THE EFFECTS OF LAND MANAGEMENT, ORGANIC COMPOST ADDITION AND SOIL SERIES ON THE SOIL ECOLOGY OF COTTON (GOSSYPIUM HIRSUTUM) FIELDS IN DRYLAND PRODUCTION IN GEORGIA (USA)

by

BREANA LEE SIMMONS

(Under the Direction of David C. Coleman)

ABSTRACT

Conservation tillage involves a reduction or elimination in tillage combined with use of a cover crop and is becoming more common in areas prone to severe erosion. A common concern when transitioning to conservation tillage is the delay in nutrient mineralization associated with a change in the soil food web. The main objective of this study was to assess the ability of a one-time compost application to accelerate the accumulation of organic matter, reducing the delay in nutrient cycling by facilitating an increase in soil biota, due to increased habitat and substrate. Additionally, we sought to differentiate between the effects of tillage and soil series using a comparative study between soils from the Piedmont and the Coastal Plain. Compost was added at three rates to five fields across a chronosequence of tillage in Coffee County, Georgia. Compost application appeared to have a minimal effect on the soil ecology at any site, but results indicate that soil biota benefit from a decrease in tillage. The conventionally tilled site had the highest C/N ratio, the lowest amount of soil organic matter, and low microbial biomass compared to sites in conservation tillage. N-mineralization was highest in sites in conservation tillage for 10 and 30 years. Fungi were typically lowest in the conventionally tilled soil, probably

due to disruption of the fungal hyphae by tillage. In all soils, microbial functional groups were most heavily influenced by soil C, % soil organic matter and soil moisture, and most sites in conservation tillage were not significantly different from each other, regardless of time in no-till. This is encouraging, because it implies that sites in transition to a reduced tillage regime may not have to wait as long as expected for stabilization of the soil food web. In the comparison study between the Piedmont and the Coastal Plain, abundances of nematodes, microarthropods and microbial community composition were assessed from each site. Results indicate that soil series has a potentially greater effect on soil food webs than tillage for most biota, and decisions about land management regime should include the best available data for that particular soil type.

INDEX WORDS: Conservation tillage, organic compost, soil series, microarthropods, nematodes, microbial community composition, FAME, N-mineralization

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DEDICATION

To Mom, Dad, Andy and Steph, who always believed in me, even when I didn't.

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Chapter 1

INTRODUCTION AND LITERATURE REVIEW

Intensive agriculture in the US

Land management practices associated with intensive agriculture directly affect the ecology of the soil. Approximately 19% of the US is currently in intensive agriculture, with concentrated activity in areas that are situated on historic mollisols, such as the Midwest and the Great Plains (Amundson et al. 2003). These areas tend to be well irrigated, flat, and high in soil organic matter. However, not all intensive cultivation is confined to the Midwest. Areas with poor soil, steep slopes, and inconsistent precipitation are also used for agriculture, and in these areas there is a need for better management techniques. In the Southeast, the crops utilizing the most space are cotton and peanut. In Georgia, cotton is the principal row crop, with approximately 1.4 million acres in cultivation (J. Gaskin, pers. comm.).

The proportion of cotton (*Gossypium hirsutum* L.) fields in dryland conditions in the southeastern USA, where soil water holding capacity is critical for successful seedling emergence, has increased in recent years, and conventional tillage is still the most common practice in these areas (Nyakatawa and Reddy 2000, Nyakatawa et al. 2000). Cotton cultivation requires a mean temperature of 21-22° C and a minimum rainfall of 500mm. Cotton is also susceptible to frost, and due to the long growing season it requires, it is grown in the southern USA to prevent loss to cold weather. Dryland agriculture is practiced in semi-arid regions of the world, and is characterized by high

evaporation, marginal, and highly variable precipitation and large diurnal temperature ranges (Tivy 1990).Such conditions makes production in these areas extremely risky, and prone to nutrient and water loss. Severe weather, such as droughts or heavy rains, can devastate fields in dryland production.

Problems with intensive agriculture

There are several current concerns about intensive agriculture, especially with a crop like cotton. Soils that are utilized for intensive agriculture often require increased inputs to compensate for poor soil fertility. Increased inputs, such as fertilizers and pesticides, often leach into groundwater system. Contamination of nearby aquatic resources is a major concern for producers, especially if the contamination source is organic, such as manure or poultry litter, which may contain harmful bacteria. Even with synthetic fertilizers, increased inputs into groundwater systems result in algal blooms, decreased oxygen content, and decreased stream functioning. In cotton, management of nutrients, specifically nitrogen, is critical to crop success (Schomberg and Endale 2004).Too much or too little fertilizer can decrease yields by reducing vegetative growth and stunting reproductive growth (Mullins and Burmester 1990).

Typically, agricultural fields are tilled and the crop residues are incorporated into the soil. Tillage is considered beneficial for rapid breakdown of residues and the release of nutrients into the soil. However, there is increasing acceptance of reduced tillage practices as a method of soil conservation in agriculture, especially in areas prone to environmental disturbance (Holland 2004). Disturbance caused by tillage and the incorporation of crop residue affects the physical, chemical and biological properties of the soil ecosystem.

Effects of tillage on soil structure and function

According to Lal (2004) the global carbon budget (2500 Gt) consists of 1550 Gt of soil organic carbon and 950 Gt of soil inorganic carbon. The global carbon cycle is being modified by human activity, mostly through the burning of fossil fuels and conversion of natural lands to agriculture (Paustian et al. 2000). Intensive disturbance to the soil ecosystem reduces carbon concentrations in the soil (Dalal and Mayer 1986). Conversion to agriculture reduces the soil carbon pools by 60-75%, where labile carbon is lost through atmospheric emissions, accelerated erosion, or increased mineralization (Lal 2004). Therefore, protection of carbon within soil aggregates is important for long term C storage and accumulation (Jastrow et al. 1998, Six et al. 1998).

Tillage increases soil exposure to oxidation and facilitates the rapid breakdown of macroaggregates, which are an important source of available carbon and ensure rapid turnover in soil food webs (Tisdall and Oades 1982). Soil microorganisms, such as mycorrhizae and saprophytic fungi, are important for the formation and stabilization of soil aggregates. Root activity and the microbial communities surrounding the roots also help to stabilize aggregates (Golchin et al. 1994, Six et al. 1998, Six et al. 2004). Microaggregates also form within earthworm casts, where the soil and litter are ingested by the earthworm and reassembled in the gut as mucus encapsulated microsites, primed for microbial colonization and aggregate formation (Shipilato and Protz 1988, Edwards and Bohlen 1996). In conventionally tilled systems, fungi and mycorrhizae are redistributed though the soil matrix, along with crop roots and their associated microbial communities. This destabilizes macroaggregates and reduces the physical protection of the labile carbon within the microaggregates (Six et al. 1998).

Breakdown of these aggregates releases clay into the soil, and causes clogging of pores and the development of a crust of seal on the soil surface, dramatically reducing infiltration of water. Soils that have large numbers of stable aggregates have low bulk densities and high porosity. Water, air, roots and soil fauna move through the soils easily. Intensively tilled soils show remarkably less resiliency, the ability to reform aggregates after disturbance, than soils that have not been tilled, due to inhibition of the formation of microaggregates within macroaggregates (Six et al. 1998).

In southern GA, the coastal plains soils are sandy and do not contain enough flocculated clay for the formation of microaggregates, which are an important storage unit for protected C (Tisdall and Oades 1982). Much like tropical ecosystems, the system relies on organic matter and biota to stabilize soil carbon and increase the soil organic carbon pool (Oelbermann et al. 2004). The formation of pores and other failure zones by biological activity, like ants and earthworms, may also be more important in soils with low amounts of clay, which can create pores due to shrinking and swelling of the clays. Soil pores are important habitat for soil fauna, such as nematodes and microarthropods (Coleman 2002), the importance of which are described later in this chapter.

Soil structure plays an important role in the ability of nutrients to remain in the system. SOM enhances the natural ability of soil to hold nutrients, and can reduce losses by leaching. SOM acts as a pH buffer in acidic or basic soils, and increases water-holding capacity, which is important for sandy soils, where nutrients are prone to leaching. Protection of nutrients within aggregates is an important function of soil organic matter in agricultural systems (Six et al. 2000). Turnover of C within macroaggregates is faster

than in microaggregates, which protect labile C and N longer than macroaggregates, which tend to contain organic matter that is microbial in origin (Six et al. 2004).

Another important consequence of regular tillage on soil structure is an increase in soil erosion. In the USA, losses due to erosion in the USA were estimated at $37.6 billion (Lal 2001) and an average decrease of 18 million Mg in productivity worldwide (Lal 2000). Loss of soil C due to erosion over the last 40 years is estimated at between 30-50%, and the rate of organic matter input is also decreasing (Davidson and Ackerman 1993, Holland 2004). This type of soil loss is a major concern for land managers. When an agricultural site is affected by wind or water erosion, there is an increased risk of runoff.

Environmental damage caused by runoff is becoming more important to growers, due to increased standards for pollution of water sources by sediment, fertilizers and pesticides (Rhoton et al. 2002). Currently, the Federal government has not established regulatory limits for suspended sediment concentrations or loads. However, the Georgia Erosion and Sedimentation Act (ESCA) of 1975 (O.C.G.A. Section 12-7-1) requires permits for activities involving disturbance of terrestrial sediments and requires that buffers be maintained between the permitted activity and the waters of the state. This act was amended in 2000, with new regulations for controlling storm water runoff from construction sites (Georgia R. & Reg. Chapter 391-3-6-.16).

A TMDL (total maximum daily load) is the amount of a specific pollutant a river, stream or lake can assimilate and still meet federal water quality standards. It is also the written document developed for impaired water bodies. A TMDL accounts for all sources of pollution: point sources (discharges from pipes, wastewater treatment facilities, etc.),

non-point sources (runoff from parking lots and agricultural fields), and natural background sources. Section 303(d) of the Clean Water Act requires that regulatory agencies determine TMDLs for all water bodies that do not meet water quality standards. TMDLs are currently being written for Georgia, and will be used to regulate sources of chemical and sediment flow into rivers and streams (Keyes and Radcliffe 2002).

Sediment, synthetic and organic inputs and organic matter can all be impacted by increased runoff. Nonpoint source pollution of surface water and through accumulation of NO_3 and P from agricultural run off is a major environmental concern, as it increases eutrophication and growth of undesirable algae (Sharpley 1995). Sediment washing also impedes the natural functioning of adjacent aquatic systems by increasing turbidity and particulate organic matter.

Similarly, incorporation of residue via tillage has major consequences for soil function. In conventional tillage systems, the amount of soil organic matter (SOM) decreases (Allmaras et al. 2000). Loss of soil organic matter can result in decreased water infiltration and storage, nutrient loss through leaching, reduced pH buffering capacity and a decrease in cation exchange capacity (CEC) (Nyakatawa and Reddy 2000). SOM is also the preferred habitat of most soil organisms, and destruction or degradation of habitat can result in disruption of the soil food web and an alteration of biotic nutrient cycling. Disruption of the soil food web leads to an unstable soil ecosystem (Moore et al. 2003).

Soil organic matter (SOM) is the foundation of the soil food web and the preferred habitat of most soil biota. Turnover of organic matter is governed by microbial activity and primary plant production. Decomposition of SOM pools by soil biota determines the efficacy of nutrient cycling in soil ecosystems, which in turn affects

aboveground productivity. This process depends on the quality and quantity of substrate provided to primary consumers, but is also driven by abiotic factors, such as climate, soil structure and land management practices.

Artificial adjustments to the organic matter pools, such as incorporation of crop residues and fertilization, alters the structure and function of SOM, often result in a reduction or shift in nutrient cycling efficiency. Incorporated plant residues and root exudates provide substrate for fungal and bacterial growth and promote the formation of biological aggregates (Jastrow et al. 1998). As the basis of the food web, these types of alterations to SOM pools cascade through the trophic levels, affecting top consumers responsible for top-down control of food web consumers.

Decomposition is typically studied as a bottom up process. The quality and quantity of the substrate drives the decomposition process, resulting in the mineralization of nutrients that become available to plants, which regulates plant growth (Swift et al. 1979, Hunt et al. 1987, Vitousek and Howarth 1991). However, it may be much more complex than a simple bottom up process, because turnover of nutrients from detritus is directly affected by biotic interactions in the soil food web (Wall and Moore 1999, Coleman 2002, Moore et al. 2003). The primary consumers decompose the substrate, immobilizing nutrients. Secondary consumers feed on bacteria and fungi, mineralizing nutrients and regulating populations (Ingham et al. 1985, Setäla and Huhta 1991). These consumers are not nitrogen limited, and therefore excrete excess nitrogen. Models of soil nutrient fluxes have estimated that grazing by soil fauna constitutes 25-40% of the total N mineralization in a given system (Hunt et al. 1987, Moore et al. 2003). Feeding on mycorrhizal fungi by soil mesofauna has been shown to be both detrimental (Warnock et

al. 1982) and beneficial (Harris and Boerner 1990, Setäla 1995) to plant growth and primary production. Top predators, such a predatory nematodes, mites, and insects may exhibit top down control of consumer populations (Moore 1988, Moore et al. 2003). This entire process also regulates the accumulation of soil organic matter as well as the efficacy of nutrient cycling within the system (Beare et al. 1992).

The effects of intensive agriculture on soil biota

The activity of soil biota is largely responsible for the mineralization of nutrients from the soil, and is therefore an important component of soil function (Ingham et al. 1985, Hunt et al. 1987, Moore 1988, Beare et al. 1992). This is especially important in low input sustainable agriculture, where increased microbial diversity is expected to increase soil quality (Parr et al. 1992, Visser and Parkinson 1992). Microbial diversity is expected to increase with a reduction in tillage, as fungal species begin to dominate the system (Hendrix et al. 1986). Moore et al (2003) refers to the two pathways of nutrient cycling as the "fast" and "slow" cycles. In systems where crop residue is buried or where labile substrate is abundant, bacteria dominate, due to their ability to break down labile carbon sources more efficiently than surface saprophytic fungi (Coleman et al. 1983, Curl and Truelove 1986, Moore 1988). In these "fast" systems, the rates of decomposition and nitrogen mineralization are accelerated (Moore and Deruiter 1991, Doles et al. 2001). In systems with a high C:N ratio, like no-till agricultural systems where residue is left on the surface, saprophytic fungi dominate, slowly breaking down more resistant substrates (Hendrix et al. 1986, Moore et al. 2003).

The ability of an ecosystem to withstand disturbance may lie in the energy pathway, where bacterial dominated systems are more resilient than fungal dominated

systems (Allen-Morley and Coleman 1989, Moore and Deruiter 1991). Moore et al (2003) postulate that recovery times of each energy channel to disturbance may be different, and result in an alteration of the food web. Several studies have found effects of land management practices on soil microbial diversity and abundance (Liljeroth et al. 1990, Frostegård et al. 1993, Kirchner et al. 1993, Zelles et al. 1994, Haslam and Hopkins 1996). In a study involving the transition from conventional to alternative agriculture, Doran (1987) found that microbial populations and activities were regulated more by crop type and rotation than by soil physical properties. In a structurally unstable soil, Gonzales et al (2003) found an increase in humification in soils in no-till as compared to those in reduced tillage, indicating that microbial populations were probably influenced by increases in organic matter. In contrast, Buyer and Kaufman (Buyer and Kaufman 1997) showed no effect of agricultural treatment on the microbial community and suggested that, due to methodology, diversity measurements may remain high in conventional agriculture despite increased disturbance.

The difficulty in assessing the effects of land management practices on soil biota is that different groups of soil animals will respond to agricultural intensification in different ways. In nematodes, this variation in response to tillage is probably due to differences in functional groups and life history habits (Wardle et al. 1995). Wardle et al (2001) found that while soil biota appeared to be driven by an increase in resource quality, the results were not consistent across higher trophic levels, with different treatments favoring different nematode taxa. Several studies have shown that bacterial feeding nematodes increase in response to organic inputs (Bongers and Ferris 1999, Porazinska et al. 1999, Bullock et al. 2002) while others have shown little or no reaction

in nematode diversity and abundance in the presence of such treatments (Forge et al. 2003, Garcia-Alvarez et al. 2004). In a study by Forge et al (2003), reduced evenness among nematode taxa resulted in an apparent reduction in nematode diversity under organic mulches.

Soil microarthropods have shown an inconsistent response to soil tillage, probably due to the extreme variation in life history, trophic levels, and functional dynamics (Wardle 1995, 2002). Physical disturbance of the soil can result in mesofauna becoming crushed or trapped within soil pores. Furthermore, tillage changes the soil climate and availability of food sources. The response of the mesofauna to this type of disturbance, and the ability of soil populations to recover, largely depend on the life history habits of each group. Collembola, consisting mostly of fungal feeders, tend to be inhibited or relatively unaffected by tillage. However, there are several different types of Collembola, and the epigeic (surface dwelling) species are highly mobile and can likely reestablish populations within a disturbed area fairly quickly. However, despite these advantages, surface dwelling species have been shown to decrease in conventional tillage as compared to reduced tillage (Winter et al. 1990, Culik et al. 2002). Soil dwelling Collembola may be more significantly affected by tillage, due to their presence in the soil pores and heavier reliance on organic matter and fungi in the rhizosphere.

Soil mites (Acari) are extremely diverse, with a wide array of trophic levels and functional groups. Different taxonomic groups respond to tillage differently, and functional groups within those taxonomic groups also vary in their response to disturbance (Wardle 1995). The Mesostigmatid mites are predatory, and are generally negatively affected by tillage. The Oribatid mites, or cryptostigmatids are commonly

considered litter transformers, but are in reality a very diverse group with a variety of feeding habits, including carnivores, omnivores, fungivores and scavengers (Maraun and Scheu 2000, Schneider et al. 2004). They are relatively slow to mature, and the effects of tillage on these mites may be more pronounced due to their inability to repopulate an area within short periods of time (Hansen 2000). Astigmatid mites, taxonomically similar to oribatids, are often found in higher numbers in conventionally tilled fields, indicating the ability to recover quickly after disturbance (Behan-Pelletier 1999). Most soil dwelling astigmatid mites feed on microbes and vegetative matter, and may potentially take advantage of the surge in bacterial growth after a plowing event, especially in moist conditions (Coleman et al. 2004). Despite this variation, populations of mites and Collembola generally decrease with tillage (Wardle 1995).

Soil tillage has the most obvious impact on large organisms, such as ants, termites, and earthworms, which are considered important litter transformers and ecosystem engineers (Giller et al. 1997, Wardle 2002). Mechanical disruption of the soil leads to the destruction of termite galleries and ant mounds, as well earthworm burrows, which are important “hot spots” of soil activity (Beare et al. 1995). Earthworms are also negatively affected by tillage due to a reduction in food supply (lower quantity and quality), a change in resource location, and a decrease in environmental protection (Kladivko 2001). Tillage has also been correlated with a decrease in populations and activity of beetles and spiders, which includes important predators as well as litter transformers (Wardle 1995, Kladivko 2001).

Conservation tillage

Conservation tillage is now fairly common in areas where decreasing erosion or moisture retention is a priority (Holland 2004). Variations of conservation tillage, including no-till, reduced till and cover cropping, is currently practiced on 45 million Ha worldwide (Lal 2000). Conventional tillage practices, in which plant residues are incorporated into the soil, increase the risk of soil erosion and contribute to contamination of water sources by leaching of phosphates and pesticides. Fields that are subjected to conventional tillage also suffer from a depletion of SOM (Keeling et al. 1989).

Conservation tillage systems use cover crops on the soil surface to add residues to maintain SOM while eliminating tillage. Implementing conservation tillage practices not only reduces erosion, but also results in increased infiltration, increased soil moisture and increased SOM. Organic matter accumulation in areas of the southern Piedmont that were previously tilled is associated with enhanced fertility and increased mineralization of soil nutrients (Beare et al. 1994, Hendrix et al. 1998). Conservation of organic matter is important to the physical, chemical and biological functions of the soil. SOM stabilizes soil pH, which is essential for nutrient uptake by plants, and is the main resource for the soil biota that are responsible for mineralizing nutrients (Campbell et al. 1996). Carbon exchange capacity, water holding capacity, microbial activity, and reduction of soil compaction are all positively influenced by increased SOM. Fields suffering from severe erosion, a common problem in the southern Piedmont, can recover with conservation tillage practices (Coleman et al. 2001). These changes can minimize inputs and maximize water use efficiency in row cropping systems.

There is also evidence that fields in conservation or no-till management are better able to sequester C from the atmosphere and could provide a sink for CO_2 (Hendrix et al. 1998, Lal et al. 1998). Soils in conservation tillage, especially those that are highly degraded and in restoration, can sequester carbon at a rate of between 100 – 1000 kg C/ha in humid and cool climates and can maintain these rates for up to 50 years (Lal 2004). This ability to sequester atmospheric carbon is directly linked to the increase in biomass and a decrease in soil disturbance that results from the elimination of tillage and the use of cover crops, green manures, mulches, biosolids, and compost (Lal 2004). Soil organic carbon is removed from systems through erosion, and typically lost to the atmosphere or adjacent aquatic systems (Lal 2003). Therefore, it is critical to control soil erosion if agricultural systems are to sequester atmospheric carbon, and conservation tillage techniques, agroforestry and the diversification of cropping systems are best suited to prevent erosion and maintain soil carbon (Paustian et al. 2000, Lal 2004).

Conservation tillage techniques combined with mulching, or the addition of organic amendments, has been shown to positively affect the soil biota. Yang et al (2003) report a slight increase in bacterial diversity under mulch. Forge et al (2003) found an increase in protozoa and bacterivorous nematode abundance under biosolids or mulch as compared to a control. Mites and Collembola tend to respond positively to a reduction in tillage (Wardle 1995). Densities of Collembola have been shown to increase in the presence of manure (Andren and Lagerlof 1980) and mulch (Wardle et al. 1993, Culik et al. 2002). A preliminary study by Coleman et al (2001) from sites in Coffee County, GA showed an increase in protozoa abundance and diversity with years in conservation

tillage. This trend was seen again in nematodes and microarthropod abundance and diversity for the same soil type (Adl et al. in press).

As with any land management technique, there are potential problems with conservation tillage. A reduction in tillage often results in a change in the weed community, and therefore a vigorous weed management program must be adopted in order to control the weed growth. This usually means an increase in herbicide use, an expensive and environmentally challenging decision. The use of genetically modified crops, such as Round-up Ready ® cotton, makes widespread herbicide use an attractive choice. However, growers have begun to find creative ways to reduce herbicide use while still keeping weeds under control, such as ridge tilling, mulching of cover crops, and on smaller farms, the use of water fowl as weed-eaters.

Another concern for growers when adopting conservation tillage regimes is the need for new equipment. Mould board plows and disk harrows must be replaced with equipment such as mulching tillers, or no-till seed drills. This problem has been solved by growers who are able to modify existing equipment for tasks like strip tilling and crimping of cover crops. However, there may be a more important deterrent for growers contemplating a change in land management, such as a delay in nutrient cycling.

When SOM increases, so do the soil biota, causing a change in the nutrient cycling patterns, which in turn supports healthy soil (Phatak et al. 1999). Many of the benefits of conservation tillage rely on the build-up of organic matter and the stabilization of the soil food web. In no-till, nutrients become stratified at the soil surface and may be released more slowly than those in conventional tillage, especially when using cereal grains as cover crops (Hargrove 1986, Schomberg and Endale 2004). A delay in the

mineralization of nutrients available to the crop is a deterrent for farmers seeking to begin conservation tillage practices.

Purpose of study

In South Georgia, cotton is grown in loamy sand soil, and conservation tillage techniques can improve the soil quality; however, accumulation of SOM and increased water holding capacity does not occur immediately. The transition from conventional tillage to conservation tillage may suffer from lag due to changes in nutrient cycling in the soil. However, the use of organic inputs may provide the necessary nutrients to speed up the transition period from conventional to conservation tillage by increasing SOM and soil fauna so that nutrient cycling patterns can be changed at a faster rate.

In this study, we investigated the use of compost to accelerate the accumulation of soil organic matter, thereby decreasing the delay associated with a change in nutrient cycling in conservation tillage. Application of organic compost in the first year should have a positive effect on nutrient availability and moisture retention, while building a solid layer of SOM that will serve as substrate for microbes and habitat for soil biota. By increasing the quality and quantity of substrate for soil biota, populations should increase and diversify, mineralizing nutrients at an accelerated pace. A diverse soil food web is beneficial in no-till systems, where monocultures and low diversity can result in outbreaks of pest species or disease.

Because of the nature of soil, an in depth study of the soil food web will allow us to gain a better understanding of the interactions between soil biota, soil characteristics and land management. Since cropping history and management practices affect nutrient management strategies, knowledge of the complex interactions within the soil food web

is important for economic and environmentally effective management practices. In this study we used Whole Soil FAME techniques to identify the microbial community at each site. We also quantified soil mesofauna and identified major functional groups within the soil agroecosystem. This type of information, coupled with data on physical and chemical properties of each site, will give us baseline ecosystem data as well as the ability to link soil food web structure and land management practices.

All factors being equal, mechanic disruption of the soil food web alters the rate of decomposition and nutrient cycling. However, no one soil performs the same way as another, so it is important to take a critical look at the soil as part of a broader system, such as the Coastal Plain and Piedmont regions of Georgia. This study will compare fields in these two dissimilar soil habitats: Horseshoe Bend, a research site on the Piedmont, and Coffee County, where five fields on the Coastal Plain are in different phases of conservation tillage.

Soils respond differently to abiotic and biotic factors based on climate, geographic range, and parent material. In the Piedmont, soil is high in clay, subject to winter frosts and consists mainly of $Fe(OH)_2^+$. On the Coastal Plain, soils are sandy, the temperatures are milder, and the most common mineral in the soil is a reduced iron oxide ($Fe(OH)_3^+$). These physical and chemical characteristics will influence the stability of the soil when disturbed. Because of these constraints on SOM pools and biotic interaction, a management technique that works for one type of soil may not work for another. Conservation tillage techniques have been shown to increase the productivity of agricultural soils, however, the behavior of functionally dissimilar soils under the same land management regime has not been fully investigated.

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CHAPTER 2

THE EFFECTS OF ORGANIC COMPOST ADDITION ON SOIL ECOLOGY IN DRYLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) FIELDS UNDER DIFFERENT TILLAGE REGIMES ON THE COASTAL PLAIN, GEORGIA (USA)[1]

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Abstract

The arable land in Georgia is highly susceptible to erosion, and may benefit from adaptation to conservation tillage, a practice that combines the reduction or elimination of tillage with a winter cover crop. The benefits of this type of system include decreased soil erosion, increased infiltration, increased soil moisture and increased soil organic matter. A common deterrent to growers wishing to transition from conventional tillage practices is a lag time in the response of soil biota to the reduction or elimination of tillage. In this study we sought to examine the ability of a one-time application of compost to accelerate the accumulation of organic matter and "jump start" the response of soil biota in cotton fields that are in different stages of conservation tillage. Organic compost was added at three rates to five sites in Coffee County, across a chronosequence of conservation tillage and soils were analyzed for differences in nutrient status, organic matter and soil biota. While effects of this compost application in this study were negligible, results indicate that soil biota benefit from a decrease in tillage. The conventionally tilled site had the highest C/N ratio, the lowest amount of soil organic matter, and low microbial biomass compared to sites in conservation tillage. Soil nutrient status and microbial C at the site in transition from conventional to conservation tillage were similar to sites already established in conservation tillage. This is encouraging, because it implies that sites in transition to a reduced tillage regime may not have to wait as long as expected for stabilization of the soil food web.

Keywords Conservation tillage, organic compost, microbial biomass, microarthropods, nematodes, Georgia Coastal Plain

Introduction

The proportion of cotton (*Gossypium hirsutum* L.) fields in dryland conditions in the southeastern USA, where soil water holding capacity is critical for successful seedling emergence, has increased in recent years. Conventional tillage is still the most common practice in these areas (Nyakatawa and Reddy 2000, Nyakatawa et al. 2000), which are characterized by high evaporation, marginal, and highly variable, precipitation and large diurnal temperature ranges. Such conditions make production in these areas extremely risky, and prone to nutrient and water loss. Severe weather, such as droughts or heavy rains, can devastate fields in dryland production. Historically, tillage practices in these areas included deep plowing to encourage infiltration; however, this only served to make the soil more susceptible to wind and water erosion (Tivy 1990).

Losses due to erosion in the USA were estimated at $37.6 billion and an average decrease of 18 million Mg in productivity worldwide (Lal 2000, 2001). Loss of soil C due to erosion over the last 40 years is between 30-50%, and the rate of organic matter input is also decreasing (Davidson and Ackerman 1993, Holland 2004). The arable land in South Georgia is highly susceptible to erosion. Water holding capacity and soil organic matter (SOM) in these sandy soils is poor, and growers are forced to increase inputs to maintain their crops. These inputs include increased pesticide use, increased irrigation, increased fertilization and increased use of expensive machinery.

Conventional tillage practices, in which plant residues are incorporated into the soil, increase the risk of soil erosion and contribute to contamination of water sources by leaching of fertilizers and pesticides. Surplus nutrients in the soil are subject to build up and run off into surface waters. A healthy soil microbial population is important in the

management of soil nutrient availability, and conservation tillage techniques increase microbial biomass (Hendrix et al. 1986, Adl et al. in press). Tillage results in rapid nutrient breakdown through decomposition of buried litter, and may promote a bacteria-dominated pathway (Hendrix et al. 1986, Beare et al. 1992, Kisselle et al. 2001).

Fields that are subjected to conventional tillage also suffer from a depletion of SOM (Keeling et al. 1989). SOM stabilizes soil pH, which is essential for nutrient uptake by plants (Campbell et al. 1996). Loss of SOM can result in decreased water holding capacity, nutrient loss through leaching, reduced PH buffering capacity and a decrease in cation exchange capacity (CEC). SOM is also the preferred habitat of most soil organisms, and destruction or degradation of habitat can result in disruption of the soil food web and an alteration of biotic nutrient cycling (Linden et al. 1994). Mega and meso fauna are more sensitive to tillage than microbes due to the physical perturbations of the soil (Wardle et al. 1999).

Conservation tillage is becoming more common in areas where decreasing erosion or moisture retention is a priority (Holland 2004). Variations of conservation tillage, including no-till, reduced till and cover cropping, are currently practiced on 45 million Ha worldwide (Lal 2003). Conservation tillage systems use cover crops on the soil surface to add residues to maintain SOM while eliminating tillage. Benefits of this type of system include decreased erosion, increased infiltration, increased soil moisture and increased soil organic matter. Fields suffering from severe erosion, a common problem in the southern Piedmont, can recover with conservation tillage practices (Coleman et al. 2001).

In previous studies, no-till practices were found to increase soil compaction and decrease soil temperature, which lead to poor seedling emergence, root penetration problems, less vigorous seedlings and poor yields (Stevens et al. 1992). However, conservation tillage is a blending of techniques designed to build SOM using cover crops and reduction of soil crusting, and has been shown to improve cotton germination, emergence and yield by increasing soil moisture (Nyakatawa and Reddy 2000). Also, a combination of conservation tillage, cover cropping, and application of poultry litter rapidly increased SOM by reducing biological oxidation of residues and increasing contributions of soil C (Nyakatawa et al. 2001).

Carbon exchange capacity, water holding capacity, microbial activity, and reduction of soil compaction are all positively influenced by increased SOM. These changes can minimize inputs and maximize water use efficiency in row cropping systems. Soil organic matter is also the foundation of the soil food web and the preferred habitat of most soil biota. Interactions within the detrital food web are important for stabilization of the soil ecosystem (de Ruiter et al. 1994) and grazing on microbial biomass is important for nutrient mineralization (Ingham et al. 1985). Decomposer organisms, such as Collembola, are found in greater numbers with conservation tillage (Culik et al. 2002). Nematode density and diversity tend to be low in conventional tillage (Yeates and Hughes 1990). Because of their sensitivity to disturbance, nematodes have been suggested as bioindicators of conservation (Yeates and Bongers 1999).

In South Georgia, cotton is grown in loamy sand soil, and conservation tillage techniques can improve the soil quality. However, accumulation of SOM and increased water holding capacity does not occur immediately. The transition from conventional

tillage to conservation tillage may suffer from lag due to changes in nutrient cycling in the soil. When SOM increases, so do the soil biota, causing a change in the nutrient cycling patterns while the soil fauna stabilize, which in turn supports healthy soil (Phatak et al. 1999). This time-lag in results is a deterrent for farmers seeking to begin conservation tillage practices. However, the use of organic inputs may provide the necessary nutrients to speed up the transition period from conventional to conservation tillage by increasing SOM and soil fauna so that nutrient cycling patterns can be changed at a faster rate.

In this study we sought to examine the ability of a one-time application of compost to accelerate the accumulation of organic matter in cotton fields that are in different stages of conservation tillage. We also investigated the effects of compost addition and long term conservation tillage on 1) soil microbial C, 2) nematode abundance and diversity, and 3) microarthropod abundance and diversity. It was our hypothesis that compost addition would have the greatest impact on a field in transition to conservation tillage. Furthermore we hypothesized that the impact of compost addition would decrease with length of time in conservation tillage, as the soil food web would already be stabilized in these systems.

Materials and Methods

Collection sites

Soil was collected from five cotton fields near Douglas in Coffee County, Georgia (USA) (31° 32’N, 82° 52’W). One site was in conventional tillage. One site reserved a small portion of the field for transition from conventional tillage to conservation tillage. Three other sites had been in conservation tillage for several years.

All fields are labeled by the number of years spent in conservation tillage at the beginning of this study: 0,1,5,10, and 30. The soils series were Fuquay (loamy, kaolinitic, thermic Arenic Plinthic Kandiudults), Pelham (loamy, siliceous, subactive, thermic Arenic Paleaquults), Cowarts/Carnegie (fine-loamy, kaolinitic, thermic Typic Kanhapludults/ fine, kaolinitic, thermic Plinthic Kandiudults), Pelham, and Tifton (fine-loamy, kaolinitic, thermic Plinthic Kandiudults), respectively (see Appendix A). Site 5, in the Cowarts/Carnegie series, is approximately 55% Carnegie and 30% Cowarts, and is so heavily mixed that separate mapping was not possible (OSD, USDA-NRCS). All fields had been continuously cropped for at least 30 years, and were planted in cotton or peanut for the duration of this study. The fields in conservation tillage use a cover crop of rye in the winter to add organic matter. Herbicides and fertilizers are used at the beginning of each crop rotation. Lime is added approximately every other year or as needed.

Experimental design

Twelve plots (2x3 m) were set up at each site, for a total of 60 experimental plots. Each plot was at least 5 m from its nearest neighbor plot. Plots were set up randomly but oriented perpendicular to row direction so that each pass of the equipment impacted the same number and type of plots. Four replicates of two compost treatments (10 and 20 tons/ha) and one control (0 tons/ha) were randomly assigned to the plots.

Organic compost was donated by GroMor Organics and consisted of high quality yard waste from Moultrie, GA. The compost was applied by hand to each plot on January 27, 2003 except in the transitional field (site 1) where conditions were too wet to disturb the soil structure. Application of compost to the plots in site 1 took place on March 3, 2003, after the soil had drained.

Sampling

Sampling occurred four times over two years (Spring 2003, Fall 2003, Spring 2004, Fall 2004), at the end of each growing season, before the crop was mowed (sites 1, 5, 10, 30) or incorporated (site 0). All samples were taken within the 1x2 center of each plot to avoid edge effects. After year 2, the grower at site 1, who experienced flooding in the area devoted to conservation tillage, incorporated the winter cover crop. This, combined with perceived minimal effect of the compost addition, contributed to the termination of the experiment before the final year. Additional microarthropod samples were taken in May 2005, one hour before the site was tilled.

Samples were taken for soil C/N from the upper 5 cm of soil using a soil probe (dia=2 cm). Samples were sealed in plastic bags and placed in a cooler for transport. Steel rings (dia=5 cm) were driven into the upper 5 cm of soil to obtain measurements of bulk density. In October 2003, May 2004 and October 2004, soil from the upper 5 cm was collected for microbial biomass C and total organic carbon (TOC) using a soil probe (dia=2 cm). Nematodes were sampled using a soil probe (dia=2 cm) from the upper 5 cm of soil, sealed in plastic bags and placed in a cooler for transport. Microarthropods were sampled from the upper 5 cm of soil using steel rings (dia 5 cm) in a specialized beveled metal corer. Samples were wrapped in aluminum foil, placed in plastic bags and stored in a cooler for transport to the lab.

Laboratory procedures

Total carbon and nitrogen were determined on soil that was air-dried, ground, and weighed into tin capsules on a Carlo Erba analyzer in the UGA Institute of Ecology Analytical Laboratory. Soil moisture values were obtained by drying soil sub samples in

an oven at 105°C for 48 hours. However, soil moisture was not used to characterize sites, because sampling was done over a 5 hour period, and soils sampled first would be naturally moister than those sampled last, rendering the data non-comparable. Despite this, moisture values were necessary for use in analyses involving the soil food web, as they characterize the conditions of the site at the time of sampling, and are therefore an important factor acting upon soil biota. An estimate of soil organic matter (SOM) was obtained by ashing soil at 450°C for 4h in a muffle furnace.

Mineralized nitrogen was determined from soils incubated over 8 weeks at 24°C. Sub samples were pressurized to 0.1 bar to calculate field capacity. One hundred gram samples were weighed, brought to field capacity, sealed in Ziploc® bags and placed in sealed 10 gallon aquariums in an incubator. Temperature and moisture were maintained within the aquariums according to Kruse et al. (2004). At weeks 0, 1, 2, 4, 6 and 8, a subsample of 5 g was removed from the bags, mixed with 30ml (1M) KCl, shaken at 142 rpm for 1 hour and filtered through #42 Whatman filter papers. The liquid samples were analyzed by the Institute of Ecology Analytical Laboratory for available nitrogen. After week 8 the samples became saturated and the experiment was discontinued.

Microbial biomass was estimated using the chloroform fumigation technique (Vance et al 1987). Samples were prepared by hand, by crumbling the wet soil and removing obvious debris. From each treatment in each field site, a subsample of 10 g was places in a beaker for fumigation (60 fumigated samples). Another subsample of 10 g was placed in an Erlenmeyer flask for extraction (60 non-fumigated samples). Samples were fumigated with chloroform according to Vance et al (1987) for 48 hours and aerated under vacuum conditions five times, or until no chloroform was detected. All samples

were extracted using 0.5M K_2SO_4, shaken for one hour and filtered through Whatman 42 ashless filter papers in plastic funnels. Extracts were analyzed using a Shimadzu 500 Total Organic Carbon analyzer at the UGA Institute of Ecology Analytical Laboratory. Microbial biomass was estimated as the difference between fumigated and non-fumigated samples using a constant (k_c) of 0.33 (Cabrera and Beare 1993, Adl et al in press). Total soluble carbon was determined using unfumigated samples only.

Nematodes were extracted using the Baermann funnel technique (Baermann 1917). A 5 g subsample of wet soil was wrapped in a Kimwipe, placed on a metal screen in water-filled, close-ended funnels. Samples were left on the funnels for 48 h. Approximately 7 ml of water from the funnel was collected into 15 ml centrifuge tubes and mixed with 7 ml of 5% formalin for preservation. Nematodes were counted under an inverted scope and categorized into feeding groups by morphological characters (Yeates et al 1993, D.H. Wall pers comm). Nematodes in samples from Spring 2003 were counted but not categorized into trophic levels because the samples were compromised before identification could take place.

Microarthropods were heat extracted over five days using modified Tullgren type funnels (Blair and Crossley 1991). Animals were collected in 70% ethanol and identified to order, suborder, or family under a dissecting microscope. Samples were prepared for permanent storage by transferring animals to 95% ethanol after identification.

Statistical analysis

Data were analyzed using a repeated measures mixed model in SAS (SAS Institute 1989). To fit assumptions of normality, microarthropod and nematode data were log transformed before analysis. Least square means were analyzed using the pdiff option

in the MIXED procedure to separate means using least significant difference. Data were also analyzed using a general linear model with slicing to elucidate within-treatment interactions. A Student-Newman-Keuls test was used to determine significance between sites and treatments at $p<0.05$. A repeated measures ANOVA was performed on the data where appropriate to determine significant interactions on time on the experiment. Analysis of biotic diversity was performed on non-transformed data using PC-ORD (McCune and Mefford 1999) and SAS (SAS Institute 1989).

Results

Soil characteristics

Bulk density at each site did not differ significantly, and averaged approximately 1.6 g/ cm^3 at all five sites, which is typical for these soils. Soil C:N ratio was significantly different between the spring and fall sampling dates (Fig 2.1). Differences in percent C, percent N and C:N ratio between each site were variable (Table 2.1). In spring 2003, percent C and C:N ratio were significantly higher in the conventionally tilled field (site 0) than in the other sites. There were no significant differences in percent N between the fields. In Fall 2003, percent C was significantly higher at site 30 as compared to the other fields. C:N ratio was significantly higher in the conventionally tilled field (site 0), while percent C was significantly higher at site 30. Percent N was variable between fields. In spring 2004, %C and %N were both significantly higher at site 0 compared to other sites. However, C:N ratio between fields varied with site 5 significantly lower than sites 0 and 2. In Fall 2004, %C and %N were significantly lower at site 5 than at other sites, while C:N ratio was significantly higher in the conventionally tilled site (site 0) compared to the other sites. The only significant difference in percent C, percent N or C:N ratio between

treatments at any site in any year was a difference in percent C at the conventionally tilled site (site 0), between the control and the compost treatment ($p = 0.019$, $p = 0.014$) The compost treatments did not differ significantly from one another at that site ($p = 0.8372$).

Overall, %SOM was variable and changed significantly over time (Table 2.1). In spring 2003, %SOM was variable across sites, with site 30 having the highest %SOM and site 1 having the lowest (Fig 2.2). In fall 2003, there were minimal differences between sites, although site 30 had the highest amount of SOM while site 5 had the lowest and site 0 experienced an increase (Fig 2.2). In spring 2004, site 30 had significantly higher %SOM than other sites, while site 5 had the lowest %SOM (Fig 2.2) compared to all sites except site 1. In fall 2004, %SOM increased at each site, although site 5 remained significantly diminished in SOM compared to the other sites except site 1 (Fig 2.2). Within sites, there were significant differences between controls and compost treatments at sites 5 ($p = 0.04$) and 10 ($p = 0.02$) in spring 2003, and between the control and highest compost treatment at site 0 in spring 2004 ($p = 0.006$).

Soil biota

Microbial biomass C decreased significantly at all sites except site 5 between fall 2003 and spring 2004 (Fig 2.3). In fall 2003, microbial biomass carbon was significantly higher at sites 1 and 30 compared to other sites, and lowest at site 5 (Table 2.2). In spring 2004, microbial biomass C was lower than in the preceding season, and was significantly higher at sites 10 and 30 compared to other sites, and was lowest in the conventionally tilled field (site 0) (Table 2.2). There was a significant difference between the control and

the compost treatments at site 30 in fall 2003 ($p = 0.007$, $p = 0.001$), but there were no other apparent effects of compost addition between other sites or years (Table 2.2).

In general, nitrate (NO_3^-) mineralized by the soil microbial biomass increased significantly over time ($F_{5,20} = 29.21$, $p<0.0001$) while the production of ammonium (NH_4^+) increased significantly during week six only ($F_{5,20} = 270.30$, $p<0.0001$). For this reason, values for NH_4^+ were not added to values for NO_3^- for statistical analysis of net N-mineralization. The amount of NO_3^- and NH_4^+ were typically highest in sites 30 and 10 (Fig 2.4). Those sites also had significantly higher amounts of NO_3^- than other sites for all dates after week 1 (Table 2.3). Site 5 never experienced any significant increases or decreases in nitrate mineralization, and after 8 weeks never regained the amount of nitrate present at time 0 (Fig 2.4). Nitrate mineralization in soils from site 1 initially declined but began to increase after week 2 (Fig 2.4). Despite this general trend, there were no significant differences between dates at site 1 (Table 2.3). Nitrate mineralization significantly increased at site 0 in the first week of incubation and maintained that general trend (Fig 2.4), although this was not significant (Table 2.3). For all sites, differences in N-mineralization between compost treatments were insignificant or inconsistent with application rates (see Appendix B).

Abundance of microarthropods was extremely variable within all sites and between all sampling dates (Table 2.4). There was no discernable effect of compost at any site on any sampling date, except at site 30 in spring 2003, between control and 10 and 20 tons ha^{-1} compost treatments ($p = 0.001$, $p = 0.003$). In general, microarthropods were most numerous in the spring 2003 (Fig 2.6), and the number of microarthropods collected on that date was significantly highest at sites 30, 10 and 1. The conventionally

tilled site (site 0) usually had the lowest number of microarthropods, although in fall 2004 none of the sites were significantly different at $p = 0.05$. Site 5 exhibited low abundance and low diversity during the first two sampling periods (Fig 2.6).

Diversity (1-D, Simpson's diversity index) of microarthropods was generally highest in the sites in conservation tillage (Table 2.5). There were no significant differences in diversity of microarthropods between treatments within sites, nor were there significant differences between sites in conservation tillage for most dates (Table 2.5). Groups of arthropods included: Collembola, Oribatids, Astigmatina, Mesostigmata, Prostigmata, Coleopterans (adults and larvae), Diplurans, Formicidae, Dipterans, Homopterans, Hemipterans, Psocopterans and Arachnids. All sites averaged at least one individual from one group for all sampling dates, although group richness (S) in spring 2004 was very low (Table 2.5).

Nematode abundances were fairly low but relatively stable at all sites throughout the study (Table 2.6). Numbers of nematodes recovered in spring 2004 were significantly lower than on other sampling dates except at site 1 (Fig 2.7). In spring 2003 there were significantly more nematodes in the highest compost treatment compared to the control at 0 ($p = 0.02$); otherwise, there were no consistent differences between treatments at any of the sites on any sampling date (Table 2.6). In general, sites 5 and 0 had the fewest nematodes per gram of soil except in fall 2004, when site 0 had the highest abundance of nematodes compared to other fields (Fig 2.7). In spring 2004, there were no significant differences between any of the sites (Table 2.6).

Nematodes were separated into 5 feeding guilds to analyze functional diversity: bacterial feeders, fungal feeders, predators, omnivores and plant feeders. Nematode

diversity was highly skewed, as bacterial and fungal feeders made up the bulk of the samples, regardless of site, treatment or sampling date (Fig 2.8). Feeding guild diversity was not significantly different within or between sites on any sampling date (Table 2.7). However, in spring 2004, site 0 and 1 were significantly different from each other ($p = 0.02$) but not from any other sites.

Discussion

The rates of compost application were chosen to reflect an upper and lower limit, based on the amount of compost required to significantly raise % soil organic matter in these fields. At the rate of 10tons/ha, the compost should have increased SOM by 1%. At the rate of 20tons/ha, SOM should have increased by 2% in all fields. The compost was not visible on the surface of the soil in Spring 2003, five months after it was applied. This could mean that the compost washed away, was rapidly transformed by the biota or was leached through the soil due to heavy rain. Precipitation was high during the winter and early spring of 2003, but decreased in frequency and intensity over the next two sampling periods. If growers wish to apply compost to fields that are very low in organic matter or highly sandy, it may be ineffectual except at very high rates of compost or at times of moderate precipitation. Organic amendments such as mulch (Wardle et al. 1993, Culik et al. 2002, Yang et al. 2003), manure (Andren and Lagerlof 1980) and bio-solids (Forge et al. 2003) have previously been shown to positively affect most soil biota on sandy loams. However, none of these experiments was conducted on fields in intensive agriculture. Therefore, it is possible that when a sandy soil is used to support rotated seasonal crops, it is not well suited to accepting loose organic amendments.

It was not surprising that percent N was not consistently different between fields (Table 2.1). Each site was fertilized at the beginning of each crop rotation. Therefore, only the amount of carbon was expected to differ between sites. The conventionally tilled field experienced a significant difference in percent C between the compost treatments and the tillage treatments (Table 2.1). This difference was not extended to the C:N ratio in that same field for that same sample date, probably due to heavy fertilization. Percent carbon, nitrogen and C:N ratio experienced significant seasonal flux, which supports findings by Adl et al (in press) for the same fields. At this time it is not known if broiler litter was added to site 5 and 10, as it has been in the past. Both sites are managed in conjunction with broiler houses, and using broiler litter to add organic matter is a fairly common practice in Coffee County (J. Gaskin pers. comm.). It will be useful to employ these percentages to create a "rule of thumb" for these particular soils, as the current 58% total carbon SOM was developed in Midwestern soils (M. Cabrera pers. comm.) and may help explain the large variation in the data.

It was expected that %SOM would be highest in the spring of 2003, because the compost addition was supposed to increase the amount of SOM in the plots. However, it does not appear that there were significant differences between treatments during that sampling period, which indicates that perhaps the compost didn't increase SOM as much as expected, but still had a small effect four months after application. SOM decreased at site 0 (Table 2.1), which was expected after spring tillage, but the sites hadn't been tilled yet, so it's possible that the organic matter was more mobile at this site than at the others, due to minimal residue on the surface. In Spring 2004, site 5 decreased significantly from the previous sampling date (Table 2.1), however, 8 fewer samples were collected from

that site during that period, due to a sampling error. Therefore, the difference may be a manifestation of fewer samples and lower statistical power, but the trend continued the next sampling period, so perhaps 4 samples were enough to elucidate changes in the data at the site.

Microbial biomass carbon was extremely variable (means: 45 ugC g $soil^{-1}$ to 246 ugC g $soil^{-1}$) and was higher than previously reported for these fields (Adl et al. in press). We expected an increase in microbial C in the spring, as microbial populations experience seasonal fluxes due to increased soil organic carbon, and breakdown of the winter residue that stimulates fungal growth. However, total organic carbon attributed to the microbial biomass decreased in the spring of 2004. This is likely related to low soil moisture. Coffee County received minimal rainfall from February 2004 to June 2004. TOC data is missing for Spring 2003 and Fall 2004. No samples were taken for TOC in the spring of 2003. If the compost had an effect on the soil microbial community, that effect should have been evident 9mo after application, in Fall 2003. There was no difference in carbon in Fall 2003 (Fig 2.3); therefore we can assume that any added C taken up from the compost had been negligible or so low as to be rapidly depleted. TOC data is also missing from Fall 2004, due to contamination of the samples. However, we have already determined that there were no differences between treatments at any of the sites after 9mo and 16mo; therefore we can infer that we would not have seen a significant difference in microbial carbon between treatments after 21mo.

Nitrate mineralization increased over time as expected (Fig 2.4). Soils from sites that had been in conservation tillage longest had the highest rates of mineralized nitrogen, most likely due to a more stable food web (Moore et al. 2003). The sieving of the soil

would not have removed protozoa from the samples, so there may have been increased grazing in those samples (Ingham et al. 1985). The environment in the incubator would have allowed protozoa to remain active throughout the study without encysting due to moisture loss (Coleman et al. 2004). Nematodes are also important grazers of microbes (Hunt et al. 1987), but the soils were in cold storage (approximately 4°C) for several weeks before the study began, and it is unlikely that nematodes would have survived both the sieving and the cold storage. Interestingly, both site 0 and site 5 experienced decreases in N-mineralization during the first week of incubation (Table 2.3). These soils are not in similar soil series or management regimes and therefore were not expected to perform in the same way. After an initial decline, site 5 had the lowest amount of mineralized NO_3^- compared to all the other sites (Table 2.3). This corroborates the trend seen in the low rates of microbial carbon (Fig 2.3), and low species richness of microbial FAMEs (Simmons 2005) at site 5. Sites 0 and 1 showed similar capabilities for N-mineralization despite being of different soil series (Table 2.3).

The transition from conventional to no-tillage agriculture has been shown to suffer from a lag in nutrient cycling as the soil microbial community equilibrates (Phatak et al. 1999), therefore the similarity in these two soils was not unexpected. It is encouraging, however, that site 1 mineralized significantly more nitrogen on most dates than site 0 (Table 2.3) and may have been able to mineralized nitrogen in amounts comparable to sites 10 and 30 had it not experienced an initial decline (Fig 2.4). In a study by Kruse et al. (2004), soils amended with cotton leaves also experienced an initial decline in N-mineralization, but this decline was not significant. If cotton residue has a negative effect on the ability of microbes to mineralize nitrogen, site 0 would have

experienced the sharpest decline due to the seasonal incorporation of cotton leaves. However, site 0 maintained a positive trend in N-mineralization (Table 2.3), therefore the presence of recalcitrant cotton residue cannot be responsible for the decline in N-mineralization at site 1.

Soil for the incubation study was not removed from the sites until 18 mo after application. The lack of a consistent, discernable effect of compost application on N-mineralization (Appendix B) at each site supports the indication that the compost was either washed away or quickly turned over, which did not allow it to have a long term effect on the soil biota. The significant pulse of NH_4 during week 6 in all samples may be an effect of encysted or resistant ciliate protozoa that emerge when conditions are favorable (Foissner 1987, Wardle et al. 1998). However, a large increase in protozoan grazing would have also been shown in nitrate mineralization (Fig 2.4), so it's unlikely that dynamics within the food web were solely responsible for the increase in NH_4. Perhaps a major turnover in microbial biomass occurs at six weeks, but again this should have been apparent in the mineralization of nitrate. The experiment itself was terminated when the samples became saturated. There is no explanation for the saturation of the samples, which were sealed in plastic bags and not visibly compromised. If the experiment had been terminated at week 4, NH_4 mineralized from the soils would have more closely resembled patterns in the mineralization of nitrate, although site 5 had higher amounts of NH_4 compared to NO_3 during week 2 (Fig 2.5).

The abundance and diversity of microarthropods was also highly variable over the course of this study (Tables 2.4, 2.5). Previous research reports high numbers of Collembola (500-7600 m^{-2}) present and up to 80,000 mites per m^2 at each site, with

oribatids accounting for 40-50,000 individuals per m^2 of those sampled (Adl et al. in press). Those results were not replicated in this study (Table 2.4). With the exception of two sampling dates (Fig 2.6), abundance of microarthropods at most sites was extremely low and patchy. One reason for this patchiness could be due to sampling error. Each of the five fields was sampled on the same day, and a large number of samples for various tests were taken within each field. Diurnal patterns of temperature and moisture cause microarthropods to move up or down through the soil profile during 24 hours. Fields were sampled in the same order each date, and those sampled at dawn would have naturally been cooler and wetter than those sampled last, closer to noon, when soil had dried down and become warm. The layer of soil most affected by these changes would be the top 5 cm; the same depth as the steel corer used to sample microarthropods. This is why extra samples were taken in the spring of 2005. All fields were sampled within 2 hours to avoid extreme heating and drying of the soil. However, total abundance of microarthropods in Spring 2005 was not significantly different from the previous fall, and except for site 5, was generally lower than in Spring 2003, when the study began (Fig 2.6). However, since microarthropods are irregularly distributed and not uniformly affected by disturbance, so patchiness and variation in the data are to be expected (Wardle 1995, Coleman et al. 2004).

Despite potential sampling error, some general trends did appear in the data, specifically, a non-linear response of the biota to the cessation of tillage. In the first year of sampling, site 1 experienced a higher abundance of microarthropods than sites 0 and 5 (Fig 2.6). These data mimic trends in % mol fraction from FAME analysis done on the same fields (Simmons 2005). It's possible that after 100 years of tillage, residue left on

the surface in year one resulted in an increase in available resources and an increase in microarthropod abundance. This would lead to higher numbers of r-selected groups, such as Collembola, that are highly mobile and can quickly exploit an increase in available resources, and Mesostigmata, a mostly predaceous group of mites. However, while site 1 did have more Collembola and Mesostigmata than sites 0 and 5, it also had more Oribatids, typically a k-selected group that has a longer life span (Hansen 2000). Before it was converted to conservation tillage, previous research showed fewer Oribatids at site 1 compared to site 5 (Adl et al. in press). It is probable that the Oribatids were already in the field but not in high numbers, and the increase is simply a manifestation of a periodic life cycle. The treatment plots were over 50m from the nearest forest or shrub edge, making it unlikely that the Oribatids were able to migrate in from nearby areas to exploit the crop residue, nor is it reasonable to assume that they were able to increase in population size in order to utilize the increased resource (Hansen 2000).

Astigmatina were expected to be in higher numbers at site 0, as they are frequently found in greater abundances in conventionally tilled soils, as they are often found in high numbers after harvest or in stored grains and laboratory cultures, indicating their ability to exploit newly available resources quickly (Behan-Pelletier 1999, Coleman et al. 2004). Because of the phoretic dispersal of immature stages, Astigmatina also tend to cluster in areas with high numbers of other animals, such as macroarthropods (K. Lamoncha, pers. comm.). However, with the exception of a single sample containing 96 individuals (site 0; Spring 2005), they were not found in significant numbers at any site. Previous research has shown great numbers of these mites at these sites in the past (Adl et al. in press), therefore it's possible that sampling later in the day (site 0 was typically

sampled fourth) prevented the collection of these mites. The soil at site 0, part of the Fuquay series, is dark in color and becomes fairly hot during the day. Without any residue on the surface, this would cause microarthropods to move down through the soil profile, perhaps at a faster rate than at other sites, where the soil is lighter in color or covered in residue.

In Spring 2005, when all fields were sampled quickly in the early morning, numbers of Oribatids and Astigmatina were higher at site 0 than had been collected in the previous two years. However, this did not hold true for other sites, such as site 1, which had fewer microarthropods in Spring 2005 compared to other years. During that collection, the grower was actively tilling the rest of the field due to concerns about flooding (R. Smith, pers. comm.), and residue from the winter cover crop was not heavy. This could have a significant impact on the soil fauna, and numbers were very low at site 1 on that sampling date (Fig 4). However, the soil at site 1 is in the Pelham series, and is usually closely aligned with site 10, in the same series and, despite higher group richness at site 10, there were no significant differences in abundance or diversity of microarthropods between those sites during spring 2005 (Tables 2.4, 2.5). Therefore, the low abundance of microarthropods at site 1 that spring may have been an effect of soil type rather than management regime.

The site that appeared to benefit greatly from early morning sampling was site 5, a field located in the Cowarts/Carnegie soil complex. These soils are prone to severe erosion, rill formation, and are dry and full of rocks and small pebbles (Appendix A). Site 5 had the highest overall microarthropod abundance in spring 2005, although species richness and diversity were greater in fall 2004. Soils in this series are characterized by

very low organic matter and are not likely to support high microarthropod diversity. In spring 2002, peanut was planted instead of cotton, and this could have affected the structure of the soil. Peanuts are required to be pulled from the soil and this moderately disrupts surface organic matter. Similarly, this type of crop rotation could have also contributed to the lower overall abundance of soil microarthropods at site 30 after Spring 2003 (Table 2.4), when peanut was substituted for cotton on the treatment plots. While diversity remained consistent, abundance decreased, possibly due to decreased substrate (Fig 2.6).

Nematode abundance and diversity was similar to microarthropod abundance and diversity, although nematode numbers were more consistent throughout the course of the study (Fig 2.7). This was unexpected, as soil moisture varied greatly among sites during collection and nematodes are presumed limited by the availability of water in the rhizosphere (Elliott et al. 1983). However, recent research has shown that nematodes may be active under lower moisture levels than previously considered (Yeates et al. 2002) and this may help them to maintain populations during times of water stress. This may have given the nematodes an advantage over the microarthropods and allowed them to feed near the root zone with less competition. Grazing of microbial populations by protozoans and nematodes has been shown to increase nutrient mineralization and stimulate bacterial turnover (Ingham et al. 1985, Setäla and Huhta 1991). Hassink (1993) determined that bacteria in coarse soils are not able to utilize small pores to escape predation. The soils in Coffee County are sandy and coarse, possibly allowing increased predation by nematodes of microbial populations that would be limited in other environments. Alternatively, if these fields really are experiencing lower numbers of microarthropods due to natural

population cycling, nematodes would have fewer predators and populations would be less regulated. However, predaceous nematodes would also be expected to increase under this scenario, and may be able to adequately regulate nematode populations.

In a previous study, while still relatively low, nematode abundance increased slightly with years in conservation tillage and was dominated by bacterial feeders (Adl et al. in press). In this study, populations changed very little between sampling dates (Table 2.7), with the exception of spring 2004, which was very dry. It is unlikely that nematode numbers were affected by diurnal changes during sampling like the microarthropods were, as nematode numbers did not noticeably increase or decrease with time of day sampled. We expected higher numbers of fungal feeders at sites 1, 5, 10, and 30, as there would be more fungal biomass in fields with higher amounts of residue. However, fungal feeders were not more abundant at sites in conservation tillage, and were found in similar numbers to bacterial feeders (Fig 2.8). Plant feeders have been shown to average up to 35% of nematodes in disturbed ecosystems (Ferris 1982), but our samples were likely not taken close enough to the root to properly sample plant feeding nematodes, and roots were not extracted for parasitic species.

It is probable that the high variation and inconsistency in the biotic data are reflective of environmental pressures, such as soil temperature, moisture, crop rotation and soil series. Due the wide range of soil types, it would be useful to compare fields that were more similar than the ones chosen for this study. Only two of the fields were within the same soil series, and sites were picked based on previous involvement with the project (Adl et al. in press), rather than on fields of the same structure, which may explain some of the differences between the sites. These sites are all within several miles of each

other, and yet they behave differently to similar treatments, which indicates that parent material and soil type may play a much bigger role in the equilibration of the food web and nutrient cycling than previously considered.

It is also possible that soil food webs in agricultural systems are more complex than previously considered (Wardle et al. 1998). Soil fauna extracted from the site in transition to conservation tillage (site 1) were not significantly different from sites that were established in conservation tillage (Tables 2.4 – 2.7). There were no groups of mesofauna excluded from any site, although site 0 experienced low overall abundance and diversity. This is encouraging, because growers who are reluctant to begin conservation tillage due to concerns about low numbers of soil biota and nutrient turnover may have the same populations and diversity of soil fauna as fields already in conservation tillage. There is a growing movement among producers to become land stewards and incentives to begin conservation programs are in demand by extension agencies, agricultural education initiatives and farm cooperatives (H. Schaumburg, pers. comm).

Conclusions

Compost, when used effectively, can reduce weeds, provide nutrients for plant growth, protect seedlings from extreme temperatures and facilitate an active soil food web. In this study, the compost was not properly managed, and was allowed to escape the system. For very sandy soils that are exposed to infrequent rain events, it may be necessary for land managers in conversion from conventional tillage to conservation tillage to incorporate the initial application of compost. A shallow disking or spading may ensure the proper placement and retention of the compost. This seems to defeat the

purpose of no-tillage agriculture, but it may be the best way to prevent loss from the system and give the soil bacteria immediate access to the organic matter. Future crop residues will add plenty of substrate for decomposition and cultivating a resilient soil food web is an important step in managing soil quality.

It may also be useful to repeat the study using larger plots and composted chicken manure, which has been shown to mineralize nitrogen at higher rates than yard waste (M. Cabrera, pers. comm.). Chicken litter has been successfully used as a fertilizer, and contributes many nutrients (N, P, K, Ca, Mg, S, Cu, Fe, Mn, B) that increase organic N and C in soils for relatively little cost (Warman and Cooper 2000). If farmers can compost chicken litter on-farm, then a potentially hazardous waste product can be safely utilized to implement a crop management regime that will ultimately benefit soil structure and function. This is extremely important to production systems in Georgia, where soil erosion is high due to low levels of SOM and poultry waste may become a major environmental problem (Edwards et al. 1992, Edwards and Daniel 1993).

However, improper use of poultry litter can be detrimental to the environment, and excessive application can lead to NO_3 contamination on the ground water (Bitzer and Sims 1988). Therefore it is important for farmers wishing to use chicken litter as fertilizer not to apply more than the plant can use. Another concern with the use of chicken litter is the tendency for increased runoff due to the hydrophobic nature of the wood particles in the litter. If water cannot infiltrate and runoff is high, the nutrients from the litter will not be available to the plants and could end up in surface water. With these concerns, the need to study the effects of poultry litter on soil dynamics becomes obvious, and it is our

belief that composted chicken manure would be a better choice for a one-time initial organic matter addition for growers seeking to begin a conservation tillage regime.

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Table 2.1. Differences in nutrient status and %SOM between sites. Values are means ± std error.

Date	Site	N	Percent N			Percent C			C/N Ratio			%SOM		
Spring '03	30	12	0.07 ± 0.07	a		1.03 ± 0.10	b		16.4 ± 0.59	bc*		1.02 ± 0.09	a	
Spring '03	10	12	0.11 ± 0.04	a		1.02 ± 0.04	b		14.6 ± 0.26	c		0.86 ± 0.08	ab*	
Spring '03	5	12	0.04 ± 0.01	a		0.66 ± 0.08	b		17.1 ± 0.82	b*		0.64 ± 0.07	b*	
Spring '03	1	12	0.59 ± 0.01	a		0.98 ± 0.06	b		16.0 ± 0.42	bc		0.60 ± 0.04	b	
Spring '03	0	12	0.09 ± 0.01	a		1.72 ± 0.18	a*		18.9 ± 0.40	a*		0.68 ± 0.04	b	
Fall '03	30	12	0.14 ± 0.01	a		1.94 ± 0.18	a*		14.3 ± 0.10	b		0.83 ± 0.04	a	
Fall '03	10	12	0.11 ± 0.01	b		1.43 ± 0.13	b		13.0 ± 0.14	b		0.66 ± 0.05	cb	
Fall '03	5	12	0.08 ± 0.10	bc		1.03 ± 0.13	b		12.0 ± 0.43	b		0.49 ± 0.06	d	
Fall '03	1	12	0.07 ± 0.01	c		1.03 ± 0.10	b		13.8 ± 1.32	b		0.53 ± 0.01	cd	
Fall '03	0	12	0.08 ± 0.01	bc		1.38 ± 0.06	b		17.4 ± 0.32	a		0.74 ± 0.02	ab	
Spring '04	30	12	0.06 ± 0.01	a		1.02 ± 0.05	a		16.7 ± 0.26	ab		0.75 ± 0.03	a	
Spring '04	10	12	0.06 ± 0.01	a		1.02 ± 0.09	a		16.5 ± 0.66	ab		0.66 ± 0.02	b	
Spring '04	5	4	0.06 ± 0.01	a		0.94 ± 0.09	a		15.3 ± 0.63	b		0.43 ± 0.19	d	
Spring '04	1	12	0.07 ± 0.01	a		1.29 ± 0.07	a		18.0 ± 0.72	a		0.49 ± 0.02	cd	
Spring '04	0	12	0.11 ± 0.01	b		2.07 ± 0.16	b		18.4 ± 0.17	a		0.55 ± 0.05	c*	
Fall '04	30	12	0.13 ± 0.01	a		1.73 ± 0.19	a		13.2 ± 0.11	bc		0.82 ± 0.06	a	
Fall '04	10	12	0.13 ± 0.01	a		1.60 ± 0.12	a		12.6 ± 0.14	c		0.70 ± 0.03	ab	
Fall '04	5	12	0.07 ± 0.01	c		0.90 ± 0.05	b		13.4 ± 0.35	bc		0.49 ± 0.01	c	
Fall '04	1	12	0.11 ± 0.01	ab		1.51 ± 0.14	a		13.7 ± 0.23	b		0.61 ± 0.03	bc	
Fall '04	0	12	0.09 ± 0.01	bc		1.40 ± 0.08	a		16.4 ± 0.36	a		0.75 ± 0.03	a	

Letters denote differences at $p<0.05$ within sampling dates only

**within site difference $p<0.05$*

Table 2.2. Differences in microbial biomass C between sites and sampling dates

Date	Site	N	ugC g soil^{-1} Mean ± SE			
Fall 2003	30	12	246.01	±	23.4	a*
Fall 2003	10	12	152.1	±	21.2	b
Fall 2003	5	12	67.41	±	9.31	c
Fall 2003	1	12	221.41	±	9.39	a
Fall 2003	0	12	82.68	±	11.6	c
Spring 2004	30	12	175.81	±	9.93	a
Spring 2004	10	12	147.32	±	9.68	a
Spring 2004	5	12	94.44	±	15.19	b
Spring 2004	1	12	113.6	±	8.13	b
Spring 2004	0	12	45.2	±	4.12	c

Letters denote differences at $p<0.05$ within sample dates only

**within site difference $p<0.05$*

Table 2.3 Inorganic nitrogen from soil samples incubated at constant temperature and moisture over eight weeks.

NO_3

Time (weeks)

Site	N	0			1			2			4			6			8		
30	12	16.77	±	0.84 d	35.29	±	4.70 b*	46.75	±	4.66 b*	53.98	±	4.81 a	64.66	±	4.84 a*	70.31	±	5.59 a
10	12	27.04	±	1.85 b	44.64	±	4.15 a*	63.08	±	4.32 a*	57.29	±	4.35 a	67.51	±	4.12 a*	67.92	±	3.29 a
5	12†	18.94	±	4.10 e	3.32	±	1.26 d	3.58	±	1.50 e	6.19	±	2.11 d	13.77	±	1.60 d	15.40	±	2.19 c
1	12	47.34	±	0.86 a	35.15	±	2.79 b	34.21	±	2.31 c	41.11	±	4.34 b	41.75	±	1.62 b	43.26	±	4.50 b
0	12	17.88	±	1.27 c	23.21	±	0.69 c*	23.16	±	1.63 d	27.85	±	6.25 c	34.97	±	2.15 c	36.19	±	2.68 b

NH_4

Time (weeks)

Site	N	0			1			2			4			6			8		
30	12	2.58	±	0.36 c	4.21	±	0.41 a	6.86	±	0.99 b	6.18	±	0.90 a	40.15	±	2.92 c*	3.95	±	0.47 a*
10	12	3.01	±	0.35 bc	4.98	±	0.60 a	11.19	±	1.14 a	6.33	±	1.02 a	20.09	±	5.14 d*	4.55	±	0.54 a*
5	12†	3.38	±	0.53 b	2.80	±	0.35 b	4.48	±	0.52 c	2.48	±	0.35 b	61.23	±	5.05 b*	2.00	±	0.19 b*
1	12	1.06	±	0.10 d	2.74	±	0.26 b	2.28	±	0.49 d	2.82	±	0.65 b	44.72	±	5.31 c*	2.73	±	0.30 b*
0	12	15.21	±	2.03 a	2.45	±	0.21 b*	1.03	±	0.12 d	1.59	±	0.19 b	80.39	±	9.16 a*	1.90	±	0.23 b*

Letters denote significant differences between means within time at $p<0.05$

** indicates significant differences in means from previous time interval at $p<0.05$*

† ; n=4 for t_0 due to contamination of samples

Table 2.4. Differences in microarthropod abundances (log transformed) per soil core

Date	Site	N	Mean ± SE			
Spring 2003	30	12	1.32	±	0.15	a
Spring 2003	10	12	1.14	±	0.11	a
Spring 2003	5	12	0.53	±	0.11	b
Spring 2003	1	12	1.04	±	0.07	a
Spring 2003	0	12	0.37	±	0.08	b
Fall 2003	30	12	0.48	±	0.11	ab
Fall 2003	10	12	0.71	±	0.07	a
Fall 2003	5	12	0.32	±	0.99	b
Fall 2003	1	12	0.43	±	0.95	ab
Fall 2003	0	12	0.19	±	0.06	b
Spring 2004	30	12	0.37	±	0.1	ab
Spring 2004	10	12	0.43	±	0.09	ab
Spring 2004	5	4	0.61	±	0.16	a
Spring 2004	1	12	0.24	±	0.11	ab
Spring 2004	0	12	0.16	±	0.06	b
Fall 2004	30	12	0.65	±	0.09	a
Fall 2004	10	12	0.8	±	0.08	a
Fall 2004	5	12	0.68	±	0.12	a
Fall 2004	1	12	0.78	±	0.09	a
Fall 2004	0	12	0.64	±	0.06	a
Fall 2005	30	12	0.59	±	0.15	ab
Fall 2005	10	12	0.66	±	0.11	ab
Fall 2005	5	12	1.05	±	0.12	a
Fall 2005	1	12	0.22	±	0.09	b
Fall 2005	0	12	0.62	±	0.22	ab

Letters denote differences at $p<0.05$ within sample dates only

Table 2.5. Differences in microarthropod diversity (D') and species richness (s) per soil core

Date	Site	N	D' Mean ± SE				s Mean ± SE			
Spring 2003	30	12	0.52	±	0.05	a	3.50	±	0.37	a
Spring 2003	10	12	0.48	±	0.06	a	3.00	±	0.23	a
Spring 2003	5	12	0.29	±	0.08	ab	1.88	±	0.29	ab
Spring 2003	1	12	0.51	±	0.06	a	3.16	±	0.32	a
Spring 2003	0	12	0.20	±	0.08	b	1.43	±	0.17	b
Fall 2003	30	12	0.38	±	0.06	a	2.00	±	0.20	a
Fall 2003	10	12	0.27	±	0.07	a	1.91	±	0.28	a
Fall 2003	5	12	0.14	±	0.07	a	1.28	±	0.14	a
Fall 2003	1	12	0.19	±	0.07	a	1.50	±	0.20	a
Fall 2003	0	12	0.08	±	0.05	a	1.20	±	0.13	a
Spring 2004	30	12	0.07	±	0.04	a	1.00	±	0.21	a
Spring 2004	10	12	0.07	±	0.05	a	1.00	±	0.17	a
Spring 2004	5	4	0.12	±	0.12	a	1.25	±	0.25	a
Spring 2004	1	12	0.04	±	0.04	a	0.42	±	0.19	a
Spring 2004	0	12	0.04	±	0.04	a	0.50	±	0.19	a
Fall 2004	30	12	0.36	±	0.08	a	2.42	±	0.45	a
Fall 2004	10	12	0.46	±	0.09	a	2.75	±	0.30	a
Fall 2004	5	12	0.42	±	0.09	a	2.91	±	0.57	a
Fall 2004	1	12	0.45	±	0.06	a	2.66	±	0.39	a
Fall 2004	0	12	0.21	±	0.08	a	1.83	±	0.39	a
Spring 2005	30	12	0.23	±	0.07	ab	1.75	±	0.46	ab
Spring 2005	10	12	0.28	±	0.09	ab	2.08	±	0.52	ab
Spring 2005	5	12	0.46	±	0.06	a	3.00	±	0.37	a
Spring 2005	1	12	0.05	±	0.05	b	0.66	±	0.26	b
Spring 2005	0	12	0.27	±	0.08	ab	2.08	±	0.68	ab

Letters denote differences at $p<0.05$ within sample dates only

Table 2.6. Differences in nematode abundance (log transformed) per g dry soil

Date	Site	N	Mean ± SE			
Spring 2003	30	12	0.99	±	0.07	a
Spring 2003	10	12	0.83	±	0.04	ab
Spring 2003	5	12	0.66	±	0.06	b
Spring 2003	1	12	0.71	±	0.08	b
Spring 2003	0	12	0.63	±	0.08	b*
Fall 2003	30	12	0.98	±	0.02	a
Fall 2003	10	12	0.85	±	0.03	a
Fall 2003	5	12	0.6	±	0.06	b
Fall 2003	1	12	0.96	±	0.09	b
Fall 2003	0	12	0.65	±	0.05	b
Spring 2004	30	12	0.58	±	0.12	a
Spring 2004	10	12	0.49	±	0.12	a
Spring 2004	5	4	0.57	±	0.07	a
Spring 2004	1	12	0.92	±	0.13	a
Spring 2004	0	12	0.37	±	0.09	a
Fall 2004	30	12	0.88	±	0.06	a
Fall 2004	10	12	0.85	±	0.08	a
Fall 2004	5	12	0.76	±	0.1	a
Fall 2004	1	12	0.89	±	0.04	a
Fall 2004	0	12	0.91	±	0.09	a

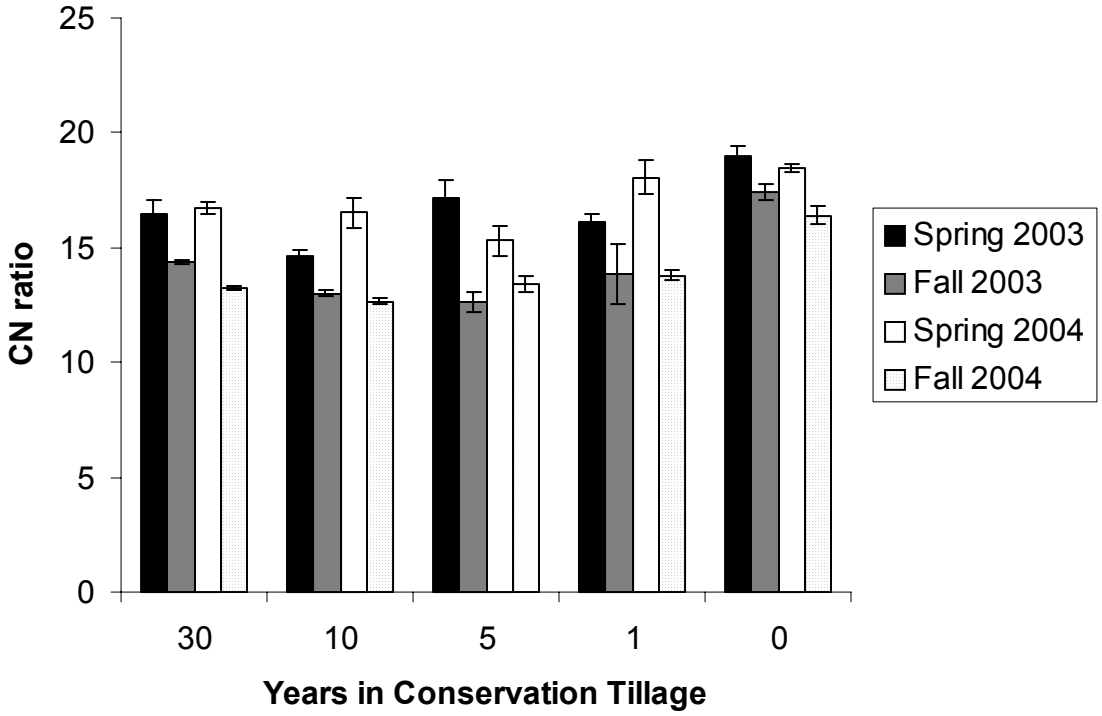
Letters denote differences at $p<0.05$ within sample dates only

**within site difference $p<0.05$*

Table 2.7. Differences in nematode feeding guild diversity (D') and richness (S) per g dry soil

Date	Site	N	D' Mean ± SE				s Mean ± SE			
Fall 2003	30	12	0.59	±	0.02	a	3.66	±	0.22	a
Fall 2003	10	12	0.65	±	0.03	a	3.25	±	0.21	a
Fall 2003	5	12	0.55	±	0.05	a	3.16	±	0.27	a
Fall 2003	1	12	0.55	±	0.06	a	3.33	±	0.41	a
Fall 2003	0	12	0.60	±	0.23	a	3.33	±	0.14	a
Spring 2004	30	12	0.49	±	0.07	a	3.00	±	0.39	a
Spring 2004	10	12	0.38	±	0.08	a	2.33	±	0.48	a
Spring 2004	5	4	0.59	±	0.02	a	3.25	±	0.43	a
Spring 2004	1	12	0.55	±	0.05	a	4.00	±	0.46	a
Spring 2004	0	12	0.29	±	0.08	a	2.90	±	0.51	a
Fall 2004	30	12	0.60	±	0.01	a	3.50	±	0.19	a
Fall 2004	10	12	0.57	±	0.05	a	3.66	±	0.37	a
Fall 2004	5	12	0.54	±	0.05	a	3.33	±	0.44	a
Fall 2004	1	12	0.63	±	0.02	a	3.91	±	0.23	a
Fall 2004	0	12	0.55	±	0.03	a	3.50	±	0.23	a

Letters denote differences at $p<0.05$ within sample dates only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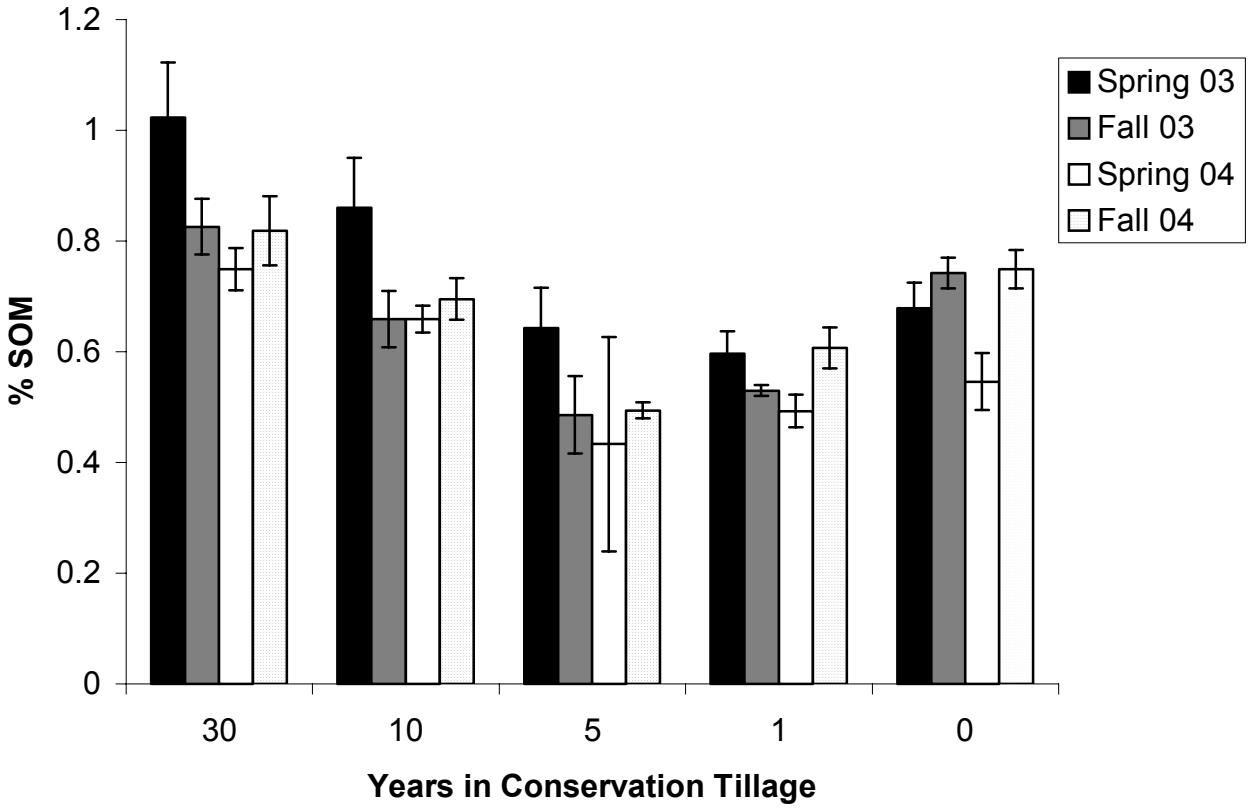
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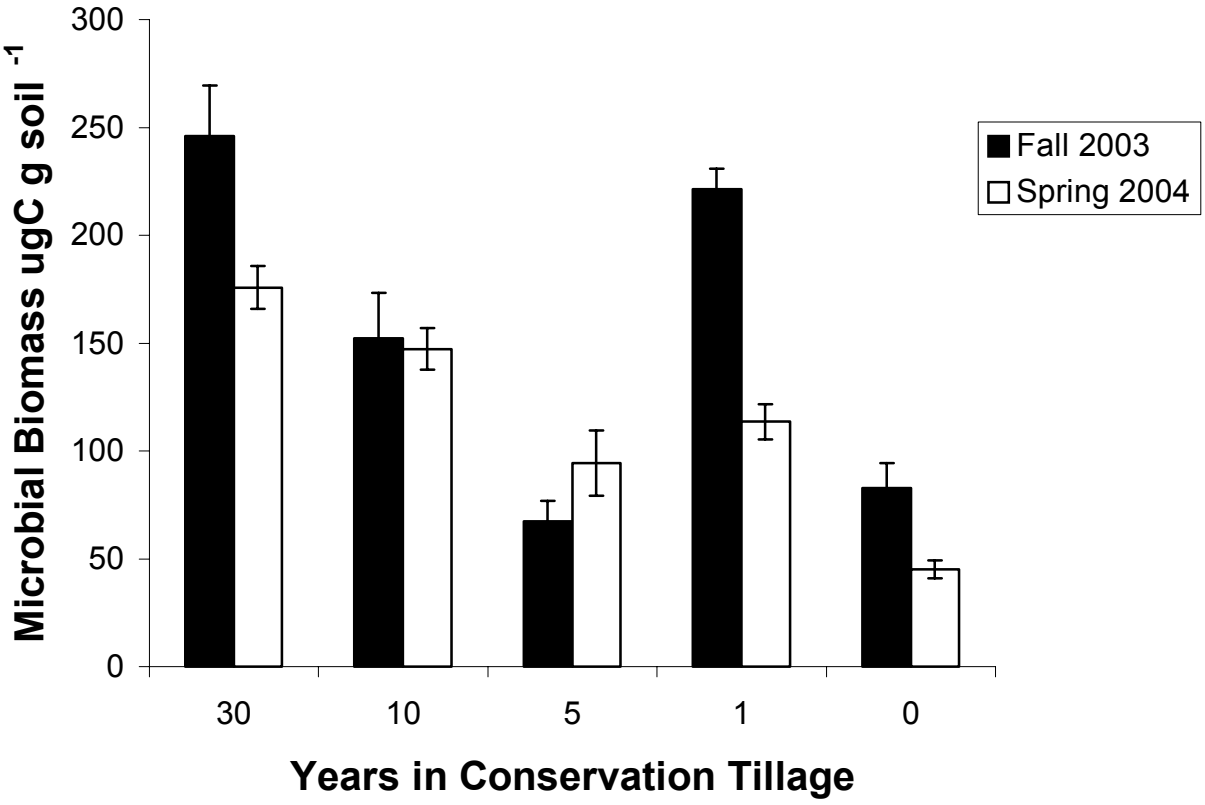
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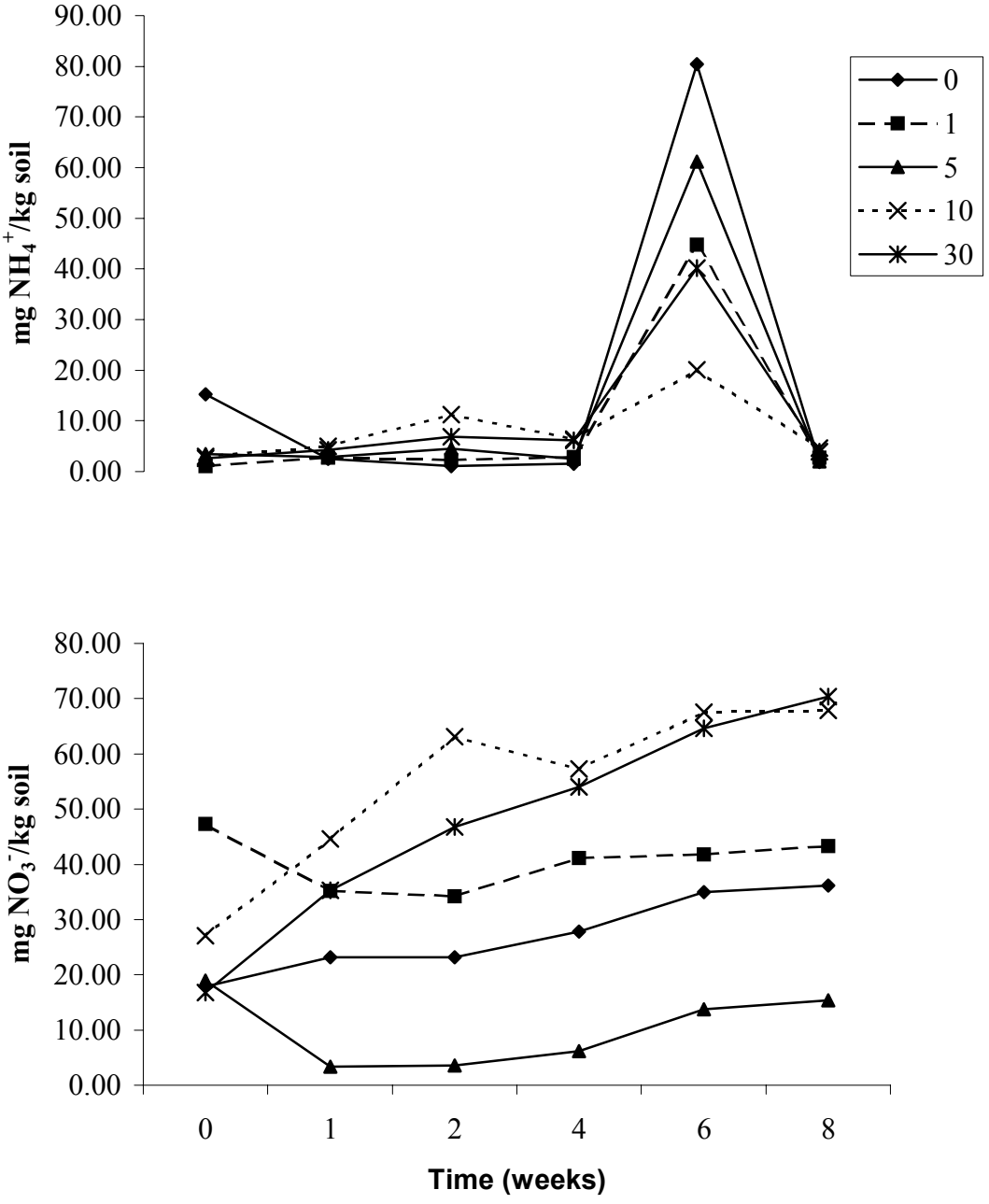
Spring 2004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mg NO_3^-/kg soil
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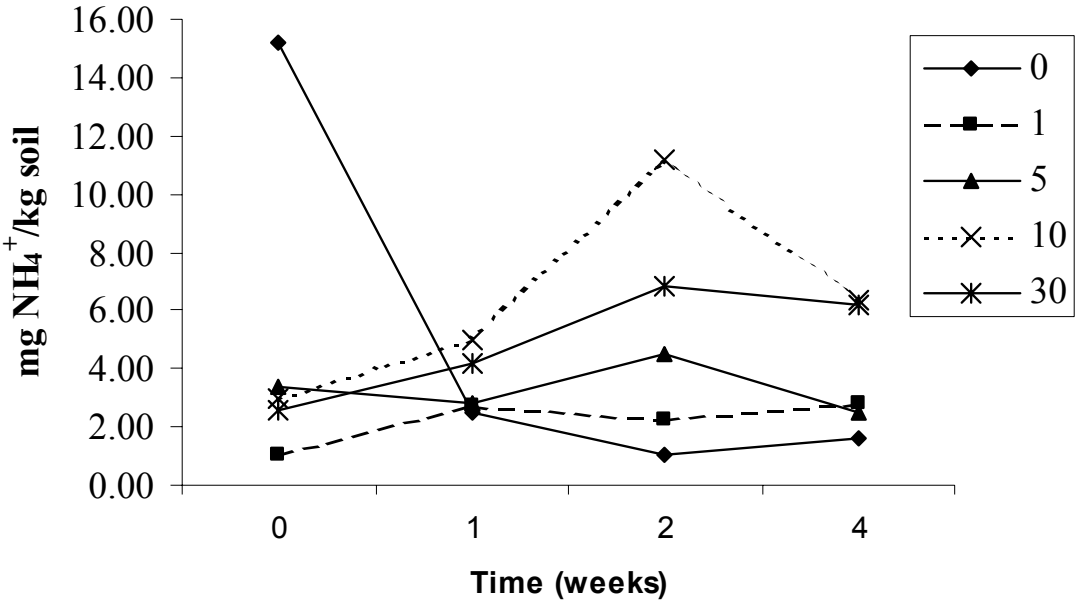
Time (weeks)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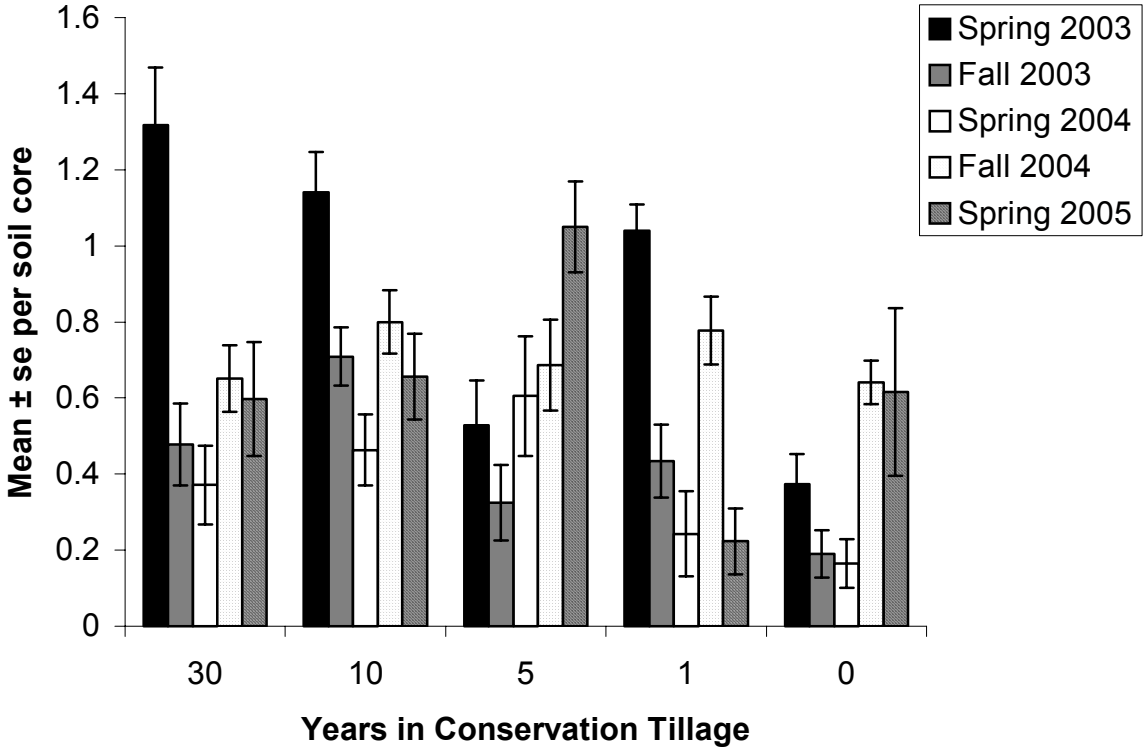
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Mean ± se per soil core
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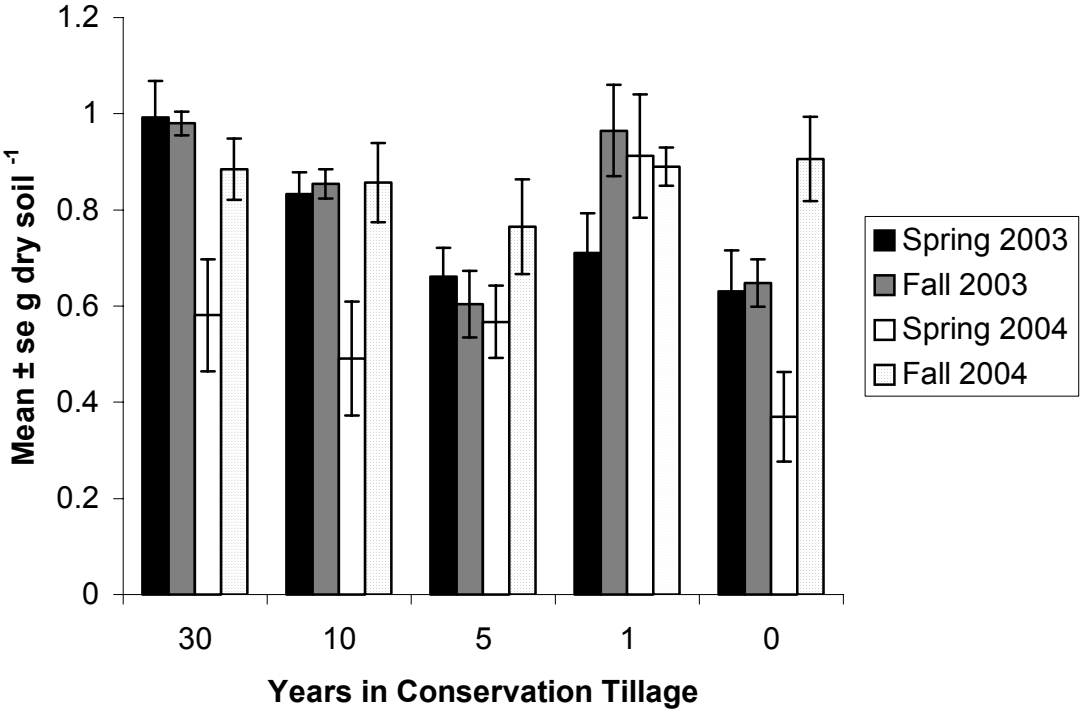
Years in Conservation Tillage
Spring 2003
Fall 2003
Spring 2004
Fall 2004
Spring 2005


1.2
1
0.8
0.6
0.4
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Mean ± se g dry soil -1
30
10
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Years in Conservation Tillage
Spring 2003
Fall 2003
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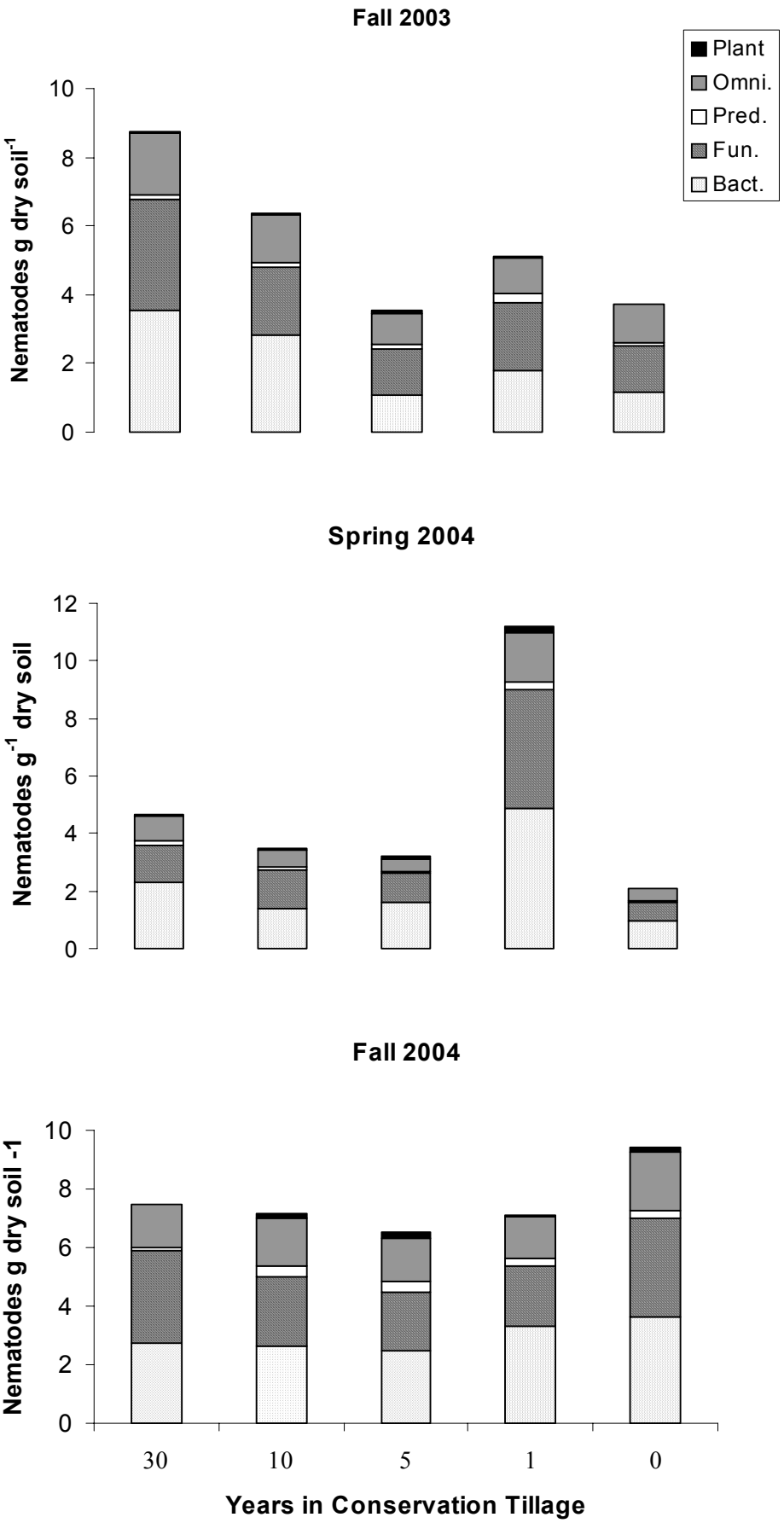
Fall 2003
Plant
Omni.
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Nematodes g dry soil-1
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2
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Spring 2004
Nematodes g-1 dry soil
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Fall 2004
Nematodes g dry soil -1
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4
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8
10
30
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5
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Years in Conservation Tillage

CHAPTER 3

CHANGES IN MICROBIAL COMMUNITIES IN RESPONSE TO COMPOST APPLICATION AND CONSERVATION TILLAGE TECHNIQUES IN AGRICULTURAL FIELDS IN COFFEE COUNTY, GEORGIA (USA)[1]

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Abstract

In the southeastern United States, intensive agricultural practices have been responsible for massive soil erosion, loss of soil organic matter, a decrease in soil fertility and a reduction in overall soil quality. In these areas, conservation tillage techniques are used to protect and replenish the soil as well as provide habitat and substrate for the soil biota, which are largely responsible for the mineralization of nutrients from the soil, and is therefore an important component of soil function. A deterrent for growers considering the transition to conservation tillage is the delay in soil response, associated with the equilibration of the soil food web. The objective of this study was to determine if the microbial community composition and biomass changed with conservation tillage, and whether this change could be facilitated by the addition of organic matter to fields in transition to conservation tillage techniques. Soils samples from five sites representing a chronosequence of conservation tillage, were collected for fatty acids analysis. Presence of microbial functional groups were significantly different between sites but similar across compost treatments. Fungi, characterized by 18:2w6, 18:1w9t, and 18:1w9c peaks, were typically lowest in the conventionally tilled soil, probably due to repeated disruption of the fungal hyphae associated with tillage. In all soils, microbial functional groups were most heavily influenced by soil C, % soil organic matter and soil moisture, and most sites in conservation tillage were not significantly different from each other, regardless of time in no-till.

Keywords Microbial community structure, microbial biomass, FAME, conservation tillage, compost, soil series, Georgia Coastal Plain

Introduction

In the southeastern United States, intensive agricultural practices have been responsible for massive soil erosion (Holland 2004), loss of soil organic matter (Allmaras et al. 2000), a decrease in soil fertility (Nyakatawa and Reddy 2000) and a reduction in overall soil quality (Parr et al. 1992). In conventional tillage systems, where crop residues are incorporated into the soil by plowing or disking, has been shown to increase decomposition of crop residues (Moore and deRuiter 1991), and change the structure of the soil food web by relocating food resources (Hendrix et al. 1986, Beare et al. 1992). Previous studies have shown that microbial community composition can be altered by a change in management practices (Visser and Parkinson 1992, Schutter and Dick 2002), substrate availability and composition (Wardle et al. 1993), and soil type (Schutter et al. 2001). Seasonal variation in soil nutrient status has also been shown to affect the microbial community (Bardgett et al. 1999, Schutter et al. 2001).

Not only are microbes important to ecosystem processes, but also they serve as an important substrate for other organisms in the soil food web (Ingham et al. 1985, Setäla and Huhta 1991). For these reasons, soil microbes can be used as an indicator of soil quality (Doran 1987, Wall and Moore 1999). However, microbes are incredibly diverse, and many cannot be studied in pure culture (Schutter et al. 2001). Extraction of fatty acid methyl esters (FAME) from whole soil samples using the MIDI protocol is simpler and less time consuming than analysis of phospholipid fatty acid (PLFA) profiles (Schutter and Dick 2000). This method has been useful for identifying microbial community composition in a number of studies (Klug and Tiedje 1993, Cavigelli et al. 1995,

Pankhurst 1997, Ibekwe and Kennedy 1999, Schutter and Dick 2000, McCulley and Burke 2004).

The activity of soil biota is largely responsible for the mineralization of nutrients from the soil, and is therefore an important component of soil function (Ingham et al. 1985, Hunt et al. 1987, Moore 1988, Beare et al. 1992). This is especially important in low input sustainable agriculture, where increased microbial diversity is expected to increase soil quality (Parr et al. 1992, Visser and Parkinson 1992). In systems where crop residue is buried or where labile substrate is abundant, bacteria dominate, due to their ability to break down labile carbon sources more efficiently than saprophytic fungi (Coleman et al. 1983, Curl and Truelove 1986, Moore et al. 2003). In these systems, the rates of decomposition and nitrogen mineralization are accelerated (Moore and deRuiter 1991, Doles et al. 2001). Microbial diversity is expected to increase with a reduction in tillage, as fungal species begin to dominate the system (Beare et al. 1992). In systems where crop residue is left on the surface, saprophytic fungi dominate, slowly breaking down more resistant substrates (Hendrix et al. 1986, Moore et al. 2003).

The ability of an ecosystem to withstand disturbance may lie in the energy pathway, where bacterial dominated systems are more resilient than fungal dominated systems (Allen-Morley and Coleman 1989, Moore and deRuiter 1991, Bardgett and Cook 1998). Moore et al (2003) postulates that recovery times of each energy channel to disturbance may be different, and result in an alteration of the food web. Several studies have found effects of land management practices on soil microbial diversity and abundance (Liljeroth et al. 1990, Frostegård et al. 1993, Kirchner et al. 1993, Zelles et al. 1994, Haslam and Hopkins 1996). In a study involving the transition from conventional

to alternative agriculture, Doran et al (1987) found that microbial populations and activities were regulated more by crop type and rotation than by soil physical properties. In a structurally unstable soil, Gonzales et al (2003) found an increase in humification in soils in no-till as compared to those in reduced tillage, indicating that microbial populations were probably influenced by increases in organic matter. In contrast, Buyer and Kaufman (1997) showed no effect of agricultural treatment on the microbial community and suggested that, due to methodology, diversity measurements may remain high in conventional agriculture despite increased disturbance.

The objective of this study was to determine if the microbial community composition and biomass changed with conservation tillage, and whether this change could be facilitated by the addition of organic matter to fields in transition to conservation tillage techniques. We hypothesized that an application of compost would help to increase the abundance and diversity of microbes in a field that is new to conservation tillage, thus accelerating the equilibration of the soil biota and establishing a strong soil food web base. Similarly, we hypothesized that for fields already in conservation tillage, the effects of compost addition would be negligible, due to higher quality and quantity of substrate already available for the soil microbes.

Methods

Collection sites

Soil was collected from five cotton fields near Douglas in Coffee County, Georgia (USA) at map coordinates 31° 21’N, 82° 52’W. One field was in conventional tillage. One field reserved a small portion of the field for transition from conventional tillage to conservation tillage. Three other fields had been in conservation tillage for several years.

All fields are labeled by the number of years spent in conservation tillage at the beginning of this study: 0,1,5,10, and 30. The soils series were Fuquay, Pelham, Cowarts/Carnegie, Pelham and Tifton, respectively. Site 5, in the Cowarts/Carnegie series, is approximately 55% Carnegie and 30% Cowarts, and is so heavily mixed that separate mapping was not possible (Appendix A). All fields had been continuously cropped for at least 30 years, and were planted in cotton or peanut for the duration of this study. The fields in conservation tillage use a cover crop of rye in the winter to add organic matter. Herbicides and fertilizers are used at the beginning of each crop rotation. Lime is added approximately every other year or as needed.

Experimental design.

Twelve plots (2x3 m) were set up at each site, for a total of 60 experimental plots. Each plot was at least 5 m from its nearest neighbor plot. Plots were set up randomly but oriented perpendicularly to row direction so that each pass of the equipment impacted the same number and type of plots. Four replicates of two compost treatments (10 and 20 tons/ha) and one control (0 tons/ha) were randomly assigned to the plots.

Organic compost was donated by GroMor Organics and consisted of high quality yard waste from Moultrie, GA. The compost was applied by hand to each plot on January 27, 2003 except in the transitional field (site 1) where conditions were too wet to disturb the soil structure. Application of compost to the plots in site 1 took place on March 3, 2003, after the soil had drained.

Sampling

Sampling for site characteristics and microbial biomass occurred four times over two years, at the end of each growing season, before the crop was mowed (sites 1, 5, 10,

30) or incorporated (site 0). After year 2, the grower at site 1, who experienced flooding in the area devoted to conservation tillage, incorporated the winter cover crop. This, combined with perceived minimal effect of the compost addition, contributed to the termination of the experiment before the final year.

Samples were taken for soil C/N from the upper 5 cm of soil using a soil probe (dia=2 cm). Samples were sealed in plastic bags and placed in a cooler for transport. Steel rings (dia=5 cm) were driven into the upper 5 cm of soil to obtain measurements of bulk density. Nematodes were sampled using a soil probe (dia=2 cm) from the upper 5cm of soil, sealed in plastic bags and placed in a cooler for transport. Microarthropods were sampled from the upper 5 cm of soil using steel rings (dia 5 cm) in a specialized beveled metal corer. Samples were wrapped in aluminum foil, placed in plastic bags and stored in a cooler for transport to the lab. Soil for FAME extraction were taken from each plot with a soil corer to a depth of 5cm and sealed in plastic bags. The samples were transported back to the lab in a cooler and air dried for the experiment.

Laboratory procedures

Total soil carbon and nitrogen were determined on a Carlo Erba analyzer in the UGA Institute of Ecology Analytical Laboratory on soil that was air-dried, ground, and weighed into tin capsules. Soil moisture values were obtained by drying soil sub samples in an oven at 105°C for 48 hours. An estimate of soil organic matter (SOM) was obtained by ashing soil at 450°C for 4 h in a muffle furnace.

Nematodes were extracted using the Baermann funnel technique (Baermann 1917). A 5 g subsample of wet soil was wrapped in a Kimwipe, placed on a metal screen in water-filled, close-ended funnels. Samples were left on the funnels for 48 h.

Approximately 7 ml of water from the funnel was collected into 15 ml centrifuge tubes and mixed with 7 ml of 5% formalin for preservation. Nematodes were counted under an inverted scope and categorized into feeding groups by morphological characters (Yeates et al 1993, Wall pers comm.). Nematodes in samples from Spring 2003 were counted but not categorized into trophic levels because the samples were compromised before identification could take place.

Microarthropods were heat extracted over five days using modified Tullgren type funnels (Blair and Crossley 1991). Animals were collected in 70% ethanol and identified to order, suborder, or family under a dissecting microscope. Samples were prepared for permanent storage by transferring animals to 95% ethanol after identification.

FAME procedures

FAME profiles were compiled using the MIDI method (Microbial ID, Inc., Newark, DE). For each sample 3.0 g of air dried soil was placed in a 30 ml glass centrifuge tube. 15mL of methanol-KOH (0.2M) was added to each tube, and the tubes were capped using Teflon-lined screw caps. The centrifuge tubes were place in a test tube rack in a 37º C water bath for 1 h. Every 10 min the tubes were vortexed for 20 sec. After the water bath, 0.5 mL of 1*N* acetic acid was repeatedly added to each tube until the pH of the solution was neutral. 10 mL of hexane was added to the soil suspension, and the mixture was vortexed for 30 sec. The tubes were centrifuged at 480 xg for 20 minutes. Approximately 7 ml of the hexane layer was transferred to a disposable test tube. The hexane was evaporated to complete dryness under a gentle stream of nitrogen. The dried extract was re-suspended in 1.0 mL of hexane and dried down again for shipment to an analytical lab in Delaware. In the analytical lab, the samples were re-suspended in a 1:1

mixture of hexane and tertiary-butyl methyl ether. The solution was transferred to a 2.0 mL gas chromatography vial and capped. The extract was analyzed with a HP 5890 gas-liquid chromatograph equipped with a HP Ultra 2 capillary column (5%-diphenyl-95%-dimethylpolysiloxane, 25 m by 0.2 mm) and a flame ionization detector.

Fatty acid methyl esters described here use the standard nomenclature for lipid markers, A:BωC. A is the number of carbon atoms, B is the number of double bonds, and ωC indicates the number of carbon atoms from the aliphatic end of the molecule and the first unsaturated bond. Isomers are denoted with the suffixes *c* (*cis*) or *t* (*trans*). Methyl branching is described by the prefixes *i* (*iso*) and *a* (*anteiso*), while methyl and cyclopropyl groups receive the notations Me and cy, respectively.

Analysis

Analysis of variance (ANOVA) was performed to determine if the total quantity and diversity of FAMEs differed between sites. Data were standardized to fit assumptions of normality and analyzed for significant differences in percentages of mol fractions between sites and between compost treatments within sites using least significant difference means separation test to determine significant effects of site and treatment interactions. These data were also used to determine if there were seasonal effects on microbial abundance using a repeated measures ANOVA. All ANOVAs were performed in SAS (SAS Institute 1989). Non-metric multidimensional scaling (NMS) was run on the mol fraction of 10 FAMES common to all samples and representing a range of microbial functional groups. Percent mol fractions were also summed for each microbial functional group and subjected to ANOVA using the pdiff option in the MIXED procedure to test for significant differences in functional groups between sampling dates,

field sites and interactions between site and compost treatments. Site characteristics (percent nitrogen, percent carbon, C/N ratio, percent soil organic matter, soil moisture) and mesofauna abundances (microarthropods and nematodes) were log transformed and used to create a secondary matrix. This secondary matrix was correlated with the main matrix and used to evaluate the effects of environmental variables on the distribution of microbial functional groups. All multivariate analyses were calculated using PC-ORD (McCune and Mefford 1999).

Results

Site characteristics

Soil nutrient status varied seasonally and between sites, with spring samples having lower C/N ratios compared to the fall samples at all sites. However, %N and %C did not change consistently with season at any site (Table 3.1). Percent SOM was always highest at site 30, and typically lowest at site 5. Soil moisture values represent changes in time as well as between sites, as the sites sampled last had typically dried down before sampling, compared to other sites (Table 3.1).

Abundance of microarthropods was extremely variable within all sites and between all sampling dates (Table 3.1). In general, microarthropods were most numerous in the spring of 2003, and the number of microarthropods collected on that date was significantly highest at sites 30, 10 and 1. The conventionally tilled site (site 0) and site 5 usually had the lowest number of microarthropods, although in fall 2004 none of the sites were significantly different. Nematode abundances were fairly low but relatively stable at all sites throughout the study, and there was no significant effect of compost application (Table 3.1). Numbers of nematodes recovered in spring 2004 were significantly lower

than on other sampling dates except at site 1. In general, sites 5 and 0 had the fewest nematodes per gram of soil except in fall 2004, when site 0 had the highest abundance of nematodes compared to other fields. In spring 2004, there were no significant differences between any of the sites (Table 3.1).

Microbial community composition

Over two years, a total of 51 different FAMEs were extracted; 48 in spring 2003, 45 in fall 2003, 33 in spring 2004 and 38 in fall 2004. For all sites, total fatty acids extracted (analyzed as the number of non-zero elements in each sample) from the samples were higher in the fall than in the spring (Fig 3.1). There were no significant effects of compost addition at any site during any sampling period. Total number of fatty acids at each site varied seasonally and between sites. During the spring sampling periods, there were no significant differences in the number of fatty acids extracted between sites (Table 3.2). In fall 2003, site 10 had significantly higher number of fatty acids compared to other fields; sites 5 and 30 had the lowest numbers (Table 3.2). In fall 2004, this trend was repeated, with site 30 experiencing an increase in total fatty acids extracted (Table 3.2).

Diversity (Simpson's D') of fatty acids extracted from each sample also varied seasonally and between sites. There were no significant differences in diversity of fatty acids extracted during the spring sampling periods (Table 3.2). In fall 2003, FAME diversity was highest at site 10 compared to other sites, and lowest at site 5 (Table 3.2). In fall 2004, diversity was highest at sites 1 and 10, and lowest at site 5 (Table 3.2).

Due to seasonal variability in the data, the non-metric multidimensional scaling (NMS) was performed separately for each sampling date. In spring 2003, the NMS

identified 3 axes that explained 93% of the variance in the FAME data (stress = 9.91). Axis 1 (Figs 3.2, 3.3) explained 18% of the data and was most negatively weighted by soil moisture (Table 3.3). Axis 2 (Figs 3.2, 3.4) explained 52% of the data and was positively weighted by soil carbon (Table 3.3). Axis 3 (Figs 3.3, 3.4) explained 22% of the data and was positively weighted by microarthropod abundance (Table 3.3). In fall 2003, NMS identified 3 axes that explained 94% of the variance in the FAME data (stress = 10.25). Axis 1 (Figs 3.5, 3.6) explained 31% of the data and was positively weighted by C/N ratio and %SOM (Table 3.3). Axis 2 (Figs 3.5, 3.7) explained 32% of the data and was negatively by soil moisture and microarthropods (Table 3.3). Axis 3 (Figs 3.6, 3.7) explained 31% of the data and was positively weighted by C/N ratio (Table 3.3). In spring 2004, NMS identified 2 axes that explained 76% of the variance in the data (stress = 10.93). Axis 1 (Fig 3.8) explained 46% of the variance and was negatively weighted by microarthropod abundance, while Axis 2 explained 30% of the variance and was negatively weighted by soil moisture (Table 3.3). In fall 2004, NMS identified 2 axes that explained 93% of the variance in the data (stress = 12.02). Axis 1 (Fig 3.9) explained 81% of the variance and was positively weighted by soil nutrients, while Axis 2 explained 12% of the variance and was positively weighted by C/N ratio (Table 3.3).

NMS weights for microbial FAME groups were variable across sites and dates. In spring 2003, Axis 1 and 3 were most positively weighted by relative abundance of fungi, while Axis 2 was positively weighted by gram-positive bacteria (Table 3.4). In fall 2003, Axis 1 and 3 were negatively weighted by relative abundances of fungi, while Axis 2 was most positively weighted by non-specific bacteria and negatively weighted by gram-negative bacteria (Table 3.4). In spring 2003, relative abundances of gram-positive

bacteria were negatively weighted on Axis 1, while fatty acid markers indicative of fungi were positively weighted on Axis 2 (Table 3.3).In fall 2004, relative abundances of fungal fatty acid markers were negatively weighted on Axis 1, while gram-positive bacteria received positive weights on Axis 2 (Table 3.4).

A repeated measures FAME indicated a significant effect of time and site on taxonomic groups (Table 3.5). Relative abundances of gram-positive and gram-negative bacteria were highest in fall 2003 and lowest in spring 2004. Relative abundances of eubacterial anaerobes was also lowest in spring 2004 but highest in spring 2003. In contrast, the relative abundance of fungi was highest in spring 2004. There were also significant effects of compost treatment on gram-negative anaerobes and the fungi (Table 3.5). In Spring 2003 there were no significant differences in FAMEs extracted between compost treatments at any site. However, the sites in conservation tillage had significantly higher relative abundances of fungi than the conventionally tilled site (Table 3.6). In fall 2003, relative abundance of fungi was higher in the control plots than the compost treatment ($p<0.005$). Overall, relative abundances of gram-positive bacteria and fungi were higher at sites in conservation tillage compared to site 0 (Table 3.6). In spring 2004, the relative abundance of gram-positive bacteria was highest in the high compost treatment and the control plots ($p<0.005$) and relative abundance of gram-negative bacteria was highest in the high compost treatment ($p<0.005$). Site 5 had the highest relative abundance of gram-positive bacteria and fungi, while site 30 had the highest relative abundance of gram-negative bacteria (Table 3.6). In fall 2003, relative abundances of all taxonomic groups were highest in the control or low compost treatments. There was no significant difference in the relative abundance of fungi that

season, and relative abundances of other taxonomic groups were variable across sites (Table 3.6).

Discussion

White et al (1996) determined that total phospholipid fatty acids (PLFA) are an indicator of viable microbial biomass, and we used the total number of FAMEs to estimate abundance and diversity of belowground organisms. While multiple fatty acid markers may indicate single species, plant material, or other organic matter, differences between these markers indicate a difference in the belowground community, and the data were analyzed accordingly. Diversity estimates were run on the relative abundance (% mol fraction) of all fatty acids present in all samples, and those samples with more fatty acids were determined to be more diverse. For quantitative analysis, this type of discrimination of the data is inappropriate, but we felt it was sufficient for the purpose of comparing sites in this experiment.

Effects of compost application, even where significant, were not consistent between sites or treatment levels. This indicates that any significant differences between variables are likely due to large variances in the dataset. The rates of compost application were chosen to reflect an upper and lower limit, based on the amount of compost required to significantly raise % SOM in these fields by 1 and 2% respectively. The compost was not visible on the surface of the soil in Spring 2003, five months after it was applied. This could mean that the compost washed away, was rapidly transformed by the biota or was leached through the soil due to heavy rain. Precipitation was high during the winter and early spring of 2003, but decreased in frequency and intensity over the next two sampling periods. Organic amendments have been shown previously to positively affect most soil

biota on sandy loams (Andren and Lagerlof 1980, Wardle et al. 1993, Culik et al. 2002, Forge et al. 2003, Yang et al. 2003). However, none of these experiments was conducted on fields in intensive agriculture. Therefore, it is possible that when a sandy soil is used to support rotated seasonal crops, or subjected to extreme precipitation, it is not well suited to accepting loose organic amendments.

Previous research in these fields indicated that microbial biomass would be greatest in the spring, due to increased soil carbon and residue from the winter cover crop exploited by microbes (Adl et al. in press). Current studies showed a decrease in C/N ratio in the fall, likely due to an increase in soil nitrogen from heavy fertilization or a field application of broiler litter (Table 3.1). Total number of fatty acids also increased in the fall, indicating a larger microbial biomass than previously expected (Table 3.2, Fig 3.1). In the spring, samples were taken at each site while the winter crop was still standing, except at site 30, where the cover was mowed and peanut planted 2 weeks prior to sampling. In the fall, samples were taken before the cotton/peanut was harvested, although usually it had already been defoliated. It is unlikely that a standing cover crop would provide microbes with enough residues to increase abundance and diversity. In the fall, microbial biomass may benefit from increased soil nitrogen from increased fertilization of the summer cash crop or slow decomposition of surface residue from the winter cover. However, those sites that didn't have a cover crop for one or more years (site 0, site 1) also experienced a seasonal increase in total fatty acids, indicating that it may be an effect of soil nutrient status rather than residue quantity or quality (Fig 3.1).

The low number of fatty acids extracted from site 5 during the spring (Table 3.2, Fig 3.1) may be explained by its location in the Cowart/Carnegie soil complex. These

soils are low in organic matter, prone to severe erosion with rapid runoff and a shallow root zone (Appendix A). Variations in soil texture due to the inconsistent mixture of soil and subsoil typical of these soils may affect the microclimate variation within the soil. Site 5 also had consistently low amounts of SOM throughout the study (Table 3.1), which negatively affects the soil food web (Linn and Doran 1984).

Total FAME diversity in the fall sampling periods was highest at site 10, where applications of broiler litter may have influenced the diversity of fatty acids extracted. In fall 2004, diversity was highest at sites 1 and 10 (Table 3.1). These two fields are both in the Pelham soil series, which is characterized by poor drainage, low fertility, high acidity and a deep root zone except in midwinter, when it is restricted by the water table. These sites are also adjacent to one another and seeds were planted with the same no-till seed drill in the spring. It is possible that the drill could have transferred a portion of soil and therefore microbes with it across the fields. However, it is also possible that as site 1 increased in "no-till age" it would begin to behave similarly to site 10 (Fig 3.1). Soils in the Pelham series are considered poor for field crops because of flooding, which restricts conventional equipment and increases the risk of seedling mortality (Appendix A). This tendency to flood should make these sites the perfect habitat for anaerobic bacteria. However, while site 10 had the highest relative abundance of eubacterial anaerobes in spring 2004, this was not a significant trend through time, for either site on the Pelham series (Table 3.6).

All sites were located in soil series that are strongly acidic (NRCS-OSD). This likely explains the lack of fatty acid markers associated with actinomycetes (Table 3.5). Actinomycetes are filamentous, gram-positive bacteria that are common in forests and

soils that are low in nitrogen. They are late colonizers that are important for decomposition of organic matter and stable humus formation. Actinomycetes are tolerant of high temperatures and low soil moisture, but intolerant of highly acidic soils, and will virtually disappear in soils with a pH lower than 6.0 (Sylvia et al 1998).

Surprisingly, nematodes did not receive any large positive or negative loadings. This may be the result of their relatively low abundance and the uniformity of the data between sites (Table 3.1). The microbial community exhibited seasonal fluctuations in relative abundance (Table 3.6). Greater relative abundance of fungi during spring 2004 (Table 3.6) was likely due to low soil moisture and high C/N ratios (Tables 3.1, 3.3). These conditions may have allowed the fungi to out compete the bacteria. Spring 2004 was very dry, and relative amounts of bacteria were lower than the year before (Table 3.6). In the NMS, microarthropod abundance received a large negative loading for that season (Table 3.3). It's possible that microarthropods, such as oribatids and collembola, are affected the fungi by both predation and competition. All sampling dates show large weights for microarthropods on at least one axis, indicating that microarthropod abundance may have a substantial influence on microbial communities (Table 3.3). This is further supported by large positive and negative weights of fungal FAMEs found on axes that were also heavily influences by microarthropod abundance (Table 3.3, 3.4). However, it is uncertain whether the microarthropods and fungi are directly or indirectly affecting one another or simply responding similarly to environmental variables. FAMEs indicative of fungi often share loading direction (+,-) with microarthropods abundances on the same axes (Table 3.3, 3.4). This also appears to be true for other FAMEs as well, and the loadings may be an effect of environmental variables such as soil moisture and

%SOM. For multivariate analyses using NMS ordination, microarthropods were placed in the secondary matrix to determine if they had a significant, consistent effect on microbial biomass.

Relative abundances of fungi were also consistently higher in sites in conservation tillage (Table 3.6). This supports research involving "fast" and "slow" energy channels in agricultural systems, where soils in no-till evolve fungal dominated, "slow" energy channels, while soils in conventional tillage break down substrate via a bacterial dominated, or "fast" energy channel (Coleman et al 1983, Curl and Truelove 1986, Hendrix et al 1986, Allen-Morley and Coleman 1989, Moore et al 1998, Doles 2000). However, because not all fatty acids were used in the taxonomic analysis, and other FAMEs have not yet been identified as specific microbial markers, it is too early to say whether "fast" or "slow" energy channels are dominant in these five soils. In a study involving the transition from conventional to alternative agriculture, Doran et al (1987) found that microbial populations and activities were regulated more by crop type and rotation than by soil physical properties. In a structurally unstable soil, Gonzalez et al (2003) found an increase in humification in soils in no-till as compared to those in reduced tillage, indicating that microbial populations were probably influenced by increases in organic matter. Schutter and Dick (2001) reported season and soil type to be dominant factors over management techniques. Buyer and Kaufman (1996) showed no effect of agricultural treatment on the microbial community and suggested that, due to methodology, diversity measurements may remain high in conventional agriculture despite increased disturbance.

Conclusions

In this study, the abundance and diversity of microbial functional groups were most heavily influenced by soil C, %SOM, and soil moisture (Table 3.3). Most sites in conservation tillage were not significantly different from one another in terms of microbial community structure (Table 3.6). This is encouraging, because it implies that the microbial community in the transitional field does not lag behind the other no-till sites, and this will benefit soil nutrient cycling. However, both the NMS and the ANOVA show consistent differences between the four sites in conservation tillage and the site in conventional tillage. The site in conventional tillage (site 0) is situated over the Fuquay series. Like all soils in this study, low fertility, low organic matter, and low pH characterize Fuquay soils. However, it also has poor water holding capacity, a deep root zone and moderate permeability (Appendix A). These characteristics should place site 0 between flood prone sites on the Pelham series (sites 1,10) and site 5, in the severely eroded Carnegie/Cowarts complex. Site 0 should also be closely aligned with site 30, in the Tifton series, which is similar to the Fuquay series but has better water holding capacity (Appendix A). Univariate and multivariate analyses in this study have shown no indication of alignment of sites along soil series. Therefore it's possible that while these five sites are arranged on four separate soil series, there is potentially something different about site 0, above and beyond belonging to the Fuquay series. Season, crop type, and management regime all play a significant role in soil nutrient status, %SOM, and soil microclimate, which in turn have a significant effect on the stability and resilience of the soil food web. More studies involving sites within the same series should be done to separate the effects of land management from the effects of soil series.

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Table 3.1. Site characteristics (0-5cm) and mesofaunal abundance (log transformed) from five fields over two years of sampling.

Date	Site	N	Percent N	Percent C	C/N ratio	%SOM	soil moisture (%)	microarthropods	nematodes
Spring 2003	30	12	0.06 ± 0.07	1.02 ± 0.10	16.48 ± 0.59	1.02 ± 0.09	11.75 ± 0.62	1.32 ± 0.15	0.99 ± 0.07
Spring 2003	10	12	0.11 ± 0.04	1.02 ± 0.04	14.65 ± 0.26	0.86 ± 0.08	14.73 ± 0.59	1.14 ± 0.11	0.83 ± 0.04
Spring 2003	5	12	0.04 ± 0.001	0.66 ± 0.08	17.11 ± 0.82	0.64 ± 0.07	9.39 ± 0.78	0.53 ± 0.11	0.66 ± 0.06
Spring 2003	1	12	0.58 ± 0.01	0.98 ± 0.06	16.07 ± 0.42	0.60 ± 0.04	7.68 ± 0.35	1.04 ± 0.07	0.71 ± 0.08
Spring 2003	0	12	0.09 ± 0.01	1.72 ± 0.18	18.99 ± 0.40	0.68 ± 0.04	10.49 ± 0.54	0.37 ± 0.08	0.63 ± 0.08
Fall 2003	30	12	0.13 ± 0.01	1.94 ± 0.18	14.39 ± 0.10	0.83 ± 0.04	7.57 ± 0.73	0.48 ± 0.11	0.98 ± 0.02
Fall 2003	10	12	0.11 ± 0.01	1.43 ± 0.13	13.02 ± 0.14	0.66 ± 0.05	15.18 ± 1.30	0.71 ± 0.07	0.85 ± 0.03
Fall 2003	5	12	0.08 ± 0.1	1.03 ± 0.13	12.60 ± 0.43	0.49 ± 0.06	5.86 ± 0.83	0.32 ± 0.99	0.6 ± 0.06
Fall 2003	1	12	0.07 ± 0.004	1.03 ± 0.10	13.86 ± 1.32	0.53 ± 0.01	17.17 ± 0.89	0.43 ± 0.95	0.96 ± 0.09
Fall 2003	0	12	0.08 ± 0.004	1.38 ± 0.06	17.42 ± 0.32	0.74 ± 0.02	4.85 ± 0.25	0.19 ± 0.06	0.65 ± 0.05
Spring 2004	30	12	0.06 ± 0.003	1.02 ± 0.05	16.69 ± 0.26	0.75 ± 0.03	5.87 ± 0.81	0.37 ± 0.1	0.58 ± 0.12
Spring 2004	10	12	0.06 ± 0.01	1.02 ± 0.09	16.52 ± 0.66	0.66 ± 0.02	5.49 ± 0.47	0.43 ± 0.09	0.49 ± 0.12
Spring 2004	5	4	0.06 ± 0.01	0.94 ± 0.09	15.30 ± 063	0.43 ± 0.19	3.79 ± 1.23	0.61 ± 0.16	0.57 ± 0.07
Spring 2004	1	12	0.07 ± 0.003	1.29 ± 0.07	18.07 ± 0.72	0.49 ± 0.02	14.61 ± 0.63	0.24 ± 0.11	0.92 ± 0.13
Spring 2004	0	12	0.11 ± 0.01	2.07 ± 0.16	18.43 ± 0.17	0.55 ± 0.05	6.22 ± 0.17	0.16 ± 0.06	0.37 ± 0.09
Fall 2004	30	12	0.13 ± 0.01	1.73 ± 0.19	13.25 ± 0.11	0.82 ± 0.06	13.56 ± 0.98	0.65 ± 0.09	0.88 ± 0.06
Fall 2004	10	12	0.12 ± 0.01	1.60 ± 0.12	12.65 ± 0.14	0.69 ± 0.03	24.20 ± 0.62	0.8 ± 0.08	0.85 ± 0.08
Fall 2004	5	12	0.07 ± 0.003	0.90 ± 0.05	13.43 ± 0.35	0.49 ± 0.01	14.36 ± 0.72	0.68 ± 0.12	0.76 ± 0.1
Fall 2004	1	12	0.11 ± 0.01	1.51 ± 0.14	13.78 ± 0.23	0.61 ± 0.03	22.96 ± 0.60	0.78 ± 0.09	0.89 ± 0.04
Fall 2004	0	12	0.08 ± 0.003	1.41 ± 0.08	16.41 ± 0.36	0.75 ± 0.03	12.90 ± 1.35	0.64 ± 0.06	0.91 ± 0.09

Values are averages ± standard error

Table 3.2. Diversity (D') and total number (s) of fatty acids extracted from 3 g samples

			D'		s		
Date	Site	N	Mean ± S.E.		Mean ± S.E.		
Spring 2003	30	12	0.87 ±	0.020 a	15.75 ±	1.890	a
Spring 2003	10	12	0.86 ±	0.030 a	14.80 ±	1.380	a
Spring 2003	5	10	0.80 ±	0.090 a	13.60 ±	2.080	a
Spring 2003	1	12	0.90 ±	0.006 a	18.40 ±	1.290	a
Spring 2003	0	12	0.90 ±	0.006 a	18.50 ±	1.420	a
Fall 2003	30	12	0.90 ±	0.003 bc	20.16 ±	1.290	c
Fall 2003	10	12	0.91 ±	0.001 a	27.58 ±	1.400	a
Fall 2003	5	12	0.89 ±	0.003 c	18.08 ±	0.640	c
Fall 2003	1	11	0.91 ±	0.003 ab	21.72 ±	0.770	bc
Fall 2003	0	12	0.91 ±	0.001 ab	24.17 ±	0.940	b
Spring 2004	30	12	0.90 ±	0.002 a	25.83 ±	0.790	a
Spring 2004	10	12	0.91 ±	0.003 a	27.33 ±	0.420	a
Spring 2004	5	4	0.88 ±	0.010 a	22.33 ±	2.690	a
Spring 2004	1	12	0.91 ±	0.008 a	23.66 ±	1.400	a
Spring 2004	0	12	0.90 ±	0.003 a	28.50 ±	0.420	a
Fall 2004	30	12	0.91 ±	0.002 b	27.83 ±	1.400	b
Fall 2004	10	12	0.92 ±	0.002 a	32.66 ±	0.880	a
Fall 2004	5	12	0.90 ±	0.004 b	23.17 ±	1.510	c
Fall 2004	1	12	0.91 ±	0.003 a	27.83 ±	1.130	b
Fall 2004	0	12	0.91 ±	0.001 ab	29.33 ±	0.210	ab

Letters denote differences at $p<0.05$ within sampling dates only

Table 3.3. Environmental variables* with high loadings (p>0.2, p<-0.2) on the first, second and third axes (where applicable)

Date	Variable	Weight
Spring 2003		Axis 1
	N	-0.323
	C	-0.33
	CNratio	-0.286
	W	-0.453
		Axis 2
	C	0.549
	CNratio	0.246
	marths	-0.207
		Axis 3
	C	-0.396
	CNratio	-0.278
	marths	0.556
Fall 2003		Axis 1
	CNratio	0.459
	SOM	0.42
	moisture	-0.387
		Axis 2
	moisture	-0.316
	marths	-0.332
		Axis 3
	CNratio	0.677
	SOM	0.452
	marths	-0.218
Spring 2004		Axis 1
	C	0.297
	CNratio	0.408
	SOM	0.292
	W	0.332
	marths	-0.35
		Axis 2
	W	-0.265
Fall 2004		Axis 1
	N	0.488
	C	0.543
	SOM	0.624
		Axis 2
	CNratio	0.45
	W	-0.237
	marths	-0.297

**N, percent nitrogen; C, percent carbon, CN, C/N Ratio; SOM, soil organic matter; W, soil moisture; marths, microarthropod abundance; nems, nematode abundance.*

Table 3.4. Microbial FAMEs with high loadings (p>0.2, p<-0.2) on the NMS axes

	Axis	1	2	3	
Date			Weights		Microbial Marker
Spring 2003	i16:0		0.484		Gram-positive bacteria
	i17:0	-0.365	-0.431		Gram-positive bacteria
	a17:0	-0.202	0.728		Gram-positive bacteria
	16:1w7c	0.619	-0.16	0.689	Gram-negative bacteria
	cy17:0	0.499	0.229		Eubacterial anaerobes (gram-)
	cy19:0	-0.618	-0.309	0.249	Eubacterial anaerobes (gram-)
	18:0	-0.332	-0.382	-0.465	Non-specific bacteria
	18:2w6	0.501	-0.333	0.31	Fungi
	18:1w9t	0.514	-0.739	0.477	Fungi
	18:1w9c	0.385	-0.73	0.481	Fungi
Fall 2003	i16:0	0.361			Gram-positive bacteria
	i17:0	-0.201	0.281	-0.305	Gram-positive bacteria
	a17:0	0.373			Gram-positive bacteria
	16:1w7c	-0.584	-0.446	-0.313	Gram-negative bacteria
	cy17:0		-0.412	0.363	Eubacterial anaerobes (gram-)
	cy19:0	0.501	0.6		Eubacterial anaerobes (gram-)
	18:0	-0.199	0.643	0.636	Non-specific bacteria
	18:2w6	-0.715	0.037	-0.587	Fungi
	18:1w9t	-0.834	-0.128		Fungi
	18:1w9c	-0.507	0.213	-0.73	Fungi
Spring 2004	i16:0	-0.465	0.492		Gram-positive bacteria
	i17:0	-0.384			Gram-positive bacteria
	a17:0	-0.502			Gram-positive bacteria
	16:1w7c	-0.33	0.286		Gram-negative bacteria
	cy17:0	-0.486			Eubacterial anaerobes (gram-)
	cy19:0				Eubacterial anaerobes (gram-)
	18:0	0.244	0.401		Non-specific bacteria
	18:2w6		0.783		Fungi
	18:1w9t	-0.214			Fungi
	18:1w9c	-0.282	0.936		Fungi
Fall 2004	i16:0	-0.055	0.57		Gram-positive bacteria
	i17:0	-0.559	0.488		Gram-positive bacteria
	a17:0	-0.159	0.358		Gram-positive bacteria
	16:1w7c	-0.876	0.021		Gram-negative bacteria
	cy17:0	0.102	-0.507		Eubacterial anaerobes (gram-)
	cy19:0	0.004	0.44		Eubacterial anaerobes (gram-)
	18:0	-0.472	0.411		Non-specific bacteria
	18:2w6	-0.72	-0.176		Fungi
	18:1w9t	-0.858	0.238		Fungi
	18:1w9c	-0.896	-0.055		Fungi

Table 3.5. ANOVA results (p-values) for date, site and treatment effects for functional groups

	Gram-positive bacteria	Gram-negative bacteria	Eubacterial anaerobes (gram-)	Fungi
Date	<0.0001	<0.0001	<0.0001	<0.0001
Site	<0.0001	<0.0001	<0.0001	<0.0001
Compost	NS	NS	NS	NS
Site x compost	NS	NS	0.0173	0.0021

NS = p>0.05.

Table 3.6. Differences in FAME % mol fraction of functional groups between sites over two years

Date	Site	N	Gram-positive	Gram-negative	Eubacterial anaerobes	Fungi
Spring 2003	30	9	8.81 ± 0.41a	8.92 ± 0.24ab	6.87 ± 0.29ab	17.74 ± 1.67a
	10	12	8.19 ± 0.37ab	8.51 ± 0.90ab	7.01 ± 0.66ab	16.01 ± 0.64a
	5	9	6.61 ± 0.63bc	9.38 ± 0.46a	8.10 ± 0.59a	19.67 ± 1.08a
	1	12	5.76 ± 0.36c	8.66 ± 0.36ab	5.61 ± 0.32b	19.38 ± 0.99a
	0	11	7.64 ± 0.20bc	6.52 ± 0.73b	6.15 ± 0.68ab	9.08 ± 0.48b
Fall 2003	30	12	8.84 ± 1.01a	10.33 ± 0.33a	7.50 ± 0.45a	18.64 ± 0.84a
	10	12	8.41 ± 0.25a	8.48 ± 0.44bc	5.23 ± 0.39bc	18.08 ± 0.84a
	5	12	9.41 ± 0.29a	9.41 ± 0.25ab	5.77 ± 0.25bc	21.36 ± 1.06a
	1	11	6.98 ± 0.21a	8.86 ± 0.35bc	4.79 ± 0.18c	18.75 ± 0.67a
	0	12	7.52 ± 0.13c	7.85 ± 0.35c	6.31 ± 0.27b	11.90 ± 0.36b
Spring 2004	30	12	7.46 ± 0.13a	7.72 ± 0.16a	4.44 ± 0.19a	27.41 ± 2.00ab
	10	12	6.82 ± 0.18b	6.96 ± 0.12b	4.09 ± 0.08a	28.02 ± 1.59ab
	5	4	7.25 ± 0.28a	7.20 ± 0.17b	3.34 ± 0.38b	30.64 ± 1.46a
	1	12	4.72 ± 0.21c	6.50 ± 0.33c	3.08 ± 0.17b	24.07 ± 1.52b
	0	11	6.60 ± 0.18b	6.19 ± 0.07c	4.49 ± 0.10a	23.80 ± 1.53b
Fall 2004	30	12	7.36 ± 0.12b	6.56 ± 0.26c	3.88 ± 0.20a	15.51 ± 0.35a
	10	12	7.81 ± 0.08a	7.49 ± 0.11b	4.36 ± 0.08b	17.13 ± 0.31a
	5	12	7.76 ± 0.24a	8.09 ± 0.18a	3.92 ± 0.10a	21.81 ± 0.51a
	1	12	6.26 ± 0.13d	7.67 ± 0.27b	4.02 ± 0.05a	16.01 ± 0.91a
	0	12	6.66 ± 0.18c	6.63 ± 0.13c	4.41 ± 0.05b	15.87 ± 0.88a

Letters denote significance at $p<0.05$

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Figure 3.7. Ordination of the fall 2003 (Axes 2,3) dataset as determined by Non-metric multidimensional scaling (NMS). N = 11 for sites 1,5, and 30 due to low relative abundance of fatty acids in three samples which were removed for analysis.

Figure 3.8. Ordination of the spring 2004 (Axes 1,2) dataset as determined by Non-metric multidimensional scaling (NMS). N = 4 for site 5; 8 samples were not collected at that site on that sampling date. N = 11 for site 10 due to low relative abundance of fatty acids in one sample which was removed for analysis.

Figure 3.9. Ordination of the fall 2004 (Axes 1,2) dataset as determined by Non-metric multidimensional scaling (NMS).

Figure 3.1

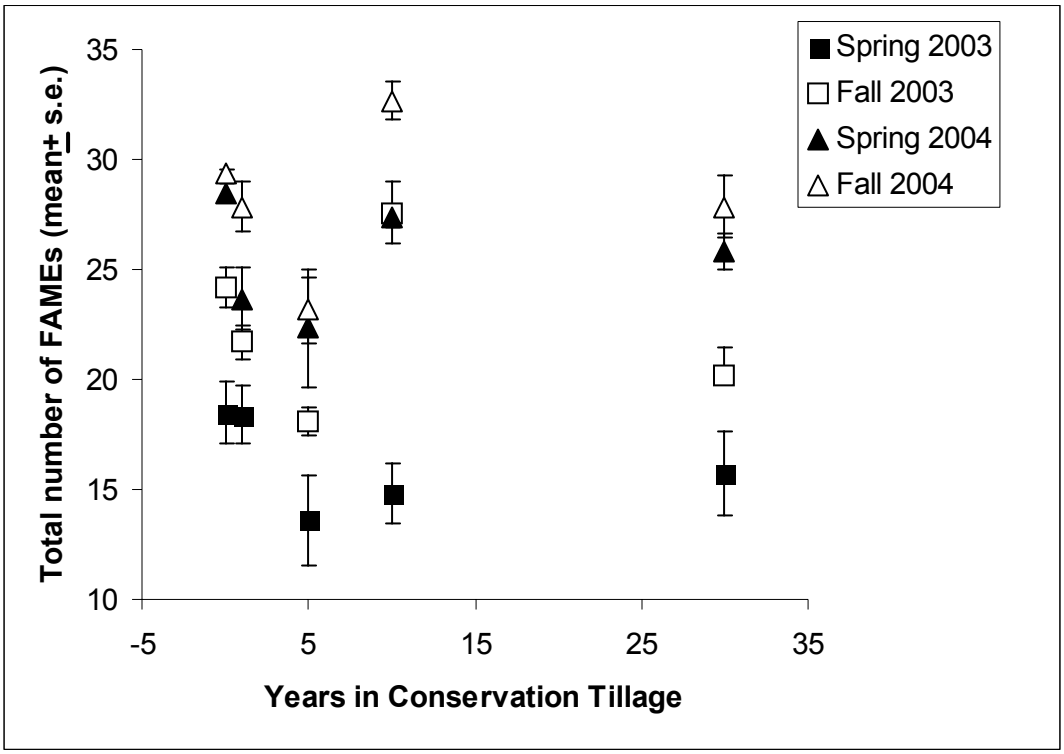

Spring 2003
Fall 2003
Spring 2004
Fall 2004
Total number of FAMEs (mean± s.e.)
35
30
25
20
15
10
-5
5
15
25
35
Years in Conservation Tillage

Figure 3.2

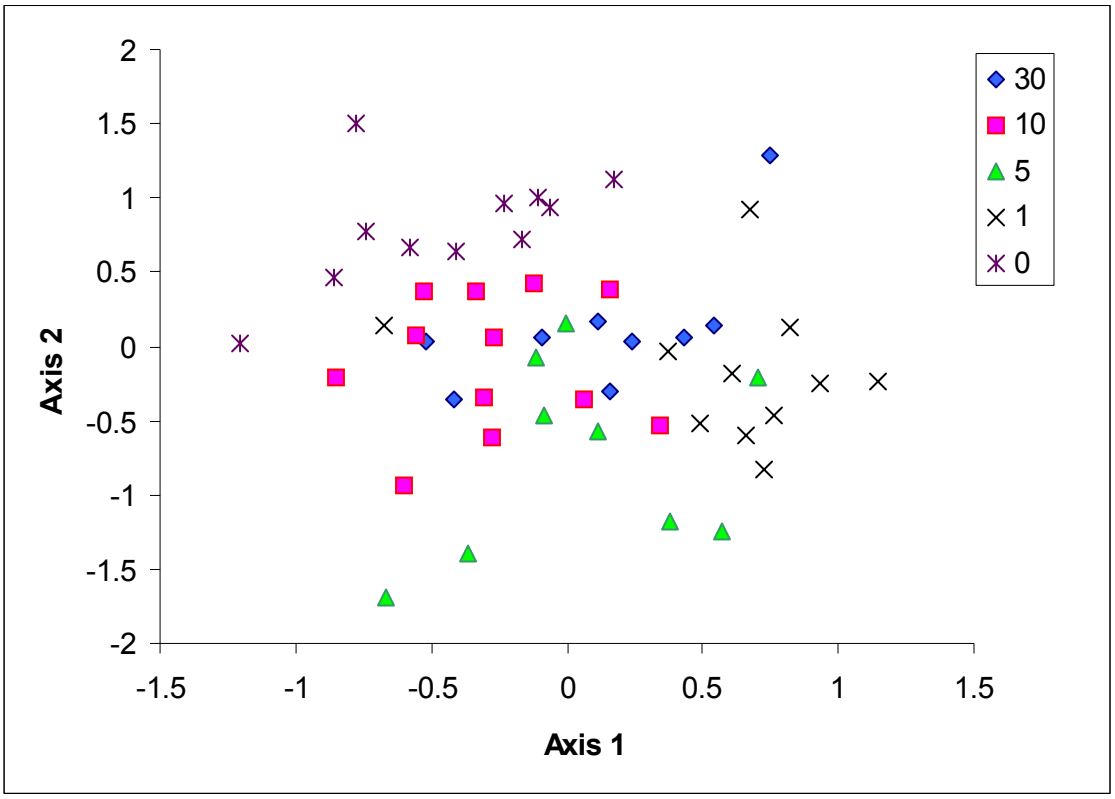


Figure 3.3

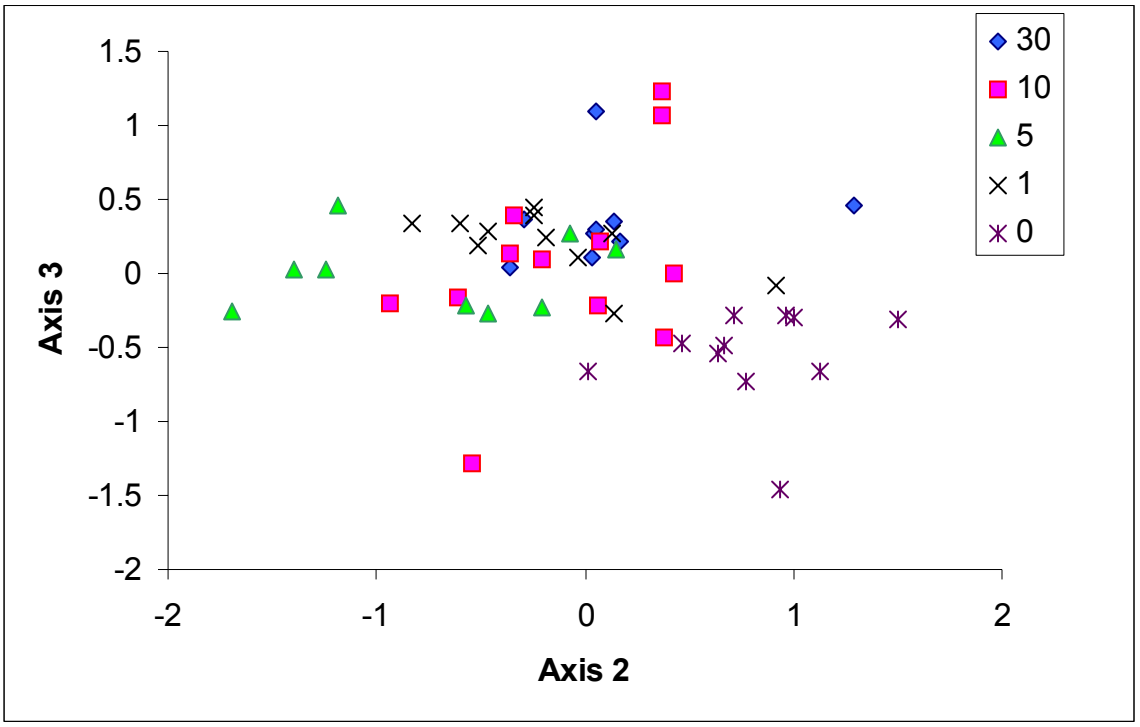


Figure 3.4

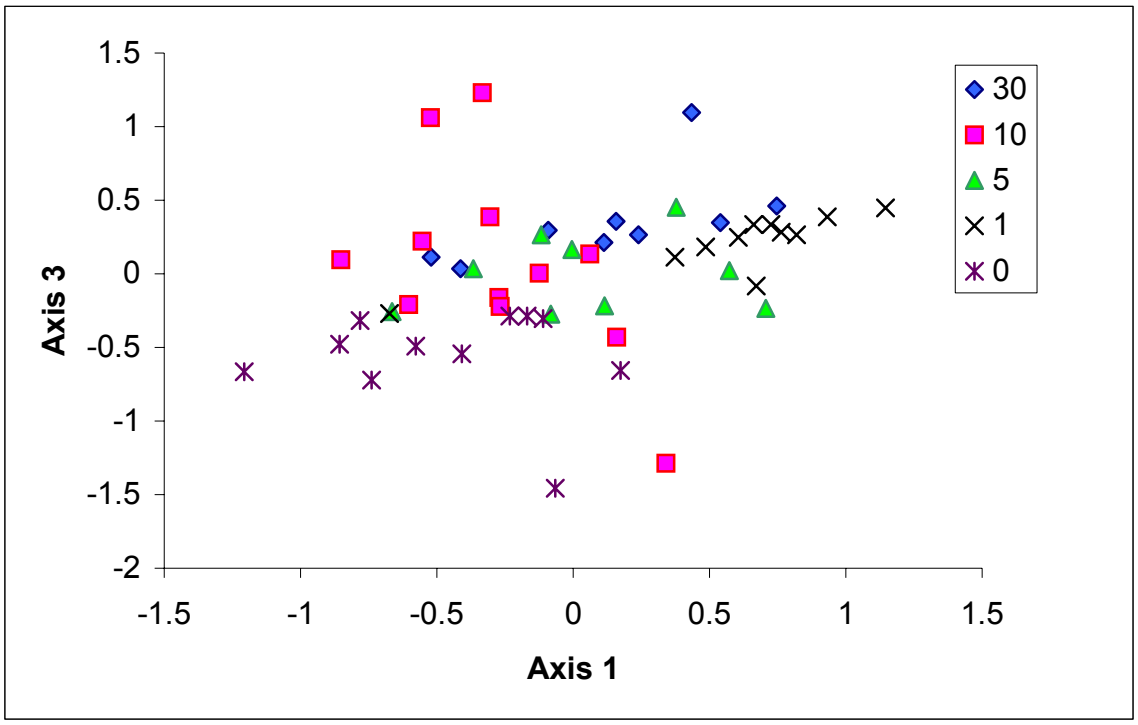


Fig 3.5

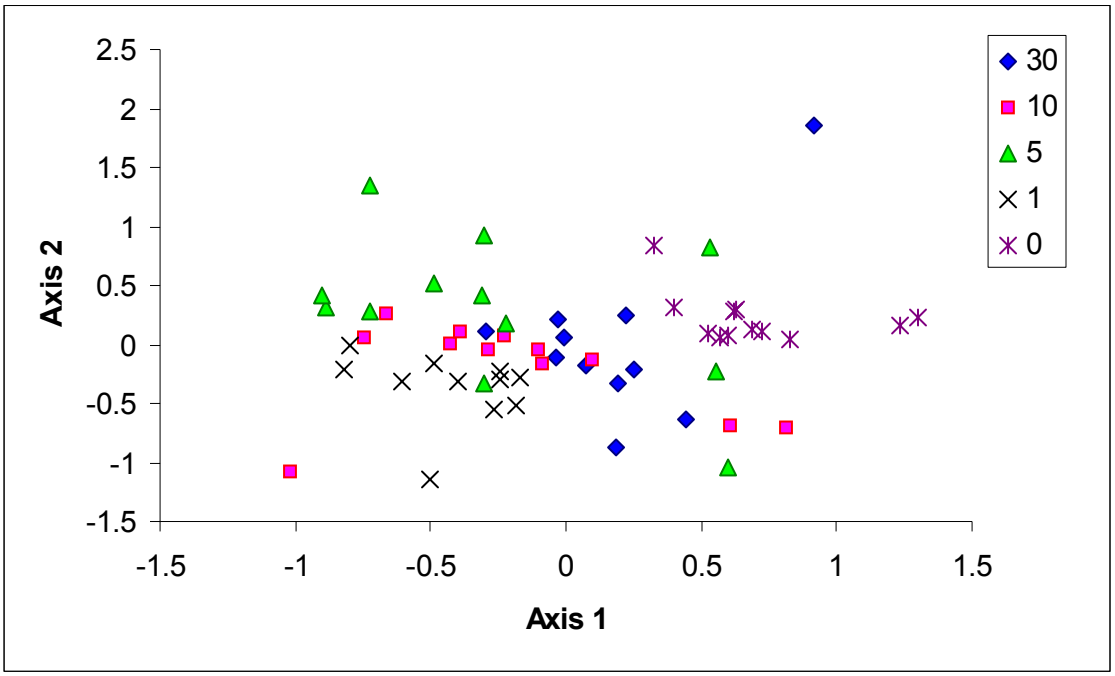


Fig 3.6

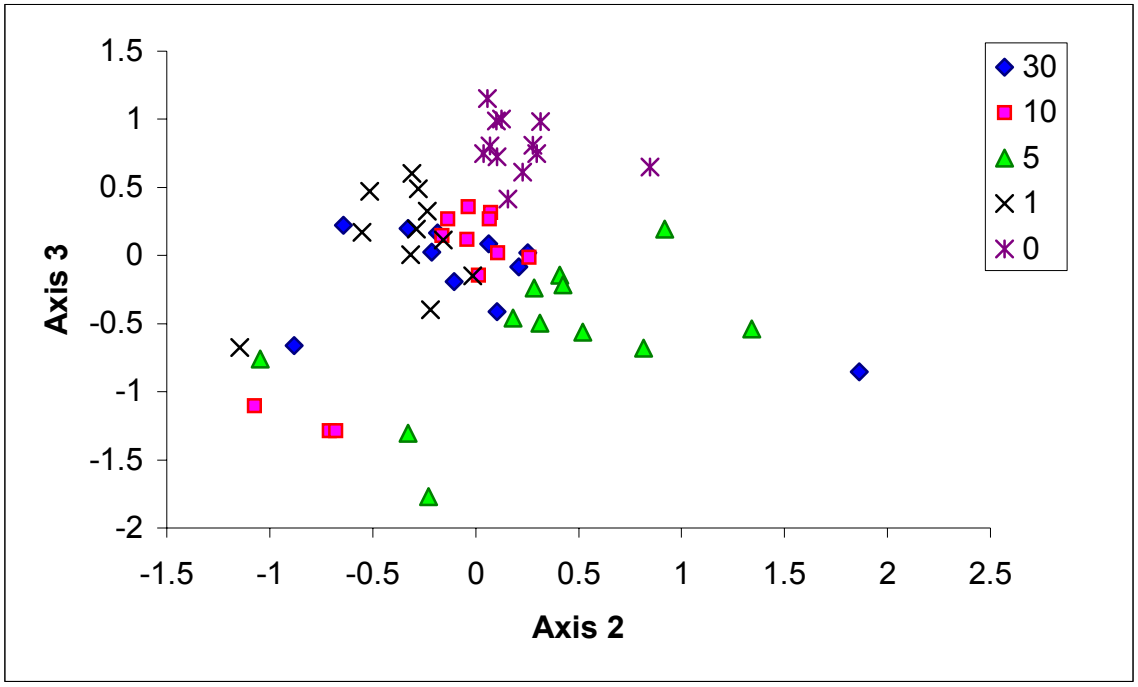


Fig 3.7

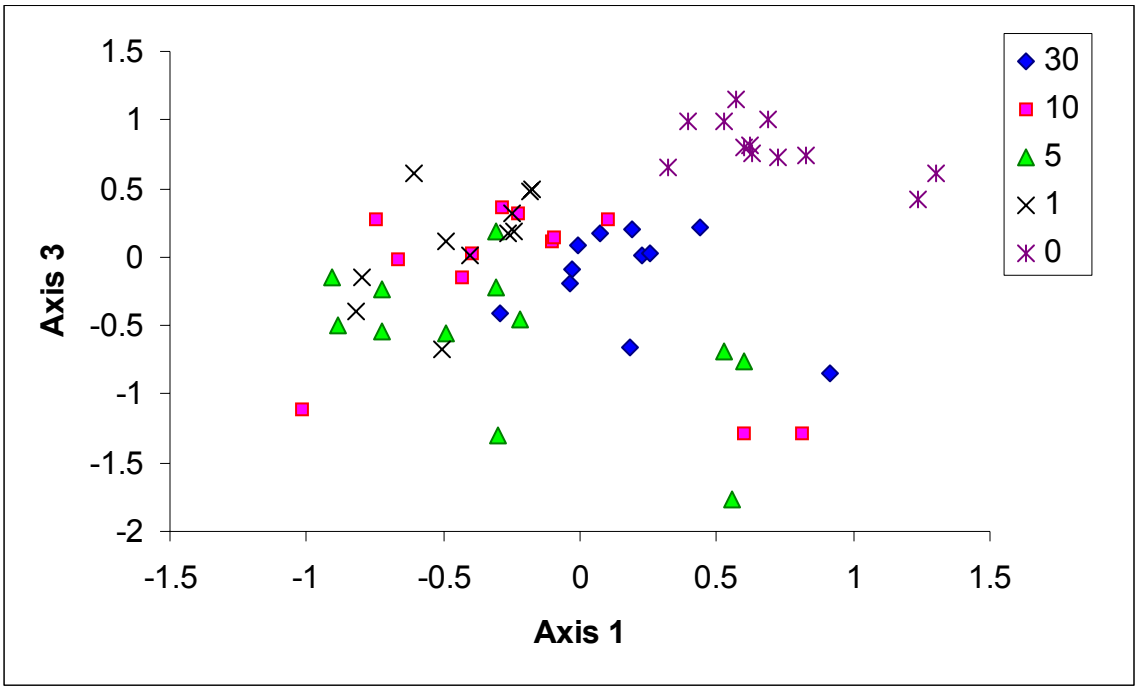


Fig 3.8

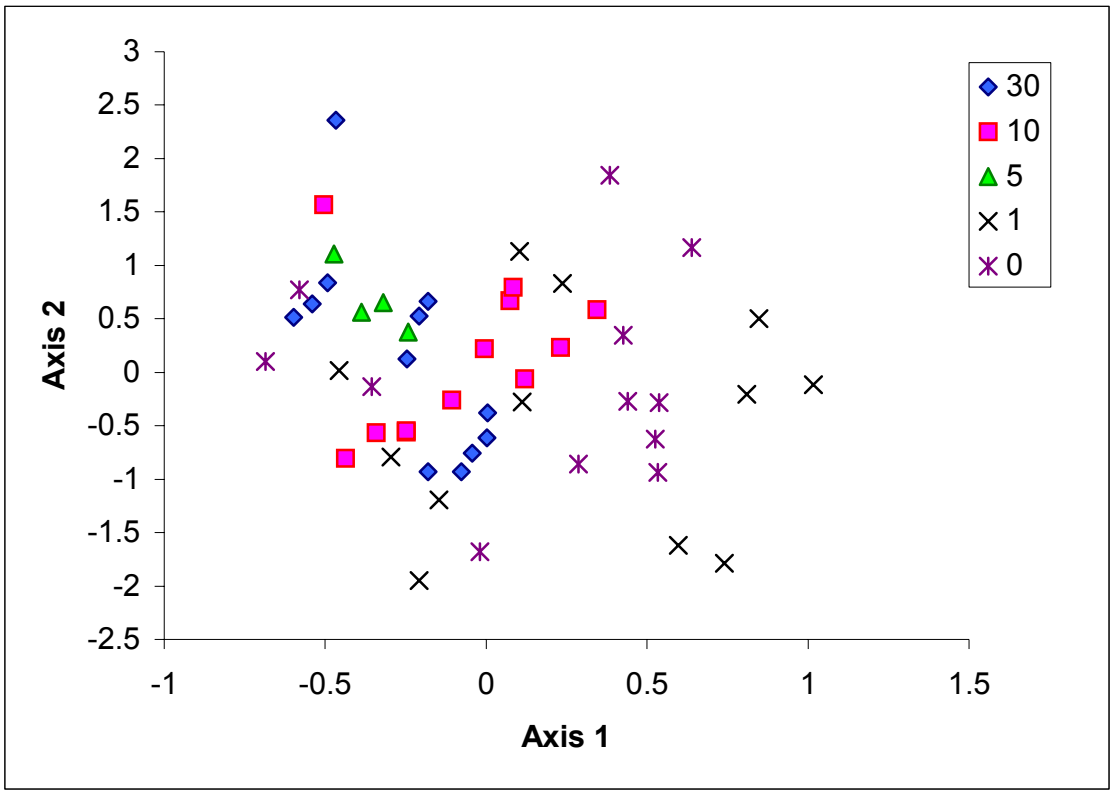
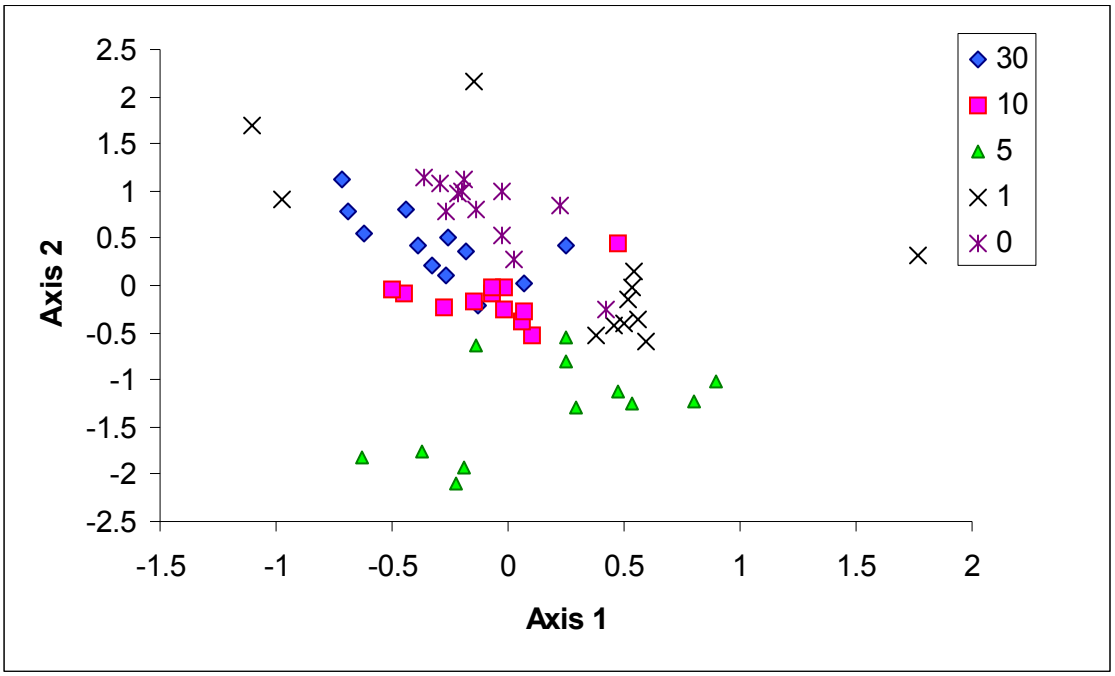


Fig 3.9



CHAPTER 4

THE EFFECTS OF AGRICULTURAL LAND MANAGEMENT AND SOIL TYPE ON SOIL FOOD WEBS: A COMPARISON OF THE PIEDMONT AND THE COASTAL PLAIN, IN GEORGIA (USA)[1]

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Abstract

Conventional tillage practices, in which plant residues are incorporated into the soil, increase the risk of soil erosion and contribute to contamination of water sources by leaching of fertilizers and pesticides. Conservation tillage, a practice that involves reduction or elimination of tillage and the use of a cover crop, is beneficial in area prone to severe erosion or loss of moisture. However, not all soil type can be expected to respond in the same way to a particular land management technique. The objective of this comparison study was to separate the effects of tillage from the inherent differences in soil type on soil food webs. Three sites in three soil series were chosen to represent Piedmont and Coastal Plains soils: an agroecology research site in the Hiwassee soil series in Clarke County, GA, a long term conservation tillage site in the Tifton soil series in Coffee County, Georgia, and a conventionally tilled site in the similar Fuquay soil series in Coffee County, Georgia. Abundances of nematodes, microarthropods and microbial community composition were assessed from each site. Results indicate that soil series has a potentially greater effect on soil food webs than tillage for most biota, and decisions about land management regime should include the best available data for that particular soil type.

Keywords conservation tillage, soil series, microarthropods, nematodes, FAME, microbial diversity, Georgia Piedmont, Georgia Coastal Plain

Introduction

Conservation tillage is now fairly common in areas where decreasing erosion or moisture retention is a priority (Holland 2004). Variations of conservation tillage, including no-till, reduced till and cover cropping, is currently practiced on 45 million Ha worldwide (Lal 2001). Disturbance caused by tillage and the incorporation of crop residue affects the physical, chemical and biological properties of the soil ecosystem. Conventional tillage practices, in which plant residues are incorporated into the soil, increase the risk of soil erosion and contribute to contamination of water sources by leaching of phosphates and pesticides. Fields that are subjected to conventional tillage also suffer from a depletion of soil organic matter (SOM) (Keeling et al. 1989).

Conservation tillage systems use cover crops on the soil surface to add residues to maintain SOM while eliminating tillage. Implementing conservation tillage practices not only reduces erosion, but also results in increased infiltration, increased soil moisture and increased SOM. Accumulation of SOM in areas of the southern Piedmont that were previously tilled is associated with enhanced fertility and increased mineralization of soil nutrients (Beare et al. 1994, Hendrix et al. 1998). Conservation of organic matter is important to the physical, chemical and biological functions of the soil. SOM stabilizes soil pH, which is essential for nutrient uptake by plants, and is the main resource for the soil biota that are responsible for mineralizing nutrients (Campbell et al. 1996). Cation exchange capacity, water holding capacity, microbial activity, and reduction of soil compaction are all positively influenced by increased SOM. Fields suffering from severe erosion, a common problem in the southern Piedmont, can recover with conservation

tillage practices (Coleman et al. 2001) These changes can minimize inputs and maximize water use efficiency in row cropping systems.

Soil organic matter (SOM) is the foundation of the soil food web and the preferred habitat of most soil biota. Turnover of organic matter is governed by microbial activity and primary plant production. Decomposition of SOM pools by soil biota determines the efficacy of nutrient cycling in soil ecosystems, which in turn affects aboveground productivity. This process depends on the quality and quantity of substrate provided to primary consumers, but is also driven by abiotic factors, such as climate, soil structure and land management practices. Artificial adjustments to the organic matter pools, such as incorporation of crop residues and fertilization, alters the structure and function of SOM, often resulting in a reduction or shift in nutrient cycling efficiency. Incorporated plant residues and root exudates provide substrate for fungal and bacterial growth and promote the formation of biological aggregates (Jastrow et al. 1998). As the basis of the food web, these types of alterations to SOM pools cascade through the trophic levels, affecting top consumers responsible for top-down control of food web consumers.

The activity of soil biota is largely responsible for the mineralization of nutrients from the soil, and is therefore an important component of soil function (Ingham et al. 1985, Hunt et al. 1987, Moore 1988, Beare et al. 1992). This is especially important in low input sustainable agriculture, where increased microbial diversity is expected to increase soil quality (Parr et al. 1992, Visser and Parkinson 1992). Microbial diversity is expected to increase with a reduction in tillage, as fungal species begin to dominate the system (Hendrix et al. 1987). The ability of an ecosystem to withstand disturbance may

lie in the energy pathway, where bacterial dominated systems are more resilient than fungal dominated systems (Allen-Morley and Coleman 1989, Moore et al. 2003). Moore et al (2003) postulated that recovery times of each energy channel to disturbance may be different, and result in an alteration of the food web. Several studies have found effects of land management practices on soil microbial diversity and abundance (Liljeroth et al. 1990, Frostegård et al. 1993, Kirchner et al. 1993, Zelles et al. 1994, Haslam and Hopkins 1996). In a study involving the transition from conventional to alternative agriculture, Doran et al (1987) found that microbial populations and activities were regulated more by crop type and rotation than by soil physical properties. Gonzales et al (2003) found an increase in humification in tropical soils in no-till as compared to those in reduced tillage, indicating that microbial populations were probably influenced by increases in organic matter. In an agricultural field in Pennsylvania, Buyer and Kaufman (1997) showed no effect of agricultural treatment on the microbial community and suggested that, due to methodology, diversity measurements may remain high in conventional agriculture despite increased disturbance.

Soils respond differently to abiotic and biotic factors based on climate, geographic range, and parent material. In the Piedmont, soil is high in clay, subject to winter frosts and consists mainly of $Fe(OH)_2^+$. On the Coastal Plain, soils are sandy, the temperatures are milder, and the most common mineral in the soil is a reduced iron oxide ($Fe(OH)_3^+$). These physical and chemical characteristics will influence the stability of the soil when disturbed. Because of these constraints on SOM pools and biotic interaction, a management technique that works for one type of soil may not work for another. The behavior of functionally dissimilar soils under the same land management regime has not

been fully investigated. Bossio et al (1998) reported that the influence of management and season on microbial communities were secondary to soil type. Differences in microbial community composition have also been shown across natural land gradients that encompass several soil types and textures in grasslands (McCulley and Burke 2004) and forests (Hackl et al. 2005).

All factors being equal, mechanistic disruption of the soil food web alters the rate of decomposition and nutrient cycling. However, no one soil performs the same way as another, so it is important to take a critical look at the soil as part of a broader system, such as the Coastal Plain and Piedmont regions of Georgia. This study compares fields in these two dissimilar soil habitats: Horseshoe Bend, a research site on the Piedmont, and Coffee County, where two fields on the Coastal Plain are in different tillage regimes.

Materials and Methods

Collection sites

For examination of the Coastal Plain, soil was collected from two cotton fields near Douglas in Coffee County, Georgia (USA), at map coordinates 31° 32′N, 82° 52′W. One field was in conventional tillage. One field was under conservation tillage for 30 years. The soils series were Fuquay (loamy, kaolinitic, thermic Arenic Plinthic Kandiudults) and Tifton (fine-loamy, kaolinitic, thermic Plinthic Kandiudults), respectively. Both fields had been continuously cropped for at least 30 years, and were planted in cotton or peanut for the duration of this study. The field in conservation tillage used a cover crop of rye in the winter to add organic matter. Herbicides and fertilizers are used at the beginning of each crop rotation. Lime is added approximately every other year or as needed.

On the Piedmont, data were collected from the Horseshoe Bend Agroecosystem Research Area, in Athens, Georgia (USA) (33° 56′N 83° 22′W). The soil is in the Hiwassee series (fine loamy, siliceous, thermic, Rhodic Kanhapudult) and has been cropped continuously since 1978. For the duration of this study the field plots at Horseshoe Bend were cropped in Bt or non-Bt cotton with a winter cover crop of rye or clover. A broad-spectrum herbicide was used in the summer to reduce weeds. No lime, fertilizers, or insecticides were added to this field during the duration of this study.

Experimental design

In Coffee County, four replicate plots were set up in each field, perpendicularly to row direction. No treatment was applied to these plots; they were control plots from a previous experiment. At Horseshoe Bend, eight subplots of a long term study on conservation tillage (Lachnicht et al. 2004) were chosen that were all in Bt cotton with a rye cover crop. Where data were unavailable or missing from long-term data sets for Bt cotton, data from subplots in non-Bt cotton with a rye cover crop were chosen.

Sampling

In Coffee County, sampling occurred four times in two years (Spring 2003, Fall 2003, Spring 2004, Fall 2004), at the end of each growing season, before the crop was mowed or incorporated. All samples were taken within the 1x2 center of each plot to avoid edge effects. Additional microarthropod samples were taken in May 2005. At Horseshoe Bend, sampling for microarthropod abundance, nematode abundance, microbial biomass and archiving are taken just before or just after the crop has been mowed, but before being incorporated in the tilled plots.

Samples were taken for soil C/N from the upper 5 cm of soil using a soil probe (dia=2 cm) and sealed in plastic bags. Soil for microbial FAME samples were taken from each plot with a soil corer (dia=2 cm) to a depth of 5 cm and sealed in plastic bags. Nematodes were sampled using a soil probe (dia=2 cm) from the upper 5cm of soil, sealed in plastic bags and placed in a cooler for transport. Microarthropods were sampled from the upper 5 cm of soil using steel rings (dia=5 cm) in a specialized beveled metal corer. Samples were wrapped in aluminum foil and sealed in plastic bags. All samples were transported to the lab in a cooler.

Comparison data from Horseshoe Bend were obtained from archived data sets representing the same time periods as the samples collected from Coffee County. Comparison of C/N data is from fall 2003 and spring 2004. For microarthropods, data are from spring and fall 2003. Nematode data sets were from fall 2003 and spring 2004. Soil was collected from both sites for FAME analysis in Fall 2004.

Laboratory procedures

Total carbon and nitrogen were determined on soil that was air-dried, ground, and weighed into tin capsules, on a Carlo Erba analyzer in the UGA Institute of Ecology Analytical Laboratory. Microarthropods were heat extracted over five days using modified Tullgren type funnels (Crossley and Blair 1991). Animals were collected in 70% ethanol and identified to order, suborder, or family under a dissecting microscope. Samples were prepared for permanent storage by transferring animals to 95% ethanol after identification.

Nematodes were extracted using the Baermann funnel technique (Baermann 1917). A 5 g subsample of wet soil was wrapped in a Kimwipe, placed on a metal screen

in water-filled, close-ended funnels. Samples were left on the funnels for 48h. Approximately 7 ml of water from the funnel was collected into 15ml centrifuge tubes and mixed with 7 ml of 5% formalin for preservation. Nematodes were counted under an inverted scope and categorized into feeding groups by morphological characters (Yeates et al. 1993). Nematodes in samples from Spring 2003 were counted and not categorized into trophic levels because the samples were compromised before identification could take place.

FAME procedures

FAME profiles were compiled using the MIDI method (Microbial ID, Inc., Newark, DE). For each sample 3.0 g of air dried soil was placed in a 30 ml glass centrifuge tube. 15 mL of methanol-KOH (0.2*N*) was added to each tube, and the tubes were capped using Teflon-lined screw caps. The centrifuge tubes were placed in a test tube rack in a 37º C water bath for 1h. Every 10min the tubes were vertexed for 20 sec. After the water bath, 0.5 mL of 1*N* acetic acid was repeatedly added to each tube until the pH of the solution was neutral. 10 mL of hexane was added to the soil suspension, and the mixture was vertexed for 30s ec. The tubes were centrifuged at 480 xg for 20 min. Approximately 7 ml of the hexane layer was transferred to a disposable test tube. The hexane was evaporated to complete dryness under a gentle stream of nitrogen. The dried extract was re-suspended in 1.0 mL of hexane and dried down again for shipment to an analytical lab in Deleware. In the analytical lab, the samples were re-suspended in a 1:1 mixture of hexane and tertiary-butyl methyl ether. The solution was transferred to a 2.0 mL gas chromatography vial and capped. The extract was analyzed with a HP 5890 gas-

liquid chromatograph equipped with a HP Ultra 2 capillary column (5%-diphenyl-95%-dimethylpolysiloxane, 25m by 0.2 mm) and a flame ionization detector.

Statistical analysis

Data were normalized using a log transformation and analyzed using a general linear model in SAS (SAS Institute 1989). Analysis of variance (ANOVA) was performed to determine if there were differences in nutrient status, and total abundances and diversity of soil mesofauna. Student-Newman-Keuls tests were used to determine significant differences in means between sites and treatments at the $p<0.05$ level. Mesofauna were also separated into feeding guilds (nematodes) or major groups (microarthropods) and analyzed for differences between sites using a general linear model in SAS. Analysis of variance (ANOVA) was performed to determine if the total number and diversity of FAMEs differed between sites. Data was standardized to fit assumptions of normality and analyzed for significant differences in percentages of mole fractions between sites using a general linear model in SAS. Principal Components Analysis (PCA) was also used to elucidate differences in microbial community composition between sites using FAMEs that were common to all three sites and represent a range of functional groups. The first and second principal components axis weights for each sample and subjected to ANOVA to test for significant differences in functional groups between the sites and soil series (McCulley and Burke 2004). ANOVA was also used on relative abundance (% mol fraction) data for microbial functional groups to test for significant differences between sites and soil series.

Results

Soil C/N ratio differed significantly between all soil series and ranged from 10 to 18 (Table 4.1). Sites on the Piedmont (Hiwassee) had significantly lower C/N ratios and the plots in conservation tillage (No-till-Hiwassee) generally had the highest percent carbon and nitrogen (Table 4.1). There were no significant differences in percent carbon or nitrogen between the no-till site on the Piedmont (Till-Hiwassee) and the sites from Coffee County (Fuquay and Tifton).

Group richness (S) and diversity (D′) of microarthropods were higher in the Hiwassee soil than in the Fuquay or Tifton soils (Table 4.2). The Fuquay soil consistently had a significantly lower number and diversity of soil microarthropod groups compared to other sites (Table 4.2). The site in conservation tillage in the Hiwassee series had the highest group richness and diversity compared to other sites, but this was not significantly different from the tilled site in the same soil series (Table 4.2). However, there were no significant differences in total abundance of each group between sites for any taxa except for Prostigmata, which were found in significantly higher numbers in the Hiwassee soil series (Table 4.3). Collembola and Prostigmata were generally higher in the no-till site in the Hiwassee series, while Oribatid, Astigmatid, and Mesostigmatid mites were generally more abundant in the Tifton soil (Table 4.2).

Principal components analysis of the microarthropods identified three axes that explained 93% of the variation in the data (Fig 4.1). Only the first and second axes are presented here. Principal Component Axis 1 (PC1) accounted for 57% of the variation in the data and was significantly related to both tillage ($df_{1,31}$, F=9.92, p=0.0037) and soil series ($df_{1,32}$, F=8.76, p=0.0011). Principal Component Axis 2 (PC2) accounted for 25%

of the variation in the data and was significantly related to soil series ($df_{2,31}$, F=9.21, p=0.0008) and but not to tillage ($df_{1,31}$, F=3.46, p=0.0729). Microarthropods groups with the highest positive weights on PC1 were Oribatids (0.707) and Mesostigmata (0.776). There were no negative weights on PC1. Microarthropod groups with the largest positive weights on PC2 were Oribatids (0.673) and Coleopterans (0.588), while groups with the largest negative weights were Astigmatina (-0.466) and Prostigmatid mites (-0.514).

Group richness (S) of nematodes was significantly higher in the Tifton and Fuquay soils compared to the Hiwassee soil (Table 4.2). Diversity (D′) of nematode feeding guilds was significantly lower in the tilled site in the Hiwassee soil series compared to other sites, and generally highest in the Fuquay and Tifton soils (Table 4.2). Abundance of bacterivores and fungivores were significantly higher in the Tifton soil compared to other soils (Table 4.4). Omnivores were found in higher numbers in the Tifton and Fuquay soils than in the Hiwassee soils (Table 4.4). Very few predatory or plant feeding nematodes were found in any sample from any site.

Principal components analysis of the nematode community identified two axes that explained 98% of the variation in the data (Fig 4.2). PC1 accounted for 95% of the variation in the data and was significantly related to soil series ($df_{2,31}$, F=9.84, p=0.0005) but not to tillage ($df_{1,31}$, F=3.75, p=0.0622). PC2 accounted for 3% of the variation in the data but was not significantly related to tillage ($df_{1,31}$, F=0.79, p=0.3813) or soil series ($df_{2,31}$, F=2.36, p=0.1123). Nematode feeding guilds with the largest negative weights on PC1 were bacterivores and fungivores. There were no positive weights on PC1. Nematode feeding guilds with the largest positive weight on PC2 was the fungivores, while the one with the largest negative weight was the bacterivores.

Total number of fatty acids extracted from the soil samples (S) was significantly higher in the Hiwassee soils than in the Fuquay or Tifton soils (Table 4.5). Diversity of fatty acids (D′) was also highest in the Hiwassee soils, and was significantly lowest in the Tifton soils (Table 4.5). Relative abundance (% mol fraction) of gram-positive bacteria was significantly higher in the Tifton soil compared to other soils (Table 4.6). Relative abundance of gram-negative bacteria was significantly higher in the Hiwassee soils compared to other soils (Table 4.6) Relative abundance of anaerobic bacteria was significantly higher in the Tifton soils compared to the Hiwassee soil, however there was no significant difference between the Fuquay soils and the Hiwassee soils (Table 4.6). There were no significant differences in relative abundance of fungi between any soil types, although the Hiwassee soils had higher values than the Fuquay or Tifton soils (Table 4.6). Relative abundance of protozoa was low in all fields, however it was significantly lower in the Tifton soil compared to other soil series (Table 4.6).

Principal components analysis of the FAME community identified two axes that explained 99% of the variation in the data (Fig 4.3). PC1 accounted for 87% of the variation in the data and was significantly related to soil series ($df_{2,31}$, F=10.15, p=0.0022) but not to tillage ($df_{1,31}$, F=0.06, p=0.8053). PC2 accounted for 12% of the variation in the data but was not significantly related to tillage ($df_{1,31}$, F=0.39, p=0.5402) or soil series ($df_{2,31}$, F=2.92, p=0.0892). FAME weights on both axes were variable and inconsistent among functional groups (Table 4.7).

Discussion

White et al. (1979) determined that total phospholipid fatty acids (PLFA) are an indicator of viable microbial biomass, and we used the total number of FAMEs to

estimate abundance and diversity of belowground organisms. While multiple fatty acid markers may indicate single species, plant material, or other organic matter, differences between these markers indicate a difference in the belowground community, and the data were analyzed accordingly. Diversity estimates were run on the percent mol fraction of all fatty acids present in all samples, and those samples with more fatty acids were determined to be more diverse. For quantitative analysis, this type of discrimination of the data is inappropriate, but we felt it was sufficient for the purpose of comparing sites in this experiment. It should also be noted that for Principal Components Analysis, only those fatty acids common to all sites and correlated with a functional group marker were used. This type of analysis necessarily leaves out certain fatty acids that may or may not have a significant effect on the data.

Soil C/N ratio was significantly different between soil series but not between tillage treatments in the same series (Table 4.1). The low C/N ratio in the Hiwassee soils may indicate a more active or opportunistic soil food web, dominated by bacteria. Hendrix et al (1986) postulated that in a no-till agricultural system, residue left on the surface will result in a high C/N ratio with an increase in surface saprophytic fungi, which slowly break down surface organic matter. This hypothesis is supported in the Hiwassee soil series, where the no-till plots had a higher C/N ratio (Table 4.1), higher species richness (Table 4.5), lower relative abundance of bacteria and higher relative abundance of fungi (Table 4.6) compared to the tilled plots. However, these differences were not significant within the soil series, and simply represent general trends (Table 4.6).

In Coffee County, the no-till soil (Tifton) had a significantly lower C/N ratio compared to the tilled soil (Fuquay) (Table 4.1) as well as lower fatty acid abundance and diversity (Table 4.5). The Tifton soil also has a significantly higher relative abundance of gram-positive bacteria compared to the Fuquay soil, and a lower relative abundance of protozoa (Table 4.6). This appears to be counterintuitive according to the above hypothesis, which predicts that soils in no-till will have a lower abundance of bacteria compared to fungi, as sites in no-till convert to the "slow" energy channel dominated by fungi (Moore et al. 2003). The Tifton site had slightly higher abundance of fungi compared to the Fuquay site, it also had higher relative abundance of bacteria. However, the PCA of the FAME data reveals that 87% of the variation in the relative abundance of common fatty acids is significantly related to soil series, not tillage (Fig 4.3). This indicates that, for the identified microbial markers used in this comparison, the effects of soil type dominate the effects of tillage regime on the soil microbial community. Based on axis weights for fatty acids, fungal markers are negatively correlated with PC1 (Table 4.7), which indicates that they may have a stronger inherent relationship with Hiwassee soils compared to Fuquay or Tifton soils (Fig 4.3).

Fungi have also been shown to become more abundant as soil pH decreases, and recalcitrant organic matter increases (Morton 1998, Coleman et al. 2004). Based on the highly acidic nature of the Fuquay and Tifton soils, it was expected that fungal biomass would be highest in those sites. However, regular liming of the soils in Coffee County to pH=6.5 and the lack of pH data from the Hiwassee soils prevents us from making conclusive statements regarding relative abundance of fungi and soil pH.

These effects were not as clear in the soil mesofauna community. Total abundance and diversity of microarthropod groups were highest in the Hiwassee soil series, although the Tifton soil was not significantly different from the Hiwassee soil in tillage (Table 4.2). The Fuquay soil had significantly lower abundance and diversity than the other fields (Table 4.2) but this is likely due to a high number of zero counts in the microarthropod community data (Table 4.3). Very few microarthropods were extracted from Fuquay soils on any date, making it difficult to assess the affects of tillage and soil series on the data. There are no significant correlations between microarthropod groups known for feeding on fungi and relative abundance of fungi, although the Hiwassee soil in no-tillage did have the highest number of Collembola and the highest relative abundance of fungi compared to other soils (Table 4.3, Table 4.6). Collembola are expected to decrease in response to tillage (Culik et al. 2002), and this was true for our study, where despite a lack of significant differences, there was a decrease in Collembola in tilled sites across soil types (Table 4.3). Mesostigmata, predatory mites generally negatively affected by tillage (Wardle et al. 1995), were found in the highest numbers in no-till soils, but this was not a significant difference (Table 4.3). The abundance of Oribatids, expected to be negatively affected by tillage (Wardle et al. 1995), was significantly lower in the Fuquay soil but not different between soils in different tillage regimes in the Hiwassee series, which means they may not be as sensitive to tillage as previously considered (Table 4.3).

Results from the PCA show that variation in microarthropod data on PC1 was related to both tillage and soil series, while PC2 was related only to soil series (Fig 4.1). This indicates that microarthropod communities may be more sensitive to mechanical

disruption than microbial communities (Fig 4.3). This was expected, due to the larger size of the microarthropods, which can become trapped or crushed in soil pores during tillage events. Oribatids had a large positive loading on both axes and likely affected the distribution, due to large disparity between the numbers of these mites extracted from the Fuquay and Tifton soils (Table 4.3).

Total abundance and diversity of nematodes was higher in the soils from the Coastal Plain compared to the Piedmont (Table 4.2). This trend was also shown in the feeding guild data, where the Tifton soil had significantly higher numbers of bacterivores, fungivores and omnivores compared to other sites (Table 4.4). This was expected for bacterivores, because the Tifton soils had higher relative abundances of both gram-positive and gram-negative bacteria (Table 4.6). Abundance of fungivores was expected to be higher in the Hiwassee soils, due to an increase in the relative abundance of fungi (Table 4.6). The increased abundance of nematodes in the Tifton soil may be related to soil moisture. The relative abundance of Eubacterial anaerobes was significantly higher in the Tifton soil (Table 4.6), which may be related to wetter conditions at that site compared to soils collected at other sites. Nematodes require a water film for locomotion, and feed in water lined pores in the soil matrix (Coleman et al. 2004). Bacterial feeding nematodes have also been shown to increase in response to organic inputs (Bullock et al. 2002). However, there were no organic inputs at the site on the Tifton series during the study period.

Results from the PCA indicate that nematodes are sensitive to soil series but not to tillage (Fig 4.2). There were no significant differences in nematode abundance or diversity between tillage treatments in the Hiwassee soil series (Tables 2, 4). The

abundance and diversity of nematodes extracted from Tifton soils is significantly different from the other two soil series (Table 4.2), and therefore it is likely that it had a large effect on the multivariate analysis. Despite normalization of the data, points representing Tifton soils are skewed to the far left, and resemble outliers (Fig 4.2). There were no nematode feeding guilds with positive loadings on PC1, and this is probably due to the nematodes found in the Tifton soils. However, when the Tifton data and data from the Hiwassee no-till plots (No-till-Hiwassee) were combined and analyzed against the tilled plots, there were no significant differences (PC1, p=0.0622; PC2, p=0.3813). This indicates that the high variation in the data from the Tifton series was not enough to carry the effects of no-tillage alone, and that there is a real significant effect of soil type on nematode community composition.

The high variability in the data appears to be related to soil series but may also be confounded by site history. The site located on the Tifton soil series was cropped in peanut during 2003, after several years in cotton. In 2004 the field had returned to cotton, but it's possible that the peanut residue was higher in nitrogen, which may have affected the decomposer community. It's also possible the mechanical harvesting of peanut, which must be pulled from the ground, disturbed the soil organic matter. Any change in the quantity or quality of organic matter will affect the microbial decomposer community and the higher trophic levels that rely on it as a food source. Schutter et al (2001) report that cover crop residues enhance fungal and protozoan populations, and this is supported by our data, which shows a lower relative abundance of fungi and protozoa in the Fuquay soil (Table 4.6), which was the only site in this study that did not use a winter cover crop. Frostegård et al. (1993) report a significant shift in acidic forest soil microbial

communities in response to lime application. Both the Tifton and the Fuquay soils were limed during the course of this study, while the Hiwassee soils had not been limed in at least ten years.

Conclusions

Soils in the Fuquay and Tifton series were chosen for this study because they are very similar to each other. Both soil series are similar in color and texture. They are also highly acidic, low in organic matter and natural fertility with moderate permeability, good tilth and deep root zones (Appendix 1). Both soils are well suited to field crops and pasture, however, available water capacity in the Fuquay soils is low while Tifton soils have moderate available water capacity. Tifton soils are in the Dothan series, while Fuquay soils have no competing series (NRCS-OSD). These soils were considered similar enough to compare with Hiwassee soils from the Piedmont to investigate the effects of soil type and land management on soil biota.

However, variation in the soil biota between sites show that there are some inherent differences between Fuquay and Tifton soils. These differences appear to dominate the effects of tillage for most soil biota. Because of the differences in soil behavior between soil series, it is important for researchers conducting on-farm comparison studies to replicate treatments on the same soil series, even when fields are closely related both specifically and within the soil families. Otherwise, it becomes difficult to separate random effects of treatments from fixed effects of soil series characteristics. However, it is still important to conduct research across soil gradients to determine regional and spatial differences in soil ecology. Dissimilar soils will respond differently to treatments such as land management, fertilization, urbanization and crop

rotation, and decisions should be made on the best available data across regional gradients and soil types. What works for one soil may not work for another, and building these regional datasets would provide land managers and county planners with important tools for making decisions about land use.

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Table 4.1. Differences in nutrient status between Piedmont and Coastal Plain soil series

Site	N	Percent N		Percent C		C/N Ratio	
Till - Hiwassee	8	0.08 ± 0.01	b	0.89 ± 0.06	ab	10.53 ± 0.10	c
No-till - Hiwassee	8	0.22 ± 0.04	a	2.58 ± 0.59	a	11.41 ± 0.43	c
Till - Fuquay	8	0.08 ± 0.01	b	1.43 ± 0.28	ab	18.35 ± 0.39	a
No-till - Tifton	8	0.11 ± 0.02	b	0.16 ± 0.15	b	15.41 ± 0.27	b

Letters denote significant differences at $p<0.05$
Values are means ± standard error

Table 4.2. Group richness (s) and diversity (D') of belowground mesofauna extracted from Hiwassee, Fuquay and Tifton soil series.

			s		D'	
Mesofauna	Site	N	Mean ± S.E.		Mean ± S.E.	
Microarthropod	Till - Hiwassee	8	3.50 ± 0.50	ab	0.53 ± 0.053	ab
Microarthropod	No-till - Hiwassee	8	4.87 ± 0.40	a	0.65 ± 0.039	a
Microarthropod	Till - Fuquay	4	1.25 ± 0.25	c	0.11 ± 0.110	c
Microarthropod	No-till - Tifton	8	2.75 ± 0.09	b	0.39 ± 0.088	b
Nematode	Till - Hiwassee	7	1.57 ± 0.20	b	0.22 ± 0.083	b
Nematode	No-till - Hiwassee	7	2.14 ± 0.26	b	0.42 ± 0.072	a
Nematode	Till - Fuquay	6	3.16 ± 0.31	a	0.58 ± 0.045	a
Nematode	No-till - Tifton	8	3.75 ± 0.25	a	0.61 ± 0.021	a

Letters denote significant differences at $p<0.05$

Table 4.3. Differences in microarthropod groups extracted from soil cores (0-5cm) in the Hiwassee, Fuquay and Tifton series.

Site	N	Collembola		Oribatida		Astigmatina		Mesostigmata		Prostigmata	
Till - Hiwassee	8	0.88 ± 0.23	a	4.00 ± 2.48	a	0.00 ± 0.00	a	2.63 ± 1.00	a	1.38 ± 0.89	ab
No-till - Hiwassee	8	4.50 ± 2.56	a	3.13 ± 1.14	a	0.00 ± 0.00	a	2.88 ± 1.20	a	3.25 ± 1.28	a
Till - Fuquay	8	0.00 ± 0.00	a	0.63 ± 0.26	a	0.00 ± 0.00	a	0.00 ± 0.00	a	0.00 ± 0.00	b
No-till - Tifton	8	1.63 ± 0.94	a	13.50 ± 6.73	a	1.25 ± 0.82	a	4.50 ± 3.26	a	0.13 ± 0.13	b

Letters denote significant differences at $p<0.05$
Values are means ± standard error

Table 4.4. Differences in nematodes feeding groups extracted from soil cores (0-5cm) between Hiwassee, Fuquay and Tifton soil series

Site	N	Bacterivorous		Fungivorous		Predatory		Omnivorous		Phytophagous	
Till - Hiwassee	7	1.21 ± 0.34	b	0.48 ± 0.37	b	0.05 ± 0.05	a	0.05 ± 0.05	b	0.00 ± 0.00	a
No-till - Hiwassee	7	1.18 ± 0.37	b	0.35 ± 0.14	b	0.20 ± 0.08	a	0.05 ± 0.05	b	0.00 ± 0.00	a
Till - Fuquay	6	0.88 ± 0.27	b	0.96 ± 0.37	b	0.05 ± 0.03	a	0.80 ± 0.28	ab	0.00 ± 0.00	a
No-till - Tifton	8	3.74 ± 1.01	a	2.64 ± 0.79	a	0.20 ± 0.09	a	1.38 ± 0.41	a	0.05 ± 0.03	a

Letters denote significant differences at $p<0.05$
Values are means ± standard error

Table 4.5. Total number (s) and Diversity (D') of fatty acids extracted.

		s		D'	
Site	N	Mean ± S.E.		Mean ± S.E.	
Till - Hiwassee	4	36.75 ± 3.20	a	0.93 ± 0.003	a
No-till - Hiwassee	4	42.25 ± 1.65	a	0.93 ± 0.003	a
Till - Fuquay	4	29.25 ± 0.25	b	0.91 ± 0.004	b
No-till - Tifton	4	27.50 ± 0.96	b	0.90 ± 0.001	c

Letters denote significant differences at $p<0.05$

Table 4.6. Differences in FAME relative abundance (% mol fraction) of microbial functional groups between Piedmont and Coastal Plain Soils

Site	N	Bacteria (gram +)		Bacteria (gram-)		Anaerobic Bacteria		Fungi		Protozoa	
Till - Hiwassee	4	5.22 ± 0.17	c	7.28 ± 0.29	a	1.66 ± 0.15	b	18.31 ± 1.22	a	1.23 ± 0.02	a
No-till - Hiwassee	4	5.02 ± 0.14	c	6.59 ± 0.07	a	1.64 ± 0.10	b	20.18 ± 0.71	a	1.18 ± 0.18	a
Till - Fuquay	4	5.97 ± 0.07	b	4.11 ± 0.71	b	1.93 ± 0.05	ab	14.70 ± 2.31	a	0.98 ± 0.02	a
No-till - Tifton	4	6.57 ± 0.13	a	4.68 ± 0.05	b	2.08 ± 0.03	a	15.60 ± 0.61	a	0.18 ± 0.01	b

Letters denote significant differences at $p<0.05$
Values are means ± standard error

Table 4.7. Microbial weights on the first and second PCA axes.

Axis 1	Weight	Functional Group Marker
i16:0	0.639	Gram-positive bacteria
i17:0	0.774	Gram-positive bacteria
a17:0	0.326	Gram-positive bacteria
16:1w7c	-0.922	Gram-negative bacteria
cy17:0	0.296	Eubacterial anaerobe (gram$^-$)
17:0	0.519	Eubacterial anaerobe (gram$^-$)
18:0	0.772	Non-specific bacteria
18:1w9t	-0.595	Fungi
18:2w6,9	-0.502	Fungi
18:1w9c	-0.926	Fungi
20:4	-0.575	Protozoa

Axis 2	Weight	Functional Group Marker
i16:0	0.354	Gram-positive bacteria
i17:0	0.414	Gram-positive bacteria
a17:0	0.45	Gram-positive bacteria
16:1w7c	-0.353	Gram-negative bacteria
cy17:0	0.353	Eubacterial anaerobe (gram$^-$)
17:0	0.58	Eubacterial anaerobe (gram$^-$)
18:0	0.484	Non-specific bacteria
18:1w9t	-0.727	Fungi
18:2w6,9	0.775	Fungi
18:1w9c	0.348	Fungi
20:4	-0.275	Protozoa

Figure legends.

Figure 4.1. Principal Components Analysis of microarthropod community composition for three soil series in two management regimes. For Fuquay soils, n=4 because four samples were eliminated from the analysis due to zero values for all microarthropods. Remaining data points were hidden behind one another and removed for ease of viewing. For all remaining soils, n=8. A single Till - Hiwassee data point was directly behind another and was eliminated for ease of viewing. Percent variation in the data explained by the principle components are shown in parentheses.

Figure 4.2. Principal Components Analysis of nematode community composition for three soil series in two management regimes. For Fuquay soils, n=6 because two samples were eliminated from the analysis due to zero values for all nematodes. For Hiwassee soils, n=7 because one sample in each data set contained all zeroes. Two data points were directly behind one another and eliminated for ease of viewing. For Tifton soils, n=8. Percent variation in the data explained by the principle components are shown in parentheses.

Figure 4.3. Principal Components Analysis of FAME community composition for three soil series in two management regimes based on relative abundance (%mol fraction) of fatty acids. For all soils, n=4 and no data points were removed for any reason. Percent variation in the data explained by the principle components are shown in parentheses.

Fig 4.1

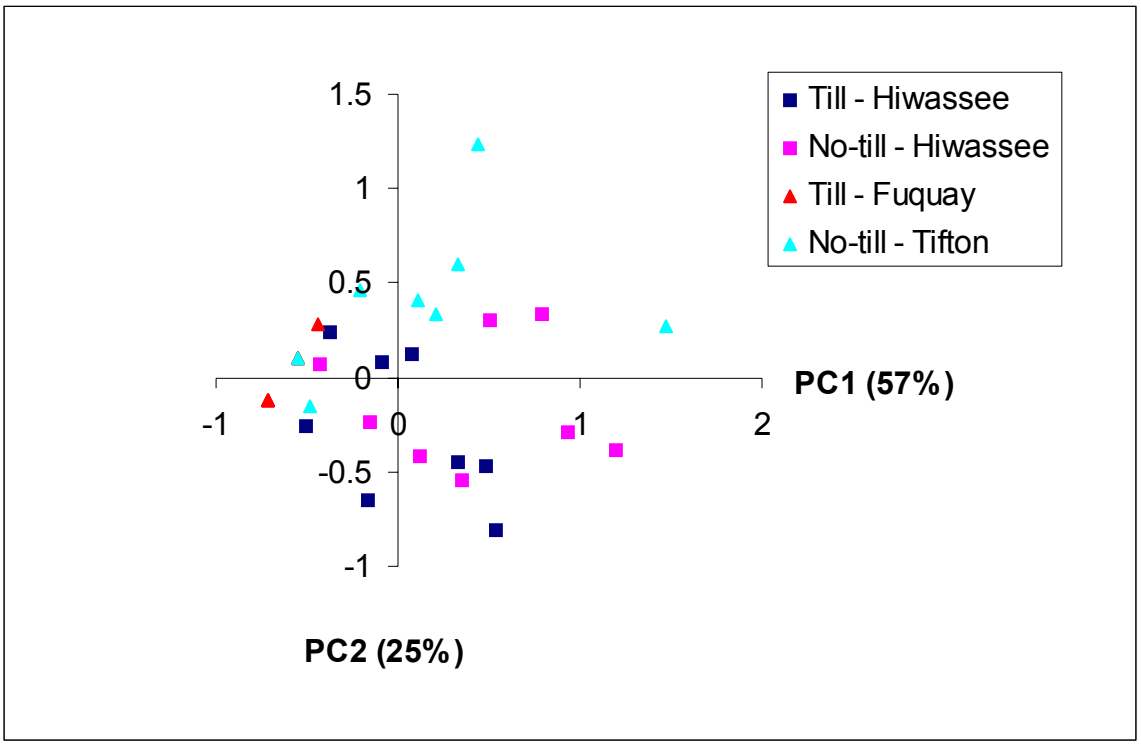

Till - Hiwassee
No-till - Hiwassee
Till - Fuquay
No-till - Tifton
1.5
1
0.5
0
-0.5
-1
-1
0
1
2
PC1 (57%)
PC2 (25%)

Fig 4.2

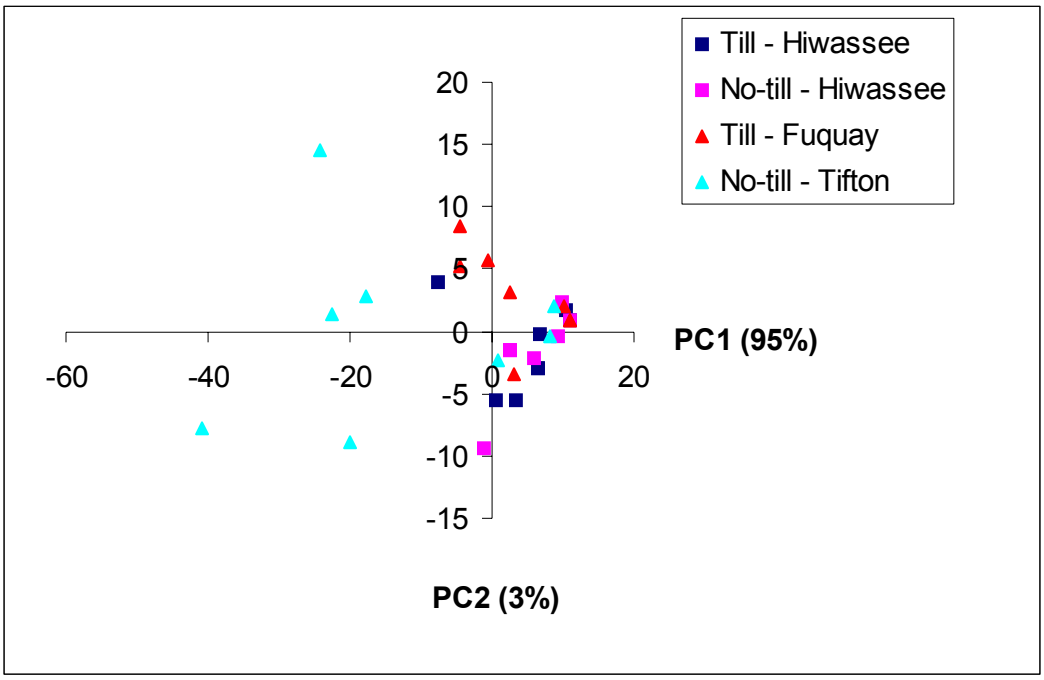
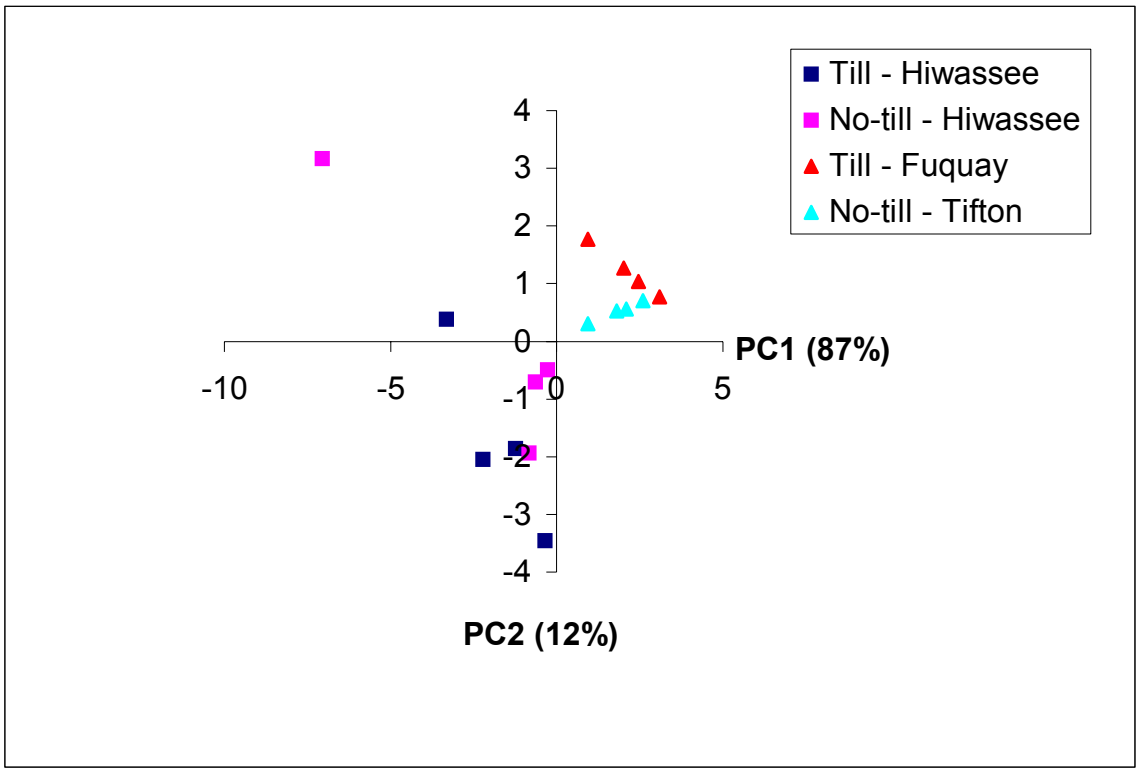

Till - Hiwassee
No-till - Hiwassee
Till - Fuquay
No-till - Tifton
20
15
10
5
0
-5
-10
-15
-60
-40
-20
0
20
PC1 (95%)
PC2 (3%)

Fig 4.3


Till - Hiwassee
No-till - Hiwassee
Till - Fuquay
No-till - Tifton
4
3
2
1
0
-1
-2
-3
-4
-10
-5
0
5
PC1 (87%)
PC2 (12%)

Chapter 5

GENERAL CONCLUSIONS

In this study I sought to examine the effects of organic compost amendment, land management regime and soil series on soil physical, chemical and biological properties. My main hypothesis was that a one-time application of high quality compost would accelerate the accumulation of organic matter in a soil in transition from conventional to conservation agriculture. Several studies have cited the benefits of conservation tillage in soils that are highly eroded or of poor quality (Hendrix et al. 1986, Parr et al. 1992, Doran and Parkin 1994, Six et al. 1998, Lal 2000, Coleman et al. 2001, Holland 2004, Adl et al. in press). However, growers are reluctant to transition from conventional agriculture due to concerns about nutrient stratification, slow release of nutrients from recalcitrant residues and a delay in nutrient cycling due to a stabilizing food web (Hargrove 1986, Phatak et al. 1999, Schomberg and Endale 2004).

I attempted to "jump start" the equilibration of the soil food web in the transitional field by applying compost at three rates in order to ascertain if an initial increase in soil organic matter would be enough to counteract the lag time (Chapter 2). I also wanted to study the effects of compost across a chronosequence of tillage to determine if compost application (a fairly costly endeavor) would benefit fields already in conservation tillage. The rates of compost application were chosen to reflect an upper and lower limit, based on the amount of compost required to significantly raise % soil organic

matter in these fields. At the rate of 10tons/ha, the compost should have increased SOM by 1%. At the rate of 20tons/ha, SOM should have increased by 2% in all fields. The uppermost rate would require more compost than a grower could typically afford, but the idea was that growers associated with poultry houses could compost their own manure on-farm, reducing the amount of waste generated by chicken houses (Nyakatawa et al. 2001).

The soil environment did differ across the chronosequence of tillage. However, it became apparent fairly early in the process that the compost may not have remained on the surface of the plots. The plots were small, and precipitation levels were severe and sporadic that spring. At most sites, the soil surface isn't conducive to the retention of particulate matter. Sites 10 and 30 would have been in the best position to retain to compost, but due to already high levels of organic matter present in the soil, it was expected that any effect of the compost would be marginal. Therefore, it becomes impossible to determine from this study whether or not compost application can reduce the lag time involved in the transition to conservation tillage. However, it is important to note that the field in transition did not differ significantly from other sites in conservation tillage for most soil factors. It is possible that soil biota are present in high enough numbers in most fields to participate in increased nutrient cycling, given appropriate amounts of substrate. Mesofauna did not differ significantly across the tillage sequence, however, this was likely the result of environmental variables. Further investigation of these fields may have provided more insight into the dynamics of the larger soil biota.
I was also interested in the composition of the microbial community and how that would change with land management and compost addition (Chapter 3). Previous studies had

shown that microbial community composition can be altered by a change in management practices (Visser and Parkinson 1992, Schutter and Dick 2002), substrate availability and composition (Wardle et al. 1993), and soil type (Schutter et al. 2001). My hypothesis that microbial community composition would shift along the chronosequence of tillage was not supported, although the field in conventional tillage had the lowest abundance and diversity of fatty acids. I expected that fungal biomass would increase across with length of time in not-till, which would support the hypothesis that in no-till systems, fungi become more dominant (Hendrix et al. 1986, Moore and deRuiter 1991, Moore et al. 2003). This relationship between bacterial and fungal biomass was not apparent in this study, but because only ten FAMEs were used to characterize the dataset, it is not possible to know how much fungal or bacterial biomass was overlooked in the analysis. However, those functional group markers that were analyzed were adequate to separate the tilled site from the sites in conservation tillage. Shifts in the microbial community can be important for the mineralization and availability of nutrients in soils, and feedback from these processes affect aboveground processes, such as plant growth and community assemblages (Mikola et al. 2001, Wardle 2002, Wardle et al. 2004). I believe it is important to continue work of this nature; as more microbial markers and techniques for identification of microbial species assemblages become available, researchers will gain insight into the complicated interactions between soil physical, chemical and biological properties.

In the course of this research I became concerned that the fields chosen for this experiment were not comparable. Studies have shown that shifts in microbial communities can be attributed to soil type (Bossio et al. 1998, Schutter et al. 2001,

McCulley and Burke 2004). The chronosequence of tillage encompassed four soil series, which were different enough from each other to potentially have an effect on the soil food web. It became important to try to tease apart the effects of tillage from that of soil series, so I chose two sites (one till and 30 year no till) from Coffee County and compared them to till and no-till soils in the Hiwassee series on the Piedmont at Horseshoe Bend (Chapter 4). I hypothesized that if tillage regime had a greater impact on soil biota compared to soil series, then sites with similar management would be more similar, regardless of soil series. Alternatively, if soil series had a greater impact on soil biota, then the data would depict three separate soil biotic communities, regardless of tillage regime. The data suggest that for most biota, soil series is more important than tillage regime (Figs 4.1, 4.2, 4.3). This becomes important when making decisions about land management. One soil may respond differently to another, due to changes in soil biotic community, and an evaluation of the soil food web structure would be a valuable tool in the decision making process. However, it would be beneficial to replicate this study across soil series, with several sites within each soil series represented to eliminate potential single site effects. Whole Soil FAME techniques allow for fairly quick processing of numerous soil samples, so it would not be labor intensive to collect soil from a large number of sites across several soil series to determine whether a no-till regime would significantly alter the microbial community.

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APPENDIX A

SOIL SERIES DESCRIPTIONS

Appendix A. Soil series descriptions from NRCS-OSD*

Soil Series	Taxonomy	Surface layer	Fertility	Organic matter	Acidity	Permeability	Water holding capacity	Tilth	Root Zone (inches)	Ironstone nodules
Cowarts/Carnegie	Fine-loamy, kaolinthic, thermic Typic Kanhapludults/ Plinthic Kandiudults	Brown sandy loam to 7 in	Low	Low	Strongly to very strongly acid	Moderately slow	Moderate with rapid runoff	Good	Limited to upper 20 in	In the surface layer and upper and middle subsoil
Fuquay	Loamy, kaolinthic, thermic Arenic Plinthic Kandiudults	Gray loamy sand to 10 in	Low	Low	Strongly to very strongly acid	Moderate, slow in lower subsoil	Low	Good	Deep	Throughout subsoil
Pelham	Loamy, siliceous, subactive, thermic Arenic Paleaquults	Dark gray loamy sand to 6 in	Low	Low	Strongly to very strongly acid	Moderate	Low	Poor, typically flooded	Deep, except when restricted by water table at 6-18 in	None
Tifton	Fine-loamy, kaolinthic, thermic Plinthic Kandiudults	Dark gray loamy sand to 9 in	Low	Low	Strongly to very strongly acid	Moderate	Moderate	Good	Deep	On surface, in surface layer and throughout subsoil

* Soil Survey Staff, Natural Resources Conservation Service, United States Department of Agriculture. Official Soil Series Descriptions [Online WWW]. Available URL: "http://soils.usda.gov/technical/classification/osd/index.html" [Accessed 5 August 2004].

APPENDIX B

COMPLETE RESULTS OF N-MINERALIZATION INCUBATION EXPERIMENT

Appendix B. Complete results of N-mineralization incubation experiment. Letters denote significant differences ($p<0.05$) between treatement means within each site for each date

			NH_4				NO_3			
Week	Site	Tx	(mg N/kg soil)				(mg N/kg soil)			
0	MC	0	1.07	±	0.11	c	22.58	±	0.53	a
0	MC	30	3.83	±	0.19	a	14.79	±	0.22	b
0	MC	60	2.82	±	0.23	b	12.92	±	0.18	c
0	MN	0	1.41	±	0.08	b	30.50	±	0.15	a
0	MN	30	3.63	±	0.09	a	26.87	±	0.64	b
0	MN	60	3.98	±	0.27	a	23.74	±	0.31	c
0	MV	0	3.48	±	0.19		13.05	±	0.87	
0	MV	0	*	±	*		*	±	*	
0	MV	0	*	±	*		*	±	*	
0	RS	0	1.23	±	0.24	a	54.66	±	0.74	a
0	RS	30	1.02	±	0.20	a	39.86	±	0.67	c
0	RS	60	0.93	±	0.07	a	47.51	±	0.44	b
0	WL	0	13.26	±	0.62	b	15.86	±	0.85	b
0	WL	30	24.22	±	0.34	a	16.27	±	0.14	b
0	WL	60	8.14	±	0.21	c	21.50	±	0.60	a
1	MC	0	3.68	±	1.01	a	37.46	±	1.10	a
1	MC	30	4.18	±	0.48	a	33.56	±	0.87	a
1	MC	60	4.77	±	0.62	a	34.86	±	0.77	a
1	MN	0	3.95	±	0.42	b	38.26	±	3.42	b
1	MN	30	5.97	±	1.45	a	50.55	±	6.03	a
1	MN	60	5.02	±	1.00	ab	45.11	±	3.49	ab
1	MV	0	2.33	±	0.49	a	5.12	±	3.06	a
1	MV	30	3.40	±	0.87	a	3.58	±	2.20	a
1	MV	60	2.67	±	0.36	a	1.25	±	0.91	a
1	RS	0	2.69	±	0.24	a	33.61	±	3.00	b
1	RS	30	2.98	±	0.36	a	21.33	±	1.38	c
1	RS	60	2.56	±	0.72	a	50.51	±	5.97	a
1	WL	0	2.44	±	0.45	a	13.22	±	1.16	b
1	WL	30	2.52	±	0.20	a	41.71	±	4.31	a
1	WL	60	2.40	±	0.47	a	14.70	±	7.20	b

App. B (cont.). Complete results of N-mineralization incubation experiment. Letters denote significant differences ($p<0.05$) between treatement means within each site for each date

			NH_4				NO_3			
Week	Site	Tx	(mg N/kg soil)				(mg N/kg soil)			
2	MC	0	8.05	±	2.19	a	51.59	±	3.82	a
2	MC	30	7.40	±	1.83	a	45.76	±	0.85	a
2	MC	60	5.14	±	1.02	a	42.90	±	0.92	a
2	MN	0	13.59	±	1.16	a	63.02	±	2.24	a
2	MN	30	8.82	±	2.46	b	56.76	±	4.03	a
2	MN	60	10.57	±	2.01	ab	67.87	±	4.24	a
2	MV	0	4.36	±	0.77	a	7.39	±	3.99	a
2	MV	30	5.29	±	0.33	a	2.46	±	0.95	a
2	MV	60	3.80	±	1.36	a	0.89	±	0.49	a
2	RS	0	2.42	±	0.43	a	35.70	±	3.83	a
2	RS	30	3.03	±	1.24	a	32.23	±	12.83	a
2	RS	60	1.37	±	0.66	a	34.69	±	4.91	a
2	WL	0	1.38	±	0.18	a	18.53	±	7.12	a
2	WL	30	0.82	±	0.16	a	31.88	±	9.86	a
2	WL	60	0.89	±	0.22	a	19.07	±	7.28	a
4	MC	0	6.07	±	1.90	a	58.96	±	19.65	a
4	MC	30	5.14	±	1.61	a	52.69	±	3.73	a
4	MC	60	7.32	±	1.42	a	50.29	±	4.01	a
4	MN	0	8.36	±	2.50	a	58.06	±	12.65	a
4	MN	30	5.33	±	1.20	a	50.10	±	2.95	a
4	MN	60	5.29	±	1.33	a	63.71	±	2.73	a
4	MV	0	3.01	±	0.94	a	11.17	±	4.60	a
4	MV	30	2.25	±	0.51	a	6.39	±	3.13	a
4	MV	60	2.18	±	0.33	a	1.01	±	0.78	a
4	RS	0	2.45	±	0.66	a	39.70	±	3.39	ab
4	RS	30	4.23	±	1.75	a	27.09	±	4.56	b
4	RS	60	1.77	±	0.27	a	56.55	±	5.48	a
4	WL	0	1.65	±	0.43	a	17.07	±	3.29	b
4	WL	30	1.92	±	0.22	a	44.47	±	5.59	a
4	WL	60	1.20	±	0.25	a	22.03	±	8.42	b

App. B (cont.). Complete results of N-mineralization incubation experiment. Letters denote significant differences ($p<0.05$) between treatement means within each site for each date

			NH_4 (mg N/kg soil)				NO_3 (mg N/kg soil)			
Week	Site	Tx								
6	MC	0	37.79	±	7.08	a	70.14	±	5.09	a
6	MC	30	41.33	±	5.31	a	63.00	±	2.99	a
6	MC	60	41.34	±	3.55	a	60.86	±	0.38	a
6	MN	0	38.42	±	10.26	a	64.61	±	3.83	a
6	MN	30	14.48	±	2.19	b	66.85	±	2.29	a
6	MN	60	7.38	±	2.01	b	71.08	±	1.38	a
6	MV	0	78.04	±	3.42	a	18.50	±	2.87	a
6	MV	30	45.41	±	7.07	b	13.42	±	2.29	a
6	MV	60	60.25	±	6.37	ab	9.38	±	0.95	a
6	RS	0	50.27	±	6.03	ab	40.48	±	2.82	b
6	RS	30	29.04	±	11.38	b	27.64	±	2.23	c
6	RS	60	54.84	±	4.23	a	57.13	±	5.26	a
6	WL	0	53.57	±	9.41	b	24.16	±	2.55	b
6	WL	30	93.08	±	10.43	a	51.97	±	5.46	a
6	WL	60	94.52	±	19.13	a	28.78	±	8.56	b
8	MC	0	3.60	±	0.71	a	69.38	±	3.46	a
8	MC	30	3.69	±	0.50	a	67.55	±	4.96	a
8	MC	60	4.55	±	1.22	a	74.02	±	5.92	a
8	MN	0	5.56	±	0.84	a	70.12	±	3.41	a
8	MN	30	3.09	±	0.51	b	60.97	±	7.25	a
8	MN	60	5.00	±	1.04	a	72.68	±	11.54	a
8	MV	0	2.19	±	0.17	a	21.75	±	3.46	a
8	MV	30	2.15	±	0.38	a	16.26	±	2.88	a
8	MV	60	1.66	±	0.38	a	8.17	±	1.10	a
8	RS	0	3.69	±	0.53	a	44.39	±	3.42	ab
8	RS	30	2.71	±	0.27	ab	30.43	±	1.93	b
8	RS	60	1.81	±	0.24	b	54.97	±	1.56	a
8	WL	0	1.14	±	0.17	a	24.84	±	7.12	b
8	WL	30	2.66	±	0.37	a	52.04	±	6.92	a
8	WL	60	1.91	±	0.18	a	31.70	±	10.56	b