



Biodiversity of Soil Microbes: Understanding the Diversity Concept and Diversity Indices

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Beneath our feet lies a living world that is far more diverse and complex than we can imagine. A handful of fertile soil contains an enormous variety of microorganisms, including bacteria, archaea, fungi, algae, protozoa and viruses. These microscopic inhabitants form the foundation of soil ecosystems, driving essential processes such as nutrient cycling, organic matter decomposition, soil fertility maintenance and plant growth promotion. Although invisible to the naked eye, soil microorganisms play a significant role in sustaining agricultural productivity and maintaining ecological balance. Soil microbial biodiversity refers to the variety and variability of microorganisms present in a particular soil environment. It encompasses differences in their genetic characteristics, species composition, functional capabilities and ecological interactions. Understanding this diversity is essential for evaluating soil health, predicting ecosystem responses to environmental changes and developing sustainable agricultural practices.

Understanding the Concept of Soil Microbial Diversity

Biodiversity is not simply a measure of how many microbial species are present in the soil. It also considers how evenly these organisms are distributed and how they differ in their genetic and functional characteristics. For example, two agricultural soils may contain the same number of bacterial species but differ considerably in their microbial communities. In one soil, a few species may dominate the population, whereas in the other, individuals may be distributed more evenly among species. Although their species richness is identical, their overall diversity may differ (Magurran, 2004).

Soil microbial diversity can be understood through three major components:

Genetic diversity: This refers to the variation in genetic material among microorganisms. Genetic diversity enables microbial populations to adapt to environmental changes, tolerate stress and develop different metabolic capabilities.

Taxonomic diversity: This represents the variety of microbial taxa present in soil, including bacteria, archaea, fungi and other microbial groups. It helps describe the composition of microbial communities.

Functional diversity: This refers to the variety of ecological functions performed by soil microorganisms, such as nitrogen fixation, phosphorus solubilization, cellulose degradation, disease suppression and greenhouse gas transformations.

These components are interconnected. A soil with diverse microbial taxa may possess a broader range of functional capabilities, although taxonomic diversity does not always translate directly into functional diversity because different microorganisms can perform similar roles.

Why Is Soil Microbial Biodiversity Important?

Soil microbial biodiversity is closely associated with the functioning and resilience of terrestrial ecosystems. Different microorganisms contribute to different biological and biochemical processes.

Nutrient cycling: Microorganisms regulate the transformation and availability of carbon, nitrogen, phosphorus and sulfur.

Organic matter decomposition: Bacteria and fungi break down plant residues and other organic materials, contributing to nutrient release and soil organic matter formation.

Plant growth promotion: Beneficial microorganisms improve plant nutrition through nitrogen fixation, phosphorus solubilization, siderophore production and phytohormone synthesis.

Disease suppression: Certain soil microorganisms inhibit plant pathogens through antibiosis, competition, parasitism and induced systemic resistance.

Soil structure and fertility: Microbial products, including extracellular polymeric substances, contribute to soil aggregation and influence soil structure.

Environmental resilience: Diverse microbial communities can support ecosystem functioning under changing environmental conditions, although resilience depends on community composition, functional redundancy and environmental conditions.

In agricultural systems, practices such as crop rotation, organic amendments, cover cropping and reduced soil disturbance can influence microbial diversity and community composition. Conversely, intensive land management, soil pollution, salinity and prolonged environmental stress may alter microbial communities and their functions. Greater microbial diversity does not automatically mean better soil health. The significance of diversity depends on the organisms present, their functions, environmental conditions and the ecosystem processes being evaluated (Fierer, 2017).

Understanding the Different Scales of Microbial Diversity

Alpha diversity: Diversity within a community

Alpha diversity describes the diversity of microorganisms within a particular soil sample or habitat. For example, the diversity of bacteria in the rhizosphere of a healthy pepper plant can be compared with that in the surrounding bulk soil. Alpha diversity is commonly assessed using species richness, the Shannon diversity index and the Simpson diversity index.

Beta diversity: Differences between communities

Beta diversity measures the differences in microbial community composition between two or more samples. For instance, researchers may compare bacterial communities in organic and conventionally managed agricultural soils. Common approaches include Bray–Curtis dissimilarity and Jaccard dissimilarity.

Gamma diversity: Diversity across a larger region

Gamma diversity represents the overall diversity across a broader geographical region or collection of habitats. The combined microbial diversity of different agricultural soils, forests, grasslands and plantation ecosystems within a region represents regional diversity (Chao, 1984).

Together, these three concepts help scientists understand microbial diversity from individual soil samples to entire landscapes.

Diversity Indices: Measuring the Invisible

Although modern molecular techniques can reveal thousands of microbial taxa in a soil sample, simply counting the number of taxa does not provide a complete picture of biodiversity. Diversity indices are mathematical tools used to describe and compare biological communities by considering species richness and, in many cases, their relative abundances (Magurran, 2004).

Species richness

Species richness is the simplest measure of diversity. It represents the total number of distinct species or taxa identified in a sample. For example, if a soil sample contains 40 distinct bacterial taxa, its observed richness is 40.

Formula: $S = \text{Total number of species or taxa}$

Higher richness indicates that more taxa have been observed. However, richness does not account for the relative abundance of each taxon and can be influenced by sampling effort and identification methods. In microbial ecology, researchers often report observed amplicon

sequence variants (ASVs) or operational taxonomic units (OTUs), rather than confirmed species.

Shannon–Wiener diversity index

The Shannon diversity index is widely used to assess microbial diversity because it incorporates both the number of taxa and their relative abundances. It reflects the uncertainty involved in predicting the identity of a randomly selected individual from the community.

$$H' = -\sum p_i \ln(p_i)$$

Where H' is the Shannon diversity index, S is the total number of taxa, p_i is the proportion of individuals belonging to the i -th taxon, and $\ln$ is the natural logarithm.

A higher Shannon index generally indicates greater diversity, reflecting a combination of richness and evenness. If all taxa are equally abundant, the Shannon index will be higher than in a community where one taxon dominates, assuming the same richness.

Simpson's diversity index

The Simpson index describes the concentration of abundance within a community and is sensitive to the dominance of common taxa. One commonly used form is:

$$D = \sum p_i^2$$

Here, D is Simpson's concentration index and p_i is the relative abundance of the i -th taxon. This form estimates the probability that two randomly selected individuals belong to the same taxon. Several versions of the Simpson index are used in ecology, and their interpretations differ. The form used must always be specified when reporting results. Simpson-based indices are useful for identifying whether a community is dominated by a few highly abundant taxa.

Pielou's evenness index

Species richness indicates how many taxa are present, but it does not reveal how evenly their abundances are distributed. Pielou's evenness index measures evenness by comparing Shannon diversity with the maximum possible Shannon diversity for the observed number of taxa.

$$J' = H' / \ln(S)$$

Here, J' is Pielou's evenness index, H' is the Shannon diversity index and S is the total number of taxa. When at least two taxa are present, the index generally ranges from 0 to 1. Values closer to 1 indicate that taxa have more similar abundances.

Margalef's richness index

Margalef's index describes taxonomic richness while accounting for the number of individuals sampled.

$$d = (S - 1) / \ln(N)$$

Here, d is Margalef's richness index, S is the number of taxa and N is the total number of individuals counted. Higher values generally indicate greater richness relative to sample size. Applying this index to sequencing data requires caution because read counts may not correspond directly to organism abundance.

Chao1 richness estimator

Many microbial taxa are rare and may not be detected consistently during sampling. The Chao1 estimator uses the frequency of rare taxa to estimate total richness, including taxa that may have gone undetected.

$$\hat{S}_{\text{Chao1}} = \text{Sobs} + [F_1(F_1 - 1)] / [2(F_2 + 1)]$$

Here, $\hat{S}_{\text{Chao1}}$ is estimated richness, Sobs is the observed number of taxa, F_1 is the number of taxa represented by one observation (singletons), and F_2 is the number represented by two observations (doubletons). The estimate depends on the sampling and detection process and should be interpreted alongside the sequencing method and data-processing procedures.

A Simple Example: Comparing Two Soil Microbial Communities

Consider two hypothetical soil samples, each containing four bacterial taxa.

Table 1: Comparison of soil microbial communities

Bacterial taxon	Soil A (%)	Soil B (%)
Taxon 1	25	70

Bacterial taxon	Soil A (%)	Soil B (%)
Taxon 2	25	10
Taxon 3	25	10
Taxon 4	25	10
Total	100	100

Both samples have the same species richness: four taxa. However, their abundance distributions are different. In Soil A, all taxa are equally abundant. In Soil B, Taxon 1 dominates the community.

Table 2: Diversity measures of two soil microbial communities

Diversity measure	Soil A	Soil B
Species richness	4	4
Shannon index (H')	1.386	0.940
Simpson's concentration (D)	0.250	0.520
Gini–Simpson index ($1 - D$)	0.750	0.480
Inverse Simpson index ($1 / D$)	4.000	1.923
Pielou's evenness (J')	1.000	0.678

Note: These are illustrative calculations based on relative abundances, not experimental measurements.

The results demonstrate that although both soils contain the same number of taxa, Soil A has higher Shannon diversity, higher Gini–Simpson diversity and greater evenness. Soil B has greater dominance by a single taxon. Biodiversity is not determined by species numbers alone; the distribution of abundance among taxa also matters.

How do scientists measure soil microbial diversity?

Traditional approaches

Culture-dependent techniques involve growing microorganisms on selective or general-purpose media under defined laboratory conditions. They help researchers isolate, identify and characterize culturable microorganisms, including plant growth-promoting bacteria and antagonistic microorganisms. However, many soil microorganisms are difficult to cultivate under routine laboratory conditions, so culture-based approaches alone cannot provide a complete picture of soil microbial diversity.

Molecular approaches

16S rRNA gene sequencing: Commonly used to characterize bacterial and archaeal communities.

ITS sequencing: Widely used to investigate fungal communities.

Shotgun metagenomic sequencing: Provides information about community composition and genetic potential across organisms represented in the sample.

Quantitative PCR: Used to quantify selected microbial genes or genetic markers.

Bioinformatics: Helps process sequence data, identify microbial taxa and calculate diversity indices.

High-throughput sequencing has transformed microbial ecology by enabling researchers to detect complex communities containing common and rare taxa. However, sequencing-based diversity estimates are influenced by DNA extraction efficiency, primer selection, sequencing depth, amplification bias and bioinformatics procedures (Delgado-Baquerizo *et al.*, 2018). The presence of a microbial gene does not necessarily mean that the corresponding function is actively being performed in the soil.

Beyond alpha diversity: understanding community differences

While alpha diversity indices describe diversity within individual samples, researchers often need to determine whether microbial communities differ between treatments. For example, an agricultural microbiologist may investigate whether organic amendments change the bacterial community of a black pepper rhizosphere. Jaccard dissimilarity is based on the presence or

absence of taxa and measures differences in taxonomic membership. Bray–Curtis dissimilarity considers differences in taxon abundances and is commonly used to compare microbial communities. These measures are often used with ordination techniques such as principal coordinates analysis (PCoA) and statistical procedures such as PERMANOVA (Thompson *et al.*, 2017).

Two soils may have similar Shannon diversity values but contain entirely different bacterial taxa. Their alpha diversity may be comparable even though their community composition differs substantially.

Factors influencing soil microbial biodiversity

Soil properties: Soil pH, moisture, texture, organic carbon, nutrient availability and salinity influence microbial growth and community composition.

Vegetation and root activity: Different plant species release different root exudates, creating distinct ecological niches in the rhizosphere.

Climate: Temperature, rainfall and seasonal fluctuations affect microbial activity, survival and distribution.

Agricultural management: Fertilizer use, pesticide application, tillage, crop rotation, irrigation and organic matter additions can alter microbial communities.

Land-use change: Conversion of forests or grasslands into agricultural land can modify soil conditions and microbial habitats.

Biotic interactions: Competition, predation, mutualism and other interactions influence which microorganisms persist and which functions they perform.

Understanding these factors helps researchers interpret diversity patterns and identify management practices that support beneficial microbial communities.

Applications of soil microbial diversity in sustainable agriculture

Soil health assessment

Comparisons of microbial diversity among soils can help identify changes associated with land use, agricultural practices or environmental disturbance. However, diversity indices should be combined with soil chemical, physical and biological measurements rather than used as standalone indicators of soil health.

Evaluation of bioinoculants

Researchers developing microbial inoculants can examine how the introduction of beneficial microorganisms affects indigenous microbial communities. For example, applying plant growth-promoting bacteria to black pepper may alter rhizosphere community composition, nutrient cycling and interactions between beneficial microorganisms and soilborne pathogens.

Monitoring environmental stress

Salinity, drought, heavy metals and other environmental stresses can influence microbial community structure. Diversity measurements can help researchers investigate these changes and identify microorganisms associated with stress-affected environments.

Development of synthetic microbial consortia

Understanding microbial diversity and community interactions provides a foundation for designing synthetic microbial consortia, in which selected microorganisms are combined to perform complementary functions. Researchers can use information about microbial identity, functional traits, interactions and environmental adaptation to select compatible members. The consortium's performance must then be evaluated experimentally under relevant soil and field conditions.

Conclusion: Every soil has a story to tell

Soil microbial biodiversity represents an essential component of ecosystem functioning, agricultural sustainability and environmental resilience. The microorganisms living beneath our feet regulate nutrient cycling, support plant growth, decompose organic matter and influence the ability of soil ecosystems to respond to environmental change. Understanding this diversity requires more than counting microbial taxa. Species richness reveals how many

taxa are present, the Shannon index integrates richness and evenness, Simpson-based indices describe dominance and diversity, and Pielou's index quantifies evenness. Meanwhile, alpha, beta and gamma diversity provide complementary perspectives on microbial diversity across different spatial scales. Modern molecular techniques and bioinformatics have greatly expanded our ability to explore the hidden microbial world. Nevertheless, diversity indices must be interpreted in the context of sampling methods, soil properties, microbial functions and ecological interactions.

Ultimately, the goal is not simply to discover how many microorganisms live in the soil, but to understand who they are, what they do and how their interactions sustain a healthy and productive ecosystem.

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