and more frequent extreme events are already destabilizing key soil processes and reducing ecosystem multifunctionality in both croplands and grasslands [8]. Even relatively small temperature increases can have measurable consequences; for example, a 1 °C rise has been associated with a 10–25% increase in pest incidence and potential reductions in major crop yields of up to 7.4% [9].

Looking ahead, the implications are substantial. The global population is projected to reach 9.8 billion by 2050 and exceed 11 billion by the end of the century [10], placing additional pressure on already stressed agricultural systems. Meeting this demand is expected to require roughly a 70% increase in caloric production [11], raising fundamental questions about whether current soil management practices are sustainable in the long term. In this context, soil health emerges not only as an environmental concern but as a central component of global food security and climate resilience.

Soil health, by integrating physical, chemical, and biological dimensions, provides a useful framework for understanding and managing soil systems in a holistic way. However, despite the rapid growth of soil-related research and policy initiatives, the global research landscape remains fragmented. Many studies focus on individual thematic areas or rely exclusively on bibliometric indicators, often overlooking the role of development investments and technological innovation. Moreover, comparative analyses that account for regional differences using normalized indicators, such as population or land area, are still limited, and relatively few studies have examined how research priorities have shifted across major policy periods.

To date, there has been no comprehensive effort to jointly integrate development investment and scientific output into a unified assessment of global soil health dynamics. To address this gap, the present study provides a multi-scalar analysis of global soil research from 1990 to 2025 by integrating international project data and scientific publications across six key thematic domains. Starting the analysis in 1990 enables a consistent

long-term assessment of global trends and captures the transition from conventional soil research to modern molecular and NGS-based approaches. Specifically, the study aims to: (i) quantify temporal trends in research and investment; (ii) evaluate thematic convergence and regional differentiation; and (iii) identify emerging research frontiers and structural imbalances. In addition, the study advances a microbiome-based framework for soil health assessment, integrating functional microbial groups with complementary indicators, and outlines a unified reference-oriented approach to support more consistent and interpretable microbiome-based evaluation of soil systems.

2. Materials and Methods

This review brings together data from international development projects, peer-reviewed scientific literature, and patent records (presented in Supplementary Materials) to capture soil health from policy, research, and innovation perspectives. The study was conducted following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) framework to ensure a transparent and consistent approach to identifying, screening, and selecting relevant projects, publications, and patents [12]. PRISMA workflows for all data sources are provided in Supplementary File S1. Records were identified through database-specific keyword searches and subsequently screened using predefined inclusion and exclusion criteria. Depending on the database, screening involved the application of temporal limits (1990–2025), language restrictions, document-type filters, subject-area restrictions, and the removal of duplicate or non-eligible records. Only records meeting all selection criteria were retained for subsequent analyses.

2.1. Projects

Project data were collected from the World Bank Group database [13] using the keywords “soil health”, “soil quality”, and “soil degradation” to capture initiatives related to soil functionality, restoration, and sustainable land management. Only projects implemented between 1990 and 2025 were included, excluding pipeline and dropped projects, resulting in 1402 active and completed projects. To account for the emerging field of soil microbiome research, additional data were obtained from the CORDIS database using the keyword “soil microbiome” [14], as no such projects were identified in the World Bank dataset. “Soil health” refers to studies addressing the overall functioning of soil as a living system, often in connection with soil organic matter. “Soil quality” reflects physico-chemical properties and traditional indicator-based assessments of soil condition. “Soil degradation” includes processes that reduce soil functionality, such as erosion, nutrient depletion, and contamination. “Soil microbiome” refers to research focusing on soil microbial communities, including diversity, composition, and functional potential. Applying the same temporal range and restricting to English-language records, 190 projects were retained and grouped into sub-periods for temporal analysis. The detailed identification, screening, exclusion, and inclusion steps for both the World Bank and CORDIS datasets are presented in Supplementary File S1 (Figure S1).

2.2. Research Papers

Scientific literature was collected from Scopus [15], Web of Science [16], and PubMed [17]. The search strategy was organized around six thematic domains: (1) “soil health” AND “soil organic matter”, (2) “soil degradation”, (3) “soil microbiome” OR “soil microbiology”, (4) “soil carbon sequestration” AND “climate change”, (5) (“nutrient management” OR “fertilizer” OR “fertilization” OR “fertilisation”) AND “soil”, and (6) (“tillage” OR “till”) AND “soil”. These domains were selected to reflect the FAO’s holistic definition of soil health as the capacity of soil to function as a living system that

sustains productivity, environmental quality, and human health [18,19]. Collectively, they capture the major dimensions of soil health, including intrinsic soil properties (“soil health and organic matter”, and the “soil microbiome”), key degradation processes (“soil degradation”), ecosystem services (“soil carbon sequestration and climate regulation”), and management interventions (“nutrient management” and “tillage”). While other important topics, such as soil biodiversity beyond microorganisms and soil water regulation, were not included as separate categories, they are embedded within these domains. This structure is consistent with both classical soil science frameworks and recent bibliometric analyses of soil research clusters, providing broad coverage of the biological, physical, chemical, and management-related dimensions of soil health while maintaining a tractable framework for global trend analysis and minimizing thematic overlap [20]. The search was limited to publications from 1990 to 2025, written in English, and classified as articles or review papers.

Although all three databases were screened, Scopus consistently provided the most extensive coverage across all thematic domains. For this reason, Scopus records were used as the primary dataset for bibliometric and quantitative analyses, while Web of Science and PubMed were retained to support comparative assessment of annual publication trends. The complete PRISMA workflow, including database-specific filtering and record retention for Scopus, Web of Science, and PubMed, is shown in Supplementary File S1 (Figure S2). Furthermore, keywords associated with scientific publications were also extracted and analyzed to capture thematic patterns in the literature. Following standardization and cleaning, keywords were ranked based on their frequency of occurrence, defined as the number of documents in which each keyword appears. For each research theme, the top 15 most frequently occurring keywords were selected to represent dominant research directions. These keywords were further grouped into thematic categories based on their conceptual similarity, enabling cross-theme comparison of major research domains.

2.3. Patents

Patent data were obtained from the World Intellectual Property Organization (WIPO) PATENTSCOPE database to capture technological innovation across soil-related domains. The search strategy followed the same six thematic areas used in the scientific literature analysis: (1) soil health and organic matter, (2) soil degradation, (3) soil microbiome, (4) soil carbon sequestration and climate change, (5) nutrient management, and (6) tillage. A consistent time filter (1990–2025) was applied across all searches.

Due to export limitations within PATENTSCOPE, records were retrieved in multiple batches and subsequently merged into a single dataset. Duplicate entries were removed using unique application identifiers, and records lacking valid application year information were excluded. For geographic analyses, non-country patent authorities and regional systems (e.g., EP, WO, PCT, ARIPO, and GCC) were excluded to ensure consistent country-level comparisons. The final dataset was used to assess patent distribution across countries. The complete patent selection workflow is presented in Supplementary File S1 (Figure S3).

2.4. Data Processing and Statistical Analysis

All data processing, statistical analyses, and visualizations were carried out in RSudio (v2025.09.0+387, R Foundation for Statistical Computing, Vienna, Austria) [21]. Data cleaning and restructuring were performed using the packages dplyr and tidyr [22,23].

Temporal analyses were based on annual aggregation of project, publication, and patent counts (1990–2025). Projects were summarized by starting year and thematic domain, with multi-topic projects counted in each relevant category. In selected analyses (Figure 1),

soil health, soil quality, and soil degradation were grouped, while soil microbiome was analyzed separately. Regional patterns were assessed using World Bank classifications and expressed as percentage shares. Trends were visualized using line plots, while cross-database comparisons combined Scopus bar plots with Web of Science and PubMed line overlays. Keywords were standardized (e.g., lowercase, removal of inconsistencies), and a subset of relevant terms was selected (see Supplementary File S1). In addition to the bibliometric and statistical analyses, a comparative visualization of microbiome differences between healthy and degraded soils was constructed based on literature-derived relative abundance data. Representative values for dominant microbial taxa were compiled across multiple soil types, including chernozem, forest, alluvial, peat, and saline soils. Paired comparisons between conditions were visualized using dumbbell plots. Additional analyses related to country-level comparisons are provided in Supplementary File S1.

3. Results and Discussions

3.1. Evolution of Soil-Related Projects

The temporal evolution of soil-related projects between 1990 and 2025 reveals distinct phases linked to shifts in global environmental governance (Figure 1). Project activity increased rapidly in the early 1990s, rising from 17 projects in 1990 to over 60 by the mid-decade, coinciding with the policy momentum of the Rio Earth Summit [24] and the establishment of the UN Convention to Combat Desertification [25], which elevated land degradation on the global agenda.

A second peak occurred between 2003 and 2006, reaching approximately 70 projects in 2004 (Figure 1a). During this period, soil-related initiatives became more closely aligned with food security, poverty reduction, and climate mitigation. In particular, the recognition of soil organic carbon as a key component of climate regulation strengthened the integration of soil governance into climate policy frameworks [26–28]. After 2010, project numbers gradually declined, particularly between 2016 and 2019. However, this trend reflects a shift toward integrated, cross-sectoral programs following the introduction of the Sustainable Development Goals [29], where soil-related activities are often embedded rather than explicitly labeled. This period coincided with the COVID-19 pandemic, which affected agricultural systems and financing priorities globally [30,31]. A modest recovery after 2020 aligns with renewed interest in regenerative agriculture and nature-based solutions [32], suggesting a process of mainstreaming rather than decline.

A comparison with soil microbiome projects highlights a clear shift in scientific focus. While traditional themes such as soil health, soil quality, and soil degradation dominated until the mid-2010s, microbiome-related research has expanded rapidly since 2015. This divergence is also evident in log-transformed trends (Figure 1b), where soil health increasingly reflects biological functioning and ecosystem resilience, while soil quality remains associated with physico-chemical properties. Microbiome research exhibits the strongest growth (CAGR = 5.72%), whereas soil quality (−2.93%) and soil health (−3.27%) show declining trends, and soil degradation remains relatively stable. These patterns indicate a shift from traditional indicator-based approaches toward biologically driven, system-oriented soil research.

At the same time, soil research exhibits a combination of thematic convergence and regional differentiation. Globally, core topics such as soil and water pollution, land management, climate change, and water resources form a shared conceptual framework, consistent with recent bibliometric evidence [33,34]. Despite this convergence, regional priorities differ substantially. East Asia and the Pacific show strong emphasis on pollution and climate-related themes, reflecting pressures from industrialization, urbanization, and intensive

land use [35,36]. In contrast, Eastern and Southern Africa focus more on disaster risk management and resilience, driven by droughts, climate variability, and land degradation [37].

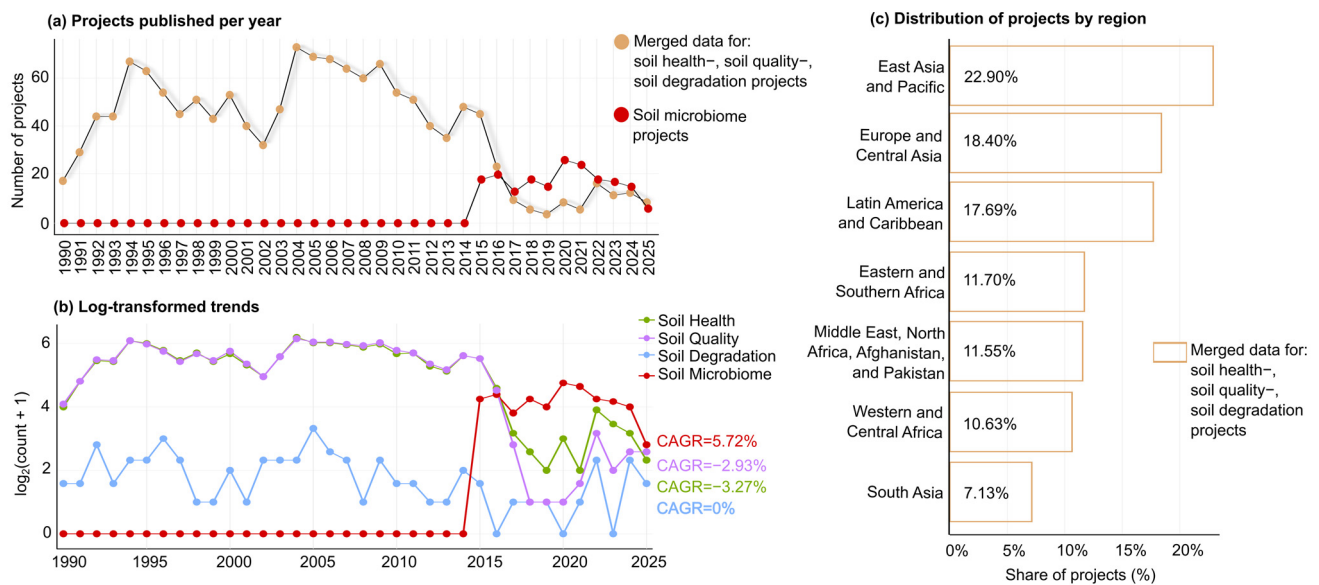


Figure 1. Temporal trends, growth dynamics, and regional distribution of soil-related projects (1990–2025). (a) Annual number of projects worldwide, comparing combined soil health, soil quality, and soil degradation projects with microbiome-related projects. (b) Log-transformed trends ($\log_2(\text{count} + 1)$) and compound annual growth rates (CAGR) of major soil themes, highlighting differences in growth dynamics across topics. (c) Regional distribution expressed as percentage share of total projects for the combined soil health, soil quality, and soil degradation domains.

Regionally, project distribution remains uneven. East Asia and the Pacific (22.90%), Europe and Central Asia (18.40%), and Latin America and the Caribbean (17.69%) dominate (Figure 1c), reflecting stronger institutional capacity and research investment [38,39]. African regions also contribute substantially, driven by vulnerability to land degradation and sustained international support [18,40,41]. In contrast, South Asia (7.13%) remains underrepresented, likely due to institutional constraints and the integration of soil-related activities into broader programs.

3.2. Three-Decade Trends in Soil Research

Building on the regional and thematic patterns described earlier, the temporal analysis provides further insight into how global soil research priorities have evolved over time. Figure 2 shows a steady increase in publication output from 1990 to 2025, with gradual growth in the early decades followed by a marked acceleration after 2010 and especially after 2020.

The largest absolute increases are observed in “soil degradation” and “nutrient management”, reflecting their central role in addressing land degradation, agricultural sustainability, and food security. These trends are closely linked to pressures from intensive agricultural practices, nutrient imbalances, and climate-driven disruptions to soil processes. Recent research further emphasizes integrated nutrient management and soil conservation strategies as key responses to these challenges [42,43].

In relative terms, however, the most rapid expansion is observed in the “soil microbiome” domain. Although initially limited, microbiome-related research has accelerated significantly since the early 2000s, with a sharp increase after 2015, positioning it as one of the fastest-growing research areas in soil science [44–46]. “Soil carbon sequestration and climate change” also show strong growth, reflecting the increasing integration of soil

processes into climate mitigation strategies. In contrast, “soil health and organic matter” display more stable and moderate growth, indicating a more mature research area.

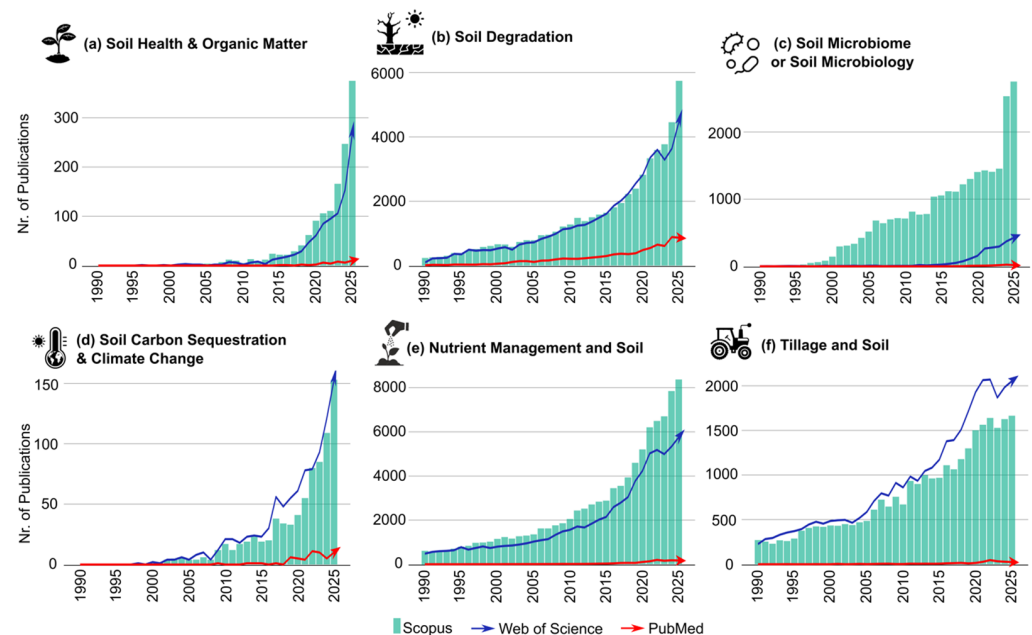


Figure 2. Temporal trends in soil research themes (1990–2025). Annual publications are shown for six topics: (a) Soil Health & Organic Matter; (b) Soil Degradation; (c) Soil Microbiome; (d) Soil Carbon Sequestration & Climate Change; (e) Nutrient Management; and (f) Tillage. Green bars (Scopus) indicate primary counts, while blue (Web of Science) and red (PubMed) lines enable comparison. The x-axis represents the study period (1990–2025), and the y-axis represents the number of publications per year.

These developments align with broader policy and institutional shifts, including the Sustainable Development Goals and the Paris Agreement, which have reinforced the role of soils in climate and sustainability agendas. The recent expansion of research activity also reflects increased global collaboration and technological advancement, despite temporary disruptions during the COVID-19 period [47,48]. These observed trends confirm a structural transition in soil research toward more integrative, biologically driven, and solution-oriented approaches, with increasing emphasis on resilience, carbon management, and microbiome-based understanding of soil systems.

3.3. Dominant Research Themes Revealed by Keyword Analysis

To better understand the primary focus of research across different soil-related themes, a keyword-based analysis was conducted. The results presented in Figure 3 reveal not only diversity but a clear dominance of specific research directions across themes. While each theme retains distinct focal points, several keywords consistently emerge as central across domains, particularly soil organic matter, soil organic carbon, and microbial communities, highlighting their foundational role in contemporary soil science. A cross-theme synthesis demonstrates a pronounced convergence toward three core dimensions: carbon dynamics, microbial processes, and agricultural management practices. This convergence reflects a fundamental shift in soil research toward integrated, function-oriented perspectives, where soil organic matter is recognized as a key regulator of ecosystem functioning [49], and microbial communities are increasingly understood as primary drivers of nutrient cycling and soil resilience [50].

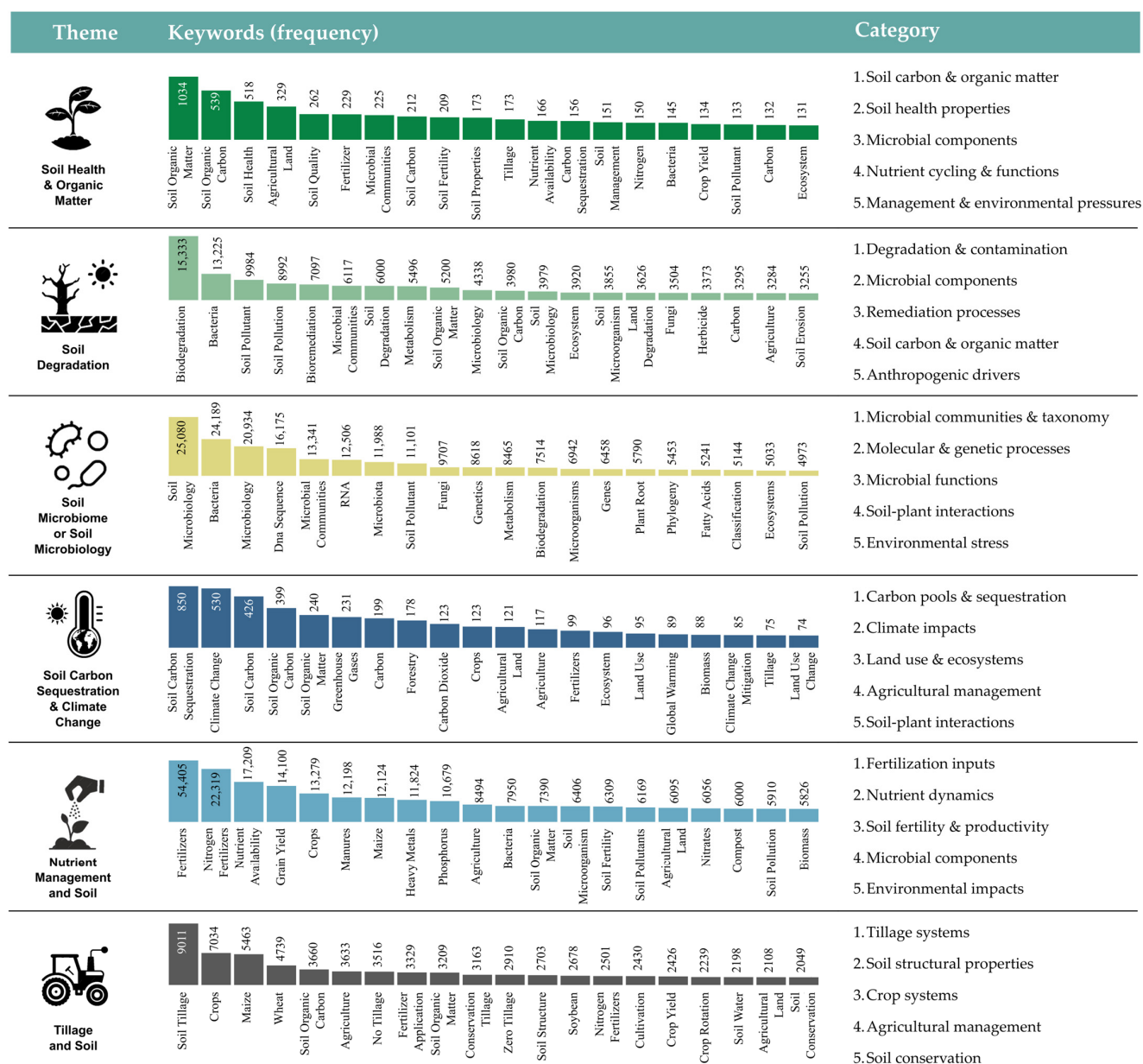


Figure 3. Keyword frequency and thematic categorization across soil research domains. Keywords were extracted from Scopus records, standardized, and ranked according to frequency of occurrence, defined as the number of documents in which each keyword appears. For each of the six predefined research themes (Soil Health & Organic Matter, Soil Degradation, Soil Microbiome, Soil Carbon Sequestration & Climate Change, Nutrient Management, and Tillage), the top 15 most frequent keywords are shown. Keywords were further grouped into broader conceptual categories based on semantic similarity. Categories represent higher-level thematic groupings of the keywords and are used to enable cross-theme comparison of dominant research domains.

However, despite this convergence, the analysis also reveals a critical limitation: the persistent fragmentation of soil health assessment approaches. Different research domains rely on isolated indicators, ranging from gene-level and biochemical measurements to management-based and environmental descriptors, without a unified framework to integrate them. This fragmentation has been widely recognized as a major challenge in soil science [51]. Additionally, the dominance of microbiome-related, carbon-focused, and environmentally driven keywords indicates not only current research priorities but also the direction in which the field is evolving. These patterns clearly demonstrate that soil health is increasingly being approached as a biologically driven and system-level concept.

Nevertheless, the absence of a standardized framework capable of integrating microbial, functional, and management-related dimensions remains a key gap. Addressing this gap is essential for advancing soil health assessment beyond descriptive indicators toward a more coherent and operational system. In this context, microbiome-based approaches emerge not merely as a growing research trend, but as a central component in the development of a multidimensional framework linking biological activity, soil function, and sustainability outcomes.

3.4. Geographical Distribution and Growth Trends in Soil Research

The continental distribution of research output reveals pronounced structural asymmetries in global soil science (Figure 4). Asia and Europe dominate across most thematic domains, with North America also maintaining a substantial presence, while Africa, South America, and Oceania remain comparatively underrepresented despite facing significant soil degradation pressures. Asia leads in key areas such as “Soil Health and Organic Matter”, “Soil Degradation”, “Soil Microbiome”, and “Nutrient Management”, reflecting intensive agricultural systems, rapid industrialization, and expanding research capacity. Europe and North America follow, supported by strong regulatory frameworks and sustained investment in soil monitoring and sustainable land management. In contrast, lower contributions from Africa, South America, and Oceania are likely linked to limitations in research infrastructure, long-term datasets, and funding availability [52,53]. This imbalance is particularly evident in “Soil Degradation” research, where Africa remains underrepresented despite high vulnerability to land degradation, consistent with previous assessments highlighting structural constraints in data availability and research capacity [19,25].

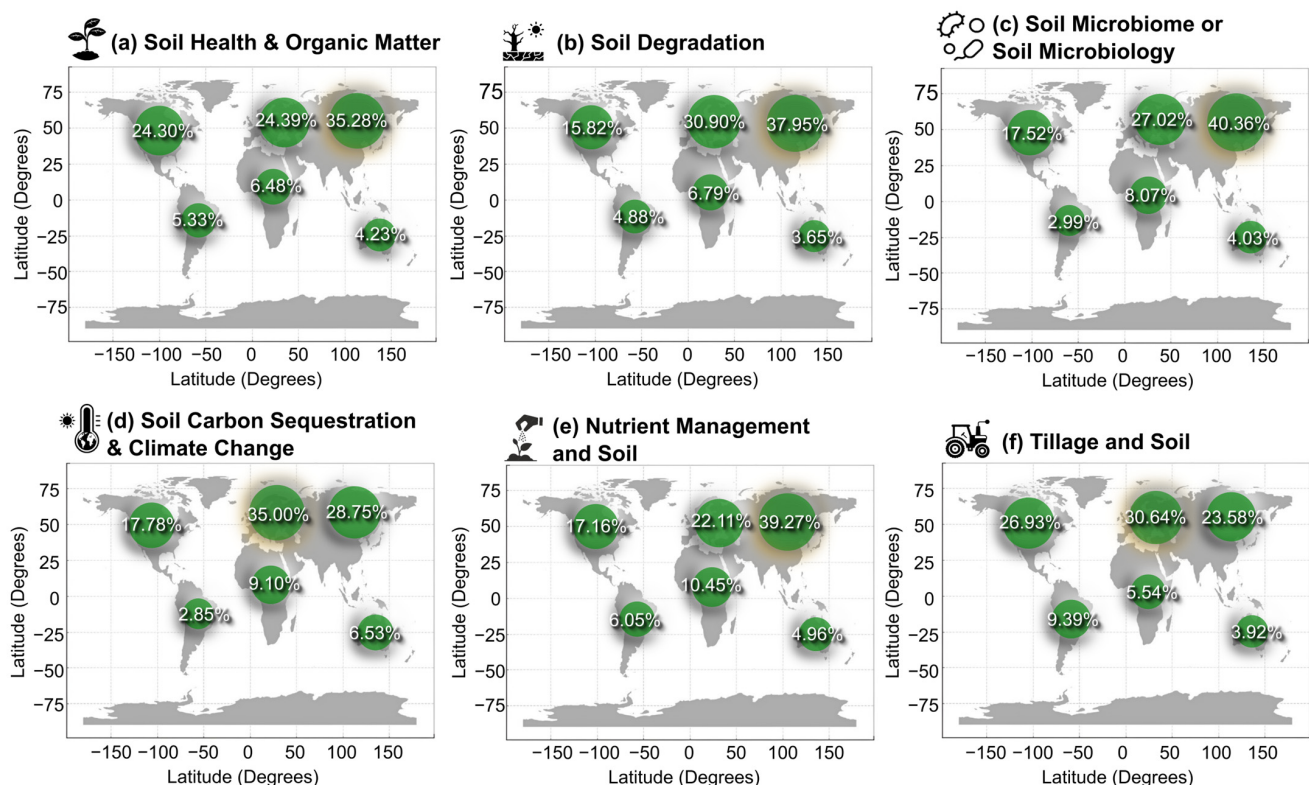


Figure 4. Global distribution and temporal growth of soil research themes (1990–2025). (a–f) Continental distribution of publications (%) across six thematic domains: Soil Health & Organic Matter, Soil Degradation, Soil Microbiome/Microbiology, Soil Carbon Sequestration & Climate Change, Nutrient Management and Soil, and Tillage and Soil. Bubble size indicates each continent’s share of total publications within a given topic.

A similar pattern is observed in “Soil Microbiome” research, where Asia shows the strongest dominance, supported by advances in sequencing infrastructure and increased investment in genomic technologies, while other regions remain constrained by limited laboratory and bioinformatics capacity [54,55]. In “Soil Carbon Sequestration and Climate Change”, Europe leads, reflecting the strong integration of soil carbon into climate policy frameworks, including carbon farming and land-use regulations [56,57]. Likewise, Europe and North America dominate “Tillage and Soil” research, supported by long-term experimental systems and mechanized agricultural practices, whereas other regions remain less represented due to structural and technological limitations [53,58].

Log-transformed trends (Figure 5) further highlight differences in growth dynamics across themes and indicate a broader shift in research focus. “Soil Microbiome” exhibits the highest growth rate (CAGR = 23.46%), followed by “Soil Carbon Sequestration and Climate Change” (20.34%) and “Soil Health and Organic Matter” (17.89%). In contrast, “Tillage” and “Nutrient Management” show more moderate growth, while “Soil Degradation” remains relatively stable. These patterns suggest a transition from traditional, practice-based approaches toward biologically driven and climate-oriented soil research, consistent with the increasing emphasis on system-level processes and ecosystem resilience. It should be noted that the bibliometric analyses were primarily based on Scopus records, which, despite providing the broadest coverage across all thematic domains, may underrepresent non-English journals and certain regional publications. As a result, research output from some regions may be underestimated, potentially influencing the observed geographic distribution patterns. Although publication trends were compared across Scopus, Web of Science, and PubMed, the regional analyses should be interpreted with consideration of database-specific coverage biases.

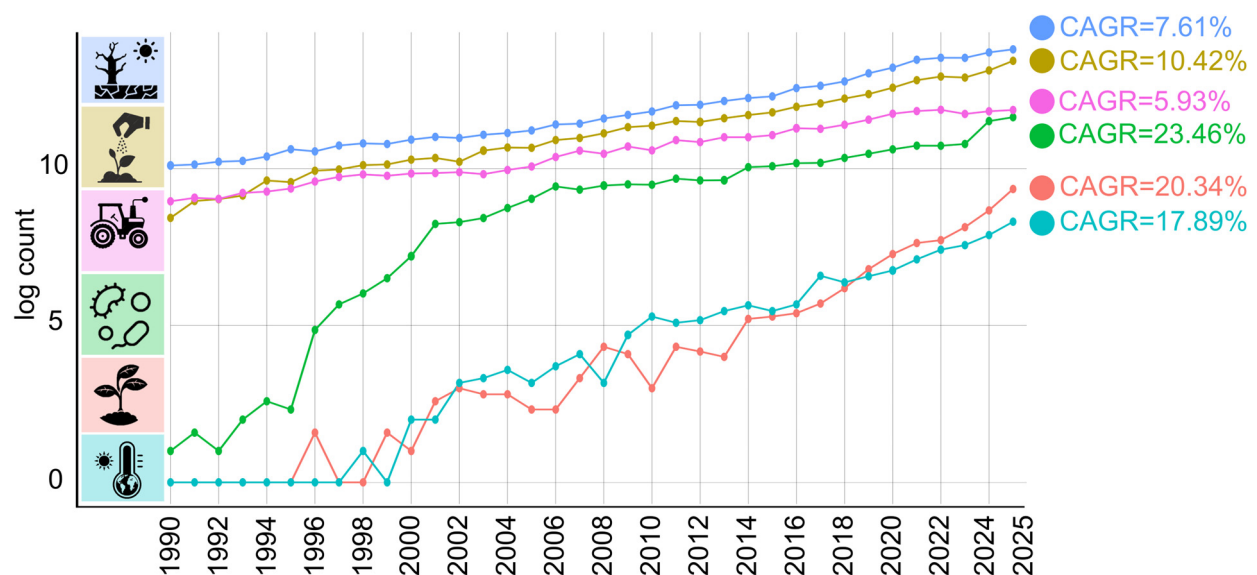


Figure 5. Log-transformed publication trends ($\log_2[\text{count} + 1]$) for all themes from 1990 to 2025. Lines represent annual outputs and CAGR values summarize long-term growth dynamics.

3.5. Technological Innovation Patterns Across Soil Research Domains

Patent activity across soil-related themes is strongly concentrated in a relatively small number of countries (Figure 6). The United States, Australia, and Canada consistently rank among the leading contributors across most domains, indicating a prominent role in the development of soil-related technologies. Other countries, including India, the United Kingdom, Israel, New Zealand, and South Africa, also contribute across multiple themes, although at lower levels. The observed geographic distribution highlights the uneven

nature of technological innovation in soil-related research. Countries with more established research systems and greater innovation capacity tend to contribute a larger share of patent activity, whereas participation from many other regions remains comparatively limited.

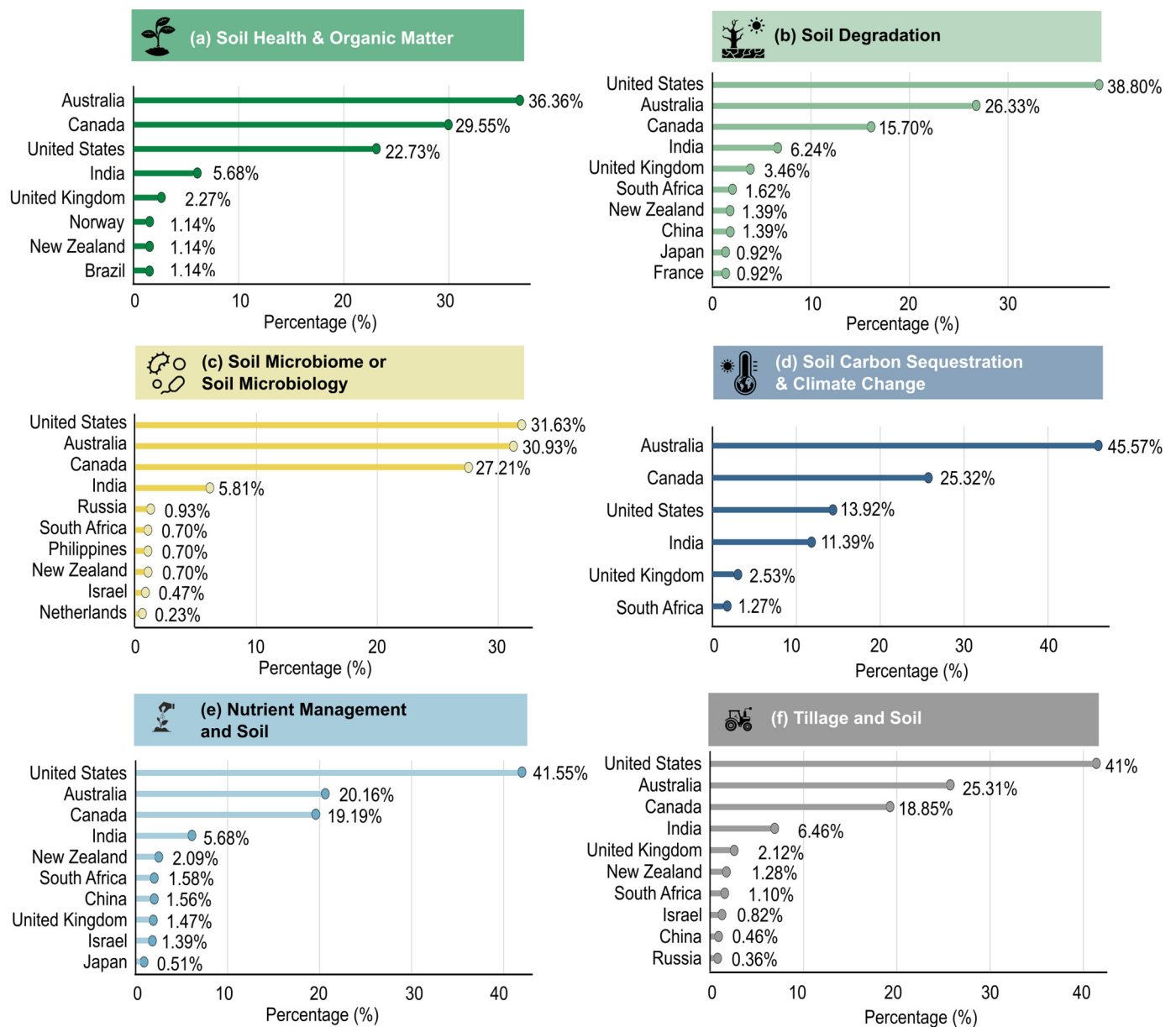


Figure 6. Geographic distribution of patent activity across soil-related research domains (1990–2025). Lollipop charts present the leading patent-contributing countries for each thematic domain. Values are expressed as percentages of the total patent records within each domain. Where fewer than ten contributing countries were identified, all countries are displayed.

3.6. Methodological Approaches in Soil Microbiome Research

Building on the trends identified in the previous sections, the increasing prominence of microbiome-related research highlights the need to examine how soil microbial communities are studied and assessed. Soil microbiome research faces several methodological challenges, including the control of soil chemical and physical variability, the selection of appropriate reference conditions, and limited comparability across studies [59]. These challenges are further exacerbated by the lack of standardized methodologies, which hinders cross-study comparison, data integration, and the development of consistent soil health indicators [60]. In addition, linking specific microbial taxa to ecological functions remains

difficult, as closely related organisms may exhibit contrasting roles depending on environmental conditions or horizontal gene transfer. Furthermore, widely used DNA-based sequencing approaches primarily reflect genetic potential rather than actual biological activity, thereby overlooking the substantial proportion of dormant microorganisms present in soils [61]. As a result, interpretations based solely on taxonomic or genomic data may not fully capture functional dynamics within soil systems.

To address these limitations, a range of analytical approaches have been developed, targeting different dimensions of the soil microbiome, including microbial biomass, community composition, functional potential, and metabolic activity. These methods vary in analytical resolution, technical complexity, and data requirements. Importantly, no single approach is sufficient to capture the full complexity of microbial functioning, reinforcing the need for methodological harmonization and the complementary use of multiple techniques depending on the specific objectives of the study. Table 1 summarizes the principal methodological categories used in soil microbiome research, highlighting their analytical targets, key strengths, and inherent limitations, and providing a basis for integrating microbial indicators into soil health assessment frameworks.

Table 1. Summary of methods used to analyze soil microbial communities and their functional attributes.

Method Category	Method	Research Question	Key Strengths	Key Limitations	References
Classical and biomass-based methods	Culture-based methods (CFU counts)	How many viable, culturable microorganisms are present?	Simple; enables strain isolation	<1 of microbes are culturable	[62,63]
	Microbial biomass C/N (fumigation–extraction)	How much living microbial biomass is present in soil?	Integrative estimate of living microbial biomass	No taxonomic or functional resolution	[64,65]
	Phospholipid fatty acid (PLFA) analysis	How large is the living microbial community and what are its major groups?	Quantitative; functional group resolution	Low taxonomic specificity	[66,67]
Molecular and sequencing methods	Metabarcoding/targeted amplicon sequencing (16S rRNA, ITS)	Who is there?	High throughput; widely comparable; cost-effective	Provides relative, not absolute abundance; limited functional insight	[68,69]
	Shotgun metagenomics	What can they do (genetic potential)?	Unbiased, stable DNA; broad functional coverage	High cost; complex data analysis, does not indicate activity	[70,71]
	Metatranscriptomics	What genes are being expressed?	Reflects real-time microbial activity	RNA instability; high technical complexity	[71,72]
	Metaproteomics	What proteins are produced?	Direct evidence of functional expression	Protein extraction, interference from humic substances, identification of low-abundance proteins	[73,74]
	Metabolomics	What are the biochemical outputs?	Captures final functional outcomes	Difficult compound identification	[75,76]
Emerging and field-deployable methods	Biosensors (aptamer-, enzyme-, or microbe-based)	What specific process or compound is active now?	Real-time, in situ monitoring	Still under development	[77,78]
	Portable qPCR/lab-on-chip systems	How much of a specific gene or pathogen is present?	Rapid field diagnostics	Limited multiplexing	[79,80]
	Soil health test kits (integrated indicators)	Is the soil generally functioning well?	Farmer-friendly	Low microbial specificity	[81,82]

3.7. Microbial Indicators Based on Key Microbially Mediated Soil Functions (MMSFs)

To address the fragmentation identified across soil research domains, this study proposes a structured microbiome-based framework for soil health assessment based on twelve key microbially mediated soil functions (12 MMSFs) (Table 2). As a central component of this framework, we systematically defined a core set of twelve key microbially mediated soil functions (12 MMSFs) representing the most critical biological processes underpinning soil

health. These MMSFs were selected based on their recurrent prominence in the literature, their ecological relevance to major soil functions, and their applicability as interpretable microbiome-linked indicators. Particular emphasis was placed on ensuring representation of the principal microbial processes involved in major soil biogeochemical cycles, especially carbon (C), nitrogen (N), and phosphorus (P) cycling, which are central to nutrient availability, organic matter turnover, soil fertility, and ecosystem stability. In addition, the selected functions were chosen to capture essential ecosystem processes related to nutrient cycling, nutrient mobilization, plant–microbe interactions, environmental resilience, and stress response under different soil conditions, and include nitrogen fixation; phosphorus solubilization; hydrocarbon degradation; potassium solubilization; phytohormone production; organic matter decomposition; siderophore production; mycorrhizal symbiosis (nutrient uptake enhancement); plant growth promotion; bioremediation; antibiotic resistance; and methane oxidation. Together, these functional groups form a comprehensive and functionally integrated representation of soil microbiome activity. To further support the operationalization of this framework, representative microbial taxa associated with each of the twelve functional groups were compiled and are presented in Supplementary File S2. This provides a clear taxonomic reference linking functional potential to microbial community composition. In practical applications, these microbial indicators should be interpreted relative to soil-specific reference conditions rather than universal thresholds. For example, healthy chernozem soils are generally characterized by higher abundances of nutrient-cycling microorganisms, including nitrogen-fixing and phosphorus-solubilizing taxa, together with greater representation of associated functional genes. In contrast, degraded chernozem soils often exhibit reduced abundance of these functional groups and lower functional potential [83]. Similarly, healthy forest soils typically show greater fungal abundance and organic matter decomposition capacity, whereas degraded forest soils are associated with reduced functional diversity and impaired nutrient cycling [84]. Therefore, microbiome-based soil health assessment should compare microbial indicators against reference datasets developed for comparable soil types, land uses, and climatic conditions rather than relying on universal indicator thresholds.

For each functional group, three complementary indicators were defined: culturable abundance (CFU-based), functional gene abundance, and relative abundance within the microbial community. These indicators reflect three distinct but complementary dimensions of soil biological status: the cultivable fraction, functional potential, and community structure. Although only a relatively small fraction of soil microorganisms is readily culturable, culture-dependent approaches remain valuable for assessing the viable and functionally active fraction of microbial communities. In contrast to sequencing-based approaches, which primarily provide information on relative abundance and genetic potential, culturable abundance can offer direct insight into metabolically active microorganisms associated with specific soil functions. Therefore, within the proposed framework, CFU-based indicators are not intended to replace NGS-based methodologies, but rather to complement molecular approaches by integrating information on viable microbial populations, functional potential, and community structure. The framework is based on the combined evaluation of these dimensions across the selected functional groups. Importantly, it is intended as a comparative and context-dependent system rather than a fixed-threshold model. In practice, soil health assessment involves interpreting indicator patterns relative to reference conditions, such as well-functioning (healthy) versus degraded soils of comparable type and land-use context. Under this approach, soil health is inferred not simply from uniformly higher or lower values, but from the extent to which microbiome profiles support balanced ecosystem functioning, including nutrient cycling, plant-associated processes, and resilience to disturbance. Conversely, deviations from these reference patterns may indicate

ecological imbalance or functional impairment. Higher microbial abundance, greater functional gene representation, and balanced community composition in healthy soils generally indicate active nutrient cycling and stable ecosystem functioning, whereas reduced values or imbalanced patterns in degraded soils reflect functional impairment. Importantly, the framework is not based on a single indicator or function, but on the integration of multiple microbial processes. This integrative approach enables a more comprehensive and operational assessment of soil health by linking measurable microbial indicators to ecosystem functions. The framework is flexible and can be adapted to different soil conditions and research contexts, allowing researchers to apply one or more indicator types across relevant functional groups. In this way, it provides a structured basis for incorporating microbiome data into soil health evaluation and supports the transition toward biologically informed, system-level assessment of soil systems.

Table 2. Illustrative examples of key microbially mediated soil functions (MMSFs) in healthy and degraded soils based on culture-dependent counts (CFU g^{−1} soil), culture-independent quantification of functional genes (qPCR gene copies), and relative abundance.

Function *	Indicator	Degraded Soil	Healthy Soil
Nitrogen fixation	CFU [85,86]	1.1×10^2	3.88×10^6
	nifH gene [87,88]	2.88×10^5 copy/g of dry soil	$1.0\text{--}4.6 \times 10^7$ copies/g of soil
	Relative abundance [89]	No data available	21.5%
	Representative species (Supplementary Table S1)	[90–120]	
Phosphorus solubilization	CFU [121,122]	10^{-2}	4×10^8
	phoD gene [123]	1.33×10^5 copies/g of dry soil	5.80×10^7 copy/g of dry soil
	gcd gene [123,124]	1.46×10^4 copy/g of dry soil	2.19×10^8 copies/g of soil
	Relative abundance [125]	0.18%	13.13%
	Representative species (Supplementary Table S1)	[113,126–175]	
Potassium solubilization	CFU [176,177]	4×10^2	75×10^4
	pqqC gene [178]	3.25×10^4 copies/g of dry soil	1.44×10^9 copies/g of dry soil
	Relative abundance [179]	5.46%	12.25%
	Representative species (Supplementary Table S1)	[159,180–198]	
Phytohormone production	CFU [199,200]	1×10^5	1.5×10^5
	acdS gene [201]	$1.0 \times 10^{1.91}$ copies/g of soil	1.0×10^{12} copies/g of soil
	Relative abundance [202,203]	7%	80%
	Representative species (Supplementary Table S1)	[98,204–206]	
Organic matter decomposition	CFU [207]	6.6×10^3	1.5×10^4
	chiA gene [208,209]	1.70×10^5 copies/g of dry soil	3.5×10^8 copies/g of dry soil
	cbhI gene [210,211]	0.17×10^4 copies/g of soil	7.2×10^4 copies/g of soil
	GH48 gene [210,211]	1.04×10^3 copies/g of soil	5.96×10^5 copies/g of soil
	Relative abundance	No data available	No data available
	Representative species (Supplementary Table S1)	[212–240]	
Siderophore production	CFU [241]	2.6×10^2	2×10^6
	PKS type I [242,243]	5.77×10^2 copies/g of dry weight of soil	9.39×10^6 copies/g of dry weight of soil
	Relative abundance [244]	47%	85%
	Representative species (Supplementary Table S1)	[245–251]	
Mycorrhizal symbiosis (Nutrient uptake enhancement)	CFU [252]	3.0×10^6	1.18×10^8
	AMF-specific 18S rRNA gene [253]	1.2×10^6 copies/g of soil	2.1×10^8 copies/g of soil
	Relative abundance [254]	0.06%	98.16%
	Representative species (Supplementary Table S1)	[123,255–291]	

Table 2. Cont.

Function *	Indicator	Degraded Soil	Healthy Soil
Plant growth promotion	CFU [292]	10^5 copies/g of soil	5.9×10^7 copies/g of soil
	phoD gene [123]	1.33×10^5 copies/g of dry soil	5.80×10^7 copies/g of dry soil
	gcd gene [123,124]	1.46×10^4 copies/g of dry soil	2.19×10^8 copies/g of dry soil
	acdS gene [201,293]	8.1×10^1 copies/g of soil	1×10^{12} copies/g of soil
	Relative abundance	No data available	No data available
	Representative species (Supplementary Table S1)	[98,112,113,143,233,294–309]	
Bioremediation	CFU [310,311]	10^3	7.32×10^6
	nahAc gene [312]	5×10^3 copies/g of soil	10^7 copies/g of soil
	arsC gene [313]	0.88×10^4 copies/ng total DNA	1.56×10^5 copies/ng total DNA
	arsM gene [314]	0.4×10^7 copies/g of dry soil	2.3×10^7 copies/g of dry soil
	Relative abundance [315]	8.63%	0.01%
	Representative species (Supplementary Table S1)	[212,316–319]	
Hydrocarbon degradation	CFU [320]	$373 \pm 56 \times 10^3$	$8 \pm 2 \times 10^3$
	alkB gene [321,322]	5.0×10^8 cells/g-soil	0.9×10^4 copies per nanogram of soil
	Nah gene [323,324]	1.1×10^8 copies/g of dry mass soil	Not detectable
	Relative abundance [325]	10%	1%
	Representative species (Supplementary Table S1)	[326–355]	
Antibiotic resistance	CFU [356]	$>2.0 \times 10^4$	6
	sulI gene [357]	4.37×10^7	2.12×10^3
	erm(B) [357]	9.57×10^8	Not detectable
	intI1 gene [357]	4.12×10^7	3.17×10^3
	Relative abundance [358]	74%	3%
	Representative species (Supplementary Table S1)	[189,319,359–371]	
Methane oxidizers	CFU [372]	1×10^2	1×10^9
	pmoA gene [373,374]	10^3	1.1×10^8
	Relative abundance [290,375]	0%	57%
	Representative species (Supplementary Table S1)	[376–393]	

* Absolute microbial abundance values vary widely depending on soil type, climate, crop, management system, and analytical method. These values were compiled from published studies and are intended as reference examples rather than universal threshold values for soil health assessment. Instead, they illustrate consistent relative trends across studies, demonstrating that healthy soils are characterized by enhanced activity and representation of key microbially mediated soil functions (MMSFs), whereas degraded soils exhibit reduced or imbalanced functional profiles. Accordingly, the proposed framework should be applied through comparisons with appropriate reference datasets for similar soil types and environmental conditions rather than fixed indicator cut-offs. Representative microbial taxa associated with each MMSF are provided in Supplementary Table S1.

Nevertheless, several limitations should be acknowledged. The comparative values summarized in Table 2 were compiled from independent studies conducted under different experimental conditions, soil types, climatic regions, sampling strategies, and analytical methodologies. Consequently, the presented framework should currently be interpreted as a conceptual and reference-oriented model rather than a fully validated universal assessment system. The purpose of the framework is to demonstrate how multiple microbiome-linked indicators and functional groups may be integrated into a structured soil health assessment approach. Accordingly, the values presented in Table 2 should be interpreted as illustrative reference examples rather than fixed criteria for classifying soil health status. Future validation will require large-scale, cross-regional studies based on standardized sampling protocols, harmonized analytical methodologies, and coordinated multi-omics datasets to establish robust reference ranges and improve comparability across soil systems. Such efforts could include cross-site comparisons across contrasting soil types and climatic regions, as well as the development of reference soil microbiome libraries to support framework calibration and benchmarking.

3.8. Toward a Unified Microbiome Reference Framework for Soil Health Interpretation

Conceptually, this approach would represent an important step toward operational soil microbiome diagnostics. Rather than asking only which taxa or functions are present, it would enable the more informative question of what a given microbiome profile means in relation to known ecological baselines and trajectories. In this sense, a unified microbiome reference framework could provide the missing interpretative layer needed to translate soil microbiome research from descriptive profiling into a comparative, scalable, and decision-supportive tool for soil health evaluation.

Although the microbial indicator framework outlined above provides a structured and functionally informed basis for soil health assessment, a major interpretative challenge remains unresolved: microbiome profiles are still difficult to evaluate meaningfully when treated as isolated measurements. Even when taxonomic composition, functional potential, and abundance-based indicators are available, there is no broadly accepted system that allows soils to be classified consistently into biologically interpretable condition categories, nor is there a robust framework for comparing microbiome states across soil types, environments, or time points. Consequently, soil microbiome data often remain descriptive rather than diagnostically actionable.

To overcome this limitation, we propose a unified, database-driven microbiome reference framework in which soil samples are interpreted relationally rather than independently. In such a system, the microbiome of an individual soil would be positioned within a multidimensional comparative space defined by previously characterized reference soils representing known pedological types and condition states. This would shift soil microbiome interpretation from a static, sample-by-sample approach toward a contextual model in which biological meaning emerges through similarity, divergence, and directional movement relative to defined reference states.

The rationale for this concept is illustrated in Figure 7, which summarizes paired comparisons of healthy and degraded soils across several soil types using a dumbbell plot format. The figure depicts the direction and magnitude of changes in the relative abundance of dominant microbial phyla within chernozem [394,395], forest [396], alluvial [397], peat [398,399], and saline soils [400,401]. These comparisons show that degradation is associated with recurring microbiome shifts, while also making clear that the structure and extent of these shifts are strongly soil-type dependent. This duality is critical: it suggests that soil health interpretation requires a reference architecture capable of capturing both broadly recurrent signatures of degradation and the ecological specificity of individual soil systems. Within such a framework, an unknown soil sample would not be judged against universal fixed thresholds alone, but against an appropriate reference background composed of biologically and environmentally comparable soils. Its condition could then be inferred from its relative position within the reference landscape, allowing classification not only into healthy or degraded states, but also into intermediate or transitional conditions. Importantly, the same framework could support longitudinal interpretation, as repeated sampling would make it possible to track directional movement of a soil microbiome toward deterioration, recovery, or stabilization over time.

A practical application of this framework would involve establishing a curated reference database that integrates microbiome profiles with standardized environmental and management metadata. At a minimum, each record should document soil type, geographic origin, climatic conditions, land use, management practices, sampling depth, and key physicochemical attributes such as pH, organic matter content, and nutrient status, alongside microbiome data generated through harmonized analytical methods. Reference samples should be drawn from well-characterized sites that encompass both healthy and degraded soils across diverse soil types and climatic zones. The similarity

between unknown samples and reference soils could then be evaluated using taxonomic, functional, and abundance-based indicators, enabling soils to be mapped within a multidimensional reference framework and classified in relation to comparable ecological contexts. To maintain consistency and reliability over time, the system would require routine updates, standardized metadata protocols, and rigorous quality control procedures.

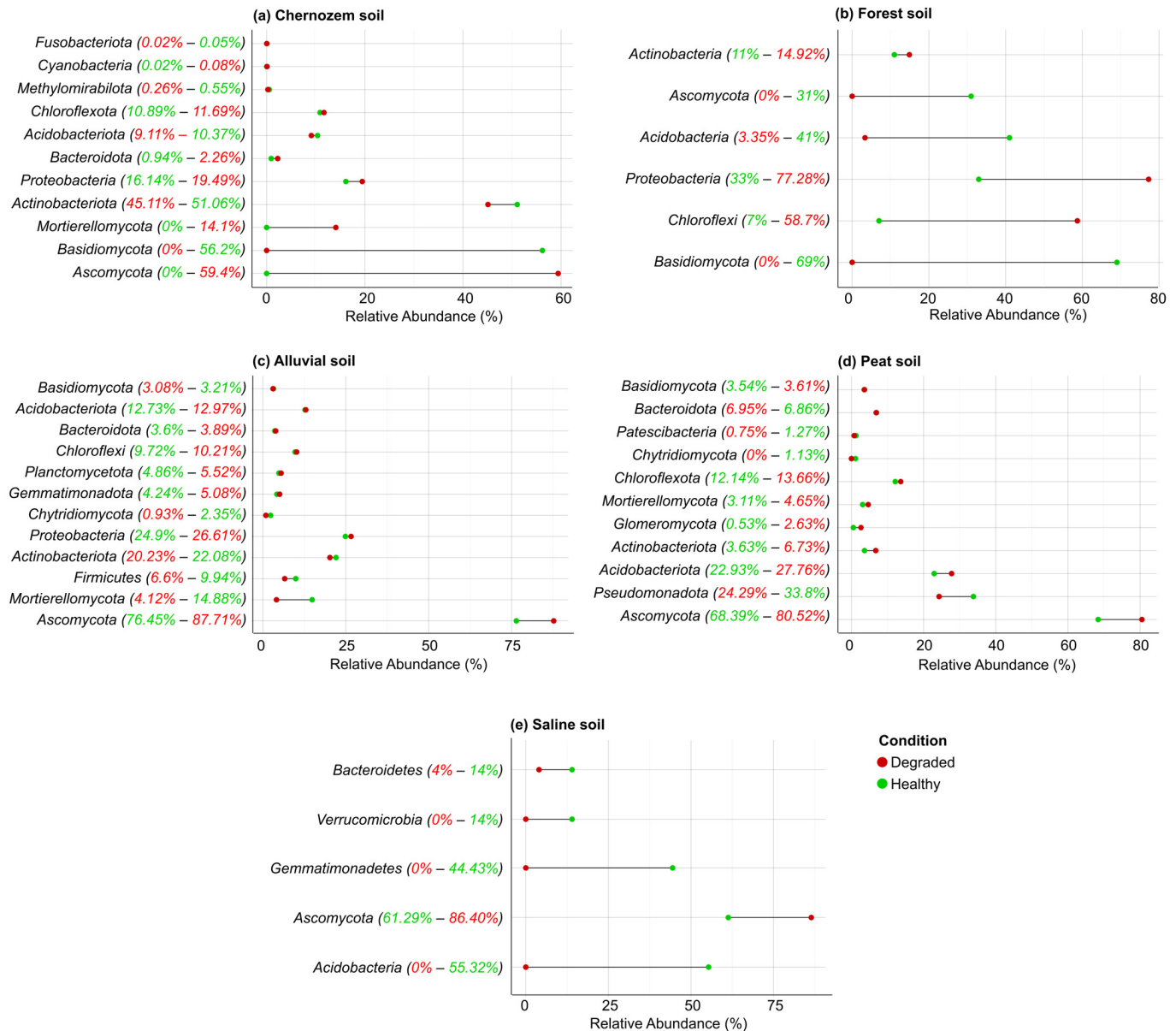


Figure 7. Microbiome-based differentiation between healthy and degraded soils across major soil types using a dumbbell plot representation. Relative abundance (%) of dominant microbial taxa is shown for paired degraded (red) and healthy (green) conditions across five soil types: (a) chernozem, (b) forest, (c) alluvial, (d) peat, and (e) saline soils. Horizontal connecting lines (dumbbells) illustrate the magnitude and direction of change between conditions for each taxon. The figure highlights both consistent and soil-type-specific shifts in microbial community composition associated with degradation, emphasizing that soil health status is reflected in relative changes in microbial abundance rather than absolute values alone. Corresponding references are provided in Supplementary Table S2.

4. Conclusions

This study analyzed global soil research dynamics over the past three decades by integrating project data, scientific publications, and patent activity. The results show a

clear expansion of soil-related research, with increasing emphasis on microbiome-driven and climate-oriented themes, while traditional areas such as soil degradation and nutrient management remain central. At the same time, persistent regional and structural imbalances highlight unequal research capacity and innovation across regions. A key finding is the strong convergence of soil research around carbon dynamics, microbial processes, and agricultural management, alongside a clear fragmentation in soil health assessment approaches. To address this gap, the study proposes a structured microbiome-based framework grounded in 12 MMSFs, providing a basis for integrating microbial indicators into soil health evaluation. Although the proposed framework offers a structured foundation for integrating microbiome-linked indicators into soil health evaluation, it remains at a proposal stage and requires further validation through standardized large-scale sampling, harmonized analytical pipelines, and cross-regional studies across diverse soil types and environmental conditions. In addition, the study highlights the need for a unified, reference-based approach in which soil microbiome data are interpreted relative to well-characterized systems, enabling more standardized, comparable, and context-aware evaluation of soil health. From a practical perspective, the proposed framework could support the integration of microbiome-based indicators into soil monitoring programs at local, regional, and national scales. By combining information on microbial activity, functional potential, and community structure, it provides a structured approach for evaluating biological aspects of soil health alongside traditional physical and chemical indicators. In addition, the use of reference-based microbiome interpretation may improve comparability across soil types and environmental conditions and support the development of more harmonized soil health assessment systems.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/agronomy16121154/s1>, Figure S1. Flow diagram of project identification, screening, and inclusion from two major databases. (a) Selection process for projects retrieved from the World Bank Group database using the keywords “soil health,” “soil quality,” and “soil degradation.” (b) Selection process for projects retrieved from the CORDIS database using the keyword “soil microbiome.” The study time frame applied in both searches was 1990–2025; Figure S2. Flow diagram of study identification, screening, and inclusion from three bibliographic databases: Scopus, Web of Science, and PubMed. For each database, records were retrieved using six keyword groups related to soil health, soil degradation, soil microbiome, soil carbon sequestration and climate change, nutrient management, and tillage. Searches were limited to the 1990–2025 time frame and restricted by subject areas, document types (articles and reviews), and English language. The diagram details the number of records identified, screened, assessed for eligibility, and ultimately included in the review for each database; Figure S3. Flow diagram of patent identification, screening, and inclusion from the WIPO PATENTSCOPE database. Searches were conducted across six thematic domains using consistent keyword strategies and a uniform time filter (1990–2025); Figure S4. Global keyword co-occurrence network of soil- and agriculture-related projects. The network is based on the top 15 most frequent keywords. Nodes represent keywords (numbered 1–15; legend on the left side), with size proportional to their contribution to total keyword occurrences (%). Edges represent keyword co-occurrence within the same projects, with thickness reflecting co-occurrence strength. Node colors indicate the dominant region in which each keyword is most frequently represented; Figure S5. Country-level distribution of soil research output across thematic domains under absolute and normalized metrics. The figure presents the top contributing countries for six soil-related themes: Soil Health & Organic Matter, Soil Degradation, Soil Microbiome, Soil Carbon Sequestration & Climate Change, Nutrient Management and Soil, and Tillage and Soil. For each theme, three complementary metrics are shown: (a) absolute publication shares by country, (b) publication shares normalized per 1 million inhabitants, and (c) publication shares normalized by land area (per 10,000 km²). Percentages represent each country’s proportional contribution within the respective thematic dataset; Table S1. Representative microbial taxa associated with the

12 microbially mediated soil functions (MMSFs) included in the proposed soil health assessment framework; Table S2. Literature sources and microbial relative abundance data used to construct Figure 7 comparing healthy and degraded soils across major soil types.

Author Contributions: Conceptualization, N.G.; methodology, N.G. and M.P.; investigation, N.G.; M.M., P.F., P.D. and F.G.; resources, N.G. and M.P.; writing—original draft preparation, N.G. and M.P.; writing—review and editing, N.G., M.P., J.R. and L.S.; visualization, N.G.; supervision, M.P., J.R. and L.S. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no funding.

Data Availability Statement: The original contributions presented in the study are included in the article, further inquiries can be directed to the corresponding author.

Acknowledgments: Supported by the University of Debrecen Program for Scientific Publication.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Telo da Gama, J. The Role of Soils in Sustainability, Climate Change, and Ecosystem Services: Challenges and Opportunities. *Ecologies* **2023**, *4*, 552–567. [CrossRef]
2. Anthony, M.A.; Bender, S.F.; van der Heijden, M.G.A. Enumerating Soil Biodiversity. *Proc. Natl. Acad. Sci. USA* **2023**, *120*, e2304663120. [CrossRef]
3. FAO. FAO Highlights the Vital Role of Soil: 95 Percent of Our Food Is Directly Produced on Soils. 2024. Available online: <https://www.fao.org/countryprofiles/news-archive/detail-news/en/c/1729967/> (accessed on 23 February 2026).
4. FAO. FAO Warns 90 per Cent of Earth’s Topsoil at Risk by 2050 | UN News. 2022. Available online: <https://news.un.org/en/story/2022/07/1123462> (accessed on 22 February 2026).
5. Robinson, J.M.; Liddicoat, C.; Muñoz-Rojas, M.; Breed, M.F. Restoring Soil Biodiversity. *Curr. Biol.* **2024**, *34*, R393–R398. [CrossRef]
6. Penuelas, J.; Coello, F.; Sardans, J. A Better Use of Fertilizers Is Needed for Global Food Security and Environmental Sustainability. *Agric. Food Secur.* **2023**, *12*, 5. [CrossRef]
7. Jin, H.; Huang, S.; Shi, D.; Li, J.; Li, J.; Li, Y.; Zhu, H. Effects of Different Tillage Practices on Soil Stability and Erodibility for Red Soil Sloping Farmland in Southern China. *Agronomy* **2023**, *13*, 1310. [CrossRef]
8. Sünemann, M.; Beugnon, R.; Breitzkreuz, C.; Buscot, F.; Cesarz, S.; Jones, A.; Lehmann, A.; Lochner, A.; Orgiazzi, A.; Reitz, T.; et al. Climate Change and Cropland Management Compromise Soil Integrity and Multifunctionality. *Commun. Earth Environ.* **2023**, *4*, 394. [CrossRef]
9. Kabato, W.; Hailegnaw, N.; Mutum, L.; Molnar, Z. Managing Soil Health for Climate Resilience and Crop Productivity in a Changing Environment. *Sci. Total Environ.* **2025**, *1000*, 180460. [CrossRef]
10. UN. World Population Projected to Reach 9.8 Billion in 2050, and 11.2 Billion in 2100. 2017. Available online: <https://www.un.org/en/desa/world-population-projected-reach-98-billion-2050-and-112-billion-2100> (accessed on 23 February 2026).
11. UN. World Must Sustainably Produce 70 per Cent More Food by Mid-Century—UN Report | UN News. 2013. Available online: <https://news.un.org/en/story/2013/12/456912> (accessed on 23 February 2026).
12. Page, M.J.; McKenzie, J.E.; Bossuyt, P.M.; Boutron, I.; Hoffmann, T.C.; Mulrow, C.D.; Shamseer, L.; Tetzlaff, J.M.; Akl, E.A.; Brennan, S.E.; et al. The PRISMA 2020 Statement: An Updated Guideline for Reporting Systematic Reviews. *BMJ* **2021**, *372*, n71. [CrossRef]
13. World Bank Projects. Available online: <https://projects.worldbank.org/en/projects-operations/projects-list> (accessed on 16 February 2026).
14. CORDIS Projects & Results | CORDIS | European Commission. Available online: <https://cordis.europa.eu/projects> (accessed on 16 February 2026).
15. Elsevier Scopus. Available online: <https://www.scopus.com/pages/home#basic> (accessed on 16 February 2026).
16. Clarivate Smart Search—Web of Science Core Collection. Available online: <https://www.webofscience.com/wos/woscc/smart-search> (accessed on 16 February 2026).
17. National Library of Medicine PubMed. Available online: <https://pubmed.ncbi.nlm.nih.gov/> (accessed on 16 February 2026).
18. FAO. *Voluntary Guidelines for Sustainable Soil Management*; FAO: Rome, Italy, 2017.
19. FAO. *Status of the World’s Soil Resources: Main Report*, 1st ed.; FAO: Rome, Italy, 2015.
20. Weil, R.; Brady, N. *The Nature and Properties of Soils*; Pearson Education, Inc.: Columbus, OH, USA, 2017; Volume 15.
21. R Core Team. *The R Project for Statistical Computing*; R Core Team: Vienna, Austria, 2024.

22. Wickham, H.; François, R.; Henry, L.; Müller, K.; Vaughan, D. *Dplyr: A Grammar of Data Manipulation*; Posit Software, PBC: Boston, MA, USA, 2026.
23. Wickham, H.; Vaughan, D.; Girlich, M.; Ushey, K. *Tidyr: Tidy Messy Data*; Posit Software, PBC: Boston, MA, USA, 2025.
24. UNCED. Summary Report 3–14 June 1992. Available online: <https://enb.iisd.org/events/unced/summary-report-3-14-june-1992> (accessed on 16 February 2026).
25. UNCCD. *United Nations Convention to Combat Desertification in Those Countries Experiencing Serious Drought and/or Desertification Particularly in Africa*; The United Nations Convention to Combat Desertification: Bonn, Germany, 1994.
26. IPCC. *Climate Change 2022 Mitigation of Climate Change*; Intergovernmental Panel on Climate Change: Geneva, Switzerland, 2022.
27. UNCCD. Sustainable Land Management Contribution to Successful Land-Based Climate Change Adaptation and Mitigation. Available online: <https://www.unccd.int/resources/reports/sustainable-land-management-contribution-successful-land-based-climate-change> (accessed on 16 February 2026).
28. UNFCCC. United Nations Framework Convention on Climate Change (UNFCCC) | Environmental Sciences | Research Starters | EBSCO Research. Available online: <https://www.ebsco.com> (accessed on 21 February 2026).
29. UN. The 17 Goals | Sustainable Development. Available online: <https://sdgs.un.org/goals> (accessed on 21 February 2026).
30. Iese, V.; Wairiu, M.; Hickey, G.M.; Ugalde, D.; Hinge Salili, D.; Walenenea, J.; Tabe, T.; Keremama, M.; Teva, C.; Navunicagi, O.; et al. Impacts of COVID-19 on Agriculture and Food Systems in Pacific Island Countries (PICs): Evidence from Communities in Fiji and Solomon Islands. *Agric. Syst.* **2021**, *190*, 103099. [CrossRef] [PubMed]
31. Koloma, Y.; Kemeze, F.H. COVID-19 and Perceived Effects on Agricultural Financing in Africa: Evidence and Policy Implications. *Afr. Dev. Rev.* **2022**, *34*, S63–S79. [CrossRef] [PubMed]
32. Das, S.; Dutta, S.; Roy Choudhury, M.; Garai, S.; Mukherjee, S.; Sengupta, S.; Jana, S.; Dey, S.; Dhar, A.; Dutta, S.; et al. Regenerating Rural Soil and Ecosystems: A 15-Year Systematic Review of Emerging Methods and Technologies. *Sci. Total Environ.* **2025**, *990*, 179926. [CrossRef]
33. Bhunia, G.S.; Sengupta, D. Cultivating Resilience: Bibliometric Analysis of Soil Health for a Sustainable Future. *Discov. Soil* **2025**, *2*, 95. [CrossRef]
34. Omer, E.; Szlatenyi, D.; Csenki, S.; Tünde, G.; Chhetri, G.; Veres, Z.; Láng, V. Soil Health for Sustainable Agriculture: A Bibliometric Review of EU Current Scientific Findings and Research Trends. *Soil Adv.* **2026**, *5*, 100097. [CrossRef]
35. FAO. UNEP Spatial Distribution of Soil Pollution in Asia and the Pacific. In *Global Assessment of Soil Pollution: Report*; FAO: Rome, Italy; UNEP: Rome, Italy, 2021; p. 846.
36. Alexandra, J.; Carter, G.; Delaney, M.; Hadobas, S.; Howden, M.; Maharjan, K.; Mahani, M.E.; Mudaliar, L.; Prinsley, R.; Rimón, A.; et al. *Inquiry into Australia's Response to the Priorities of Pacific Island Countries and the Pacific Region*; ANU Institute for Climate, Energy & Disaster Solutions: Canberra, Australia, 2024.
37. SADC; IUCN; UNCCD. *Drought Risk Management and Mitigation Strategy (DRIMMS) 2022–2032*; SADC: Gaborone, Botswana; IUCN: Gland, Switzerland; UNCCD: Bonn, Germany, 2022.
38. Erdogan, H.E.; Havlicek, E.; Dazzi, C.; Montanarella, L.; Van Liedekerke, M.; Vrščaj, B.; Krasilnikov, P.; Khasankhanova, G.; Vargas, R. Soil Conservation and Sustainable Development Goals (SDGs) Achievement in Europe and Central Asia: Which Role for the European Soil Partnership? *Int. Soil Water Conserv. Res.* **2021**, *9*, 360–369. [CrossRef]
39. FAO. FAO Marks World Soil Day 2025, Underlines Rising Soil Sealing Across Asia and the Pacific. Available online: <https://www.fao.org/asiapacific/news/news-detail/fao-marks-world-soil-day-2025--underlines-rising-soil-sealing-across-asia-and-the-pacific/en> (accessed on 21 February 2026).
40. GEF. *Report of the Global Environment Facility to the Fifteenth Session of the Conference of the Parties to the United Nations Convention to Combat Desertification*; GEF: Washington, DC, USA, 2022.
41. UNCCD. Great Green Wall Initiative. Available online: <https://www.unccd.int/our-work/ggwi> (accessed on 21 February 2026).
42. Yimer, A.H.; Tarnawa, A. Advancing Nutrient Management Strategies for Sustainable Crop Productivity in a Changing Climate: A Systematic Review. *Sci. World J.* **2025**, *2025*, 7101060. [CrossRef] [PubMed]
43. Ge, G.; Chen, X.; Ma, H.; Zhang, X.; Shi, J.; Wang, X.; Zhao, X.; Wang, M.; Xian, F.; Lu, Z.; et al. Bibliometric Analysis of Research Trends in Agricultural Soil Organic Carbon Components from 2000 to 2023. *Front. Plant Sci.* **2024**, *15*, 1457826. [CrossRef]
44. Reznikova, D.A.; Barannikova, M.V.; Shnakhova, L.M.; Mitkin, N.A.; Vatlin, A.A. Next-Generation Sequencing Approaches for Soil Microbiome Research. *Front. Soil Sci.* **2026**, *5*, 1706999. [CrossRef]
45. Romero, F.; Labouyrie, M.; Orgiazzi, A.; Ballabio, C.; Panagos, P.; Jones, A.; Tedersoo, L.; Bahram, M.; Eisenhauer, N.; Sünemann, M.; et al. The Soil Microbiome as an Indicator of Ecosystem Multifunctionality in European Soils. *Nat. Commun.* **2025**, *17*, 705. [CrossRef]
46. Mc, G.; Kn, S.; Yadahalli, V.R. Emerging Techniques in Soil Microbiome Analysis for Sustainable Agriculture. *Int. J. Adv. Biochem. Res.* **2025**, *9*, 350–355. [CrossRef]

47. Jesus, E.d.C.; Coelho, M.R.R.; Chaer, G.M.; Mendes, I.d.C.; Oliveira, M.I.L.d.; Malaquias, J.V.; Silva, O.D.D.d.; Oliveira, I.v.d.W.A.; Eugenio, N.R.; Brown, G.G. A Bibliometric Analysis on Soil Microbial Diversity and Processes: Global Trends and Methodologies. *Soil Org.* **2025**, *97*, 65–77. [\[CrossRef\]](#)
48. Zhao, S.; Zhang, J. Microplastics in Soils during the COVID-19 Pandemic: Sources, Migration and Transformations, and Remediation Technologies. *Sci. Total Environ.* **2023**, *883*, 163700. [\[CrossRef\]](#)
49. Lal, R. Soil Health and Carbon Management. *Food Energy Secur.* **2016**, *5*, 212–222. [\[CrossRef\]](#)
50. Delgado-Baquerizo, M.; Eldridge, D.J.; Liu, Y.-R.; Liu, Z.-W.; Coleine, C.; Trivedi, P. Soil Biodiversity and Function under Global Change. *PLoS Biol.* **2025**, *23*, e3003093. [\[CrossRef\]](#)
51. Rinot, O.; Levy, G.J.; Steinberger, Y.; Svoray, T.; Eshel, G. Soil Health Assessment: A Critical Review of Current Methodologies and a Proposed New Approach. *Sci. Total Environ.* **2019**, *648*, 1484–1491. [\[CrossRef\]](#)
52. Cherubin, M.R.; Pinheiro Junior, C.R.; Souza, L.F.N.; Canisares, L.P.; Ferreira, T.O.; Cerri, C.E.P.; Minasny, B.; Smith, P. Global Blind Spots in Soil Health Research Overlap with Environmental Vulnerability Hotspots. *Commun. Earth Environ.* **2025**, *6*, 651. [\[CrossRef\]](#)
53. Sellami, M.H.; Mori, M.; Terribile, F. Mapping the Conceptual and Intellectual Structure of Soil Health Research (1996–2021): A Terms Co-Occurrence and Co-Cited Reference Network Analysis. *Front. Soil Sci.* **2025**, *5*, 1549290. [\[CrossRef\]](#)
54. Delgado-Baquerizo, M.; Hu, H.-W.; Maestre, F.T.; Guerra, C.A.; Eisenhauer, N.; Eldridge, D.J.; Zhu, Y.-G.; Chen, Q.-L.; Trivedi, P.; Du, S.; et al. The Global Distribution and Environmental Drivers of the Soil Antibiotic Resistome. *Microbiome* **2022**, *10*, 219. [\[CrossRef\]](#)
55. Li, Y.; Duan, Y.; Zhang, J.; Petropoulos, E.; Zhao, J.; Wu, F.; Wang, L.; Chen, Y.; Wang, X. Structure and Function of the Topsoil Microbiome in Chinese Terrestrial Ecosystems. *Front. Microbiol.* **2025**, *16*, 1595810. [\[CrossRef\]](#)
56. Böttcher, H.; Zell-Ziegler, C.; Herold, A.; Siemons, A. *EU LULUCF Regulation Explained Summary of Core Provisions and Expected Effects*; Öko-Institut: Berlin, Germany, 2019.
57. EU. Regulation (EU) 2024/3012 of the European Parliament and of the Council of 27 November 2024 Establishing a Union Certification Framework for Permanent Carbon Removals, Carbon Farming and Carbon Storage in Products; EU: Brussels, Belgium, 2024.
58. Huang, B.; Gao, J.; Zhang, W.; Gan, C.; Bao, X.; Xu, M.; Wu, L. Impacts of Conservation Tillage on Soil Organic Carbon and Crop Yield in Black Soil Region of Northeast China: Integrated Regulation by Climate, Management and Soil Properties. *J. Agric. Food Res.* **2025**, *24*, 102388. [\[CrossRef\]](#)
59. Leite, M.F.A.; van den Broek, S.W.E.B.; Kuramae, E.E. Current Challenges and Pitfalls in Soil Metagenomics. *Microorganisms* **2022**, *10*, 1900. [\[CrossRef\]](#) [\[PubMed\]](#)
60. Ferrocino, I.; Ferrara, M.; Garelo, M.; Turchetti, B.; Andreolli, M.; Arena, M.P.; Alduina, R.; Aloï, F.; Bevivino, A.; Bruno, E.; et al. Standardizing Microbiome Research: Interlaboratory Validation of SOPs for Sample Preparation and DNA Extraction from Food and Environmental Ecosystems. *Environ. Microbiome* **2025**, *21*, 14. [\[CrossRef\]](#)
61. Sergaki, C.; Lagunas, B.; Lidbury, I.; Gifford, M.L.; Schäfer, P. Challenges and Approaches in Microbiome Research: From Fundamental to Applied. *Front. Plant Sci.* **2018**, *9*, 1205. [\[CrossRef\]](#) [\[PubMed\]](#)
62. Hill, G.T.; Mitkowski, N.A.; Aldrich-Wolfe, L.; Emele, L.R.; Jurkonie, D.D.; Ficke, A.; Maldonado-Ramirez, S.; Lynch, S.T.; Nelson, E.B. Methods for Assessing the Composition and Diversity of Soil Microbial Communities. *Appl. Soil Ecol.* **2000**, *15*, 25–36. [\[CrossRef\]](#)
63. Martiny, A.C. High Proportions of Bacteria Are Culturable across Major Biomes. *ISME J.* **2019**, *13*, 2125–2128. [\[CrossRef\]](#)
64. FAO. *Standard Operating Procedure for Soil Microbial Biomass (Carbon): Chloroform Fumigation-Extraction Method*; FAO: Rome, Italy, 2024.
65. Joergensen, R.G. Microbial Biomass Estimation by Fumigation Extraction and ATP—A Review in Memoriam of Phil Brookes. *Biol. Fertil. Soils* **2025**, *61*, 1287–1299. [\[CrossRef\]](#)
66. Quideau, S.A.; McIntosh, A.C.S.; Norris, C.E.; Lloret, E.; Swallow, M.J.B.; Hannam, K. Extraction and Analysis of Microbial Phospholipid Fatty Acids in Soils. *J. Vis. Exp.* **2016**, *114*, 54360. [\[CrossRef\]](#)
67. van Galen, L.G.; Smith, G.R.; Margenot, A.J.; Waldrop, M.P.; Crowther, T.W.; Peay, K.G.; Jackson, R.B.; Yu, K.; Abrahão, A.; Ahmed, T.A.; et al. A Global Database of Soil Microbial Phospholipid Fatty Acids and Enzyme Activities. *Sci. Data* **2025**, *12*, 1568. [\[CrossRef\]](#)
68. Machado, M.S.; Rühlemann, M.; Reitmeier, S.; Kacprowski, T.; Frost, F.; Haller, D.; Baumbach, J.; List, M. On the Limits of 16S rRNA Gene-Based Metagenome Prediction and Functional Profiling. *Microb. Genom.* **2024**, *10*, 001203. [\[CrossRef\]](#)
69. Microbiome Insights 16S rRNA Gene Sequencing vs. Shotgun Metagenomic Sequencing. Available online: <https://blog.microbiomeinsights.com/16s-rrna-sequencing-vs-shotgun-metagenomic-sequencing> (accessed on 31 March 2026).
70. Lugli, G.A.; Ventura, M. A Breath of Fresh Air in Microbiome Science: Shallow Shotgun Metagenomics for a Reliable Disentangling of Microbial Ecosystems. *Microbiome Res. Rep.* **2022**, *1*, 8. [\[CrossRef\]](#)
71. Terrón-Camero, L.C.; Gordillo-González, F.; Salas-Espejo, E.; Andrés-León, E. Comparison of Metagenomics and Metatranscriptomics Tools: A Guide to Making the Right Choice. *Genes* **2022**, *13*, 2280. [\[CrossRef\]](#)

72. Josephs-Spaulding, J.; Rettig, H.C.; Zimmermann, J.; Chkonia, M.; Mischnik, A.; Franzenburg, S.; Graspeuntner, S.; Rupp, J.; Kaleta, C. Metatranscriptomics-Based Metabolic Modeling of Patient-Specific Urinary Microbiome during Infection. *npj Biofilms Microbiomes* **2025**, *11*, 183. [\[CrossRef\]](#)
73. Ascandari, A.; Aminu, S.; Safdi, N.E.H.; El Allali, A.; Daoud, R. A Bibliometric Analysis of the Global Impact of Metaproteomics Research. *Front. Microbiol.* **2023**, *14*, 1217727. [\[CrossRef\]](#)
74. Tartaglia, M.; Bastida, F.; Sciarrillo, R.; Guarino, C. Soil Metaproteomics for the Study of the Relationships Between Microorganisms and Plants: A Review of Extraction Protocols and Ecological Insights. *Int. J. Mol. Sci.* **2020**, *21*, 8455. [\[CrossRef\]](#)
75. Johnson, C.H.; Ivanisevic, J.; Siuzdak, G. Metabolomics: Beyond Biomarkers and towards Mechanisms. *Nat. Rev. Mol. Cell Biol.* **2016**, *17*, 451–459. [\[CrossRef\]](#) [\[PubMed\]](#)
76. Song, Y.; Yao, S.; Li, X.; Wang, T.; Jiang, X.; Bolan, N.; Warren, C.R.; Northen, T.R.; Chang, S.X. Soil Metabolomics: Deciphering Underground Metabolic Webs in Terrestrial Ecosystems. *Eco-Environ. Health* **2024**, *3*, 227–237. [\[CrossRef\]](#)
77. Divyasorubini, S.; Kandage, S.M.; Liyanage, S.; Rajapakse, C.; Silva, G.N. Microbial Biosensors for Real-Time Monitoring of the Bioremediation Processes. In *Bioremediation of Environmental Pollutants: Emerging Trends and Strategies*; Suyal, D.C., Soni, R., Eds.; Springer International Publishing: Cham, Switzerland, 2022; pp. 111–144.
78. Huang, C.-W.; Lin, C.; Nguyen, M.K.; Hussain, A.; Bui, X.-T.; Ngo, H.H. A Review of Biosensor for Environmental Monitoring: Principle, Application, and Corresponding Achievement of Sustainable Development Goals. *Bioengineered* **2023**, *14*, 58–80. [\[CrossRef\]](#) [\[PubMed\]](#)
79. Araz, M.K.; Tentori, A.M.; Herr, A.E. Microfluidic Multiplexing in Bioanalyses. *SLAS Technol.* **2013**, *18*, 350–366. [\[CrossRef\]](#) [\[PubMed\]](#)
80. Hariharasudha, H.K.R.S.; Chandrasekaran, M.; Baskaran, C.M.; Govindarajan, D.K.; Kandaswamy, K. Lab-on-a-Chip Devices for Bacterial Systems: Tracking Biofilm Growth and Antimicrobial Interactions. *Total Environ. Microbiol.* **2025**, *1*, 100042. [\[CrossRef\]](#)
81. Fierer, N.; Wood, S.A.; Bueno de Mesquita, C.P. How Microbes Can, and Cannot, Be Used to Assess Soil Health. *Soil Biol. Biochem.* **2021**, *153*, 108111. [\[CrossRef\]](#)
82. Nicholls, C.I.; Altieri, M.A.; Dezanet, A.; Lana, M.; Feistauer, D.; Ouriques, M. A Rapid, Farmer-Friendly Agroecological Method to Estimate Soil Quality and Crop Health in Vineyard Systems. *Biodynamics* **2004**, 33–39.
83. Shuliko, N.N.; Kiselyova, A.A.; Tukmacheva, E.V.; Korchagina, I.A.; Kubasova, E.V.; Timokhin, A.Y.; Yusova, O.A. Associative Nitrogen Fixation in the Rhizosphere of Cereals During Seed Inoculation by Bacteria *Arthrobacter mysorens* 7 and *Flavobacterium* sp. *Sib. J. Life Sci. Agric.* **2024**, *16*, 361–384. [\[CrossRef\]](#)
84. Mayer, M.; Rewald, B.; Matthews, B.; Sandén, H.; Rosinger, C.; Katzensteiner, K.; Gorfer, M.; Berger, H.; Tallian, C.; Berger, T.W.; et al. Soil Fertility Relates to Fungal-Mediated Decomposition and Organic Matter Turnover in a Temperate Mountain Forest. *New Phytol.* **2021**, *231*, 777–790. [\[CrossRef\]](#)
85. Wu, S.; Jie, H.; Jie, Y. Role of Rhizosphere Soil Microbes in Adapting Ramie (*Boehmeria nivea* L.) Plants to Poor Soil Conditions through N-Fixing and P-Solubilization. *Agronomy* **2021**, *11*, 2096. [\[CrossRef\]](#)
86. Lomtadze, Z.; Gioshvili, I. Distribution Characteristics of Free-Living Nitrogen-Fixing Bacteria in Solonetz Soil Types. *Asian J. Agric. Hortic. Res.* **2025**, *12*, 149–155. [\[CrossRef\]](#)
87. Silva, D.F.; Cardoso, E.J.B.N.; Huang, L.; Erikson, C.; Silva, A.M.M.; Araujo, V.L.V.P.; Silva, D.E.O.; Melo, V.M.M.; Araujo, A.S.F.; Pereira, A.P.A.; et al. Functional Genes Related to N and P Cycling in Degraded and Restored Areas from Brazilian Drylands. *Appl. Soil Ecol.* **2024**, *196*, 105316. [\[CrossRef\]](#)
88. Bouffaud, M.-L.; Renoud, S.; Moëne-Loccoz, Y.; Muller, D. Is Plant Evolutionary History Impacting Recruitment of Diazotrophs and nifH Expression in the Rhizosphere? *Sci. Rep.* **2016**, *6*, 21690. [\[CrossRef\]](#)
89. Jia, R.; Wang, K.; Li, L.; Qu, Z.; Shen, W.; Qu, D. Abundance and Community Succession of Nitrogen-Fixing Bacteria in Ferrihydrite Enriched Cultures of Paddy Soils Is Closely Related to Fe(III)-Reduction. *Sci. Total Environ.* **2020**, *720*, 137633. [\[CrossRef\]](#) [\[PubMed\]](#)
90. Rodrigues, E.P.; Rodrigues, L.d.S.; de Oliveira, A.L.M.; Divan Baldani, V.L.; Teixeira, K.R.d.S.; Urquiaga, S.; Reis, V.M. *Azospirillum amazonense* Inoculation: Effects on Growth, Yield and N₂ Fixation of Rice (*Oryza sativa* L.). *Plant Soil* **2009**, *316*, 323. [\[CrossRef\]](#)
91. Okon, Y.; Heytler, P.G.; Hardy, R.W.F. N₂ Fixation by *Azospirillum brasilense* and Its Incorporation into Host *Setaria italica*. *Appl. Environ. Microbiol.* **1983**, *46*, 694–697. [\[CrossRef\]](#)
92. Reinhold, B.; Hurek, T.; Fendrik, I.; Pot, B.; Gillis, M.; Kersters, K.; Thielemans, S.; De Ley, J. *Azospirillum halopraeferens* sp. Nov., a Nitrogen-Fixing Organism Associated with Roots of Kallar Grass (*Leptochloa fusca* (L.) Kunth). *Int. J. Syst. Evol. Microbiol.* **1987**, *37*, 43–51. [\[CrossRef\]](#)
93. Karpati, E.; Kiss, P.; Ponyi, T.; Fendrik, I.; de Zamaroczy, M.; Orosz, L. Interaction of *Azospirillum lipoferum* with Wheat Germ Agglutinin Stimulates Nitrogen Fixation. *J. Bacteriol.* **1999**, *181*, 3949–3955. [\[CrossRef\]](#)
94. Kargar, M.; Kargar, M.; Noerooznejad, M.; Ayazpour, K. The Role of *Azotobacter chroococcum* and *Azotobacter paspali* on Wheat Growth in Fars Province. *Adv. Environ. Biol.* **2014**, *8*, 837–841.

95. Hamilton, T.L.; Ludwig, M.; Dixon, R.; Boyd, E.S.; Dos Santos, P.C.; Setubal, J.C.; Bryant, D.A.; Dean, D.R.; Peters, J.W. Transcriptional Profiling of Nitrogen Fixation in *Azotobacter vinelandii*. *J. Bacteriol.* **2011**, *193*, 4477–4486. [\[CrossRef\]](#)
96. Salas, A.; Tortosa, G.; Hidalgo-García, A.; Delgado, A.; Bedmar, E.J.; Richardson, D.J.; Gates, A.J.; Delgado, M.J. The Hemoglobin B_{jgb} from *Bradyrhizobium diazoefficiens* Controls NO Homeostasis in Soybean Nodules to Protect Symbiotic Nitrogen Fixation. *Front. Microbiol.* **2020**, *10*, 2915. [\[CrossRef\]](#)
97. Bitire, T.D.; Abberton, M.; Oyatomi, O.; Babalola, O.O. Effect of *Bradyrhizobium japonicum* Strains and Inorganic Nitrogen Fertilizer on the Growth and Yield of Bambara Groundnut (*Vigna subterranea* (L.) Verdc) Accessions. *Front. Sustain. Food Syst.* **2022**, *6*, 913239. [\[CrossRef\]](#)
98. Li, Z.; Henawy, A.R.; Halema, A.A.; Fan, Q.; Duanmu, D.; Huang, R. A Wild Rice Rhizobacterium *Burkholderia cepacia* BRDJ Enhances Nitrogen Use Efficiency in Rice. *Int. J. Mol. Sci.* **2022**, *23*, 10769. [\[CrossRef\]](#)
99. Potrikus, C.J.; Breznak, J.A. Nitrogen-Fixing *Enterobacter agglomerans* Isolated from Guts of Wood-Eating Termites. *Appl. Environ. Microbiol.* **1977**, *33*, 392–399. [\[CrossRef\]](#) [\[PubMed\]](#)
100. Ji, C.; Liu, Z.; Hao, L.; Song, X.; Wang, C.; Liu, Y.; Li, H.; Li, C.; Gao, Q.; Liu, X. Effects of *Enterobacter Cloacae* HG-1 on the Nitrogen-Fixing Community Structure of Wheat Rhizosphere Soil and on Salt Tolerance. *Front. Plant Sci.* **2020**, *11*, 1094. [\[CrossRef\]](#) [\[PubMed\]](#)
101. Alloisio, N.; Kucho, K.; Pujic, P.; Normand, P. The *Frankia alni* Symbiotic Transcriptome. In *Biological Nitrogen Fixation*; John Wiley & Sons, Ltd.: Hoboken, NJ, USA, 2015; pp. 757–768.
102. Kucho, K.; Taniyama, K. Characterization of *Frankia casuarinae* Mutants Defective in Vesicle Envelope Development. *Microbes Environ.* **2025**, *40*, ME25037. [\[CrossRef\]](#)
103. Tian, G.; Pauls, K.; Dong, Z.; Reid, L.; Tian, L. Colonization of the Nitrogen-Fixing Bacterium *Gluconacetobacter diazotrophicus* in a Large Number of Canadian Corn Plants. *Can. J. Plant Sci.* **2009**, *89*, 1009–1016. [\[CrossRef\]](#)
104. Pedrolo, A.M.; Matteoli, F.P.; Soares, C.R.F.S.; Arisi, A.C.M. Comparative Genomics Reveal the High Conservation and Scarce Distribution of Nitrogen Fixation *nif* Genes in the Plant-Associated Genus *Herbaspirillum*. *Microb. Ecol.* **2023**, *86*, 563–574. [\[CrossRef\]](#)
105. Klassen, G.; de Oliveira Pedrosa, F.; de Souza, E.M.; Yates, M.G.; Rigo, L.U. Nitrogenase Activity of *Herbaspirillum seropedicae* Grown under Low Iron Levels Requires the Products of *nifXorf1* Genes. *FEMS Microbiol. Lett.* **2003**, *224*, 255–259. [\[CrossRef\]](#) [\[PubMed\]](#)
106. Temme, K.; Zhao, D.; Voigt, C.A. Refactoring the Nitrogen Fixation Gene Cluster from *Klebsiella oxytoca*. *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 7085–7090. [\[CrossRef\]](#)
107. Benjelloun, I.; Thami Alami, I.; El Khadir, M.; Douira, A.; Udupa, S.M. Co-Inoculation of *Mesorhizobium ciceri* with Either *Bacillus* sp. or *Enterobacter aerogenes* on Chickpea Improves Growth and Productivity in Phosphate-Deficient Soils in Dry Areas of a Mediterranean Region. *Plants* **2021**, *10*, 571. [\[CrossRef\]](#)
108. Shimoda, Y.; Hirakawa, H.; Sato, S.; Saeki, K.; Hayashi, M. Whole-Genome Sequence of the Nitrogen-Fixing Symbiotic Rhizobium *Mesorhizobium loti* Strain TONO. *Genome Announc.* **2016**, *4*, e01016-16. [\[CrossRef\]](#) [\[PubMed\]](#)
109. Zhivotchenko, A.G.; Nikonova, E.S.; Jørgensen, M.H. Effect of Fermentation Conditions on N₂ Fixation by *Methylococcus capsulatus*. *Bioprocess. Eng.* **1995**, *14*, 9–15. [\[CrossRef\]](#)
110. Canto-Encalada, G.; Tec-Campos, D.; Tibocha-Bonilla, J.D.; Zengler, K.; Zepeda, A.; Zuñiga, C. Flux Balance Analysis of the Ammonia-Oxidizing Bacterium *Nitrosomonas europaea* ATCC19718 Unravels Specific Metabolic Activities While Degrading Toxic Compounds. *PLoS Comput. Biol.* **2022**, *18*, e1009828. [\[CrossRef\]](#)
111. Stepień, A.; Wojtkowiak, K.; Kolankowska, E. Effect of Commercial Microbial Preparations Containing *Paenibacillus azotofixans*, *Bacillus megaterium* and *Bacillus subtilis* on the Yield and Photosynthesis of Winter Wheat and the Nitrogen and Phosphorus Content in the Soil. *Appl. Sci.* **2022**, *12*, 12541. [\[CrossRef\]](#)
112. Daud, N.S.; Mohd Din, A.R.J.; Rosli, M.A.; Azam, Z.M.; Othman, N.Z.; Sarmidi, M.R. *Paenibacillus polymyxa* Bioactive Compounds for Agricultural and Biotechnological Applications. *Biocatal. Agric. Biotechnol.* **2019**, *18*, 101092. [\[CrossRef\]](#)
113. Soren, T.; Sarkar, A.; Mondal, T.; Ghosh, S.K.; Mondal, S.; Pal, P.; Maiti, T.K. The Rhizospheric Strain *Paraburkholderia kururiensis* WP2T3 Efficiently Degrades Para-Nitrophenol and Exhibits Plant Growth-Promoting Characters. *Microbe* **2025**, *9*, 100550. [\[CrossRef\]](#)
114. Esmaeel, Q.; Miotto, L.; Rondeau, M.; Leclère, V.; Clément, C.; Jacquard, C.; Sanchez, L.; Barka, E.A. *Paraburkholderia phytofirmans* PsJN-Plants Interaction: From Perception to the Induced Mechanisms. *Front. Microbiol.* **2018**, *9*, 2093. [\[CrossRef\]](#) [\[PubMed\]](#)
115. Casas-Román, A.; Lorite, M.-J.; Werner, M.; Muñoz, S.; Gallegos, M.-T.; Sanjuán, J. The *Gap* Gene of *Rhizobium etli* Is Required for Both Free Life and Symbiosis with Common Beans. *Microbiol. Res.* **2024**, *284*, 127737. [\[CrossRef\]](#) [\[PubMed\]](#)
116. Janczarek, M.; Koziół, M.; Adamczyk, P.; Buczek, K.; Kalita, M.; Gromada, A.; Mordzińska-Rak, A.; Polakowski, C.; Bieganski, A. Symbiotic Efficiency of *Rhizobium leguminosarum* Sv. *Trifolii* Strains Originating from the Subpolar and Temperate Climate Regions. *Sci. Rep.* **2024**, *14*, 6264. [\[CrossRef\]](#)

117. Demtröder, L.; Pfänder, Y.; Masepohl, B. *Rhodobacter capsulatus* AnfA Is Essential for Production of Fe-Nitrogenase Proteins but Dispensable for Cofactor Biosynthesis and Electron Supply. *MicrobiologyOpen* **2020**, *9*, e1033. [\[CrossRef\]](#)
118. Arashida, H.; Kugenuma, T.; Watanabe, M.; Maeda, I. Nitrogen Fixation in *Rhodopseudomonas palustris* Co-Cultured with *Bacillus subtilis* in the Presence of Air. *J. Biosci. Bioeng.* **2019**, *127*, 589–593. [\[CrossRef\]](#)
119. Temprano-Vera, F.; Rodríguez-Navarro, D.N.; Acosta-Jurado, S.; Perret, X.; Fossou, R.K.; Navarro-Gómez, P.; Zhen, T.; Yu, D.; An, Q.; Buendía-Clavería, A.M.; et al. *Sinorhizobium fredii* Strains HH103 and NGR234 form Nitrogen Fixing Nodules with Diverse Wild Soybeans (*Glycine soja*) from Central China but Are Ineffective on Northern China Accessions. *Front. Microbiol.* **2018**, *9*, 2843. [\[CrossRef\]](#)
120. Marcela, D.; Fourment, J.; Lucas, A.; Bergès, H.; Kahn, D. Nitrogen Regulation in *Sinorhizobium meliloti* Probed with Whole Genome Arrays. *FEMS Microbiol. Lett.* **2004**, *241*, 33–40. [\[CrossRef\]](#)
121. Peix, A.; Rivas, R.; Santa-Regina, I.; Mateos, P.F.; Martínez-Molina, E.; Rodríguez-Barrueco, C.; Velázquez, E. *Pseudomonas lutea* sp. Nov., a Novel Phosphate-Solubilizing Bacterium Isolated from the Rhizosphere of Grasses. *Int. J. Syst. Evol. Microbiol.* **2004**, *54*, 847–850. [\[CrossRef\]](#)
122. Widawati, S. Diversity and Phosphate Solubilization by Bacteria Isolated from Laki Island Coastal Ecosystem. *Biodiversitas J. Biol. Divers.* **2011**, *12*, 17–21. [\[CrossRef\]](#)
123. Zhao, X.; Zhang, Y.; Cui, Z.; Peng, L.; Cao, C. Dynamics of phoD- and Gcd-Harboring Microbial Communities Across an Age Sequence of Biological Soil Crusts Under Sand-Fixation Plantation. *Front. Microbiol.* **2022**, *13*, 831888. [\[CrossRef\]](#)
124. Wan, W.; Qin, Y.; Wu, H.; Zuo, W.; He, H.; Tan, J.; Wang, Y.; He, D. Isolation and Characterization of Phosphorus Solubilizing Bacteria with Multiple Phosphorus Sources Utilizing Capability and Their Potential for Lead Immobilization in Soil. *Front. Microbiol.* **2020**, *11*, 752. [\[CrossRef\]](#)
125. Azziz, G.; Bajsa, N.; Haghjou, T.; Taulé, C.; Valverde, Á.; Igual, J.M.; Arias, A. Abundance, Diversity and Prospecting of Culturable Phosphate Solubilizing Bacteria on Soils Under Crop–Pasture Rotations in a No-Tillage Regime in Uruguay. *Appl. Soil Ecol.* **2012**, *61*, 320–326. [\[CrossRef\]](#)
126. Zhang, L.; Ge, A.-H.; Tóth, T.; Yang, F.; Wang, Z.; An, F. Enrichment of Keystone Fungal Taxa after Flue Gas Desulphurization Gypsum Application Drives Reclamation of the Saline-Sodic Soil. *Land Degrad. Dev.* **2023**, *34*, 2276–2287. [\[CrossRef\]](#)
127. Zampieri, E.; Pesenti, M.; Nocito, F.F.; Sacchi, G.A.; Valè, G. Rice Responses to Water Limiting Conditions: Improving Stress Management by Exploiting Genetics and Physiological Processes. *Agriculture* **2023**, *13*, 464. [\[CrossRef\]](#)
128. Dobbratz, M.; Jungers, J.M.; Gutknecht, J.L.M. Seasonal Plant Nitrogen Use and Soil N Pools in Intermediate Wheatgrass (*Thinopyrum intermedium*). *Agriculture* **2023**, *13*, 468. [\[CrossRef\]](#)
129. Rodriguez, H.; Gonzalez, T.; Goire, I.; Bashan, Y. Gluconic Acid Production and Phosphate Solubilization by the Plant Growth-Promoting Bacterium *Azospirillum* spp. *Naturwissenschaften* **2004**, *91*, 552–555. [\[CrossRef\]](#)
130. Kumar, V.; Kumar Behl, R.; Narula, N. Establishment of Phosphate-Solubilizing Strains of *Azotobacter chroococcum* in the Rhizosphere and Their Effect on Wheat Cultivars under Green House Conditions. *Microbiol. Res.* **2001**, *156*, 87–93. [\[CrossRef\]](#)
131. Ciopińska, J.; Bezak-Mazur, E. Phosphorus Solubilizing Bacteria—Review Article. *Struct. Environ.* **2018**, *10*, 278–287. [\[CrossRef\]](#)
132. Velazquez, L.E.; Perez-Rios, R.; Munguia, N.E.; Zepeda, D.S.; Neudert, C.; Esquer, J. Environmental Approach for Energy Audits on Government Buildings: A Mexican Case for the Air Conditioning System. *J. Environ. Prot.* **2018**, *9*, 278–293. [\[CrossRef\]](#)
133. Mohamed, E.A.H.; Farag, A.G.; Youssef, S.A. Phosphate Solubilization by *Bacillus subtilis* and *Serratia marcescens* Isolated from Tomato Plant Rhizosphere. *J. Environ. Prot.* **2018**, *9*, 266–277. [\[CrossRef\]](#)
134. Grodzicki, P.; Bacia, J.; Piątkowska, K.; Piechowicz, B. Do Glycogen Content and Thermal Preference in Worker Bees Vary Depending on Geographical Origin? A Comparison of Carniolan Honeybees, Central European Honeybees and Caucasian Honeybees. *Agriculture* **2023**, *13*, 492. [\[CrossRef\]](#)
135. Piepel, M.-F.; Olfs, H.-W. Development of a Physicochemical Test Kit for On-Farm Measurement of Nutrients in Liquid Organic Manures. *Agriculture* **2023**, *13*, 477. [\[CrossRef\]](#)
136. Saeid, A.; Prochownik, E.; Dobrowolska-Iwanek, J. Phosphorus Solubilization by *Bacillus* Species. *Molecules* **2018**, *23*, 2897. [\[CrossRef\]](#) [\[PubMed\]](#)
137. Davison, N.; Brown, A.; Ross, A. Potential Greenhouse Gas Mitigation from Utilising Pig Manure and Grass for Hydrothermal Carbonisation and Anaerobic Digestion in the UK, EU, and China. *Agriculture* **2023**, *13*, 479. [\[CrossRef\]](#)
138. Sawicka, M.; Latocha, P.; Łata, B. Peel to Flesh Bioactive Compounds Ratio Affect Apple Antioxidant Potential and Cultivar Functional Properties. *Agriculture* **2023**, *13*, 478. [\[CrossRef\]](#)
139. Yan, Z.; Wang, M.; Li, X.; Jiang, H. Impact of African Swine Fever Epidemic on the Cost Intensity of Pork Production in China. *Agriculture* **2023**, *13*, 497. [\[CrossRef\]](#)
140. Méndez-León, J.R.; Camarena-Gómez, D.M.J.; Salgado-Beltrán, L. Competitive Positioning of Mexican Pork in Japan. *Agriculture* **2023**, *13*, 505. [\[CrossRef\]](#)

141. Wu, B.; Wu, Y.; Dong, R.; Sato, K.; Ikuno, S.; Nishimura, S.; Jin, Q. Behavioral Analysis of Mowing Workers Based on Hilbert–Huang Transform: An Auxiliary Movement Analysis of Manual Mowing on the Slopes of Terraced Rice Fields. *Agriculture* **2023**, *13*, 489. [\[CrossRef\]](#)
142. Chi, L.; Zhu, M.; Shen, C.; Zhang, J.; Xing, L.; Zhou, X. Does the Winner Take All in E-Commerce of Agricultural Products Under the Background of Platform Monopoly? *Agriculture* **2023**, *13*, 476. [\[CrossRef\]](#)
143. Hashemi, F.; Zalaghi, R.; Enayatizamir, N. Using Zeolite, Molasses, and PGP Microorganisms to Improve Apatite Solubility and Increase Phosphorus Uptake by *Sorghum bicolor* L. (*Speedfed cultivar*). *Sci. Rep.* **2025**, *15*, 19352. [\[CrossRef\]](#)
144. Borham, A.; Belal, E.; Salem, M.; El-Gremy, S. Phosphate Solubilization by *Enterobacter Cloacae* and Its Impact on Growth and Yield of Wheat Plants. *J. Sustain. Agric. Sci.* **2017**, *43*, 89–103. [\[CrossRef\]](#)
145. Geneva, M.; Hristozkova, M.; Kirova, E.; Sichanova, M.; Stancheva, I. Response to Drought Stress of In Vitro and In Vivo Propagated *Physalis peruviana* L. Plants Inoculated with Arbuscular Mycorrhizal Fungi. *Agriculture* **2023**, *13*, 472. [\[CrossRef\]](#)
146. Bieniek, A.; Bieniek, A.; Bielska, N. Variation in Fruit and Seed Morphology of Selected Biotypes and Cultivars of *Elaeagnus multiflora* Thunb. in North-Eastern Europe. *Agriculture* **2023**, *13*, 495. [\[CrossRef\]](#)
147. Cheng, T.; Cao, X.; Wang, Y.; Zhao, L. Development of CRISPR-Cas9-Based Genome Editing Tools for Non-Model Microorganism *Erwinia persicina*. *Synth. Syst. Biotechnol.* **2025**, *10*, 555–563. [\[CrossRef\]](#) [\[PubMed\]](#)
148. Silva, L.I.d.; Pereira, M.C.; Carvalho, A.M.X.d.; Buttrós, V.H.; Pasqual, M.; Dória, J. Phosphorus-Solubilizing Microorganisms: A Key to Sustainable Agriculture. *Agriculture* **2023**, *13*, 462. [\[CrossRef\]](#)
149. Correa-Garcia, S.; Constant, P.; Yergeau, E. The Forecasting Power of the Microbiome. *Trends Microbiol.* **2023**, *31*, 444–452. [\[CrossRef\]](#)
150. Liu, R.; Liang, B.; Zhao, H.; Zhao, Y. Impacts of Various Amendments on the Microbial Communities and Soil Organic Carbon of Coastal Saline–Alkali Soil in the Yellow River Delta. *Front. Microbiol.* **2023**, *14*, 1239855. [\[CrossRef\]](#) [\[PubMed\]](#)
151. Khalid, M.; Sarfraz, M.S.; Iqbal, U.; Aftab, M.U.; Niedbala, G.; Rauf, H.T. Real-Time Plant Health Detection Using Deep Convolutional Neural Networks. *Agriculture* **2025**, *15*, 510. [\[CrossRef\]](#)
152. Gabilondo, R.; Sánchez, J.; Muñoz, P.; Montero-Muñoz, I.; Mauri, P.V.; Marín, J.; Mostaza-Colado, D. Evaluation of Biostimulatory Activity of Commercial Formulations on Three Varieties of Chickpea. *Agriculture* **2023**, *13*, 474. [\[CrossRef\]](#)
153. Hao, M.; Lu, C.; Zhou, X.; Xu, J. How Agricultural Farmers Respond to Risks During the COVID-19 Pandemic: An Exploration Through the Dual Social Capitals Approach. *Agriculture* **2023**, *13*, 485. [\[CrossRef\]](#)
154. Sharma, S.; Gupta, S.; Kumari, D.; Kothari, S.L.; Jain, R.; Kachhwaha, S. Exploring Plant Tissue Culture and Steviol Glycosides Production in *Stevia rebaudiana* (Bert.) Berton: A Review. *Agriculture* **2023**, *13*, 475. [\[CrossRef\]](#)
155. Pei, J.; Liu, P.; Fang, H.; Gao, X.; Pan, B.; Li, H.; Guo, H.; Zhang, F. Estimating Yield and Economic Losses Induced by Ozone Exposure in South China Based on Full-Coverage Surface Ozone Reanalysis Data and High-Resolution Rice Maps. *Agriculture* **2023**, *13*, 506. [\[CrossRef\]](#)
156. Lal, M.; Munda, S.; Begum, T.; Pandey, S.K. Identification and Registration of the Novel High-Rhizome-Yielding Variety Bharamputra-1 of *Kaempferia galanga* L. *Agriculture* **2023**, *13*, 482. [\[CrossRef\]](#)
157. Mubeen, S.; Ni, W.; He, C.; Yang, Z. Agricultural Strategies to Reduce Cadmium Accumulation in Crops for Food Safety. *Agriculture* **2023**, *13*, 471. [\[CrossRef\]](#)
158. Hu, J.; Li, G.; Mo, H.; Lv, Y.; Qian, T.; Chen, M.; Lu, S. Crop Node Detection and Internode Length Estimation Using an Improved YOLOv5 Model. *Agriculture* **2023**, *13*, 473. [\[CrossRef\]](#)
159. Wang, Y.; Guo, Y.; Wang, X.; Song, C.; Song, Y.; Liu, Z.; Wang, S.; Gao, S.; Ma, G. Mineral Protection Controls Soil Organic Carbon Stability in Permafrost Wetlands. *Sci. Total Environ.* **2023**, *869*, 161864. [\[CrossRef\]](#)
160. Tang, F.; Li, Q.; Yue, J.; Ge, F.; Li, F.; Liu, Y.; Zhang, D.; Tian, J. *Penicillium oxalicum* Augments Soil Lead Immobilization by Affecting Indigenous Microbial Community Structure and Inorganic Phosphate Solubilization Potential During Microbial-Induced Phosphate Precipitation. *Environ. Pollut.* **2023**, *319*, 120953. [\[CrossRef\]](#)
161. Qureshi, T.M.; Nadeem, M.; Iftikhar, J.; Salim-ur-Rehman; Ibrahim, S.M.; Majeed, F.; Sultan, M. Effect of Traditional Spices on the Quality and Antioxidant Potential of Paneer Prepared from Buffalo Milk. *Agriculture* **2023**, *13*, 491. [\[CrossRef\]](#)
162. Tomatis, F.; Egerer, M.; Correa-Guimaraes, A.; Navas-Gracia, L.M. Urban Gardening in a Changing Climate: A Review of Effects, Responses and Adaptation Capacities for Cities. *Agriculture* **2023**, *13*, 502. [\[CrossRef\]](#)
163. Shruti; Shukla, A.; Rahman, S.S.; Suneja, P.; Yadav, R.; Hussain, Z.; Singh, R.; Yadav, S.K.; Rana, J.C.; Yadav, S.; et al. Developing an NIRS Prediction Model for Oil, Protein, Amino Acids and Fatty Acids in Amaranth and Buckwheat. *Agriculture* **2023**, *13*, 469. [\[CrossRef\]](#)
164. Park, K.-H.; Lee, C.-Y.; Son, H.-J. Mechanism of Insoluble Phosphate Solubilization by *Pseudomonas fluorescens* RAF15 Isolated from Ginseng Rhizosphere and Its Plant Growth-promoting Activities. *Lett. Appl. Microbiol.* **2009**, *49*, 222–228. [\[CrossRef\]](#)
165. Osei, E.; Jafri, S.H.; Gassman, P.W.; Saleh, A.; Gallego, O. Climate Change Impacts on Surface Runoff and Nutrient and Sediment Losses in Buchanan County, Iowa. *Agriculture* **2023**, *13*, 470. [\[CrossRef\]](#)

166. Costa-Gutierrez, S.B.; Adler, C.; Espinosa-Urgel, M.; de Cristóbal, R.E. *Pseudomonas putida* and Its Close Relatives: Mixing and Mastering the Perfect Tune for Plants. *Appl. Microbiol. Biotechnol.* **2022**, *106*, 3351–3367. [[CrossRef](#)] [[PubMed](#)]
167. López-Ortega, M.D.P.; Criollo-Campos, P.J.; Gómez-Vargas, R.M.; Camelo-Runsique, M.; Estrada-Bonilla, G.; Garrido-Rubiano, M.F.; Bonilla-Buitrago, R. Characterization of Diazotrophic Phosphate Solubilizing Bacteria as Growth Promoters of Maize Plants. *Rev. Colomb. Biotechnol.* **2013**, *15*, 115–123. [[CrossRef](#)]
168. Abril, A.; Zurdo-Piñero, J.L.; Peix, A.; Rivas, R.; Velázquez, E. Solubilization of Phosphate by a Strain of *Rhizobium leguminosarum* Bv. Trifolii Isolated from *Phaseolus vulgaris* in El Chaco Arido Soil (Argentina). In *First International Meeting on Microbial Phosphate Solubilization*; Velázquez, E., Rodríguez-Barrueco, C., Eds.; Developments in Plant and Soil Sciences; Springer: Dordrecht, The Netherlands, 2007; Volume 102, pp. 135–138.
169. Marra, L.M.; Oliveira, S.M.d.; Soares, C.R.F.S.; Moreira, F.M.d.S. Solubilisation of Inorganic Phosphates by Inoculant Strains from Tropical Legumes. *Sci. Agric.* **2011**, *68*, 603–609. [[CrossRef](#)]
170. Akhtar, M.N.; Ansari, E.; Alhady, S.S.N.; Abu Bakar, E. Leveraging on Advanced Remote Sensing- and Artificial Intelligence-Based Technologies to Manage Palm Oil Plantation for Current Global Scenario: A Review. *Agriculture* **2023**, *13*, 504. [[CrossRef](#)]
171. Ropelewska, E.; Rutkowski, K.P. The Classification of Peaches at Different Ripening Stages Using Machine Learning Models Based on Texture Parameters of Flesh Images. *Agriculture* **2023**, *13*, 498. [[CrossRef](#)]
172. Piechowicz, B.; Kwiatek, A.; Sadło, S.; Zareba, L.; Kozirowska, A.; Kloc, D.; Balawejder, M. Use of Gas Chromatography and SPME Extraction for the Differentiation Between Healthy and *Paenibacillus larvae* Infected Colonies of Bee Brood—Preliminary Research. *Agriculture* **2023**, *13*, 487. [[CrossRef](#)]
173. Gidey, E.; Dikinya, O.; Sebego, R.; Segosebe, E.; Zenebe, A.; Mussa, S.; Mhangara, P.; Birhane, E. Land Use and Land Cover Change Determinants in Raya Valley, Tigray, Northern Ethiopian Highlands. *Agriculture* **2023**, *13*, 507. [[CrossRef](#)]
174. Kan, H.; Qu, S.; Dong, K.; Wang, S.; Xu, C.; Wang, Y.; Hua, S. Integrated Metabolome and Transcriptome Analysis Unveils the Underlying Molecular Response of *Panax ginseng* Plants to the *Phytophthora cactorum* Infection. *Agriculture* **2023**, *13*, 509. [[CrossRef](#)]
175. Chen, N.; Zhao, X.; Dou, S.; Deng, A.; Zheng, C.; Cao, T.; Song, Z.; Zhang, W. The Tradeoff between Maintaining Maize (*Zea mays* L.) Productivity and Improving Soil Quality under Conservation Tillage Practice in Semi-Arid Region of Northeast China. *Agriculture* **2023**, *13*, 508. [[CrossRef](#)]
176. Kavya, V.; Jayaprakash, R.; Shankar, M. Effect of Potassium Solubilizing Bacteria and Foliar Application of Potassium on Soil Nutrient Status and Soil Biological Properties in Paddy (*Oryza sativa*) in Coastal Acid Soils of Karnataka. *Int. J. Res. Agron.* **2025**, *8*, 403–408. [[CrossRef](#)]
177. Sani, S.; Bairwa, R.; Abdulkadir, A.I.; Lawal, A.U.; Gurjar, O.P.; Regar, C.L.; Meena, V.S.; Alhassan, S. A Comparative Assessment of Potassium Mineralization from Waste Mica by Application of KSB and FYM in Alluvial and Black Soils. *Res. Sq.* **2025**. [[CrossRef](#)]
178. Zheng, J.; Shi, G.; Dini-Andreote, F.; Yang, Y.; Jiang, Y. Root-Derived Low Molecular Weight Organic Acids Modulate Keystone Microbial Taxa Impacting Plant Phosphorus Acquisition. *J. Adv. Res.* **2026**, *81*, 95–109. [[CrossRef](#)]
179. Dong, X.; Lv, L.; Wang, W.; Liu, Y.; Yin, C.; Xu, Q.; Yan, H.; Fu, J.; Liu, X. Differences in Distribution of Potassium-Solubilizing Bacteria in Forest and Plantation Soils in Myanmar. *Int. J. Environ. Res. Public Health* **2019**, *16*, 700. [[CrossRef](#)]
180. Pratama, D.; Anas, I.; Suwarno, S. Ability of Potassium-Solubilising Microbes to Solubilise Feldspar and Their Effects on Sorghum Growth. *Malays. J. Soil Sci.* **2016**, *20*, 163–175.
181. Zhang, C.; Kong, F. Isolation and Identification of Potassium-Solubilizing Bacteria from Tobacco Rhizospheric Soil and Their Effect on Tobacco Plants. *Appl. Soil Ecol.* **2014**, *82*, 18–25. [[CrossRef](#)]
182. Lian, B.; Wang, B.; Pan, M.; Liu, C.; Teng, H.H. Microbial Release of Potassium from K-Bearing Minerals by Thermophilic Fungus *Aspergillus fumigatus*. *Geochim. Cosmochim. Acta* **2008**, *72*, 87–98. [[CrossRef](#)]
183. Lopes-Assad, M.L.; Avansini, S.H.; Rosa, M.M.; de Carvalho, J.R.P.; Ceccato-Antonini, S.R. The Solubilization of Potassium-Bearing Rock Powder by *Aspergillus niger* in Small-Scale Batch Fermentations. *Can. J. Microbiol.* **2010**, *56*, 598–605. [[CrossRef](#)] [[PubMed](#)]
184. Ashrafi-Saiedlou, S.; Rasouli-Sadaghiani, M.; Samadi, A.; Barin, M.; Sepehr, E. *Aspergillus niger* as an Eco-Friendly Agent for Potassium Release from K-Bearing Minerals: Isolation, Screening and Culture Medium Optimization Using Plackett-Burman Design and Response Surface Methodology. *Heliyon* **2024**, *10*, e29117. [[CrossRef](#)]
185. Gao, G.; Li, X.; Ma, J.; Cui, Y.; Ying, M.; Huang, L.; Li, M. *Bacillus amyloliquefaciens* SQ-2 and Biochar: A Promising Combination for Enhancing Rice Growth in Pb/Al-Contaminated Acidic Soils. *Microorganisms* **2025**, *13*, 1556. [[CrossRef](#)] [[PubMed](#)]
186. Tian, Y.; Jiang, W.; Chen, G.; Wang, X.; Li, T. Gypsum and Organic Materials Improved Soil Quality and Crop Production in Saline-Alkali on the Loess Plateau of China. *Front. Environ. Sci.* **2024**, *12*, 1434147. [[CrossRef](#)]
187. Etesami, H.; Emami, S.; Alikhani, H.A. Potassium Solubilizing Bacteria (KSB): Mechanisms, Promotion of Plant Growth, and Future Prospects—A Review. *J. Soil Sci. Plant Nutr.* **2017**, *17*, 897–911. [[CrossRef](#)]

188. Romero-Munar, A.; Aroca, R. A Non-K⁺-Solubilizing PGPB (*Bacillus megaterium*) Increased K⁺ Deprivation Tolerance in *Oryza sativa* Seedlings by up-Regulating Root K⁺ Transporters. *Plant Physiol. Biochem.* **2023**, *196*, 774–782. [\[CrossRef\]](#)
189. Nguyen, N.K.; Vo, D.T.V.; Le, T.X.; Morton, L.W.; Tran, H.-T.; Robotjazi, J.; Lasar, H.G.W.; Tecimen, H.B. Isolation, and Selection of Indigenous Potassium Solubilizing Bacteria from Vietnam Mekong Delta Rhizospheric Soils and Their Effects on Diverse Cropping Systems. *Biocatal. Agric. Biotechnol.* **2024**, *58*, 103200. [\[CrossRef\]](#)
190. Kumar, P.; Singh, A.B.; Singh, R. Seasonal Variation and Size Distribution in the Airborne Indoor Microbial Concentration of Residential Houses in Delhi and Its Impact on Health. *Aerobiologia* **2021**, *37*, 719–732. [\[CrossRef\]](#)
191. Boubekri, K.; Soumare, A.; Mardad, I.; Lyamlouli, K.; Hafidi, M.; Ouhdouch, Y.; Kouisni, L. The Screening of Potassium- and Phosphate-Solubilizing Actinobacteria and the Assessment of Their Ability to Promote Wheat Growth Parameters. *Microorganisms* **2021**, *9*, 470. [\[CrossRef\]](#) [\[PubMed\]](#)
192. Zhang, A.; Zhao, G.; Gao, T.; Wang, W.; Li, J.; Zhang, S.; Zhu, B. Solubilization of Insoluble Potassium and Phosphate by *Paenibacillus kribensis* CX-7: A Soil Microorganism with Biological Control Potential. *Afr. J. Microbiol. Res.* **2013**, *7*, 41–47. [\[CrossRef\]](#)
193. Zhuang, J.; Liu, C.; Wang, X.; Xu, T.; Yang, H. *Penicillium simplicissimum* NL-Z1 Induced an Imposed Effect to Promote the Leguminous Plant Growth. *Front. Microbiol.* **2021**, *12*, 738734. [\[CrossRef\]](#) [\[PubMed\]](#)
194. Ashrafi-Saeidlou, S.; Samadi, A.; Rasouli-Sadaghiani, M.; Barin, M.; Sepehr, E. Optimization of Potassium Dissolution by *Pseudomonas fluorescens* Using Placket-Burman Design and Response Surface Methodology. *J. Water Soil* **2019**, *33*, 647–658. [\[CrossRef\]](#)
195. Yaghoubi Khanghahi, M.; Pirdashti, H.; Rahimian, H.; Nematzadeh, G.; Ghajar Sepanlou, M. The Role of Potassium Solubilizing Bacteria (KSB) Inoculations on Grain Yield, Dry Matter Remobilization and Translocation in Rice (*Oryza sativa* L.). *J. Plant Nutr.* **2019**, *42*, 1165–1179. [\[CrossRef\]](#)
196. Chouyia, F.E.; Ventrino, V.; Pepe, O. Diversity, Mechanisms and Beneficial Features of Phosphate-Solubilizing Streptomyces in Sustainable Agriculture: A Review. *Front. Plant Sci.* **2022**, *13*, 1035358. [\[CrossRef\]](#)
197. El-Egami, H.M.; Hegab, R.H.; Montaser, H.; El-Hawary, M.M.; Hasanuzzaman, M. Impact of Potassium-Solubilizing Microorganisms with Potassium Sources on the Growth, Physiology, and Productivity of Wheat Crop under Salt-Affected Soil Conditions. *Agronomy* **2024**, *14*, 423. [\[CrossRef\]](#)
198. Kumari, M.D.H.M.; Athukorala, A.D.S.N.P.; Vishwajith, H.K.I.S.; Rajapakse, R.M.G. Potassium Solubilizers, *Aspergillus* sp. and *Trichoderma* sp. Promote Growth in Tomato. *Proc. Int. For. Environ. Symp.* **2023**, *27*, 132. [\[CrossRef\]](#)
199. Ei, S.L.; Lwin, K.M.; Padamyar, Khaing, H.O.; Yu, S.S. Study on IAA Producing Rhizobacterial Isolates and Their Effect in Talc-Based Carrier on Some Plants. *J. Soil Sci. Plant Health* **2000**, *2*, 1–7.
200. Yuliatin, E.; Ardyati, T.; Suharjono, S. Effect of Soil Physicochemical Properties on PGPR Density at A Coffee Plantation in Malang, Indonesia. *IOP Conf. Ser. Earth Environ. Sci.* **2019**, *391*, 012071. [\[CrossRef\]](#)
201. Gruet, C.; Abrouk, D.; Börner, A.; Muller, D.; Moënné-Loccoz, Y. D Genome Acquisition and Breeding Have Had a Significant Impact on Interaction of Wheat with ACC Deaminase Producers in Soil or ACC Deaminase Potential Activity in the Rhizosphere. *Soil Biol. Biochem.* **2024**, *193*, 109392. [\[CrossRef\]](#)
202. Uzma, M.; Nisar, A.; Iqbal, A.; Hasnain, S.; Mahmoud, M.H.; Rahim, M.A.; Gull, T.; Castro-Muñoz, R.; Zongo, E. Exploring the Efficacy of Drought Tolerant, IAA-Producing Plant Growth-Promoting Rhizobacteria for Sustainable Agriculture. *Plant Signal. Behav.* **2025**, *20*, 2452331. [\[CrossRef\]](#)
203. Wang, X.; Chi, Y.; Song, S. Important Soil Microbiota's Effects on Plants and Soils: A Comprehensive 30-Year Systematic Literature Review. *Front. Microbiol.* **2024**, *15*, 1347745. [\[CrossRef\]](#)
204. Egamberdieva, D.; Wirth, S.J.; Alqarawi, A.A.; Abd_Allah, E.F.; Hashem, A. Phytohormones and Beneficial Microbes: Essential Components for Plants to Balance Stress and Fitness. *Front. Microbiol.* **2017**, *8*, 2104. [\[CrossRef\]](#)
205. Neelam, A.; Tabassum, S. Optical Sensing Technologies to Elucidate the Interplay between Plant and Microbes. *Micromachines* **2023**, *14*, 195. [\[CrossRef\]](#)
206. Zaheer, M.S.; Ali, H.H.; Iqbal, M.A.; Erinle, K.O.; Javed, T.; Iqbal, J.; Hashmi, M.I.U.; Mumtaz, M.Z.; Salama, E.A.A.; Kalaji, H.M.; et al. Cytokinin Production by *Azospirillum brasilense* Contributes to Increase in Growth, Yield, Antioxidant, and Physiological Systems of Wheat (*Triticum aestivum* L.). *Front. Microbiol.* **2022**, *13*, 886041. [\[CrossRef\]](#)
207. Nghia, N.K.; Robotjazi, J.; Vy, V.D.T.; Tecimen, H.B.; Lasar, H.G.W.; Lesueur, D.; Bai, S.H.; Tran, H.-T.; Thien, N.H.; Luan, D.T. Effect of Organic Farming Practices on Soil Health Improvement of Coconut Farms. *Environ. Technol. Innov.* **2025**, *38*, 104067. [\[CrossRef\]](#)
208. Allingham, S.M.; Drake, S.J.; Ramsey, A.; Field, C.D.; Nwaishi, F.C.; Elliott, D.R. Changes in Nitrogen Functional Genes and Microbial Populations in Soil Profiles of a Peatland under Different Burning Regimes. *Appl. Soil Ecol.* **2024**, *200*, 105426. [\[CrossRef\]](#)
209. Cretoiu, M.S.; Korthals, G.W.; Visser, J.H.M.; van Elsas, J.D. Chitin Amendment Increases Soil Suppressiveness toward Plant Pathogens and Modulates the Actinobacterial and Oxalobacteraceal Communities in an Experimental Agricultural Field. *Appl. Environ. Microbiol.* **2013**, *79*, 5291–5301. [\[CrossRef\]](#)

210. Jiang, L.; Xu, B.; Wang, Q. Functional Characteristics and Cellulose Degradation Genes of the Microbial Community in Soils with Different Initial pH Values. *Agriculture* **2025**, *15*, 1068. [[CrossRef](#)]
211. Li, G.; Wei, M.; Wei, G.; Chen, Z.; Shao, Z. Efficient Heterotrophic Nitrification by a Novel Bacterium *Sneathiella aquimaris* 216LB-ZA1-12T Isolated from Aquaculture Seawater. *Ecotoxicol. Environ. Saf.* **2023**, *266*, 115588. [[CrossRef](#)] [[PubMed](#)]
212. Kalwasinska, A.; Keszy, J.; Donderski, W.; Lalke-Porczyk, E. Biodegradation of Carbendazim by Planktonic and Benthic Bacteria of Eutrophic Lake Chełmżyńskie. *Pol. J. Environ. Stud.* **2008**, *17*, 515–523.
213. Singh, R.; Upadhyay, S.K. A Study on the Plant Litter Decomposition Using Mycoflora for Sustainable Environment. *Plantae Sci.* **2019**, *2*, 11–14. [[CrossRef](#)]
214. Fang, W.; Latgé, J.-P. Microbe Profile: *Aspergillus Fumigatus*: A Saprotrophic and Opportunistic Fungal Pathogen. *Microbiology* **2018**, *164*, 1009–1011. [[CrossRef](#)]
215. Heidarzadeh, M.H.; Amani, H.; Javadian, B. Improving Municipal Solid Waste Compost Process by Cycle Time Reduction through Inoculation of *Aspergillus niger*. *J. Environ. Health Sci. Eng.* **2019**, *17*, 295–303. [[CrossRef](#)]
216. Jiang, J.; Tang, M.; Chen, J.; Yang, Y. Identification and Degradation Characteristics of *Bacillus cereus* Strain WD-2 Isolated from Prochloraz-Manganese-Contaminated Soils. *PLoS ONE* **2019**, *14*, e0220975. [[CrossRef](#)] [[PubMed](#)]
217. Su, J.; Zhou, K.; Chen, W.; Xu, S.; Feng, Z.; Chang, Y.; Ding, X.; Zheng, Y.; Tao, X.; Zhang, A.; et al. Enhanced Organic Degradation and Microbial Community Cooperation by Inoculating *Bacillus licheniformis* in Low Temperature Composting. *J. Environ. Sci.* **2024**, *143*, 189–200. [[CrossRef](#)]
218. Alshelmani, M.I.; Loh, T.C.; Foo, H.L.; Lau, W.H.; Sazili, A.Q. Characterization of Cellulolytic Bacterial Cultures Grown in Different Substrates. *Sci. World J.* **2013**, *2013*, 689235. [[CrossRef](#)] [[PubMed](#)]
219. Sobolczyk-Bednarek, J.; Choińska-Pulit, A.; Łaba, W. Composting Poultry Feathers with Keratinolytic *Bacillus subtilis*: Effects on Degradation Efficiency and Compost Maturity. *Materials* **2025**, *18*, 4667. [[CrossRef](#)]
220. Zafar, H.; Peleato, N.; Roberts, D. Bioaugmentation with *Bacillus subtilis* and *Cellulomonas fimi* to Enhance the Biodegradation of Complex Carbohydrates in MFC-Fed Fruit Waste. *Biomass Bioenergy* **2023**, *174*, 106843. [[CrossRef](#)]
221. Bowen, R.M.; Harper, S.H.T. Decomposition of Wheat Straw and Related Compounds by Fungi Isolated from Straw in Arable Soils. *Soil Biol. Biochem.* **1990**, *22*, 393–399. [[CrossRef](#)]
222. Li, X.; Han, C.; Li, W.; Chen, G.; Wang, L. Insights into the Cellulose Degradation Mechanism of the Thermophilic Fungus *Chaetomium thermophilum* Based on Integrated Functional Omics. *Biotechnol. Biofuels* **2020**, *13*, 143. [[CrossRef](#)]
223. Ha-Tran, D.M.; Nguyen, T.T.M.; Huang, C.-C. *Clostridium thermocellum* as a Promising Source of Genetic Material for Designer Cellulosomes: An Overview. *Catalysts* **2021**, *11*, 996. [[CrossRef](#)]
224. Olajuyigbe, F.M.; Nlekerem, C.M.; Ogunyewo, O.A. Production and Characterization of Highly Thermostable β -Glucosidase during the Biodegradation of Methyl Cellulose by *Fusarium oxysporum*. *Biochem. Res. Int.* **2016**, *2016*, 3978124. [[CrossRef](#)] [[PubMed](#)]
225. Ladevèze, S.; Haon, M.; Villares, A.; Cathala, B.; Grisel, S.; Herpoël-Gimbert, I.; Henrissat, B.; Berrin, J.-G. The Yeast *Geotrichum candidum* Encodes Functional Lytic Polysaccharide Monooxygenases. *Biotechnol. Biofuels* **2017**, *10*, 215. [[CrossRef](#)] [[PubMed](#)]
226. Zhu, N.; Zhu, Y.; Li, B.; Jin, H.; Dong, Y. Increased Enzyme Activities and Fungal Degraders by *Gloeophyllum trabeum* Inoculation Improve Lignocellulose Degradation Efficiency during Manure-Straw Composting. *Bioresour. Technol.* **2021**, *337*, 125427. [[CrossRef](#)]
227. Bhairamkar, S.; Kadam, P.; Anjulal, H.; Joshi, A.; Chaudhari, R.; Bagul, D.; Javdekar, V.; Zinjarde, S. Comprehensive Updates on the Biological Features and Metabolic Potential of the Versatile Extremophilic Actinomycete *Nocardioopsis dassonvillei*. *Res. Microbiol.* **2024**, *175*, 104171. [[CrossRef](#)]
228. Waeonukul, R.; Kyu, K.L.; Sakka, K.; Ratanakhanokchai, K. Isolation and Characterization of a Multienzyme Complex (Cellulosome) of the *Paenibacillus curdlanolyticus* B-6 Grown on Avicel under Aerobic Conditions. *J. Biosci. Bioeng.* **2009**, *107*, 610–614. [[CrossRef](#)]
229. Wolski, E.A. The Versatility of *Penicillium* Species to Degrade Organic Pollutants and Its Use for Wastewater Treatment. *SIF* **2023**, *8*, 2. [[CrossRef](#)]
230. Martinez, D.; Larrondo, L.F.; Putnam, N.; Gelpke, M.D.S.; Huang, K.; Chapman, J.; Helfenbein, K.G.; Ramaiya, P.; Detter, J.C.; Larimer, F.; et al. Genome Sequence of the Lignocellulose Degrading Fungus *Phanerochaete chrysosporium* Strain RP78. *Nat. Biotechnol.* **2004**, *22*, 695–700. [[CrossRef](#)]
231. Li, F.; Ma, F.; Zhao, H.; Zhang, S.; Wang, L.; Zhang, X.; Yu, H. A Lytic Polysaccharide Monooxygenase from a White-Rot Fungus Drives the Degradation of Lignin by a Versatile Peroxidase. *Appl. Environ. Microbiol.* **2019**, *85*, e02803-18. [[CrossRef](#)]
232. Kameshwar, A.K.S.; Qin, W. Molecular Networks of *Postia placenta* Involved in Degradation of Lignocellulosic Biomass Revealed from Metadata Analysis of Open Access Gene Expression Data. *Int. J. Biol. Sci.* **2018**, *14*, 237–252. [[CrossRef](#)] [[PubMed](#)]
233. Zhou, Q.; Fransen, A.; de Winde, H. Lignin-Degrading Enzymes and the Potential of *Pseudomonas Putida* as a Cell Factory for Lignin Degradation and Valorization. *Microorganisms* **2025**, *13*, 935. [[CrossRef](#)]

234. Sabar, M.A.; Ali, M.I.; Fatima, N.; Malik, A.Y.; Jamal, A.; Farman, M.; Huang, Z.; Urynowicz, M. Degradation of Low Rank Coal by *Rhizopus oryzae* Isolated from a Pakistani Coal Mine and Its Enhanced Releases of Organic Substances. *Fuel* **2019**, *253*, 257–265. [\[CrossRef\]](#)
235. Ahmad, M.; Roberts, J.N.; Hardiman, E.M.; Singh, R.; Eltis, L.D.; Bugg, T.D.H. Identification of DypB from *Rhodococcus jostii* RHA1 as a Lignin Peroxidase. *Biochemistry* **2011**, *50*, 5096–5107. [\[CrossRef\]](#)
236. Chater, K.F.; Biró, S.; Lee, K.J.; Palmer, T.; Schrempf, H. The Complex Extracellular Biology of Streptomyces. *FEMS Microbiol. Rev.* **2010**, *34*, 171–198. [\[CrossRef\]](#)
237. Hernandez-Pérez, G.; Goma, G.; Rols, J.L. Enhanced Degradation of Lignosulfonated Compounds by *Streptomyces viridosporus*. *Water Sci. Technol.* **1998**, *38*, 289–297. [\[CrossRef\]](#)
238. Zainudin, M.H.M.; Gan, H.M.; Tokura, M. Genome Sequence of Thermophilic Cellulolytic Actinobacterium *Thermobifida fusca* Strain UPMC 901 Producing Thermostable Cellulases. *Gene Rep.* **2024**, *35*, 101900. [\[CrossRef\]](#)
239. Tišma, M.; Žnidaršič-Plazl, P.; Šelo, G.; Tolj, I.; Šperanda, M.; Bucić-Kojić, A.; Planinić, M. *Trametes versicolor* in Lignocellulose-Based Bioeconomy: State of the Art, Challenges and Opportunities. *Bioresour. Technol.* **2021**, *330*, 124997. [\[CrossRef\]](#)
240. Li, J.-X.; Zhang, F.; Jiang, D.-D.; Li, J.; Wang, F.-L.; Zhang, Z.; Wang, W.; Zhao, X.-Q. Diversity of Cellulase-Producing Filamentous Fungi from Tibet and Transcriptomic Analysis of a Superior Cellulase Producer *Trichoderma harzianum* LZ117. *Front. Microbiol.* **2020**, *11*, 1617. [\[CrossRef\]](#)
241. Reza, M.M. Assessing the Effect of Siderophore Producing Bacteria for the Iron Nutrition in Lentil and Pea. Master's Thesis, University of Saskatchewan, Saskatoon, SK, Canada, 2017.
242. Yi, X.; Wang, M.; Zhou, Z. The Potential Impact of Naturally Produced Antibiotics, Environmental Factors, and Anthropogenic Pressure on the Occurrence of *Erm* Genes in Urban Soils. *Environ. Pollut.* **2019**, *245*, 282–289. [\[CrossRef\]](#)
243. Le, T.-H.; Sivachidambaram, V.; Yi, X.; Li, X.; Zhou, Z. Quantification of Polyketide Synthase Genes in Tropical Urban Soils Using Real-Time PCR. *J. Microbiol. Methods* **2014**, *106*, 135–142. [\[CrossRef\]](#)
244. Majewska, M.; Słomka, A.; Hanaka, A. Siderophore-Producing Bacteria from Spitsbergen Soils—Novel Agents Assisted in Bioremediation of the Metal-Polluted Soils. *Environ. Sci. Pollut. Res.* **2024**, *31*, 32371–32381. [\[CrossRef\]](#)
245. Sharma, M.; Mishra, V.; Rau, N.; Sharma, R.S. Increased Iron-Stress Resilience of Maize through Inoculation of Siderophore-Producing *Arthrobacter globiformis* from Mine. *J. Basic Microbiol.* **2016**, *56*, 719–735. [\[CrossRef\]](#) [\[PubMed\]](#)
246. Xie, B.; Wei, X.; Wan, C.; Zhao, W.; Song, R.; Xin, S.; Song, K. Exploring the Biological Pathways of Siderophores and Their Multidisciplinary Applications: A Comprehensive Review. *Molecules* **2024**, *29*, 2318. [\[CrossRef\]](#)
247. Timofeeva, A.M.; Galyamova, M.R.; Sedykh, S.E. Bacterial Siderophores: Classification, Biosynthesis, Perspectives of Use in Agriculture. *Plants* **2022**, *11*, 3065. [\[CrossRef\]](#)
248. Suneja, S.; Lakshminarayana, K.; Narula, N. Optimization of Cultural Conditions for Hydroxamate Type of Siderophore Production by *Azotobacter chroococcum*. *Microbiol. Res.* **1994**, *149*, 385–390. [\[CrossRef\]](#)
249. Nouiou, I.; Cortés-albayay, C.; Carro, L.; Castro, J.F.; Gtari, M.; Ghodhbane-Gtari, F.; Klenk, H.-P.; Tisa, L.S.; Sangal, V.; Goodfellow, M. Genomic Insights Into Plant-Growth-Promoting Potentialities of the Genus *Frankia*. *Front. Microbiol.* **2019**, *10*, 1457. [\[CrossRef\]](#)
250. Ferreira, C.M.H.; Vilas-Boas, Â.; Sousa, C.A.; Soares, H.M.V.M.; Soares, E.V. Comparison of Five Bacterial Strains Producing Siderophores with Ability to Chelate Iron Under Alkaline Conditions. *AMB Express* **2019**, *9*, 78. [\[CrossRef\]](#)
251. Barona-Gómez, F.; Lautru, S.; Francou, F.-X.; Leblond, P.; Pernodet, J.-L.; Challis, G.L. Multiple Biosynthetic and Uptake Systems Mediate Siderophore-Dependent Iron Acquisition in *Streptomyces coelicolor* A3(2) and *Streptomyces ambifaciens* ATCC 23877. *Microbiology* **2006**, *152*, 3355–3366. [\[CrossRef\]](#) [\[PubMed\]](#)
252. Bolaji, A.S.; Liasu, M.O.; Ayandele, A.A.; Amao, J.A. Assessing the Synergistic Relationship of Mycorrhiza and Bacteria for the Degradation of Spent Engine Oil in Maize Grown Soil. *Bull. Natl. Res. Cent.* **2020**, *44*, 43. [\[CrossRef\]](#)
253. Park, S.H.; Kang, B.R.; Kim, J.; Lee, Y.; Nam, H.S.; Lee, T.K. Enhanced Soil Fertility and Carbon Dynamics in Organic Farming Systems: The Role of Arbuscular Mycorrhizal Fungal Abundance. *J. Fungi* **2024**, *10*, 598. [\[CrossRef\]](#) [\[PubMed\]](#)
254. Zou, G.; Liu, Y.; Kong, F.; Liao, L.; Deng, G.; Jiang, X.; Cai, J.; Liu, W. Depression of the Soil Arbuscular Mycorrhizal Fungal Community by the Canopy Gaps in a Japanese Cedar (*Cryptomeria japonica*) Plantation on Lushan Mountain, Subtropical China. *PeerJ* **2021**, *9*, e10905. [\[CrossRef\]](#)
255. Pawar, P.B.; Melo, J.S.; Kotkar, H.M.; Kulkarni, M.V. Role of Indigenous Mycorrhizal Species in Enhancing Physiological and Biochemical Status, Nutrient Acquisition and Yield Pattern of Groundnut (*Arachis hypogaea* L.). *J. Crop Sci. Biotechnol.* **2018**, *21*, 23–33. [\[CrossRef\]](#)
256. Bücking, H.; Liepold, E.; Ambilwade, P. The Role of the Mycorrhizal Symbiosis in Nutrient Uptake of Plants and the Regulatory Mechanisms Underlying These Transport Processes. In *Plant Science*; IntechOpen: London, UK, 2012.
257. Chen, X.; Song, F.; Liu, F.; Tian, C.; Liu, S.; Xu, H.; Zhu, X. Effect of Different Arbuscular Mycorrhizal Fungi on Growth and Physiology of Maize at Ambient and Low Temperature Regimes. *Sci. World J.* **2014**, *2014*, 956141. [\[CrossRef\]](#)
258. Sauter, M.; Hager, A. The Mycorrhizal Fungus *Amanita Muscaria* Induces Chitinase Activity in Roots and in Suspension-Cultured Cells of Its Host *Picea Abies*. *Planta* **1989**, *179*, 61–66. [\[CrossRef\]](#)

259. Sun, Q.; Fu, Z.; Finlay, R.; Lian, B. Transcriptome Analysis Provides Novel Insights into the Capacity of the Ectomycorrhizal Fungus *Amanita pantherina* to Weather K-Containing Feldspar and Apatite. *Appl. Environ. Microbiol.* **2019**, *85*, e00719–19. [\[CrossRef\]](#) [\[PubMed\]](#)
260. Aučina, A.; Rudawska, M.; Leski, T.; Skridaila, A.; Riepšas, E.; Iwanski, M. Growth and Mycorrhizal Community Structure of *Pinus Sylvestris* Seedlings Following the Addition of Forest Litter. *Appl. Environ. Microbiol.* **2007**, *73*, 4867–4873. [\[CrossRef\]](#)
261. Nasslahsen, B.; Prin, Y.; Ferhout, H.; Smouni, A.; Duponnois, R. Mycorrhizae Helper Bacteria for Managing the Mycorrhizal Soil Infectivity. *Front. Soil Sci.* **2022**, *2*, 979246. [\[CrossRef\]](#)
262. Aguilera, P.; Becerra, N.; Alvear, M.; Ortiz, N.; Turrini, A.; Azcón-Aguilar, C.; López-Gómez, M.; Romero, J.K.; Massri, M.; Seguel, A.; et al. Arbuscular Mycorrhizal Fungi from Acidic Soils Favors Production of Tomatoes and Lycopene Concentration. *J. Sci. Food Agric.* **2022**, *102*, 2352–2358. [\[CrossRef\]](#)
263. Brambilla, S.; Stritzler, M.; Soto, G.; Ayub, N. A Synthesis of Functional Contributions of Rhizobacteria to Growth Promotion in Diverse Crops. *Rhizosphere* **2022**, *24*, 100611. [\[CrossRef\]](#)
264. Castillo-Esparza, J.F.; Bandala, V.M.; Ramos, A.; Desgarennes, D.; Carrión, G.; César, E.; Montoya, L.; Ortiz-Castro, R. *Pisolithus tinctorius* Extract Affects the Root System Architecture through Compound Production with Auxin-like Activity in *Arabidopsis thaliana*. *Rhizosphere* **2021**, *19*, 100397. [\[CrossRef\]](#)
265. Domínguez-Núñez, J.A. Leguminous Trees for Sustainable Tropical Agroforestry. In *Advances in Legumes for Sustainable Intensification*; Academic Press: Cambridge, MA, USA, 2022; pp. 483–504.
266. Frey, S.D. Mycorrhizal Fungi as Mediators of Soil Organic Matter Dynamics. *Annu. Rev. Ecol. Evol. Syst.* **2019**, *50*, 237–259. [\[CrossRef\]](#)
267. Gan, X.; Janus, J.; Willbold, S.; Dombinov, V.; Kuhn, A.J.; Amelung, W.; Reinecke, D.; Calahan, D.; Nedbal, L.; Klose, H.; et al. Wheat Growth and Phosphorus Uptake from Polyculture Algal Biofilms Are Synergistically Modulated by Arbuscular Mycorrhizal Fungi and *Serendipita vermifera*. *Plant Soil* **2025**, *514*, 1923–1940. [\[CrossRef\]](#)
268. Gunjal, A.B. Chemistry of Plant Microbe Synergy in the Rhizosphere. In *Unravelling Plant-Microbe Synergy*; Academic Press: Cambridge, MA, USA, 2023; pp. 283–294.
269. Hambleton, S.; Sigler, L. *Meliniomyces*, a New Anamorph Genus for Root-Associated Fungi with Phylogenetic Affinities to *Rhizoscyphus ericae* (Å% *Hymenoscyphus ericae*), *Leotiomyces*. *Stud. Mycol.* **2005**, *53*, 1–27. [\[CrossRef\]](#)
270. Hilszczanska, D.; Sierota, Z. Persistence of Ectomycorrhizas by *Thelephora terrestris* on Outplanted Scots Pine Seedlings. *Acta Mycol.* **2013**, *41*, 313–318. [\[CrossRef\]](#)
271. Jangir, P.; Shekhawat, P.K.; Bishnoi, A.; Ram, H.; Soni, P. Role of *Serendipita indica* in Enhancing Drought Tolerance in Crops. *Physiol. Mol. Plant Pathol.* **2021**, *116*, 101691. [\[CrossRef\]](#)
272. Jha, S.S. Evaluating Mycorrhizal Association of *Funnelliformis mosseae* and *Glomus macrocarpum* with *Solanum melongena* L. (Brinjal) Using Proteomics and System Biology Approaches. *bioRxiv* **2025**, preprint. [\[CrossRef\]](#)
273. Klinsukon, C.; Ekprasert, J.; Boonlue, S. Using Arbuscular Mycorrhizal Fungi (*Gigaspora margarita*) as a Growth Promoter and Biocontrol of Leaf Blight Disease in Eucalyptus Seedlings Caused by *Cylindrocladium quinqueseptatum*. *Rhizosphere* **2021**, *20*, 100450. [\[CrossRef\]](#)
274. Kusakabe, R.; Yamato, M. Isolation and Identification of an Arbuscular Mycorrhizal Fungus Specifically Associated with Mycoheterotrophic Seedlings of *Gentiana zollingeri* (*Gentianaceae*). *Mycoscience* **2023**, *64*, 55–62. [\[CrossRef\]](#)
275. Ladeyn, I.; Plassard, C.; Staunton, S. Mycorrhizal Association of Maritime Pine, *Pinus pinaster*, with *Rhizopogon roseolus* Has Contrasting Effects on the Uptake from Soil and Root-to-Shoot Transfer of ¹³⁷Cs, ⁸⁵Sr and ^{95m}Tc. *J. Environ. Radioact.* **2008**, *99*, 853–863. [\[CrossRef\]](#) [\[PubMed\]](#)
276. Malicka, M.; Magurno, F.; Posta, K.; Chmura, D.; Piotrowska-Seget, Z. Differences in the Effects of Single and Mixed Species of AMF on the Growth and Oxidative Stress Defense in *Lolium perenne* Exposed to Hydrocarbons. *Ecotoxicol. Environ. Saf.* **2021**, *217*, 112252. [\[CrossRef\]](#) [\[PubMed\]](#)
277. Mello, A.; Lumini, E.; Napoli, C.; Bianciotto, V.; Bonfante, P. Arbuscular Mycorrhizal Fungal Diversity in the *Tuber melanosporum* Brûlé. *Fungal Biol.* **2015**, *119*, 518–527. [\[CrossRef\]](#) [\[PubMed\]](#)
278. Midgley, D.J.; Rosewarne, C.P.; Greenfield, P.; Li, D.; Vockler, C.J.; Hitchcock, C.J.; Sawyer, N.A.; Brett, R.; Edwards, J.; Pitt, J.I.; et al. Genomic Insights into the Carbohydrate Catabolism of *Cairneyella variabilis* Gen. Nov. sp. Nov., the First Reports from a Genome of an Ericoid Mycorrhizal Fungus from the Southern Hemisphere. *Mycorrhiza* **2016**, *26*, 345–352. [\[CrossRef\]](#)
279. Mikheev, V.S.; Struchkova, I.V.; Churkina, L.M.; Brilkina, A.A.; Berezina, E.V. Several Characteristics of *Oidiodendron maius* G.L. Barron Important for Heather Plants' Controlled Mycorrhization. *J. Fungi* **2023**, *9*, 728. [\[CrossRef\]](#) [\[PubMed\]](#)
280. Oliveira, T.C.; Cabral, J.S.R.; Santana, L.R.; Tavares, G.G.; Santos, L.D.S.; Paim, T.P.; Müller, C.; Silva, F.G.; Costa, A.C.; Souchie, E.L.; et al. The Arbuscular Mycorrhizal Fungus *Rhizophagus clarus* Improves Physiological Tolerance to Drought Stress in Soybean Plants. *Sci. Rep.* **2022**, *12*, 9044. [\[CrossRef\]](#) [\[PubMed\]](#)
281. Orfanoudakis, M.; Wheeler, C.T.; Hooker, J.E. Both the Arbuscular Mycorrhizal Fungus *Gigaspora rosea* and *Frankia* Increase Root System Branching and Reduce Root Hair Frequency in *Alnus glutinosa*. *Mycorrhiza* **2010**, *20*, 117–126. [\[CrossRef\]](#)

282. Pagano, M.C.; Cabello, M.N.; Scotti, M.R. Arbuscular Mycorrhizal Colonization and Growth of *Eremanthus incanus* Less. in a Highland Field. *Plant Soil Environ.* **2010**, *56*, 412–418. [\[CrossRef\]](#)
283. Parise, A.G.; De Oliveira, V.H.; Tibbett, M.; Pickles, B.J. The Pitfalls of Ectomycorrhizal Microcosms: Lessons Learnt for Future Success. *Plant Signal. Behav.* **2025**, *20*, 2527378. [\[CrossRef\]](#)
284. Perotto, S.; Daghino, S.; Martino, E. Ericoid Mycorrhizal Fungi and Their Genomes: Another Side to the Mycorrhizal Symbiosis? *New Phytol.* **2018**, *220*, 1141–1147. [\[CrossRef\]](#)
285. Peterson, R.L.; Currah, R.S. Synthesis of Mycorrhizae between Protocorms of *Goodyera repens* (Orchidaceae) and *Ceratobasidium cereale*. *Can. J. Bot.* **1990**, *68*, 1117–1125. [\[CrossRef\]](#)
286. Pujasatria, G.C.; Miura, C.; Yamaguchi, K.; Shigenobu, S.; Kaminaka, H. Colonization by Orchid Mycorrhizal Fungi Primes Induced Systemic Resistance against Necrotrophic Pathogen. *Front. Plant Sci.* **2024**, *15*, 1447050. [\[CrossRef\]](#)
287. Rineau, F.; Roth, D.; Shah, F.; Smits, M.; Johansson, T.; Canbäck, B.; Olsen, P.B.; Persson, P.; Grell, M.N.; Lindquist, E.; et al. The Ectomycorrhizal Fungus *Paxillus involutus* Converts Organic Matter in Plant Litter Using a Trimmed Brown-Rot Mechanism Involving Fenton Chemistry. *Environ. Microbiol.* **2012**, *14*, 1477–1487. [\[CrossRef\]](#)
288. Sun, X.; Chen, W.; Ivanov, S.; MacLean, A.M.; Wight, H.; Ramaraj, T.; Mudge, J.; Harrison, M.J.; Fei, Z. Genome and Evolution of the Arbuscular Mycorrhizal Fungus *Diversispora epigaea* (Formerly *Glomus versiforme*) and Its Bacterial Endosymbionts. *New Phytol.* **2019**, *221*, 1556–1573. [\[CrossRef\]](#)
289. Timonen, S.; Peterson, R.L. Cytoskeleton in Mycorrhizal Symbiosis. *Plant Soil* **2002**, *244*, 199–210. [\[CrossRef\]](#)
290. Wang, P.; Kuzyakov, Y.; Wang, Y.; Liu, Y.; Liu, J.; Qi, Z.; He, Y.; Jiang, Q. Quantifying Microbial Necromass Contributions to Soil Carbon Sequestration Under Diverse Cropland Management Practices: A Meta-Analysis. *J. Environ. Manag.* **2025**, *388*, 126008. [\[CrossRef\]](#)
291. Wu, Q.-S.; Zou, Y.-N.; Huang, Y.-M. The Arbuscular Mycorrhizal Fungus *Diversispora spurca* Ameliorates Effects of Waterlogging on Growth, Root System Architecture and Antioxidant Enzyme Activities of Citrus Seedlings. *Fungal Ecol.* **2013**, *6*, 37–43. [\[CrossRef\]](#)
292. Jeon, J.; Lee, S.; Kim, H.; Ahn, T.-S.; Song, H.-G. Plant Growth Promotion in Soil by Some Inoculated Microorganisms. *J. Microbiol.* **2003**, *41*, 271–276.
293. Bouffaud, M.-L.; Renoud, S.; Dubost, A.; Moënné-Loccoz, Y.; Muller, D. 1-Aminocyclopropane-1-Carboxylate Deaminase Producers Associated to Maize and Other *Poaceae* Species. *Microbiome* **2018**, *6*, 114. [\[CrossRef\]](#) [\[PubMed\]](#)
294. Alexandre, F.S.; Della Flora, L.V.; Henrique, I.G.; da Silva, D.C.; Mercedes, A.P.; Cardoso Silva, A.; Silva de Oliveira, A.; Bondespacho da Silva, M.P.; Formelh Ronning, B.P.; Dreher, D.R.; et al. Arbuscular Mycorrhizal Fungi (*Rhizophagus clarus*) and Rhizobacteria (*Bacillus subtilis*) Can Improve the Clonal Propagation and Development of Teak for Commercial Plantings. *Front. Plant Sci.* **2021**, *12*, 628769. [\[CrossRef\]](#)
295. David, B.V.; Chandrasehar, G.; Selvam, P.N. *Pseudomonas fluorescens*: A Plant-Growth-Promoting Rhizobacterium (PGPR) with Potential Role in Biocontrol of Pests of Crops. In *Crop Improvement Through Microbial Biotechnology*; Elsevier: Amsterdam, The Netherlands, 2018; pp. 221–243.
296. Du, Y.; Wang, T.; Jiang, J.; Wang, Y.; Lv, C.; Sun, K.; Sun, J.; Yan, B.; Kang, C.; Guo, L.; et al. Biological Control and Plant Growth Promotion Properties of *Streptomyces albidoflavus* St-220 Isolated from *Salvia miltiorrhiza* Rhizosphere. *Front. Plant Sci.* **2022**, *13*, 976813. [\[CrossRef\]](#) [\[PubMed\]](#)
297. Fanai, A.; Bohia, B.; Lalremruati, F.; Lalhriatpuii, N.; Lalrokimi; Lalmuanpuii, R.; Singh, P.K.; Zothanpuia. Plant Growth Promoting Bacteria (PGPB)-Induced Plant Adaptations to Stresses: An Updated Review. *PeerJ* **2024**, *12*, e17882. [\[CrossRef\]](#)
298. Kakabouki, I.; Mavroeidis, A.; Tataridas, A.; Kousta, A.; Efthimiadou, A.; Karydogianni, S.; Katsenios, N.; Roussis, I.; Papastilianou, P. Effect of *Rhizophagus irregularis* on Growth and Quality of *Cannabis sativa* Seedlings. *Plants* **2021**, *10*, 1333. [\[CrossRef\]](#)
299. Ma, N.; Yokoyama, K.; Marumoto, T. Promotion of Host Plant Growth and Infection of Roots with Arbuscular Mycorrhizal Fungus *Gigaspora margarita* by the Application of Peat. *Soil Sci. Plant Nutr.* **2006**, *52*, 162–167. [\[CrossRef\]](#)
300. Magesh, S.; Hurley, A.I.; Nepper, J.F.; Chevrette, M.G.; Schroppe, J.H.; Li, C.; Beebe, D.J.; Handelsman, J. Surface Colonization by *Flavobacterium johnsoniae* Promotes Its Survival in a Model Microbial Community. *mBio* **2024**, *15*, e03428-23. [\[CrossRef\]](#)
301. Noel, T.C.; Sheng, C.; Yost, C.K.; Pharis, R.P.; Hynes, M.F. *Rhizobium leguminosarum* as a Plant Growth-Promoting Rhizobacterium: Direct Growth Promotion of Canola and Lettuce. *Can. J. Microbiol.* **1996**, *42*, 279–283. [\[CrossRef\]](#)
302. Oleńska, E.; Małek, W.; Wójcik, M.; Swiecicka, I.; Thijs, S.; Vangronsveld, J. Beneficial Features of Plant Growth-Promoting Rhizobacteria for Improving Plant Growth and Health in Challenging Conditions: A Methodical Review. *Sci. Total Environ.* **2020**, *743*, 140682. [\[CrossRef\]](#)
303. Pallucchini, M.; Franchini, M.; El-Ballat, E.M.; Narraido, N.; Pointer-Gleadhill, B.; Palframan, M.J.; Hayes, C.J.; Dent, D.; Cocking, E.C.; Perazzolli, M.; et al. *Gluconacetobacter diazotrophicus* AZ0019 Requires Functional *nifD* Gene for Optimal Plant Growth Promotion in Tomato Plants. *Front. Plant Sci.* **2024**, *15*, 1469676. [\[CrossRef\]](#) [\[PubMed\]](#)

304. Ruiz-Güereca, D.A.; Sánchez-Saavedra, M.d.P. Growth and Phosphorus Removal by *Synechococcus elongatus* Co-Immobilized in Alginate Beads with *Azospirillum brasilense*. *J. Appl. Phycol.* **2016**, *28*, 1501–1507. [\[CrossRef\]](#)
305. Stassinou, P.M.; Rossi, M.; Borromeo, I.; Capo, C.; Beninati, S.; Forni, C. Amelioration of Salt Stress Tolerance in Rapeseed (*Brassica napus*) Cultivars by Seed Inoculation with *Arthrobacter globiformis*. *Plant Biosyst.-Int. J. Deal. All Asp. Plant Biol.* **2022**, *156*, 370–383. [\[CrossRef\]](#)
306. Viscardi, S.; Ventorino, V.; Duran, P.; Maggio, A.; De Pascale, S.; Mora, M.L.; Pepe, O. Assessment of Plant Growth Promoting Activities and Abiotic Stress Tolerance of *Azotobacter chroococcum* Strains for a Potential Use in Sustainable Agriculture. *J. Soil Sci. Plant Nutr.* **2016**, *16*, 848–863. [\[CrossRef\]](#)
307. Yadav, M.; Divyanshu, K.; Dubey, M.K.; Rai, A.; Kumar, S.; Tripathi, Y.N.; Shukla, V.; Upadhyay, R.S. Plant Growth Promotion and Differential Expression of Defense Genes in Chilli Pepper against *Colletotrichum truncatum* Induced by *Trichoderma asperellum* and *T. harzianum*. *BMC Microbiol.* **2023**, *23*, 54. [\[CrossRef\]](#)
308. Zhang, J.; Diao, F.; Hao, B.; Xu, L.; Jia, B.; Hou, Y.; Ding, S.; Guo, W. Multiomics Reveals *Claroideoglomus etunicatum* Regulates Plant Hormone Signal Transduction, Photosynthesis and La Compartmentalization in Maize to Promote Growth under La Stress. *Ecotoxicol. Environ. Saf.* **2023**, *262*, 115128. [\[CrossRef\]](#)
309. Hashem, A.; Tabassum, B.; Fathi Abd Allah, E. *Bacillus subtilis*: A Plant-Growth Promoting Rhizobacterium That Also Impacts Biotic Stress. *Saudi J. Biol. Sci.* **2019**, *26*, 1291–1297. [\[CrossRef\]](#)
310. Nozari, M.; Samaei, M.; Dehghani, M.; Ebrahimi, A. Bioremediation of Alkane Hydrocarbons Using Bacterial Consortium from Soil. *Health Scope* **2018**, in press. [\[CrossRef\]](#)
311. Helmy, Q.; Kardenia, E. Enhancing Field-Scale Bioremediation of Weathered Petroleum Oil-Contaminated Soil with Biocompost as a Bulking Agent. *Case Stud. Chem. Environ. Eng.* **2024**, *9*, 100735. [\[CrossRef\]](#)
312. Park, J.-W.; Crowley, D.E. Dynamic Changes in *nahAc* Gene Copy Numbers during Degradation of Naphthalene in PAH-Contaminated Soils. *Appl. Microbiol. Biotechnol.* **2006**, *72*, 1322–1329. [\[CrossRef\]](#)
313. Sun, Y.; Polishchuk, E.A.; Radoja, U.; Cullen, W.R. Identification and Quantification of *arsC* Genes in Environmental Samples by Using Real-Time PCR. *J. Microbiol. Methods* **2004**, *58*, 335–349. [\[CrossRef\]](#) [\[PubMed\]](#)
314. Gu, Y.; Nostrand, J.D.V.; Wu, L.; He, Z.; Qin, Y.; Zhao, F.-J.; Zhou, J. Bacterial Community and Arsenic Functional Genes Diversity in Arsenic Contaminated Soils from Different Geographic Locations. *PLoS ONE* **2017**, *12*, e0176696. [\[CrossRef\]](#)
315. Kim, J.-W.; Hong, Y.-K.; Kim, H.-S.; Oh, E.-J.; Park, Y.-H.; Kim, S.-C. Metagenomic Analysis for Evaluating Change in Bacterial Diversity in TPH-Contaminated Soil after Soil Remediation. *Toxics* **2021**, *9*, 319. [\[CrossRef\]](#)
316. Ayilara, M.S.; Babalola, O.O. Bioremediation of Environmental Wastes: The Role of Microorganisms. *Front. Agron.* **2023**, *5*, 1183691. [\[CrossRef\]](#)
317. Dell'Anno, F.; Rastelli, E.; Sansone, C.; Brunet, C.; Ianora, A.; Dell'Anno, A. Bacteria, Fungi and Microalgae for the Bioremediation of Marine Sediments Contaminated by Petroleum Hydrocarbons in the Omics Era. *Microorganisms* **2021**, *9*, 1695. [\[CrossRef\]](#)
318. Jangra, B.; Dwivedi, V.; Kaur, G.; Bhadrecha, P. Decoding Genomic Potential of *Streptomyces* spp. for Sustainable Environment and Industries. *S. Afr. J. Bot.* **2025**, *184*, 480–494. [\[CrossRef\]](#)
319. Zeng, Y.; Feng, R.; Huang, C.; Liu, J.; Yang, F. Antibiotic Resistance Genes in Agricultural Soils: A Comprehensive Review of the Hidden Crisis and Exploring Control Strategies. *Toxics* **2025**, *13*, 239. [\[CrossRef\]](#)
320. Wang, X.; Cai, Z.; Zhou, Q.; Zhang, Z.; Chen, C. Bioelectrochemical Stimulation of Petroleum Hydrocarbon Degradation in Saline Soil Using U-Tube Microbial Fuel Cells. *Biotechnol. Bioeng.* **2012**, *109*, 426–433. [\[CrossRef\]](#) [\[PubMed\]](#)
321. Fukuhara, Y.; Horii, S.; Matsuno, T.; Matsumiya, Y.; Mukai, M.; Kubo, M. Distribution of Hydrocarbon-Degrading Bacteria in the Soil Environment and Their Contribution to Bioremediation. *Appl. Biochem. Biotechnol.* **2013**, *170*, 329–339. [\[CrossRef\]](#)
322. Kloos, K.; Munch, J.C.; Schlöter, M. A New Method for the Detection of Alkane-Monooxygenase Homologous Genes (*alkB*) in Soils Based on PCR-Hybridization. *J. Microbiol. Methods* **2006**, *66*, 486–496. [\[CrossRef\]](#) [\[PubMed\]](#)
323. Liu, Q.; Tang, J.; Bai, Z.; Hecker, M.; Giesy, J.P. Distribution of Petroleum Degrading Genes and Factor Analysis of Petroleum Contaminated Soil from the Dagang Oilfield, China. *Sci. Rep.* **2015**, *5*, 11068. [\[CrossRef\]](#)
324. Tuomi, P.M.; Salminen, J.M.; Jørgensen, K.S. The Abundance of *nahAc* Genes Correlates with the ¹⁴C-Naphthalene Mineralization Potential in Petroleum Hydrocarbon-Contaminated Oxidic Soil Layers. *FEMS Microbiol. Ecol.* **2004**, *51*, 99–107. [\[CrossRef\]](#) [\[PubMed\]](#)
325. Ezemba, C.C.; Ekwealor, C.C.; Ekwealor, I.A.; Ozokpo, C.A.; Chukwujekwu, C.E.; Anakwenze, V.N.; Anukwu, C.G.; Archibong, E.J. Utilization of Hydrocarbons by Bacteria Isolated from Oil-Contaminated and Uncontaminated Soil in South-East Nigeria. *Int. J. Curr. Res. Biosci. Plant Biol.* **2015**, *2*, 12–19.
326. Abo-State, M.A.M.; Osman, M.E.; Khattab, O.H.; El-Kelani, T.A.; Abdel-Rahman, Z.M. Degradative Pathways of Polycyclic Aromatic Hydrocarbons (PAHs) by *Phanerochaete chrysosporium* Under Optimum Conditions. *J. Radiat. Res. Appl. Sci.* **2021**, *14*, 507–520. [\[CrossRef\]](#)
327. Al-Otibi, F.; Al-Zahrani, R.M.; Marraiki, N. Biodegradation of Selected Hydrocarbons by *Fusarium* Species Isolated from Contaminated Soil Samples in Riyadh, Saudi Arabia. *J. Fungi* **2023**, *9*, 216. [\[CrossRef\]](#) [\[PubMed\]](#)

328. Asemoloye, M.D.; Tosi, S.; Daccò, C.; Wang, X.; Xu, S.; Marchisio, M.A.; Gao, W.; Jonathan, S.G.; Pecoraro, L. Hydrocarbon Degradation and Enzyme Activities of *Aspergillus oryzae* and *Mucor irregularis* Isolated from Nigerian Crude Oil-Polluted Sites. *Microorganisms* **2020**, *8*, 1912. [\[CrossRef\]](#) [\[PubMed\]](#)
329. Barathi, S.; Vasudevan, N. Utilization of Petroleum Hydrocarbons by *Pseudomonas fluorescens* Isolated from a Petroleum-Contaminated Soil. *Environ. Int.* **2001**, *26*, 413–416. [\[CrossRef\]](#)
330. Brown, W.A.; Cooper, D.G. Hydrocarbon Degradation by *Acinetobacter calcoaceticus* RAG-1 Using the Self-Cycling Fermentation Technique. *Biotechnol. Bioeng.* **1992**, *40*, 797–805. [\[CrossRef\]](#)
331. Chikwem, I.; Christopher, N.U.; Ekwenye, U.; Stanley, O.; Irene, E.; Duru, I. Biodegradation Potential of *Aspergillus niger* on Crude Oil Contaminated Soil. *Int. J. Sci. Res. Sci. Technol.* **2017**, *3*, 405–414.
332. Dyksterhouse, S.E.; Gray, J.P.; Herwig, R.P.; Lara, J.C.; Staley, J.T. *Cycloclasticus pugetii* Gen. Nov., sp. Nov., an Aromatic Hydrocarbon-Degrading Bacterium from Marine Sediments. *Int. J. Syst. Bacteriol.* **1995**, *45*, 116–123. [\[CrossRef\]](#)
333. Fredslund, L.; Sniegowski, K.; Wick, L.Y.; Jacobsen, C.S.; De Mot, R.; Springael, D. Surface Motility of Polycyclic Aromatic Hydrocarbon (PAH)-Degrading Mycobacteria. *Res. Microbiol.* **2008**, *159*, 255–262. [\[CrossRef\]](#)
334. Hu, K.; Peris, A.; Torán, J.; Eljarrat, E.; Sarrà, M.; Blánquez, P.; Caminal, G. Exploring the Degradation Capability of *Trametes versicolor* on Selected Hydrophobic Pesticides Through Setting Sights Simultaneously on Culture Broth and Biological Matrix. *Chemosphere* **2020**, *250*, 126293. [\[CrossRef\]](#)
335. Ibrahim, S.Y.; Abdelhamid, E.A.; El-Hagrassi, A.M.; Kamal, N.M. Statistical Optimization of Crude Oil Bioremediation Using *Streptomyces aurantiogriseus* Isolated from Egypt's Western Desert. *Biodegradation* **2025**, *36*, 68. [\[CrossRef\]](#) [\[PubMed\]](#)
336. Kadri, T.; Magdoui, S.; Rouissi, T.; Brar, S.K. Ex-Situ Biodegradation of Petroleum Hydrocarbons Using *Alcanivorax borkumensis* Enzymes. *Biochem. Eng. J.* **2018**, *132*, 279–287. [\[CrossRef\]](#)
337. Khan, S.R.; Nirmal, J.I.K.; Kumar, R.N.; Patel, J.G. Biodegradation of Kerosene: Study of Growth Optimization and Metabolic Fate of *P. janthinellum* SDX7. *Braz. J. Microbiol.* **2015**, *46*, 397–406. [\[CrossRef\]](#)
338. Kim, S.-J.; Kweon, O.; Jones, R.C.; Edmondson, R.D.; Cerniglia, C.E. Genomic Analysis of Polycyclic Aromatic Hydrocarbon Degradation in *Mycobacterium vanbaalenii* PYR-1. *Biodegradation* **2008**, *19*, 859–881. [\[CrossRef\]](#) [\[PubMed\]](#)
339. Li, H.; Yang, Y.; Zhang, D.; Li, Y.; Zhang, H.; Luo, J.; Jones, K.C. Evaluating the Simulated Toxicities of Metal Mixtures and Hydrocarbons Using the Alkane Degrading Bioreporter *Acinetobacter baylyi* ADPWH_recA. *J. Hazard. Mater.* **2021**, *419*, 126471. [\[CrossRef\]](#) [\[PubMed\]](#)
340. Li, L.; Liu, Y.; Zhang, Y.; Wang, X.; Liu, H.; Liu, Q.; Chen, S.; Zhou, G. Dynamic Responses in *Pseudomonas stutzeri* M3 Bioaugmentation of Crude-Oil-Contaminated Soil: Hydrocarbons, Microbial Community Structures, and Functional Genes. *J. Environ. Chem. Eng.* **2024**, *12*, 111863. [\[CrossRef\]](#)
341. Lopez, E.S.; Elufisan, T.O.; Bustos, P.; Charles, C.P.M.; Mendoza-Herrera, A.; Guo, X. Complete Genome Report of a Hydrocarbon-Degrading *Sphingobium yanoikuyae* S72. *Appl. Sci.* **2022**, *12*, 6201. [\[CrossRef\]](#)
342. Mayans, B.; Antón-Herrero, R.; García-Delgado, C.; Delgado-Moreno, L.; Guirado, M.; Pérez-Esteban, J.; Escolástico, C.; Eymar, E. Bioremediation of Petroleum Hydrocarbons Polluted Soil by Spent Mushroom Substrates: Microbiological Structure and Functionality. *J. Hazard. Mater.* **2024**, *473*, 134650. [\[CrossRef\]](#)
343. Mounier, J.; Camus, A.; Mitteau, I.; Vaysse, P.-J.; Goulas, P.; Grimaud, R.; Sivadon, P. The Marine Bacterium *Marinobacter hydrocarbonoclasticus* SP17 Degrades a Wide Range of Lipids and Hydrocarbons through the Formation of Oleolytic Biofilms with Distinct Gene Expression Profiles. *FEMS Microbiol. Ecol.* **2014**, *90*, 816–831. [\[CrossRef\]](#)
344. Oh, K.-B.; Mar, W.; Chang, I.-M. Biodegradation of Hydrocarbons by an Organic Solvent-Tolerant Fungus, *Cladosporium resinae* NK-1. *J. Microbiol. Biotechnol.* **2001**, *11*, 56–60.
345. Okoro, C.; Amund, O. Biodegradation of Produced Water Hydrocarbons by *Aspergillus fumigatus*. *J. Am. Sci.* **2009**, *6*, 143–149.
346. Lamprea Pineda, P.A.; Demeestere, K.; Alvarado-Alvarado, A.A.; Devlieghere, F.; Boon, N.; Van Langenhove, H.; Walgraeve, C. Degradation of Gaseous Hydrocarbons in Aerated Stirred Bioreactors Inoculated with *Rhodococcus erythropolis*: Effect of the Carbon Source and SIFT-MS Method Development. *J. Environ. Sci.* **2025**, *147*, 268–281. [\[CrossRef\]](#) [\[PubMed\]](#)
347. Purnomo, A.S.; Rizqi, H.D.; Harmelia, L.; Anggraeni, S.D.; Melati, R.E.; Damayanti, Z.H.; Shafwah, O.M.; Kusuma, F.C. Biodegradation of Crude Oil by *Ralstonia pickettii* Under High Salinity Medium. *Malays. J. Fundam. Appl. Sci.* **2019**, *15*, 377–380. [\[CrossRef\]](#)
348. Radwan, S.S.; Barabás, G.; Sorkhoh, N.A.; Damjanovich, S.; Szabó, I.; Szöllősi, J.; Matkó, J.; Penyige, A.; Hirano, T.; Szabó, I.M. Hydrocarbon Uptake by *Streptomyces*. *FEMS Microbiol. Lett.* **1998**, *169*, 87–94. [\[CrossRef\]](#) [\[PubMed\]](#)
349. Ramdass, A.C.; Rampersad, S.N. Draft Genome of Hydrocarbon-Degrader *Burkholderia cepacia* BCTT, Isolated from Soil Chronically Polluted with Crude Oil in Trinidad. *Microbiol. Resour. Announc.* **2024**, *13*, e00902-24. [\[CrossRef\]](#)
350. Romanowska, I.; Kwapisz, E.; Mitka, M.; Bielecki, S. Isolation and Preliminary Characterization of a Respiratory Nitrate Reductase from Hydrocarbon-Degrading Bacterium *Gordonia alkanivorans* S7. *J. Ind. Microbiol. Biotechnol.* **2010**, *37*, 625–629. [\[CrossRef\]](#)

351. Sonia, S.; Abdelkader, B.; Zoulikha, B.; Vogel, T.; Navarro, E.; Sonia, I. The Diversity of Cultivable Hydrocarbon-Degrading Bacteria Isolated from Crude Oil Contaminated Soil and Sludge from Arzew Refinery in Algeria. *J. Microbiol. Biotechnol. Food Sci.* **2019**, *9*, 70–77. [[CrossRef](#)]
352. Trögl, J.; Esuola, C.O.; Kříženecká, S.; Kuráň, P.; Seidlová, L.; Veronesi-Dáňová, P.; Popelka, J.; Babalola, O.O.; Hrabák, P.; Czinnerová, M.; et al. Biodegradation of High Concentrations of Aliphatic Hydrocarbons in Soil from a Petroleum Refinery: Implications for Applicability of New Actinobacterial Strains. *Appl. Sci.* **2018**, *8*, 1855. [[CrossRef](#)]
353. Xu, X.; Liu, W.; Tian, S.; Wang, W.; Qi, Q.; Jiang, P.; Gao, X.; Li, F.; Li, H.; Yu, H. Petroleum Hydrocarbon-Degrading Bacteria for the Remediation of Oil Pollution Under Aerobic Conditions: A Perspective Analysis. *Front. Microbiol.* **2018**, *9*, 2885. [[CrossRef](#)]
354. Yang, S.; Zhang, J.; Liu, Y.; Feng, W. Biodegradation of Hydrocarbons by *Purpureocillium lilacinum* and *Penicillium chrysogenum* from Heavy Oil Sludge and Their Potential for Bioremediation of Contaminated Soils. *Int. Biodeterior. Biodegrad.* **2023**, *178*, 105566. [[CrossRef](#)]
355. Zylstra, G.J.; Kim, E. Aromatic Hydrocarbon Degradation by *Sphingomonas yanoikuyae* B1. *J. Ind. Microbiol. Biotechnol.* **1997**, *19*, 408–414. [[CrossRef](#)] [[PubMed](#)]
356. Roy, S.; Dawson, R.A.; Bradley, J.A.; Hernández, M. Prevalence and Dynamics of Antimicrobial Resistance in Pioneer and Developing Arctic Soils. *BMC Microbiol.* **2025**, *25*, 50. [[CrossRef](#)] [[PubMed](#)]
357. Meyers, M.A.; Durso, L.M.; Gilley, J.E.; Waldrip, H.M.; Castleberry, L.; Millmier-Schmidt, A. Antibiotic Resistance Gene Profile Changes in Cropland Soil After Manure Application and Rainfall. *J. Environ. Qual.* **2020**, *49*, 754–761. [[CrossRef](#)]
358. Symochko, L.; Demyanyuk, O.; Symochko, V.; Grulova, D.; Fejer, J.; Mariychuk, R. The Spreading of Antibiotic-Resistant Bacteria in Terrestrial Ecosystems and the Formation of Soil Resistome. *Land* **2023**, *12*, 769. [[CrossRef](#)]
359. Crowley, P.D.; Vaillant, J.J.; Shirley, J.D.; Wengenack, N.L.; Jo Kasten, M. Rapidly Growing Knowledge of *Mycobacterium smegmatis*: A Case Series and Review of Antimicrobial Susceptibility Patterns. *J. Clin. Tuberc. Other Mycobact. Dis.* **2024**, *37*, 100489. [[CrossRef](#)]
360. Holmes, A.H.; Govan, J.; Goldstein, R. Agricultural Use of Burkholderia (Pseudomonas) Cepacia: A Threat to Human Health? *Emerg. Infect. Dis. J.* **1998**, *4*, 221. [[CrossRef](#)]
361. Jensen, G.B.; Hansen, B.M.; Eilenberg, J.; Mahillon, J. The Hidden Lifestyles of *Bacillus cereus* and Relatives. *Environ. Microbiol.* **2003**, *5*, 631–640. [[CrossRef](#)] [[PubMed](#)]
362. Kisková, J.; Juhás, A.; Galušková, S.; Maliničová, L.; Kolesárová, M.; Píknová, M.; Pristaš, P. Antibiotic Resistance and Genetic Variability of *Acinetobacter* spp. from Wastewater Treatment Plant in Kokšov-Bakša (Košice, Slovakia). *Microorganisms* **2023**, *11*, 840. [[CrossRef](#)]
363. Kyselková, M.; Chroňáková, A.; Němec, J.; Kotrbová, L.; Elhottová, D. Isolation and Antibiotic Susceptibility Testing of Rapidly-Growing Mycobacteria from Grassland Soils. *J. Microbiol. Biotechnol. Food Sci.* **2013**, *3*, 76–80.
364. Lewandowska, W.; Mahillon, J.; Drewnowska, J.M.; Swiecicka, I. Insight into the Phylogeny and Antibiotic Resistance of *Pseudomonas* spp. Originating from Soil of the Białowieża National Park in Northeastern Poland. *Front. Microbiol.* **2025**, *16*, 1454510. [[CrossRef](#)]
365. Mahapatra, S.; Yadav, R.; Ramakrishna, W. *Bacillus subtilis* Impact on Plant Growth, Soil Health and Environment: Dr. Jekyll and Mr. Hyde. *J. Appl. Microbiol.* **2022**, *132*, 3543–3562. [[CrossRef](#)] [[PubMed](#)]
366. Nirwati, H.; Sinanjung, K.; Fahrurissa, F.; Wijaya, F.; Napitupulu, S.; Hati, V.P.; Hakim, M.S.; Meliala, A.; Aman, A.T.; Nuryastuti, T. Biofilm Formation and Antibiotic Resistance of *Klebsiella pneumoniae* Isolated from Clinical Samples in a Tertiary Care Hospital, Klaten, Indonesia. *BMC Proc.* **2019**, *13*, 20. [[CrossRef](#)] [[PubMed](#)]
367. Peleg, A.Y.; Seifert, H.; Paterson, D.L. *Acinetobacter baumannii*: Emergence of a Successful Pathogen. *Clin. Microbiol. Rev.* **2008**, *21*, 538–582. [[CrossRef](#)]
368. Silverio, M.P.; Schultz, J.; Parise, M.T.D.; Parise, D.; Viana, M.V.C.; Nogueira, W.; Ramos, R.T.J.; Góes-Neto, A.; Azevedo, V.A.D.C.; Brenig, B.; et al. Genomic and Phenotypic Insight into Antimicrobial Resistance of *Pseudomonas fluorescens* from King George Island, Antarctica. *Front. Microbiol.* **2025**, *16*, 1535420. [[CrossRef](#)]
369. Twomey, E.; Fields, D.; Begley, M. Investigating Soil Bacteria for Novel Antimicrobials Which Inhibit the Opportunistic Pathogen, *Staphylococcus epidermidis*. *Access Microbiol.* **2019**, *1*, 778. [[CrossRef](#)]
370. Zhang, X.; Ma, Z.; Hao, P.; Ji, S.; Gao, Y. Characteristics and Health Impacts of Bioaerosols in Animal Barns: A Comprehensive Study. *Ecotoxicol. Environ. Saf.* **2024**, *278*, 116381. [[CrossRef](#)]
371. Zhao, Y.; Li, L.; Huang, Y.; Xu, X.; Liu, Z.; Li, S.; Zhu, L.; Hu, B.; Zhang, T. Global Soil Antibiotic Resistance Genes Are Associated with Increasing Risk and Connectivity to Human Resistome. *Nat. Commun.* **2025**, *16*, 7141. [[CrossRef](#)]
372. Svenning, M.M.; Warttinen, I.; Hestnes, A.G.; Binnerup, S.J. Isolation of Methane Oxidising Bacteria from Soil by Use of a Soil Substrate Membrane System. *FEMS Microbiol. Ecol.* **2003**, *44*, 347–354. [[CrossRef](#)] [[PubMed](#)]
373. Thomas, C.; Frossard, V.; Perga, M.-E.; Tofield-Pasche, N.; Hofmann, H.; Dubois, N.; Belkina, N.; Zobkova, M.; Robert, S.; Lyautey, E. Lateral Variations and Vertical Structure of the Microbial Methane Cycle in the Sediment of Lake Onego (Russia). *Inland Waters* **2019**, *9*, 205–226. [[CrossRef](#)]

374. Deng, Y.; Che, R.; Wang, F.; Conrad, R.; Dumont, M.; Yun, J.; Wu, Y.; Hu, A.; Fang, J.; Xu, Z.; et al. Upland Soil Cluster Gamma Dominates Methanotrophic Communities in Upland Grassland Soils. *Sci. Total Environ.* **2019**, *670*, 826–836. [\[CrossRef\]](#)
375. de Groot, T.R.; Engelmann, J.C.; Ramond, P.; Dorigo, J.; van Bleijswijk, J.; Niemann, H. Adaptation of Methane-Oxidizing Bacteria to Environmental Changes: Implications for Coastal Methane Dynamics. *Biogeosciences* **2025**, *22*, 5173–5191. [\[CrossRef\]](#)
376. van Teeseling, M.C.F.; Pol, A.; Harhangi, H.R.; van der Zwart, S.; Jetten, M.S.M.; Op den Camp, H.J.M.; van Niftrik, L. Expanding the Verrucomicrobial Methanotrophic World: Description of Three Novel Species of *Methylococcoides* Gen. Nov. *Appl. Environ. Microbiol.* **2014**, *80*, 6782–6791. [\[CrossRef\]](#)
377. Picone, N.; Mohammadi, S.S.; Waajen, A.C.; van Alen, T.A.; Jetten, M.S.M.; Pol, A.; Op den Camp, H.J.M. More Than a Methanotroph: A Broader Substrate Spectrum for *Methylococcoides fumariolicum* SolV. *Front. Microbiol.* **2020**, *11*, 604485. [\[CrossRef\]](#)
378. Hou, S.; Makarova, K.S.; Saw, J.H.; Senin, P.; Ly, B.V.; Zhou, Z.; Ren, Y.; Wang, J.; Galperin, M.Y.; Omelchenko, M.V.; et al. Complete Genome Sequence of the Extremely Acidophilic Methanotroph Isolate V4, *Methylococcoides infernorum*, a Representative of the Bacterial Phylum Verrucomicrobia. *Biol. Direct* **2008**, *3*, 26. [\[CrossRef\]](#)
379. Ratnadevi, C.M.; Erikstad, H.-A.; Kruse, T.; Birkeland, N.-K. *Methylococcoides kamchatkense* Gen. Nov., sp. Nov., an Extremely Acidophilic and Moderately Thermophilic Methanotroph Belonging to the Phylum Verrucomicrobiota. *Int. J. Syst. Evol. Microbiol.* **2023**, *73*, 006060. [\[CrossRef\]](#)
380. Smith, G.J.; Angle, J.C.; Solden, L.M.; Borton, M.A.; Morin, T.H.; Daly, R.A.; Johnston, M.D.; Stefanik, K.C.; Wolfe, R.; Gil, B.; et al. Members of the Genus *Methylobacter* Are Inferred to Account for the Majority of Aerobic Methane Oxidation in Oxic Soils from a Freshwater Wetland. *mBio* **2018**, *9*, e00815-18. [\[CrossRef\]](#)
381. Feisthauer, S.; Vogt, C.; Modrzyński, J.; Szlenkier, M.; Krüger, M.; Siegert, M.; Richnow, H.-H. Different Types of Methane Monooxygenases Produce Similar Carbon and Hydrogen Isotope Fractionation Patterns during Methane Oxidation. *Geochim. Cosmochim. Acta* **2011**, *75*, 1173–1184. [\[CrossRef\]](#)
382. Delherbe, N.A.; Pearce, D.; But, S.Y.; Murrell, J.C.; Khmelenina, V.N.; Kalyuzhnaya, M.G. Genomic Insights into Moderately Thermophilic Methanotrophs of the Genus *Methylocaldum*. *Microorganisms* **2024**, *12*, 469. [\[CrossRef\]](#) [\[PubMed\]](#)
383. Schmider, T.; Hestnes, A.G.; Brzykcy, J.; Schmidt, H.; Schintlmeister, A.; Roller, B.R.K.; Teran, E.J.; Söllinger, A.; Schmidt, O.; Polz, M.F.; et al. Physiological Basis for Atmospheric Methane Oxidation and Methanotrophic Growth on Air. *Nat. Commun.* **2024**, *15*, 4151. [\[CrossRef\]](#)
384. Peterse, I.F.; Pol, A.; Cremers, G.; Berben, T.; van Alen, T.A.; Op den Camp, H.J.M.; Veraart, A.J.; Lückner, S. Hydrogen Oxidation Benefits Alphaproteobacterial Methanotrophs Under Severe Methane Limitation. *Environ. Microbiol.* **2025**, *27*, e70163. [\[CrossRef\]](#) [\[PubMed\]](#)
385. Im, J.; Lee, S.-W.; Yoon, S.; DiSpirito, A.A.; Semrau, J.D. Characterization of a Novel Facultative *Methylocystis* Species Capable of Growth on Methane, Acetate and Ethanol. *Environ. Microbiol. Rep.* **2011**, *3*, 174–181. [\[CrossRef\]](#)
386. Bordel, S.; Rodríguez, Y.; Hakobyan, A.; Rodríguez, E.; Lebrero, R.; Muñoz, R. Genome Scale Metabolic Modeling Reveals the Metabolic Potential of Three Type II Methanotrophs of the Genus *Methylocystis*. *Metab. Eng.* **2019**, *54*, 191–199. [\[CrossRef\]](#)
387. del Cerro, C.; García, J.M.; Rojas, A.; Tortajada, M.; Ramón, D.; Galán, B.; Prieto, M.A.; García, J.L. Genome Sequence of the Methanotrophic Poly-β-Hydroxybutyrate Producer *Methylocystis parvus* OBBP. *J. Bacteriol.* **2012**, *194*, 5709–5710. [\[CrossRef\]](#)
388. Cáceres, M.; Gentina, J.C.; Aroca, G. Oxidation of Methane by *Methylococcoides albus* and *Methylocystis* sp. in the Presence of H₂S and NH₃. *Biotechnol. Lett.* **2014**, *36*, 69–74. [\[CrossRef\]](#)
389. Akberdin, I.R.; Thompson, M.; Hamilton, R.; Desai, N.; Alexander, D.; Henard, C.A.; Guarnieri, M.T.; Kalyuzhnaya, M.G. Methane Utilization in *Methylococcoides alcaliphilum* 20Z^R: A Systems Approach. *Sci. Rep.* **2018**, *8*, 2512. [\[CrossRef\]](#)
390. Stone, K.; Hilliard, M.; Badr, K.; Bradford, A.; He, Q.P.; Wang, J. Comparative Study of Oxygen-Limited and Methane-Limited Growth Phenotypes of *Methylococcoides buryatense* 5GB1. *Biochem. Eng. J.* **2020**, *161*, 107707. [\[CrossRef\]](#)
391. Sly, L.I.; Bryant, L.J.; Cox, J.M.; Anderson, J.M. Development of a Biofilter for the Removal of Methane from Coal Mine Ventilation Atmospheres. *Appl. Microbiol. Biotechnol.* **1993**, *39*, 400–404. [\[CrossRef\]](#)
392. Sang, Y.; Hao, Q.; Zhang, Y.; Wang, O.; Zheng, S.; Liu, F. Simultaneous Removal of Methane and High Nitrite from the Wastewater by *Methylobacter* sp. with Soluble Methane Monooxygenase. *Bioresour. Technol.* **2025**, *418*, 131972. [\[CrossRef\]](#)
393. Park, Y.R.; Yoo, H.S.; Song, M.Y.; Lee, D.-H.; Lee, S.J. Biocatalytic Oxidations of Substrates through Soluble Methane Monooxygenase from *Methylobacterium sporium* 5. *Catalysts* **2018**, *8*, 582. [\[CrossRef\]](#)
394. Poshvina, D.V.; Balkin, A.S.; Teslya, A.V.; Dilbaryan, D.S.; Stepanov, A.A.; Kravchenko, S.V.; Vasilchenko, A.S. Structural and Functional Differences in the Bacterial Community of Chernozem Soil Under Conventional and Organic Farming Conditions. *Agriculture* **2024**, *14*, 2127. [\[CrossRef\]](#)
395. Khrapai, E.S.; Kolesnikov, S.I.; Kuzina, A.A.; Kazeev, K.S.; Minnikova, T.V.; Demin, K.A.; Kocharovskaya, Y.N.; Delegan, Y.A.; Bogun, A.G.; Minkina, T.M.; et al. Metagenomic Profiling of the Soil Microbiological Community in the Impact Area of the Urup Mining and Processing Plant Tailings (Karachay-Cherkess Republic). *Eurasian Soil Sci.* **2025**, *58*, 119. [\[CrossRef\]](#)

396. Wang, C.; Lin, W.; Jia, S.; Chen, S.; Xiong, D.; Xu, C.; Yang, Z.; Liu, X.; Yang, Y. Effects of Litter and Root Inputs on Soil Microbial Community Structure in Subtropical Natural and Plantation Forests. *Plant Soil* **2025**, *513*, 823–838. [[CrossRef](#)]
397. Yao, R.; Gao, Q.; Liu, Y.; Li, H.; Yang, J.; Bai, Y.; Zhu, H.; Wang, X.; Xie, W.; Zhang, X. Deep Vertical Rotary Tillage Mitigates Salinization Hazards and Shifts Microbial Community Structure in Salt-Affected Anthropogenic-Alluvial Soil. *Soil Tillage Res.* **2023**, *227*, 105627. [[CrossRef](#)]
398. Liang, X.; Zhong, D.; Zhang, C.; Pan, Y.; Zhang, C.; Guo, H.; Zhu, X.; Li, X.; He, Y.; Huang, S.; et al. Effects of Different Cultivation Substrates on the Growth of *Podocarpus macrophyllus* and the Rhizosphere Soil Microbial Community Structure. *Agronomy* **2025**, *15*, 1055. [[CrossRef](#)]
399. Bautista, D.; García, D.; Dávila, L.; Caro-Quintero, A.; Cotes, A.M.; González, A.; Zuluaga, A.P. Studying the Microbiome of Suppressive Soils Against Vascular Wilt, Caused by *Fusarium oxysporum* in Cape Gooseberry (*Physalis peruviana*). *Environ. Microbiol. Rep.* **2023**, *15*, 757–768. [[CrossRef](#)]
400. Sun, Y.; Ji, L.; Chang, J.; Li, Y.; Wang, H.; Lu, D.; Tian, C. Compositional and Functional Succession of Soil Bacterial Communities during Long-Term Rice Cultivation on Saline-Alkali Soils: Insights Derived from a New Perspective on Core Bacterial Taxa. *Pedosphere* **2025**, *35*, 641–654. [[CrossRef](#)]
401. Li, Y.; Gu, M.; Xu, W.; Zhu, J.; Chu, M.; Tang, Q.; Yi, Y.; Zhang, L.; Li, P.; Zhang, Y.; et al. Whole-Genome Analysis of *Halomonas* sp. H5 Revealed Multiple Functional Genes Relevant to Tomato Growth Promotion, Plant Salt Tolerance, and Rhizosphere Soil Microecology Regulation. *Microorganisms* **2025**, *13*, 1781. [[CrossRef](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.