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Soil Microbial Communities as Indicators of Soil Health

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Abstract: Healthy soil supports ecosystem function. The health of arid soils is impacted by disturbances and perturbations, which can influence the physical, chemical and biological components of soil. The health of arid soils can be degraded by erosion, desertification, salinization, sodification and other soil contaminants, all of which influence the soil microbial community. Soil organic matter dynamics, nutrient cycling and soil structure are all influenced by microbial processes and are often negatively affected by management. Soil microbial communities often change more rapidly with management and environment. The soil microbial community is more diverse than any other group of organisms, but we know so little about this diverse genetic resource. The functions of these diverse communities range from nutrient cycling and residue decomposition, to soil structural component, to plant growth effects. Management can have a large effect on microbial processes and community structure. New methods are available or emerging that will enhance our knowledge of what is happening underground. Community and process level studies, as well as investigations at the ecosystem and functional level, are needed to develop management systems that include soil biota for successful sustainable systems. As indicated in this manuscript, research is needed to increase our understanding of the diversity and function of microbial communities in ecosystems. Investigations will enhance the understanding of microbial diversity and increase our knowledge of the functional roles of microbial communities in ecosystem health and productivity.

Key words: Diversity; ecosystem management, bacteria, fungi, community, molecular, soil quality.

Healthy soil supports the functions of ecosystems by enhancing the health of plants and animals. A healthy microbial community is vital to fertility, productivity, and sustainability of an ecosystem; however, we cannot yet comprehend what fully constitutes a healthy microbial community. The health of arid soils is impacted by disturbances and perturbations, which can influence the physical, chemical and biological components of soil in different ways depending on the level of the disturbance or change (Fig. 1). Microbial diversity considerations need to be included in investigations of soil quality and soil health (Kennedy and Papendick, 1995). The soil biota is difficult to study due to their small size, vast number and diversity, and the challenges associated with identifying the soil's biotic community and its functioning (Hawksworth and Mound, 1991). The health of arid soils can be degraded by erosion, desertification, salinization, sodification and other soil contaminants, all of which influence the soil microbial community. Soil organic

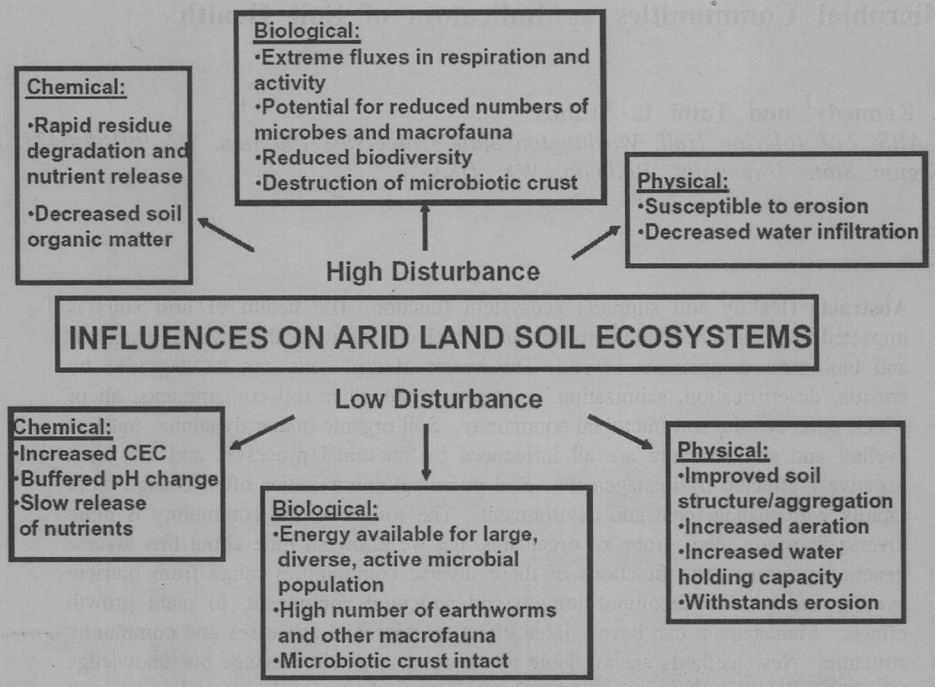

Fig. 1. The effects of disturbance on chemical, biological and physical components of arid land ecosystems.

matter (SOM) dynamics, nutrient cycling and soil structure are all influenced by microbial processes and are often negatively affected by management. Soil microbial communities often change more rapidly with changes in management and environment than soil physical and chemical characteristics, and as a result they are excellent indicators of soil health.

Soil Microorganisms

The presence of a diverse soil microbial community is crucial to the productivity of any ecosystem, since microorganisms affect all levels within the ecosystem. While potential harmful effects from soil microorganisms include plant diseases, production of plant-suppressive compounds, and loss of plant-available nutrients (Bruehl, 1987), the majority of soil microorganisms are beneficial to plant growth (Lynch, 1983). Soil bacteria improve plant performance by increasing mineral solubilization (Okon, 1982) and dinitrogen fixation (Albrecht *et al.*, 1981), producing hormones (Brown, 1972) and antibiotics, and suppressing pathogens (Bruehl, 1987). The composition of the microbial community influences the rate of residue decomposition and nutrient cycling (Beare *et al.*, 1993). Fungi and bacteria are decomposers in soil (Beare *et al.*, 1993), and are crucial to mineralization of nutrients, making them available to plants and other organisms (Henriksen and Breland, 1999). Actinomycetes are a specialized group of

soil bacteria that are able to degrade plant materials such as cellulose and mineralize nutrients. Some actinomycetes produce antibiotics. Microorganisms break down complex organic compounds into simple and possibly recalcitrant compounds. They are a part of the dynamic nutrient sources and sinks in ecosystems. These various groups of microorganisms are part of the larger food web where all of the members are influenced by environment and management, and are useful in soil quality assessments.

Beneficial mycorrhizal fungi can enhance plant growth and are often key players in the soil community. Mycorrhizal fungi are responsible for translocation of nutrients, especially soil phosphorus, and increase nutrient (Ocampo, 1986) and water uptake (Tinker, 1976). These associations are of greatest importance in stressed environments, drought conditions, phosphorus deficient soils, eroded sites, and acidic or reclaimed lands (Barea, 1991). The interactions involving mycorrhizal fungi and rhizobia may further affect the host plant by increasing nitrogen and phosphorus nutrition (Allen, 1992). The presence or absence of mycorrhizae may influence plant growth, especially in stressed soils or low in nutrients, and can be considered as indicators of soil quality.

Microbial communities play a major role in soil structure and consequently will influence soil quality (Lynch and Bragg, 1985). Soil bacteria aid in weathering soil minerals, contribute to soil formation, and secrete polysaccharides to hold soil particles together and promote aggregate stability. Fungi and actinomycetes produce hyphal threads that bind soil particles together as well as produce extracellular polysaccharides. These binding actions reduce erosion, allow for increased water infiltration and maintain adequate aeration of the soil.

Arid and semi-arid lands comprise 33-40% of the Earth's land surface (Kassas, 1995). Microbiotic crusts are common to these lands, and are dominated by cyanobacteria, algae, heterotrophic bacteria, actinomycetes, fungi, xanthophytes and diatoms, lichens and mosses. Microbiotic crusts are crucial to soil fertility in arid lands. Some of the organisms in these crusts are capable of dinitrogen fixation, and they may be a source of N for these ecosystems (Evans and Johansen, 1999). The composition of the microbial community in a crust determines the amount of dinitrogen fixation, the stability of the crust, its ability to prevent soil erosion, and the ability of the crust to withstand disturbance by humans, livestock and fire. Water-film organisms, such as ciliates, amoeba, protozoa and a few nematodes from microbiotic crusts can also contribute to N cycling in soils and influence plant health and growth (Bamforth, 2004).

Protection of soils from wind and water erosion is one of the vital roles of microbiotic crusts in arid ecosystems (Evans and Johansen, 1999). Soil organisms provide stability to crusts in two ways; first by the production of extracellular polysaccharides that help to aggregate soil particles, and also through the filaments of cyanobacteria, rhizoids of mosses and fungal hyphae of lichens that help to stabilize soil particles (Evans and Johansen, 1999; Schulten, 1985). Particles of soil can be

held together for as long as two years after the organism has died (Schulten, 1985). Microbiotic crusts take many years to establish and are extremely sensitive to disturbance from grazing, land use changes, recreation or fire (Evans and Johansen, 1999; Jeffries and Klopatek, 1987). The detrimental effects of disturbance require many years for recovery (Jeffries and Klopatek, 1987). Lichens and mosses seem to be the slowest to recover, while cyanobacteria, algae and diatoms can recover in just a few years (Evans and Johansen, 1999). Measurement of the communities found in crusts and their reappearance, albeit slow, may be excellent indicators of soil quality changes of these lands.

The rhizosphere is that dynamic zone surrounding the root that is influenced by root exudation and water/nutrient uptake. Microbial populations may be 10- to 100-fold higher in the rhizosphere than in soil with no growing plants (Bottomley, 1998). This high concentration of microorganisms in the rhizosphere leads to larger numbers of nematodes and protozoa that feed on bacteria and fungi, and in turn, high populations of microarthropods that prey on nematodes and protozoa. While population numbers of the various groups are high, the overall types of microorganisms stimulated by and inhabiting the rhizosphere may be limited and thus the overall diversity may be lower than one might expect. The quality of residue, like the quality of exudates in the rhizosphere, influences the populations of micro- and mesofauna that colonize residue (van Vliet *et al.*, 2000). The rhizosphere and the community in that zone can directly or indirectly affect soil quality and soil quality indicators.

Diverse soil microbial communities and the dynamics within and among these communities can be used to indicate changes in soil health. The issue though is whether their increase or the decrease in activity and diversity of a given community indicates degradative or aggregative processes of the soil.

Soil Microbial Diversity

Soil microbial community diversity is often difficult to comprehend due to the spatial differences present in the soil system, but diversity and diversity indicators may be useful indicators of soil health. There are several different habitats in soil: the spermosphere, rhizoplane, rhizosphere, residue or SOM, aggregates, bulk soil, and lastly the soil horizons across a landscape or across a watershed. Microbial diversity will vary across all these habitats and be influenced by the action of other trophic levels.

The extent and dimension of the soil microbial diversity is not truly known (Holben and Tiedje, 1988; Torsvik *et al.*, 1990). Taxonomic diversity relies on characterization of known phenotypic or genetic characterizations that possibly have little bearing on soil processes (Lee and Pankhurst, 1992). The functioning of microorganisms can be more significant than the number of species in regulating ecosystem processes (Grime, 1997; Wardle *et al.*, 1997; Bardgett and Shine, 1999). Although variation in species richness may not be discernible in many environments, differences may be indicative in stressed

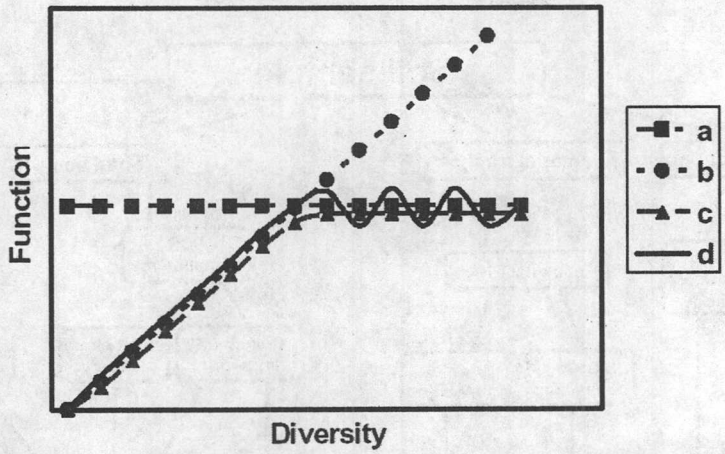

Fig. 2. The potential relationships between function and diversity in soils. a) Function independent of diversity. b) Function and diversity increase with each other, c) Function increases with diversity up to a maximum, d) Function increases with increasing diversity to an upper limit and then fluctuates due to restrictive factors.

systems or when conditions are altered (Yachi and Loreau, 1999). If all functional groups are present, higher microbial diversity may not lead to improved ecosystem functioning, thus diversity indices along with additional soil information is needed to determine the status of a soil.

Several different scenarios can explain the relationship between diversity and function (Fig. 2). As diversity increases, the functioning of a system can either be maintained at a constant level (a) or increased (b). A third scenario could be that function increases with diversity to some maximum, possibly regulated by limiting resources or other factors, but diversity continues to increase (c). A fourth possibility, which may be the more likely relationship, is one in which function and diversity increase to some level, and diversity changes with inputs or stresses, with the amplitude of that change dependent upon the environment (d). A major question can be what level of diversity is needed for a stable soil microbial community and can we assess that with soil health indicators?

Microbial diversity impacts ecosystem functioning due to many microbial processes. Microbial diversity can directly influence plant productivity and diversity by influencing plant growth and development, plant competition and nutrient and water uptake (Price, 1988). Diversity measurements are made up of richness (How many species or genotypes?) and evenness (How are the species or genotypes distributed within the populations?). Estimates of diversity need to be identified as to whether species, groups, organism types or functions are being used as the gauge for measurement. Measurements need to be equivalent, and samples of equivalent

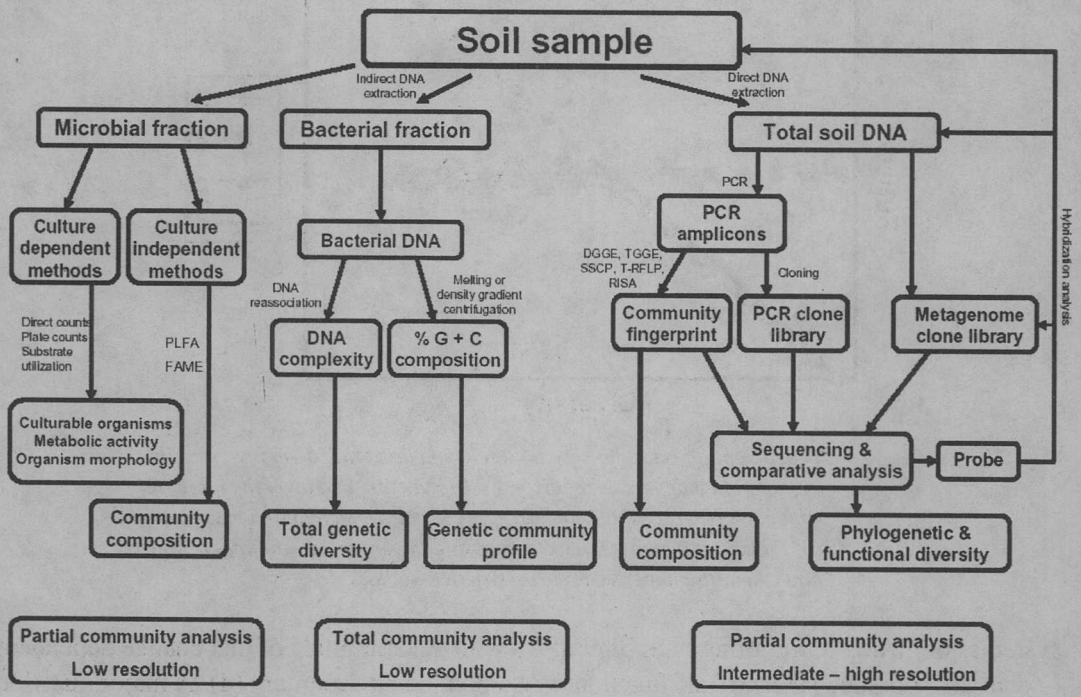

Fig. 3. An overview of culture dependent and culture independent methods for the analyses of microbial communities. Adapted from Lynch et al., 2004. FAME Fatty acid methyl ester; PLFA Phospholipid fatty acid methyl ester; PCR Polymerase chain reaction, DGGE Denaturing gradient gel electrophoresis, TGGE Thermal gradient gel electrophoresis, SSCP single-strand conformation polymorphism, T-RFLP Terminal-restriction fragment length polymorphism, RISA Ribosomal intergenic spacer analysis, % G + C mole % guanine + cytosine.

size used, especially when diversity is low (Grunwald *et al.*, 2003). The values used in diversity estimates need to truly represent unique species or function and not simply biomarkers or unknown measurements. Microbial diversity and functional diversity may contribute greatly to the understanding of soil quality and the development of sustainable ecosystems (Hawksworth, 1991). Soil organisms are useful in classifying disturbed or contaminated systems, since diversity can be affected by minute changes in the ecosystem. The use of microorganisms and their functioning for examination of environmental stress and declining biological diversity can be used in ecosystem management and as indicators of soil health (OTA, 1987).

A remaining question is: How much diversity is required to ensure sustainable

Table 1. Comparison of microbial community analyses.

Method	Test	Extent	Specificity/ resolution	Application	Select citations
Plate counts; Direct counts	Culturability	Functional main group	Low		Torsvik *et al.*, 1996
CLPP; Substrate utilization	Community level physiological profiles; Culturability	C source utilization, functional diversity	Low	Excludes fungi	Garland, 1996; Zak *et al.*, 1994; Bossio and Scow, 1995
PLFA	Phospholipid fatty acid; Cell wall	Structural fingerprinting, predominant active members	Low	May be overlap in marker PLFA	Petersen and Klug, 1994; Frostegard and Baath, 1996
FAME	Fatty acid methyl ester	Structural fingerprinting	Low	Limited to total fatty acids, not specific	Kennedy and Busacca, 1995; Cavigelli *et al.*, 1995
DNA reassociation	Nucleic acid	Total genetic diversity	Low	Genetic potential, changes in composition	Torsvik, 1995
Mole % G + C	% guanine + cytosine	Genetic profile	Low	Changes in composition	Torsvik *et al.*, 1996
DGGE/ TGGE	Denaturing/ Thermal gradient gel electrophoresis; sequencing of individual bands	Genetic fingerprinting, predominant members	Medium	Community structure, spatial and temporal changes in composition	Muyzer *et al.*, 1993; Muyzer and Smalla, 1998
SSCP	Single-strand confirmation polymorphism; sequencing of individual bands	Genetic fingerprinting, predominant members	Medium	Community structure, spatial and temporal changes in composition	Lee *et al.*, 1996
ARDRA	Amplified ribosomal DNA restriction analysis	Genetic fingerprinting of simple communities, populations or phylogenetic groups; lower species levels	High	Microbial population dynamics, diversity within phylogenetic or functional groups	Avaniss-Aghajani *et al.*, 1994; Massol-Deya *et al.*, 1995; Sandaa *et al.*, 2001

Table 1 contd.....

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Method	Test	Extent	Specificity/ resolution	Application	Select citations
RISA	Ribosomal intergenic spacer analysis	Genetic fingerprinting of populations or phylogenetic groups	High	Microbial population dynamics, diversity within phylogenetic or functional groups	Borneman and Triplett, 1997; Ranjard *et al.*, 2000
rDNA	Cloning and sequencing	Phylogenetic diversity, identification of members	High	Phylogenetic diversity of members	Johnsen *et al.*, 2001
PCR functional genes	Cloning and sequencing	Functional diversity	High	Functional potential	Amann *et al.*, 1990
RNA slot/ dot blot hybridization		Phylogenetic identification of metabolic active members	Medium	Qualitative and quantitative analysis of metabolic active populations; phylogenetic information on active members	Manz *et al.*, 1992; Amann *et al.*, 1995
FISH	Fluorescence in situ hybridization	Detection and species counting of metabolic active microbes	Medium	Community structure; identification of active cells; direct phylogenetic information on members	Amann *et al.*, 1990

and efficient SOM turnover? Further use of diversity indices is limited by absence of detailed information on microbial species composition in soil (Torsvik *et al.*, 1990). Diverse systems are thought to have higher agricultural productivity, resilience to stress, greater sustainability and protection from risk (Giller *et al.*, 1997; Wolters, 1997). A diverse system has a wider range of function with more interactions among microorganisms that influence each other to varying degrees. A greater number of different types of organisms present in a system are able to perform various processes and fill a niche that may not be filled if a particular group is inhibited by stress

(Andren *et al.*, 1995). However, there may be an upper limit of diversity that allows for efficient functioning of the total system.

Diversity may function as an indicator of stress or change, and therefore soil health. Diversity indices can be used to indicate the effect of disturbance; however, greater diversity may not always be desirable. Greater diversity should not be equated with a more stable system, rather the changes in diversity with management may be more informative of the status of a soil microbial community. Basic shifts in large groups in an ecosystem may indicate a change, but may not be able to address functioning of that altered system. Microbial communities and their processes need to be examined, not only in relation to the individuals that comprise the community, but also with regards to the effect of perturbations or environmental stresses on those communities.

Methods to Assess Microbial Communities and Diversity

Many methods are currently used by researchers to help quantify the microbial community and its function and diversity, and to compare the effects of management practices (Fig. 3). They may range from simple and limited plate counts to more inclusive and higher resolution nucleic acid analysis of total soil DNA to estimate functional diversity (Table 1) (Lynch *et al.*, 2004). Studies of soil microbial community structure will often use a combination of both traditional, cultural techniques along with newer, molecular techniques. While new technology is continually being developed, methods will advance and improve indicators of changes in the soil microbial community.

Substrate utilization patterns have been used to obtain "fingerprints" of community structure (Garland, 1996; Bossio and Scow, 1995; Haack *et al.*, 1995; Wunsche *et al.*, 1995; Zak *et al.*, 1994). These measures can also indicate functional diversity, metabolic potential (Degens, 1999; Haack *et al.*, 1995; Wunsche *et al.*, 1995) and nutritional strategies (Zak *et al.*, 1994). Substrate utilization patterns rely on the growth of populations once in the presence of the substrate, and changes to the community may occur during incubation that could lead to incorrect conclusions. This method is an indicator for bacteria and not fungi; however, it is very useful in identifying functional groups based on substrate use and catabolic versatility (Burkhardt *et al.*, 1993; Degens and Harris, 1997). Community-level physiological profiling (CLPP) can be used to determine the physiological capacity of a community by substrate use of the whole community (Garland and Mills, 1991). A more time-consuming, but information-yielding method can be performed on the whole community by assessing substrate-induced respiration (Degens and Harris, 1997). The active and fast-growing subsets of soil microbial populations are the targets for these methods. While there is an upper limit of soil organic C, a relationship was found between soil organic C and functional diversity using substrate utilization (Yan *et al.*, 2000). Their results illustrate that substrate utilization can be used as an indicator of soil health.

The fatty acids of cell membranes are varied and unique, and thus can be used

in community analysis. Whole soil fatty acid methyl ester (FAME) analysis is used in community investigations to fingerprint the community. FAME can differentiate soils by geographic region (Kennedy and Busacca, 1995) and cropping pattern (Cavigelli *et al.*, 1995). Results of this analysis may give more of a biological history rather than the current microbial community, and results depend on what fraction of the soil is actually used. The living microbiological component of a soil community can be estimated by phospholipid fatty acid (PLFA) analyses (Zelles *et al.*, 1994). The PLFA method provides biomarkers of the community, but this technique is limited in identifying functional groups or functioning unless coupled with stable isotope methods. Fungi to bacteria ratios can be used as an indicator of shifts in these two groups, and while not identical to fungal:bacterial biomass, they are still indicators of changes in the soil microbial community (Frostegård and Bååth, 1996). Both methods are rapid, reproducible and relatively easy to use.

Molecular genetic techniques are continually evolving as tools for characterizing soil microbial communities and can identify both culturable and non-culturable organisms. Extraction of DNA can be dependent not only on the extraction procedure but also on soil type, humic acids and clay minerals present. Total genomic DNA analyses of soil communities have shown that several thousand independent genomes can be present in one gram of soil (Torsvik *et al.*, 1990). Microbial diversity as determined by small sub-unit (SSU) rDNA illustrated that diversity among the dominant soil microorganisms was high and not randomly distributed among the major taxa (Borneman *et al.*, 1996). Relative diversity in bacterial communities can be measured from single-strand conformation polymorphism (SSCP) of the PCR products of 16S rRNA genes (Lee *et al.*, 1996). Denaturing/thermal gradient gel electrophoresis (DGGE/TGGE) and SSCP are each based on separating of nucleic acid molecules to analyze the individuals and communities of a particular soil (Muyzer and Uitterlinden, 1993). These methods are widely used in community analysis.

The use of 16S rRNA methods has evolved as a set of strategies to estimate soil microbial diversity. This method has not only profiled the diversity of dominant microorganisms in soil, which was much higher than predicted, but also demonstrated that diversity is not randomly distributed (Borneman *et al.*, 1996). A hybridization technique that provided similarity indices and measures of relative diversity of two samples from whole soil community DNA showed that extracted bacteria and whole community DNA had a 75% similarity to each other (Griffiths *et al.*, 1996). Improved hybridization signals have allowed the use of whole community DNA to profile soil microbial community structure. DNA microarray technology has been used to rapidly analyze microbial communities based on phylogenetic groupings (Guschin *et al.*, 1997). The use of probes is of medium resolution and specificity and can quantify target microbial species or detect minimum taxonomic composition present in soil microbial communities.

Terminal-restriction fragment length polymorphism (T-RLFP) uses restriction

enzyme digestion of PCR-amplified DNA that is fluorescently labeled at one end to produce a fingerprint of the community. Specific species or rank of these components can be identified from this method (Osborn *et al.*, 2000). Amplified ribosomal DNA restriction analysis (ARDRA) is a method of rapidly fingerprinting the soil microbial community based on restriction patterns of ribosomal DNA (Massol-Deya *et al.*, 1995; Tiedje *et al.*, 1999). The procedure is versatile because it can be used on a range of samples from soil DNA to isolates from pure culture. Community DNA can also be analyzed by ribosomal intergenic spacer analysis (RISA) band pattern for bacteria, and internal transcribed spacer analysis (ITS) for fungi, and give profiles of the community (Ranjard *et al.*, 2001). A drawback of these methods is that no calculation of richness or evenness can be made as a single bacterium or fungi may actually be responsible for more than one band.

Reassociation kinetics of soil bacterial DNA estimated that 4,000 bacterial genomic types were present, with a potential of 40,000 species (Torsvik *et al.*, 1990). Total genomic DNA analyses (% G + C in DNA) can also be used in assessing the microbial community (Torsvik *et al.*, 1996). This method has lower resolution; however, changes in microbial community profile can be determined, especially when diversity is low. This method does not indicate species composition, rather base composition profiles are constructed. If different base composition is found between samples it is likely that species are different as well. This method is useful in situations where only a general indication of change is needed. The less dominant species of a community are represented by this method.

These methods produce copious amounts of data and often the statistical analysis is the more challenging portion of the research. There are many different ordination methods for multivariate analysis that include principal component analysis, correspondence analysis and multi-dimensional scaling, etc. With the assumptions for each analysis, strengths and weaknesses need to be considered before drawing conclusions (Jongman *et al.*, 1995; McCune and Grace, 2002).

The methods that can be used in ecological studies are as varied as the organisms found in the soil. As advances in the technology of molecular microbial ecology continue, so too will our understanding of the dynamics and complexity of the soil microbial community. These have promise as indicators of the status of a soil. Reproducibility, assumptions, ample replication and amplification bias are the issues that need to be resolved with each study and group of soils being investigated. Microbial diversity indices can function as bioindicators of the stability of a community and can be used to describe the ecological dynamics of a community and the impact of stress on that community (Mills and Wassel, 1980).

Environmental Influences

The diversity of the microbial community, as well as the functions within communities, influences the stability and resilience of the soil system and thus the health of that soil. Microbiological properties can identify changes in overall soil health before changes occur that

influence overall plant productivity (Visser and Parkinson, 1992). Fluxes in microbial diversity and functional diversity may contribute greatly to the understanding of soil quality and the development of sustainable ecosystems (Hawksworth, 1991).

Microbial diversity may be linked to susceptibility and resiliency of soil to stress, and thus may affect some soil functions, such as OM decomposition. Partial fumigation of grassland soils produced differing degrees of diversity, with longer fumigation times producing soils with less diversity. There was no direct correlation between diversity and overall function; however, soils with lower diversity had decreased ability to decompose added grass residue (Griffiths *et al.*, 2000). Organically farmed soils initially contained a more abundant and diverse microbial community; however, when organic amendments were added, soil from the conventionally farmed system had increased microbial activity and abundance compared to the soil in the organic system (Gunapala *et al.*, 1998). Reduction in aboveground plant diversity, which occurs with severe disturbance such as tillage, overgrazing, and pollutants, may decrease microbial diversity (Christensen, 1989). However, in a study of the diversity of native prairie and cultivated soils, diversity indices were greater with tillage when compared to grassland (Kennedy and Smith, 1995). With the substrate exposed by tillage, more surface area was available for colonization and more microbial activity occurred rather than less.

Fumigation was used to alter functional diversity in a grassland soil and *in situ* catabolic potential measurements were used to characterize the ability of the soil community to metabolize C substrates with substrate added to the soil directly (Degens and Harris, 1997). The functional indices were different among fumigated, unfumigated, or fumigated and inoculated with untreated soil. Functional diversity and decomposition of added wheat straw were not well correlated, indicating that water potential may have been the limiting factor in that system.

Soil biodiversity and nutrient cycling were not linked in a study of Nigerian tropical soils (Swift *et al.*, 1998). Native bush soils had higher diversity of soil fauna than those under cultivation, but the soils were similar in the decomposition of surface residues. However, the quality and quantity of substrate may affect community structure. The microbial community changed as substrate loading increased, and fungi dominated rather than bacteria in high substrate conditions. Ecosystem function and microbial communities are influenced by environment. Severe disturbances, such as those caused by heavy tillage, overgrazing, and pollutants may reduce aboveground plant diversity and without the carbon source as food, may decrease microbial functioning (Fig. 4) (Christensen, 1989; Zak, 1992). The changes in the physical and chemical properties of soil resulting from tillage greatly alter the matrix supporting growth of the microbial population. No-till increased microbial biomass (Drijber *et al.*, 2000), increased the ratio of fungi:bacteria, and provided for a more diverse population of residue decomposers and a slower release of nutrients than under conventional tillage (Altieri, 1991). The composition of the

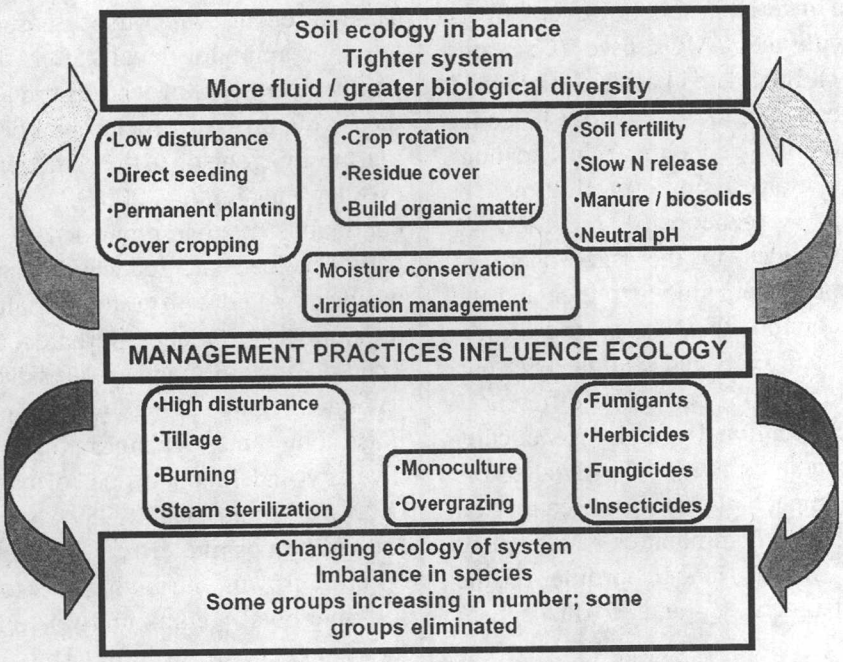

Fig. 4. The effect of management on soil biology. Practices that favor build-up of soil organic matter may lead to greater biological diversity, while practices that involve high disturbance or stress from chemicals may result in limited microbial diversity, or elimination of some biological groups.

microbial community influenced the rate of residue decomposition and nutrient cycling in both no-till and tillage-based systems (Beare *et al.*, 1993). Fungi dominate decomposition in a no-till system, while the bacterial component is responsible for a greater portion of the decomposition of residue with tillage. Microbial community analyses such as PLFA, substrate utilization, DNA microarray technology, etc. are useful in distinguishing among specific populations associated with conventional, minimum and no-tillage cropping systems.

Grazing can also affect soil microbial communities by shifting plant populations from perennial species to annual grasses (DiTomaso, 2000). Overgrazed rangelands in Argentina had the lowest soil OM and microbial activity (Abril and Bucher, 1999). These results are case-specific however, as microbial diversity and microbial activities of intensely grazed grasslands in New Mexico were not different from non-grazed lands (Liu *et al.*, 2000).

Differences in soil properties are evident with the introduction of some genetically modified organisms (GMOs), but the impact of these differences on the soil microbial community and soil quality is situation specific, and long-term impacts are not clear. Functional and community differences were seen with the persistence of genetically

engineered material in soil; however, effects differed with the GMOs used (Gagliardi *et al.*, 2001). Inoculated bacterial biological control agents and the indigenous bacterial community colonized transgenic and non-transgenic potatoes similarly (Lottman *et al.*, 2000). A genetically modified *P. fluorescens* added to the rhizosphere of pea affected soil enzyme activities and the microbial community (Naseby and Lynch, 1998). Using FAME and Biolog, Dunfield and Germida (2003) compared differences among conventional and genetically modified canola cultivars. They studied the ecological impact of transgenic canola on soil microbial communities and found differences in the FAME profile of the soil, rhizoplane, and rhizosphere community.

The soil microbial community can be influenced by plant species, succession, or species sequence and degree of cropping intensity. Plants may be a selective force for rhizosphere microbial populations through their influences on exudation patterns (Meharg and Killham, 1995) and soil nutrients (Jensen and Nybroe, 1999; Pennanen *et al.*, 1999), and the composition of the plant community may drive the make up of the soil microbial community (Minamisawa *et al.*, 1999; Achouak *et al.*, 2000). Likewise, soil microorganisms affect plant growth and influence plant competition among species (Westover *et al.*, 1997). Microbial communities can be responsive to soil characteristics, as well as plant species (Wardle *et al.*, 1999; Degens *et al.*, 2000). An example of this is the decline of the wheat disease take-all (*Gaeumannomyces graminis* var. *tritici*) that is the result of a change in the soil microbial community. Take-all occurs when the disease develops to a maximum level after numerous consecutive years of wheat production, and then is suppressed as microbial populations that are antagonistic to the pathogen increase (Weller *et al.*, 2002). Conversely, continuous monocropping led to increased pathogen load and reduced barley growth when compared with grains in multiple-crop rotation (Olsson and Gerhardson, 1992). The populations and aggressiveness of pathogens can be altered with crop rotation, illustrating the changes in microbial diversity and function due to management (El Nashaar and Stack, 1989). Studies have shown the positive effects of crop rotation on crop growth, attributing this to changes in microbial community composition (Johnson *et al.*, 1992). The microbial diversity of soils under wheat preceded by a legume crop (red clover, *Trifolium pratense* L. or peas, *Pisum sativum* L.) was higher than in wheat preceded by summer fallow or continuous wheat (Lupwayi *et al.*, 1998). In a study where fields in Brazil had not received inoculant of the nitrogen-fixing bacterium *Bradyrhizobium* for more than 15 years, no-till combined with crop rotations containing soybeans (*Glycine max* L.) resulted in higher populations and greater diversity and activity of *Bradyrhizobium* than cropping systems without soybeans (Ferreira *et al.*, 2000).

The impacts of biosolids on soil quality are varied and investigations of the soil microbial community may assist in assessing the impact of these applications. Applications of biosolids to the soil surface provide an avenue for recycling of sewage sludge, wastewater, and animal wastes

(Barbarick *et al.*, 2004), and remediation of contaminated soils (Perez-de-Mora *et al.*, 2006), while potentially enhancing soil fertility with increased nutrients, higher crop yields and improved soil quality through increased SOM levels (Speir *et al.*, 2004). However, biosolids may be damaging to soil health and cause shifts in the soil microbial community if they are contaminated with levels of heavy metals (Fließbach *et al.*, 1994; Kao *et al.*, 2006), or animal or human pathogens (Gerba and Smith, 2005). Heavy metal contamination varies with type of biosolids applied, level of contamination and specific metal (such as Cd, Pb, Zn, Cu, Ni), and soil type. Fließbach *et al.* (1994) found that sewage sludge with low levels of metal contamination had favorable effects on microbial biomass C and soil microbial activity; however, sludge with high levels of contamination led to a decrease in microbial biomass C. Respiration and metabolic quotient increased with increasing metals concentration (Fließbach *et al.*, 1994). Microbial biomass C:N ratio increased toward the conclusion of the experiment, as the microbial population had shifted from primarily bacteria to predominantly fungi, which are better able to withstand high metal concentrations (Kao *et al.*, 2006). A similar shift in the microbial community was observed by Fließbach *et al.* (1994) as fungi contributed more to soil respiration. In response to application of metal enriched sewage sludge, Khan and Scullion (2002) also noticed a shift in the microbial community from bacteria to fungi, along with increased mineralization of SOM, and decreased utilization of mineralized N. Chemically or heavy-metal-stressed soils were found to decrease in microbial diversity depending on the type of chemical applied (Reber, 1992). Greater susceptibility to copper toxicity was found with lower diversity (Griffiths *et al.*, 2000). Soils may be contaminated with pathogenic organisms from the application of biosolids from animal feeding operations, wastewater treatment plant effluents, and on-site treatment systems (Gerba and Smith, 2005). These materials require that wastes be handled and treated properly with methods in place to detect pathogens (Gerba and Smith, 2005).

Salt concentrations can influence the health of arid soils. Catabolic response profiles were calculated from the soil respiration response due to added simple C substrates. Catabolic diversity was low in cropped soils compared to pasture, and salt stress caused much greater negative effect in catabolic evenness in the crop soil (low evenness) than the pasture soil (high evenness) (Degens *et al.*, 2001). The microbial community in the cropped system was less resilient than the pasture counterpart. In the assessment of health of California salt marshes, metals were found to have a greater impact on the microbial community and diversity than organic pollutants. Pollutant concentrations correlated with microbial indicators, indicating the potential for using microbial community analyses as indicators of ecosystem health (Córdova-Kreylos *et al.*, 2006). Microbial diversity as measured by *in situ* phospholipid fatty acids was higher in uncontaminated sediments. Microbial PLFA diversity did not differ in the contaminated sediments among the different plant species or unvegetated area. In salt

marshes, two plant species influenced sediment microbial community function (dehalogenation capabilities), even though the disturbed and undisturbed sediments varied in microbial community composition (Ravit *et al.*, 2005). Rehabilitation of mined sand dunes in South Africa was studied using metabolic diversity of the soil microflora. Organic C content influenced PLFA relationships to the greatest extent; and the greatest diversity was found in soils under native forest or those mined sites with the longest rehabilitation time (Graham and Haynes, 2004). The microbial communities of those sand dunes rehabilitated for a short time period had the lowest diversity and were different from the native site and the 25 year rehabilitated site. Bacterial functional redundancy as determined from active growth on selected carbon substrates was determined along a reclamation gradient from mine site to native forest in Brazil (Yin *et al.*, 2000). The highest functional redundancy was found in the native and new growth forest soils. Bacterial functional redundancy increased with the growth of plant communities, which represents a critical event in the restoration of soil biology to mine spoils.

Conclusions

The soil microbial community is more diverse than any other group of organisms, but we know so little about this diverse genetic resource. The functions of these diverse communities range from nutrient cycling and residue decomposition, to soil structural component, to plant growth effects. Soil crusts provide a source of added carbon and nutrients in arid soils as well as protecting the soil from wind and water erosion. Management can have a large effect on microbial processes and community structure. While only a small portion of the microorganisms in soil can be collected and studied, new methods are available that will enhance our knowledge of what is happening underground. Functional groups rather than only taxonomic units are now being studied. Community and process level studies, as well as investigations at the ecosystem and functional level, are needed to develop management systems that include soil biota for successful sustainable systems. Research is needed to increase our understanding of the diversity and function of microbial communities in ecosystems. Identification of functional genes and their use in diversity studies will assist in more meaningful assessments of soil health. Before soil microbial communities can be used as indicators we need to identify, for a given soil, the level of microbial diversity and community composition that withstands stress and maintains a quality ecosystem. Ecological investigations will enhance the understanding of microbial diversity and increase our knowledge of the functional roles of microbial communities in ecosystem health and productivity.

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