Influence of Herbicide-Desiccated Cover Crops on Biological Soil Quality in the Mississippi Delta

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Abstract

The effect of crop residue management (CRM) systems on selected biological properties (microbial biomass/populations and soil enzyme activity) of Dundee soils under two cropping systems was investigated. In a cotton *(Gossypium hirsutum* L.) study, the influence of conventional tillage (CT) and no-tillage (NT) with and without an annual ryegrass cover crop *(Lolium multiforum* Lam.) on these properties was determined. Annual ryegrass residues in cotton stimulated total and Gram-negative bacteria, fluorescent pseudomonads, and total fungi for all sampling periods under both tillage systems. Soil aryl acylamidase, esterase, and phosphatase activity were greatest in the NT-ryegrass treatment. The second study addressed the effects of rye *(Secale cereale* L.) and hairy vetch *(Vicia villosa* Roth) cover crops in soybean [Glycine max (L.) Merr.]. The presence of cover crops initially enhanced total and Gram-negative bacteria, fluorescent pseudomonads, and microbial biomass N in Dundee surface soils (0-2 cm), with hairy vetch having the greatest effect. Both cover crops in soybeans enhanced surface soil esterase and phosphatase activities for the first 21 days after planting, with hairy vetch initially enhancing activity more than rye. Soils with cover crop had consistently higher sulfatase activity than soils in the bare ground control. In both studies, use of herbicide-desiccated cover crops enhanced microbial biomass/populationsand soil enzyme activity, thereby improving soil quality.

Introduction

The use of CRM as a tool to improve soil quality is not a new concept. However, as national attention to sustainable agriculture continues to grow, increasing numbers of farmers are considering and adopting CRM systems. Cover crops used as green manure have been a component of southern farming systems. Recent attention has focused on direct seeding of crops into soils with herbicide-desiccated cover crops or planting into residues of the previous crop (e.g. soybean-wheat doublecrop).

Several reports have shown that cover crop residues remaining on the soil surface can provide weed control and minimize soil erosion (Liebl et al., 1992). Herbicide-desiccated cover crops may impact microbial activity. Since microorganisms play a considerable role in soil processes that directly affect soil quality (Paul and Clark, 1989), the effect of this approach to CRM on parameters of biological soil quality in the Mississippi Delta warranted investigation.

We investigated the effect of cover crops on microbial population dynamics, microbial biomass, and soil enzyme activities in cotton and soybean production systems, both very important in Mississipppi agriculture.

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Materials and Methods

A randomized complete block (4 replicates) cotton study was established in 1990 near Stoneville, Mississippi, with plots maintained in NT and CT. In the fall of 1993, a split-block (10-m by 12-m subplots) arrangement of treatments with the presence or absence of annual ryegrass was imposed on the study. All plots were treated with 1.1 kg/ha glyphosate one month prior to planting cotton the following spring. CT treatments were subsoiled and then disked twice; beds were prepared 2 weeks prior to planting and cultivated three times. Soils from two depths (0-2 and 2-10 cm) collected at planting and at 2, 5, and 8 weeks after planting were assessed for microbial populations and enzyme activities.

The soybean cover crop study was established in fall 1993. Three treatments [RCB design of four replicates] consisted of tilled bare ground (BG); and untilled soil with rye (RC) and hairy vetch (VC) cover crops. All plots were treated with 1.1 kg/ha paraquat at soybean planting, and received no additional herbicides during this study. Soils and cover crop residues were collected at soybean planting and at 3, 6, and 11 weeks after planting.

Moist soils were sieved through a #6 sieve and stored at 4 "C until microbial assays could be performed. Microbial populations were estimated by serial dilution spiral plating. Soils were diluted in 0.1 M phosphate buffer (pH 7.0) and plated on 10%tryptic soy agar (TSA) for total bacteria, TSA with 2 g/mL crystal violet for Gram-negative bacteria, and S-1 agar for fluorescent pseudomonads (Gould et al., 1985).

Fungi were enumerated on rose bengal potato dextrose agar with streptomycin (Martin, 1950). Esterase activity was determined using the fluorescein diacetate (FDA) hydrolysis method of Schunrer and Roswall (l982). Phosphatase and sulfatase activities were determined by colorimetric methods using nitrophenyl phosphate and sulfate, respectively, as substrates (Tabatabai, 1982). Aryl acylamidase activity was determined in cotton soils using 2-nitroacetanilide as substrate (Zablotowicz et al., 1995). Microbial biomass N was determined by chloroform fumigation, K_2SO_4 extraction, and ninhydrin reaction as described by Joergensen and Brookes (1990).

Results and Discussion

In the cotton study, annual ryegrass residues in both CT and NT significantly enhanced all measured microbial populations (Table 1). Stimulation of soil microorganisms was more persistent in the surface soil (0-2 cm) in NT- ryegrass, while greater microbial populations were observed in the 2-10 cm depth of CT-ryegrass plots. Increased total soil bacterial populations were specifically due to the proliferation of Gram-negative bacteria, such as fluorescent pseudomonads.

In the soybean cover crop study, both rye and vetch cover crops stimulated soil bacterial populations in the surface soil (0-2 cm) (Table 2). However, the effect of cover crop was significant only for the first 3 weeks after planting. The greatest stimulatory effects were observed in VC plots, where significantly greater bacterial populations were initially observed. Total bacteria and pseudomonad populations were significantly greater in surface soils of RC plots than in those of BG plots. Bacterial populations in cover crop residues were 50- to 1,000-fold greater than in the underlying soils in all samples taken from both the cotton and soybean studies (Table 3, only data at planting are shown).

In the soybean study, surface soils from VC and RC plots exhibited significantly greater microbial biomass than did those from BG plots (Table 2). Soils from VC plots initially had the greatest microbial biomass; however, the soils in RC maintained higher levels of microbial biomass than did soils in BG plots in later samplings. In the cotton study, microbial biomass in the surface soil from NT-ryegrass plots was significantly greater than in the surface soil from the other treatments at planting (2 09, 109, 91, and 60 g microbial biomass N/g soil for NT-ryegrass, NT-bare, CT-ryegrass, and CT-bare, respectively).

Following 4 years of NT, organic carbon content of the surface 0-2 cm of soil was 74-108% greater than the corresponding CT soils in the cotton study. The effect of cover crop on soil organic carbon was not significant in the first year of the soybean study (Table 4).

Adoption of practices that increase soil organic matter accumulation affects soil microorganisms. Long-term NT soils cropped with corn in several locations across the United States had populations of aerobic bacteria, facultative anaerobes, nitrite oxidizers, and fungi that were higher than those found in soils under CT (Doran, 1980). Only slight increases in microbial populations were observed after 4 years of NT in

Table 1. Effect of tillage and annual ryegrass cover crop on microbial populations of a Dundee silt loam, cotton study, 1994.

Tillage	Total Bacteria*		Gram Negative Bacteria[1]		Fluorescent Pseudomonads[2]		Total Fungi[2]	
Cover Crop[1]	0-2 cm	2-10 cm	0-2 cm	2-10 cm	0-2 cm	2-10 cm	0-2 cm	2-10 cm
Week 0								
NT-ryegrass	8.16 a[3]	7.92 b	6.68 a	6.70 b	6.27 a	6.12 b	5.25 a	4.95 a
CT-ryegrass	8.17 a	8.17 a	7.03 a	7.09 a	6.58 a	6.76 a	4.94 a	4.90 a
NT-bare	7.71 b	7.42 c	6.12 b	6.05 c	5.46 b	5.41 c	4.29 b	3.86 b
CT-bare	7.66 b	7.46 c	5.78 b	5.73 d	4.96 b	5.28 c	3.87 b	3.78 b
Week 2								
NT-ryegrass	8.26 a	7.90 b	7.15 a	6.28 b	5.93 a	5.46 b	5.52 a	4.93 a
CT-ryegrass	8.20 a	8.10 a	6.89 ab	6.86 a	5.91 a	6.22 a	5.08 ab	5.11 a
NT-bare	7.94 b	7.82 b	6.39 bc	6.02 c	5.11 b	5.01 c	4.52 b	4.31 b
CT-bare	7.94 b	7.79 b	6.28 c	5.98 c	4.96 b	5.17 bc	4.80 ab	4.72 ab
Week 5								
NT-ryegrass	8.25 a	7.87 a	7.02 a	6.41 a	5.70 a	5.37 a	4.09 a	3.57 a
CT-ryegrass	7.88 b	7.77 b	6.23 b	6.37 a	5.05 b	5.20 a	3.79 b	3.30 b
NT-bare	7.96 b	7.71 b	6.40 b	6.07 a	5.05 b	4.93 a	3.82 b	3.23 b
CT-bare	7.53 c	7.63 b	5.93 c	6.03 a	4.58 c	5.08 a	3.36 c	3.00 c
Week 8								
NT-ryegrass	7.98 a	7.80 a	5.94 a	6.20 a	2.35 a	5.14 a	4.29 a	4.22 ab
CT-ryegrass	7.73 b	7.66 a	5.99 a	6.22 a	1.59 ab	4.97 a	4.01 ab	4.37 a
NT-bare	7.62 bc	7.66 a	5.42 b	6.10a	1.67 ab	4.44 b	3.83 b	3.69 c
CT-bare	7.59 c	7.48 b	5.38 b	5.99 a	1.40 b	4.52 b	3.45 c	3.70 bc

INT = no tillage, CT = conventional tillage.

[2] Log (10) colony forming units per g soil 0.d.

[3] Means within a column and sample period followed by the same letter do not differ at the 95% level.

Table 2. Effect of rye and vetch cover crops on microbial populations and microbial biomass of a Dundee silt loam (0-2 cm), soybean study, 1994.

Sample Time	Treatment[1]	Total Bacteria[2]	Gram Negative Bacteria*	Fluorescent Pseudomonads[2]	Total Fungi[2]	Microbial Biomass[3]
Planting	Bare	8.12 c[4]	6.59 b	5.04 c	3.22 a	76 b
	Rye	8.31 b	6.75 b	5.48 b	4.46 a	117 b
	Vetch	8.70 a	7.13 a	6.48 a	4.89 a	266 a
Week 3	Bare	7.51 b	5.93 a	4.53 b	3.48 a	81 b
	Rye	7.65 ab	6.13 a	4.64 b	3.94 a	121 a
	Vetch	8.03 a	6.45 a	5.42 a	4.16 a	114 a
Week 6	Bare	7.67 a	6.11 a	4.74 a	2.97 a	41 b
	Rye	7.47 a	5.89 a	4.00 a	2.72 a	74 a
	Vetch	7.26 b	5.94 a	4.53 a	3.44 a	59 ab
Week 11	Bare	1.56 a	6.35 a	4.98 a	3.47 a	91 c
	Rye	7.49 a	6.23 a	4.67 a	3.35 a	133 a
	Vetch	7.41 b	6.42 a	4.82 a	3.44 a	122 b

[1]BG = bareground, RC = rye cover crop soil, VC = vetch cover crop soil.
[2]log (10) colony forming units per g soil 0.d.
[3]μg ninhydrin reactive N released following chloroform fumigation per g soil 0.d.
[4]Means within a column and sample period followed by the same letter do not differ at the 95% level.

our Mississippi cotton study, although soils under NT had significantly greater organic carbon than those under CT. Major changes in microbial populations were associated with the ryegrass cover crop. Likewise, in the soybean study, both rye and vetch cover crops enhanced soil bacterial populations and microbial biomass.

Table 3. Bacterial populations of cover crop residues compared to underlying soils (at planting).

	Ryegrass[1]		Rye[1]		Vetch[1]	
Bacterial Group	Residue	Soil	Residue	Soil	Residue	Soil
Total	10.73	8.16	10.09	8.31	10.29	8.70
Gram Negative	9.42	6.68	9.12	6.75	8.86	7.73
Fl. Pseudomonads	8.22	6.27	7.95	5.48	7.59	6.48

[1]log (10) colony forming units per g material 0.d.

Table 4. Soil organic carbon content of the cotton and soybean studies at planting, 1994.

Treatment[1]	Organic Carbon (g/kg) 0-2 cm	2 - 10 cm
Cotton Study		
NT-Ryegrass	19.8 a[2]	5.1 a
NT-Bare	13.9 b	3.5 b
CT - Ryegrass	9.6 c	5.2 a
CT - Bare	8.0 c	4.5 ab
Soybean Study		
BG	13.6 a	9.9 a
RC	14.6 a	10.1 a
VC	15.3 a	9.4a

[1]NT = no-tillage, CT = conventional-tillage, BG = bareground, RC = rye cover crop soil, VC = vetch cover crop soil.
[2]Means within a column and cropping system followed by the same letter do not differ at the 95% level.

Results from both studies are similar to those of Kirchner et al. (1993) who demonstrated that a fall-seeded clover *(Trifolium incarnatum* L.) temporarily enhanced total bacterial and fungal populations. Our studies indicated that certain Gram-negative bacteria such as fluorescent pseudomonads are most affected by cover crops.

Herbicide-desiccated cover crops also enhanced soil enzyme activities in the surface soil (0-2 cm) in both studies. In the cotton study, soil in the NT-ryegrass treatment had greater esterase, phosphatase, and aryl acylamidase activity than soil in all other plots at all sample periods, while minimal effects of ryegrass were measured in CT soils (Table 5). In the absence of ryegrass, significantly greater enzyme activities were measured in NT than in CT plots at certain sampling times. Dick (1984) also found higher soil enzyme levels in NT soils than in CT soils. In the soybean study, both rye and vetch enhanced soil esterase, phosphatase, and aryl sulfatase activity compared to BG soils (Table 6). Soils from VC plots initially had significantly greater esterase and phosphatase activity than did soils from RC and BG plots; however, effects of the rye cover crop were more persistent.

Esterase activity is highly correlated with respiration and is a general indicator of microbial activity (Schunrer and Rosswall, 1982). Increased levels of phosphatase and aryl sulfatase, as well as other hydrolytic enzymes have been associated with soils previously cropped with clover (Kirchner et al., 1993). Phosphatase and sulfatase activity are indicators of potential nutrient availability since these enzymes release phosphate and sulfate, respectively, from organic pools. Enzymes such as esterase, aryl acylamidase, and aryl sulfatase may also be indicators of the potential for hydrolytic catabolism of several families of soil-applied herbicides.

Both studies demonstrated that herbicide-desiccated cover crops enhanced descriptors of biological soil quality, name-

Table 5. Effect of tillage and ryegrass cover crop on soil enzyme activities of a Dundee silt loam (0-2 cm), cotton study, 1994.

Tillage/ Cover Crop[1]	Esterase[2]	Aryl Acylamidase[3]	Alkaline Phosphatase[3]
Week 0			
NT-ryegrass	1096 a[4]	44.9 a	1219 a
CT-ryegrass	345 bc	9.9 b	565 b
NT-bare	507 b	15.3 b	896 b
CT-bare	233 c	9.9 b	565 b
Week 2			
NT-ryegrass	408 a	31.0 a	1187 a
CT-ryegrass	234 b	14.3 bc	864 b
NT-bare	220 bc	18.4 b	869 b
CT-bare	114 c	10.1 c	565 b
Week 5			
NT-ryegrass	526 a	26.1 a	1191 a
CT-ryegrass	221 bc	6.7 c	566 c
NT-bare	318 b	17.8 b	857 b
CT-bare	153 c	3.8 c	527 c
Week 8			
NT-ryegrass	201 a	3.1 a	nd
CT-ryegrass	122 bc	0.8 b	nd
NT-bare	141 b	0.5 b	nd
CT-bare	76 c	0.1 b	nd

[1]NT = no-tillage, CT = conventional-tillage.
[2]μmole/h/g soil o.d.
[3]nmoles/h/g soil o.d.
[4]Means within a column and sample period followed by the same letter do not differ at the 95% level.

Table 6. Effect of rye and vetch cover crops on soil enzyme activities of a Dundee silt loam (0-2 cm), soybean study, 1994.

Cover Crop[1]	Esterase[2]	Alkaline Phosphatase[3]	Aryl Sulfatase[3]
Week 0			
BG	88.1 c	494.8 c	143.8 b
RC	172.0 b	685.7 b	264.4 a
VC	242.4 a	859.8 a	263.6 a
Week 3			
BG	81.8 b	522.5 b	152.2 b
RC	154.4 a	634.7 a	266.8 a
VC	166.5 a	687.2 a	248.9 a
Week 6			
BG	78.2 b	470.5 ab	153.3 b
RC	139.6 a	564.4 a	260.2 a
VC	106.4 b	435.8 b	242.0 a
Week 11			
BG	97.1 b	504.4 ab	228.4 b
RC	139.8 a	641.5 a	311.7 a
VC	145.4 b	465.2 b	271.7 a

[1]BG = bareground, RC = rye cover crop soil, VC = vetch cover crop soil.
[2]μmole/h/g soil o.d.
[3]nmoles/h/g soil o.d.
[4]Means within a column and sample period followed by the same letter do not differ at the 95% level.

ly microbial biomass, microbial populations, and soil enzyme activities. These factors can potentially affect the availability of plant nutrients, organic matter transformations, and the fate of pesticides in the environment (Locke et al., 1995), all of which are important in the development of sustainable agricultural systems.

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