Soil Organic Matter Dynamics and Microbiological Interactions

P. D. Millner and D. D. Kaufman
Agricultural Research Service U. S. Department of Agriculture, Beltsville, Maryland, USA

Abstract

Soil organic matter (SOM) undergoes continuous decomposition over many years and the decomposition process is characterized by a series of stages. Plant, animal, and microbial constituents and residues are the building blocks of SOM. Soil microbial biomass (SMB) is that portion of the organic matter associated with the living soil microbial (bacterial fungi, and fauna) populations. SMB is a major source and sink for nutrients, and it controls the rate of turnover and mineralization of nutrients. Soil mesofauna (microarthropods) break residues into ever smaller particles so that they may be accessed more easily by enzymes and, thereby, decomposition is facilitated. The soil hyphae of mycorrhizal fungi effectively increase the rhizosphere around plant roots, and the active nutrient absorption zone and surface area of plants in soil. Thus, the measurement and evaluation of the biological aspects of SOM cycling relative to soil quality are quite complex and challenging. Recent advances in quantitative techniques need to be applied to assess SOM and microbial interactions and their consequences.

Introduction

Soil organic matter is widely recognized as a critical component of soil quality and productivity (Arshad and Coen, 1992; Granatstein and Bezdicek, 1992) because of its value in nutrient cycling processes and soil physical properties. Soil quality, like air and water quality, is a key to environmental quality; indeed, water quality depends in part on soil quality (NRC, 1993). This paper focuses on some of the major effects of soil organic matter (SOM) on soil quality, and it highlights the associated major microbial groups. Biomarkers for soil microbial activity, biomass and enzymatic processes are discussed along with their relevance to the concept of nutrient cycling and sustainable agriculture. Terminology used here will generally be that which is used by microbial ecologists. Although these terms are somewhat different from those used by soil scientists, the phenomena described are the same.

Interactions of Soil Organisms

Soil organic matter dynamics, i.e., transformations, have long been known to involve interactions among many different groups of soil organisms. The interdependence of life forms in soil affects the reproduction, growth, dispersal, and survival of the entities involved. Except for photosynthetic forms like algae and a few bacteria, microorganisms depend on organic matter for their growth and other metabolic processes.

Soil organic matter has been defined by Stevenson (1982) as the total organic constituents in soil excluding undecomposed plant and animal tissues, their “particle decomposition” products, i.e., organic residues, and soil biomass, i.e., microbial biomass. Jenkinson and Raynor (1977) described five fractions of organic material and their associated half-lives in soil: (1) fresh residues from plants and animals, 0.17 years; (2) lignin from previous additions of organic materials, 2.3 years; (3) soil biomass including microbial cells with their metabolic by-products, 1.7 years; (4) colloidally-sorbed materials, 50 years; and (5) old humus, 2.0 years. When SOM becomes so thoroughly modified by decomposition that it no longer resembles any of the starting materials macroscopically, microscopically, or molecularly, it is then referred to as humus, which is characterized by the abundance of humic substances (Stevenson, 1982). Microbial decomposition of plant lignins and microbial biosynthesis are thought to be the principal means by which humic substances are produced.

The diverse sources and compositions of SOM result in a correspondingly diverse array of microbes and exoenzymes involved in multiple chemical and biochemical transformations that yield the humic substances. Although resistant to rapid degradation, humic substances can serve as nutrient

sources for bacteria, fungi, blue-green algae, and protozoa. Various microbes utilize different organic constituents in humus at different rates and to different extents. The biological activity status of a soil is dynamically responsive to environmental conditions such as changes in temperature, nutrients, and water availability. Additions of organic material, whether as complex polysaccharides (e.g., straw) or as simple sugars (e.g., glucose), stimulate the decomposition of native organic matter as well as the added substrate (Jenkinson, 1966.; Dalenberg and Jager, 1981). In a healthy soil system, however, this loss of native organic matter is offset by larger inputs to the stable organic matter from the dynamic pool (as illustrated by the arrows in Figure 1). In the short-run, this process results in an increased respiration rate by the soil biomass and a consequent change in the carbon dioxide (CO_2) output. After the readily available substrate is depleted, the respiration rate will re-equilibrate itself in accord with the availability of nutrients and the prevailing environmental conditions. Often, this is at a lower rate than that which occurred after the introduction of a readily metabolizable substrate.

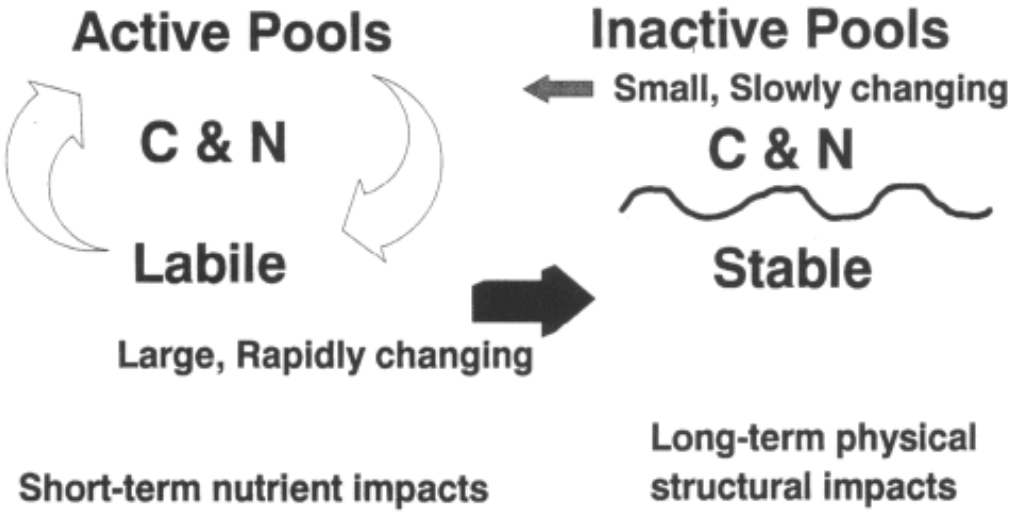

Figure 1. The Formation and Turnover of Soil Organic Matter (SOM) Containing Carbon (C) and Nitrogen (N) can be Characterized by at Least two Different Pools of Organic Matter, Distinguished by Their Relative Rates of Decomposition. One is a Stable Pool with a Very Slow Rate of Organic Matter Turnover. The Other is a Labile Pool with a Rapid Rate of Decomposition that Comprises the Active, Dynamic Fraction of SOM and may be an Indicator of the Long-Term Effects of Management on SOM and Soil Quality. The Labile Pool Has Been Measured in Terms of Microbial Biomass, Specific Respiration (CO_2C per Unit Biomass C per Unit Time) and Particulate Organic Matter.

Soil microbial biomass (SMB) and its measurement have been the subject of considerable research simply because SMB is an important source and sink for nutrients, and its activity controls the rate of turnover and mineralization of organic substrates. Competition between plants and soil microbes for N and P released during mineralization of SOM can be intense, and a good balance is necessary to sustain plant and soil productivity. Among the standard methods (Table 1) the chloroform fumigation-incubation technique for measuring SMB (Jenkinson and Powlson, 1976) has been used extensively along with other methods (Sikora et al., 1994; Turco et al., 1994) to show that SMB is a large and labile pool, but it is relatively inactive because of the low level of readily available nutrients. Recent advances in technology have lead to development and use of new methods, procedures, and techniques for measuring SMB (Ritz et al., 1994). Several of these new techniques, which depend on the measurement of specific biochemical moieties that serve as markers of broad groupings of microorganisms, are shown in Table 2.

Table 1. Five Types of Biological Activity and the Corresponding Methods Used to Measure the Activities

Type of Biological Activity	Measurement Method(s)
Soil respiration, i.e., CO_2 production	Chloroform fumigation/incubation/ or substrate induced respiration of *in-situ*, intact cores, bulk soil, and/or rehydrated cores
CO_2/biomass N	Release of CO_2 and NH_4^+ in biomarkers upon rehydration of dry soil
ATP	Intensity of luciferin fluorescence
Dehydrogenase	Reduction of 2,3,5-triphenyltetrazolium chloride (TTC) to triphenylformazan
Esterase	Fluorescein diacetate hydrolysis

Table 2. A Partial List of Biomarkers (Biochemical Markers) Used in Ecological and Soil Microbial Studies to Measure the Biomass of Various Groups of Microorganisms (also see Ritz et al., 1994).

Biomarker	Type of Biomass Measured
Phospholipid (16:0)	Total biomass: eukaryotes and prokaryotes
Glycerol release from phospholipid	Bacteria
Cyclopropyl fatty acids	Bacteria
Lipopolysaccharides (LPS)	Gram-negative bacteria
Teichoic Acid	Gram-positive bacteria
Muramic Acids	Bacteria
Polyenoic fatty acids	Eukaryotes/gliding bacteria
Phytopigments	Photoautotrophs
16S rDNA amplified by PCR	Genera: bacteria/actinomycetes
ATP	Bacteria
N-acetylglucosamine	Fungi
Ergosterol	Fungi
Chitin	Nematodes

In addition to microbes, the soil mesofauna are important in the whole process of humification and SOM nutrient cycling (Linden et al., 1994) because they facilitate decomposition by breaking plant, insect, and other residues into smaller particles to increase the active surface area upon which microbes can access nutrients. The mesofauna also serve as vectors for decomposer microbes.

Thus, SOM dynamics involve interactions across different trophic levels of the soil ecosystem; these interactions include direct and indirect effects on SOM and can result from by-products of the collective metabolic activities of macro-, meso-, and microflora and fauna. The broad range of organisms that are involved in cycling of organic matter (Crossley et al, 1989; Lee, 1991) make the effort of measuring and evaluating soil quality exceptionally challenging.

For soil microorganisms, the classical approach to assess the effects of various soils, crops, climates, cultural practices, etc. on the standing “crop” of microbes is to count them. Serial dilutions (in water or buffer) of a soil sample are either spread onto gelling agents such as agar, or mixed with various types of nutrient media containing agar (Jensen, 1968). When grown to easily discernable size, individual colonies are counted, selections are established in pure culture on standardized media,

and then the microorganisms are identified by taxonomic name or by physiological properties. Colony counts are reported as colony-forming units (CFU) and are used with the dilution factor to calculate the number of CFU's per gram of soil, usually on a dry weight basis.

Bacterial identifications usually require characterization of their biological activities and their enzymatic/metabolic capabilities along with their colony and cell morphology. Some examples of broad biogeochemical groups and types of associated microbes are shown in Table 3. Identification of fungi requires observation and recordation of morphological traits, and usually requires microscopic examination with occasional use of metabolic characteristics (Domsch et al., 1980). Meso- and macrofauna are enumerated by appropriate standard methods (Stork and Eggleton, 1992), although reports on the biomass and phosphorus content of some soil invertebrates have also appeared (McKercher et al., 1979). Collection, detection, identification, characterization, and quantification of the micro-, meso-, macroflora and fauna community is a daunting task for soil ecologists. For this reason, the newly developed biomarker approaches (Table 2) are being more widely used.

Some investigators suggest that nitrogen and its flux through soil-crop systems is an appropriate indicator of the fitness of the biological soil system (Yakovchenko et al., 1995). Others note that carbon mineralization and specifically the particulate organic matter carbon are sensitive indicators of the influence of crop-soil management practices on SOM (Elliott et al., 1994) and hence of the system. In actuality, both C and N are critical in determining the biological status of soils because as nutrient elements they are interdependent (spatially and temporally) in the transformation of SOM through their cycles as illustrated in Figure 2.

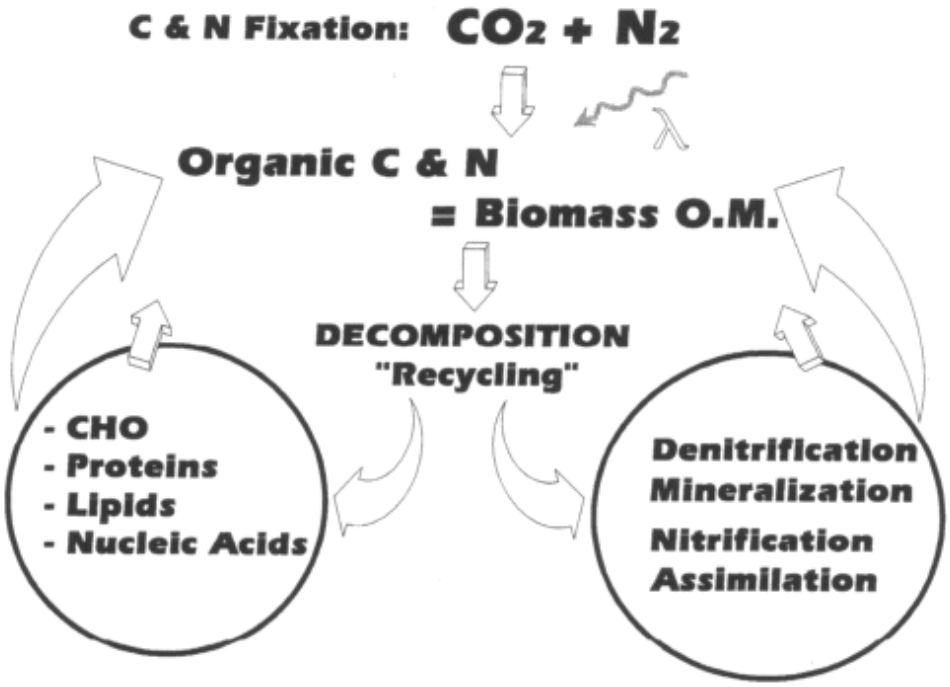

Figure 2. A Simplified Version of the Collateral Recycling or Organic Carbon and Nitrogen Forms that were Initially Fixed from Gaseous States by Plants and Decomposed to Various Organic Constitutents (Carbohydrates, Proteins, etc.) by a Wide Variety of Microbes that Utilize Diverse Mechanisms (Denitrification, Mineralization, etc.).

Table 3. Biogeochemical Groups of Soil Microbes Involved in Carbon Decomposition, and Nitrate Oxidation and Reduction in Soil.

Substrate	Examples of Decomposer Microbes	
Carbon	**Decomposers**	
Cellulose	Bacteria:	*Cellulomonas*
	Fungi:	*Trichoderma, Chaetomium*
Lignin	Basidiomycetous fungi:	*white rot type*
Pectins	Bacteria:	*Erwinia*
	Actinomycetes:	Streptom*yces*
	Fungi:	*Fusarium*
Chitin	Bacteria:	*Bacillus*
	Actinomyces:	Nocard*ia*
	Fungi:	*Beauvaria*
Protein	Bacteria:	Pseud*omonas*
	Actinomycetes:	Streptom*yces*
	Fungi:	*Aspergillus*
Lipids	Bacteria:	*Clostridium*
	Actinomycetes:	*Nocardia*
Nitrogen	**Oxidizers**	
Ammonia	Bacteria:	*Nitrosomonas*
	Actinomycetes:	*Streptomyces*
	Fungi:	*Aspergillus*
Nitrate	Bacteria:	*Nitrobacter*
Nitrogen	**Reducers**	
Nitrate	Bacteria:	*Achromobacter, Pseudomonas, Thiobacillus*

Mycorrhizosphere

The soil immediately adjacent to the root surface is known as the rhizosphere and has a significantly higher level of biological activity than bulk soils not containing roots or fresh plant or animal debris. Much of this activity is due to the abundance of various organic substrates, growth factors and nutrients that are available from sloughed-off root cells and root exudates or secretions. When roots are colonized by mycorrhizal fungi, the active absorptive and secretory surface area of the rhizosphere increases by virtue of the mycorrhizal hyphae that grow into the soil beyond the immediate zone of nutrient depletion around the roots. Numerous secondary benefits accrue to the soil's biological community as a result of the development of mycorrhizal associations and the exudation and secretion of carbon by their soil hyphae. Soil structure and organic matter turnover improves significantly through the increased biotic activity around soil hyphae (Griffiths, 1965; Oades, 1984; Schwab et al., 1984; Jakobsen and Rosendahl, 1990).

With such positive benefits associated with SOM-microbial interactions, numerous investigators have explored the possibilities of optimizing microbial processes in soil by increasing the populations of soil microbes. The two major strategies considered are 1) introduction of specially selected isolates, singly or in combination, and 2) management of crop/soil conditions to enhance the beneficial activities of the indigenous isolates. Inconsistent results in field soil inoculation tests with batch cultured isolates delivered to the soil by one of several means, are common (Baker and Cook, 1982; Rodriguez-Kabana et al., 1987). Competition between the introduced isolates and the already successfully-adapted indigenous ones often impedes the establishment of perennial populations of the inoculants in soil (Clark, 1965). Inclusion of suitable microbial substrates in the inoculation matrix can overcome the competition factors enough to support the growth and/or production of beneficial metabolites (e.g., antibiotics) or enzymes by inoculated biocontrol microbes (Lumsden et al., 1992). Such nutrient supplementation of inoculants (a practice also used with Kyusei Nature Farming products in agriculture) provides more reliable and higher

concentrations of effective microorganisms (EM). It also provides readily available sources of C, N, and P for soil microbes that are indigenously present through the root-mycorrhizal fungus hyphae-soil environment system. A conceptual model of the latter system has been presented by Wright and Millner (1992) as the mycorrhizosystem.

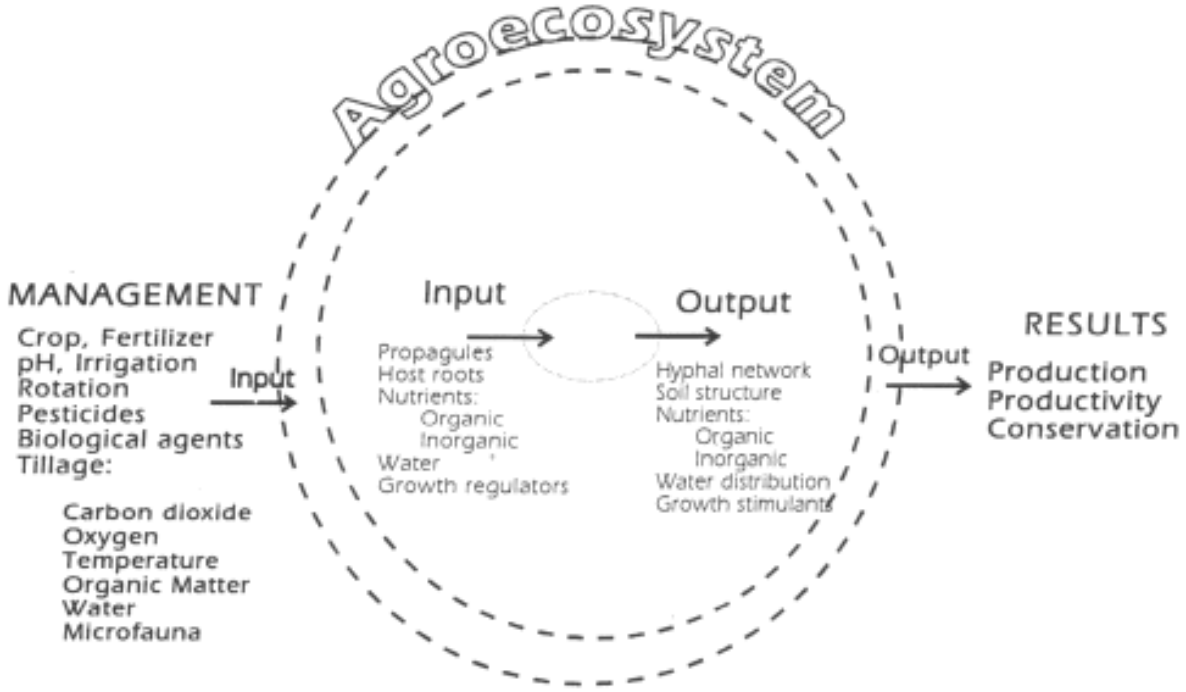

Figure 3. A Diagram Representing a Functioning Agroecosystem with Inputs of Management and Environmental Factors and Outputs Affecting Such Things as Productivity. Central to the Scheme are the Possible Impacts on Mycorrhizae that Mediate Events Which Determine the Health of Plant and SoilSystems.

Figure 3 illustrates some of the possible ways in which specific crop-soil system management practices (inputs) can be used to influence or control the desired system outputs. From such a model and from studies of biological control agents and SOM cycling, one conclusion that emerges is that single-isolate or consortium inoculants may be beneficial in specific crop production situations. Also, multiple-isolate inoculants may benefit a wider range of situations. However, it would be highly unlikely that even a multiple-isolate inoculant would be sufficiently robust to benefit all crop systems equally well. Furthermore, from our knowledge of the mycorrhizosystem and plant disease-biocontrol processes, we postulate that establishment of beneficial soil microbes in agricultural soils would require inclusion into standard cropping practices of a means to sustain the types and amounts of organic matter necessary to feed them. In all likelihood, many of the intensive production practices now prevalent would need modification (NRC, 1989) to provide for SOM maintenance and then to account for the nutrients that become available to plants through microbial mineralization of SOM.

Agricultural systems that purposely strive for balance among the various outputs reflected in the mycorrhizosystem model must also inherently achieve better balance among the array of inputs which impact so critically on soil microbial and ecological processes. The cycling, accumulation, and loss of active and inactive pools of SOM by microbes are key processes in dynamically sustainable agriculture.

Summary
Soil organic matter is as variable qualitatively and quantitatively across soils, habitats, climatic regions, and agroecosystems as are the soil microbes that utilize and synthesize them. In the process of creating sustainable agricultural systems with high quality soils, we know that SOM plays a key role, but quantitating this role remains a formidable challenge. Several recent advances in quantitative and qualitative techniques can and should be used to assess SOM and microbial interactions, and their outcomes.
Some of the central questions that agricultural scientists and policymakers are currently struggling with may be summarized as follows: How can we sustain the long-term fitness and integrity of our agricultural system while meeting the short-term goals of production, profitability, and safety? What kinds and amounts of outputs and inputs are acceptable in ecological, economic, and social terms? As soil microbiologists we might ask: What input interventions mediated by microbial activity most critically influence these system-level outputs, not just the primary productivity output? Tools to measure active pools of organic matter, carbon, and nitrogen, types and quantities of SOM, SMB, and micro- and macrofauna show promise as a means by which to measure the system-level microbial effects and interactions.

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