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Effects of Switchgrass (*Panicum virgatum*) Rotations with Peanut (*Arachis hypogaea* L.) on Nematode Populations and Soil Microflora

N. Kokalis-Burelle,[1] W. F. Mahaffee,[2] R. Rodríguez-Kábana,[3] J. W. Kloepper,[4] and K. L. Bowen[5]

Abstract: A 3-year field rotation study was conducted to assess the potential of switchgrass (*Panicum virgatum*) to suppress root-knot nematodes (*Meloidogyne arenaria*), southern blight (*Sclerotium rolfsii*), and aflatoxigenic fungi (*Aspergillus* sp.) in peanut (*Arachis hypogaea* L.) and to assess shifts in microbial populations following crop rotation. Switchgrass did not support populations of root-knot nematodes but supported high populations of nonparasitic nematodes. Peanut with no nematicide applied and following 2 years of switchgrass had the same nematode populations as continuous peanut plus nematicide. Neither previous crop nor nematicide significantly reduced the incidence of pods infected with *Aspergillus*. However, pod invasion by *A. flavus* was highest in plots previously planted with peanut and not treated with nematicide. Peanut with nematicide applied at planting following 2 years of switchgrass had significantly less incidence of southern blight than either continuous peanut without nematicide application or peanut without nematicide following 2 years of cotton. Peanut yield did not differ among rotations in either sample year. Effects of crop rotation on the microbial community structure associated with peanut were examined using indices for diversity, richness, and similarity derived from culture-based analyses. Continuous peanut supported a distinctly different rhizosphere bacterial microflora compared to peanut following 1 year of switchgrass, or continuous switchgrass. Richness and diversity indices for continuous peanut rhizosphere and geocarposphere were not consistently different from peanut following switchgrass, but always differed in the specific genera present. These shifts in community structure were associated with changes in parasitic nematode populations.

Key words: *Arachis hypogaea* L, *Aspergillus*, microbial community, microbial diversity, nematode, *Panicum virgatum*, peanut, rhizosphere ecology, root-knot nematode, *Sclerotium rolfsii*, southern blight, switchgrass.

Annually, 1.5 million acres of peanuts are harvested in the United States, and more than 1.3 billion pounds are consumed. The crop value exceeds $1 billion each year, and approximately 65% of domestically produced peanuts are grown in the southeastern United States. Peanut production in the Southeast is limited by damage from the root-knot nematode (*Meloidogyne arenaria*) and southern blight (*Sclerotium rolfsii*, teleomorph = *Athelia rolfsii*), and the value of production is decreased due to contamination with fungi that produce aflatoxins (*Aspergillus* spp.).

Annual yield losses due to root-knot nematodes in the Southeast have been estimated to be greater than 5% of the total peanut crop, while southern blight causes an estimated loss of 6% to 20% annually (Bowen et al., 1992). In addition, *S. rolfsii* and nematodes interact synergistically to damage peanuts and reduce yield (Culbreath et al., 1991). *Aspergillus flavus* and *A. parasiticus* are closely related species that produce highly carcinogenic aflatoxins (Diener et al., 1982). These fungi are ubiquitous in soils and are found on peanut plants throughout most growing seasons (Diener et al., 1987). Seed invasion by aflatoxigenic fungi is aggravated by pod damage resulting from natural cracking and feeding by soilborne insects (Bowen and Mack, 1993; Lynch and Wilson, 1991; Widstrom, 1979) and nematodes (Jackson and Minton, 1968; Minton et al., 1969; Minton and Jackson, 1969). Root-knot nematodes, *S. rolfsii*, and aflatoxigenic fungi constitute an interactive group of pests that combine to limit profitability and sustainability of peanut production in the southeastern United States.

The most effective control for root-knot nematodes is use of resistant varieties. However, availability of root-knot nematode-resistant peanut varieties is limited. Rotations of peanut with certain soybean varieties, cotton, sorghum, or corn can effectively suppress populations of *M. arenaria* (Rodríguez-Kábana and Canullo, 1992). Fumigant nematicides used for control of root-knot nematodes in peanut include 1,3-dichloropropene (1,3-D) and metam sodium; nonfumigant nematicides available for use on peanut include aldicarb, carbofuran, phenamiphos, ethoprop, and fensulfothion. Control of southern blight with resistant varieties is becoming more feasible with the development of the cultivar Southern Runner, which reduces disease incidence by 50% compared to Florunner. Rotations with grass crops including corn, sorghum, and pasture are also effective for controlling *S. rolfsii* (Rodríguez-Kábana et al., 1988; Rodríguez-Kábana et al., 1994). Fungicides with activity against *S. rolfsii* include PCNB, tebuconazole, propiconazole, and flutolanil. *Aspergillus flavus* can be effective controlled only by irrigation although early harvest during drought years may provide some relief of extensive contamination.

Switchgrass (*Panicum virgatum*) is an outstanding native forage species (Burns et al., 1984). Switchgrass requires low fertilizer inputs, is widely adapted to different soils, has good soil conservation properties, has a deep root system and a long growing season, and serves as excellent wildlife habitat. Grass rotations may also alter soil microbial communities and, thereby, phytoparasitic nematode communities. Increased use of perennial forages in rotation with annual crops could result in less contamination of groundwater with nemati-

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[1] Research Ecologist, USDA-ARS Horticultural Research Lab, 2001 South Rock Rd., Ft. Pierce, FL 34945.
[2] Research Plant Pathologist, USDA-ARS Horticulture Crop Research Lab, 3420 NW Orchard Ave., Corvallis, OR 97330.
[3] Professor, Department of Plant Pathology, Auburn University, AL 36849-5409.
[4] Professor and Director, Biological Control Institute, Department of Plant Pathology, Auburn University, AL 36849-5409.
[5] Professor, Department of Plant Pathology, Auburn University, AL 36849-5409.
E-mail: nburelle@saa.ars.usda.gov
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cides, increased soil organic matter, less soil erosion, and a more economically sustainable, integrated crop and livestock production system.

The objectives of this research were to: (i) evaluate the usefulness of incorporating switchgrass into peanut rotations for management of diseases caused by root-knot nematodes and southern blight, and contamination by aflatoxigenic fungi and; (ii) determine the impact of switchgrass rotations on soil microbial communities.

Materials and Methods

Field experiment design: A 3-year crop rotation experiment was established at the Auburn University Wiregrass Substation in Headland, Alabama. The field location had been cropped in continuous peanut production with winter fallow for 10 years. The soil was a sandy loam with pH 6.2, organic matter content <1.0%, and cation exchange capacity <10 meq per 100 g of soil. Eight different 3-year rotation practices were compared. All crops were planted in the spring of the initial year. Planting generally occurred from mid-April to mid-May, and harvesting occurred from mid-September to mid-October, depending on weather. Crop rotation sequences were: (i) 3 years of continuous peanut without nematicide (PPP–), (ii) 3 years of continuous peanut with nematicide (PPP+), (iii) 1 year of switchgrass followed by 1 year of peanut without nematicide followed by 1 year of switchgrass (SP–S), (iv) 1 year of switchgrass followed by 1 year of peanut with nematicide followed by 1 year of switchgrass (SP+S), (v) 2 years of switchgrass followed by 1 year of peanut without nematicide (SSP–), (vi) 2 years of switchgrass followed by 1 year of peanut with nematicide (SSP+), (vii) 1 year of cotton followed by 1 year of peanut without nematicide followed by 1 year of cotton (CP–C), and (viii) 2 years of cotton followed by 1 year of peanut without nematicide (CCP–). The nematicide used was aldicarb (Temik® 15G, Aventis CropScience, Research Triangle Park, NC). Nematicide was applied in a 20-cm-wide band at 3 g a.i. per 10-m row (3.3 kg a.i./ha) and incorporated into the top 5 to 10 cm of soil. Plots were arranged in a randomized complete block design with eight replications per treatment (cropping system). Each plot was eight rows wide and 10 m long, with a total area of 73 m^2. Switchgrass seed was broadcast at 28 kg per ha and received no pesticides. During each year of the study, cultural practices, fertilization, control of insects, weeds, and foliar diseases of peanut and cotton were performed according to recommendations for peanut and cotton production in south Alabama. Cultural practices were consistent over the 3-year duration of the study. During the third growing season, peanut plots were sampled for nematodes, *A. flavus*, and microbial populations. Yields were collected for peanut and cotton from the center two rows of each plot in each replication. Switchgrass was not harvested but was mowed and disked into the soil at the end of the season.

Nematode extractions from field trials: Nematodes were extracted from soil samples collected 2 to 3 weeks before harvest from each plot, each year. Samples consisted of 16 to 20 combined soil cores taken with a 2.5-cm-diam. probe to a depth of 20 to 25 cm in the plant root zone. Soil subsamples (100 cm^3) were evaluated for phytoparasitic and nonparasitic nematode populations using a modified Baermann technique (Rodríguez-Kábana and Pope, 1981). Predominant parasitic species were identified to genus using standard morphological characteristics. Nonparasitic nematodes were not identified further. Populations were expressed as nematodes per 100 cm^3 of soil.

*Field evaluation of southern blight (*Sclerotium rolfsii*) incidence:* Incidence of southern blight in peanut was assessed by counting the number of disease loci in the center two rows of each plot immediately after digging and inversion of the plants at harvest. A disease locus is defined as ≤30 cm of row with peanut plants killed by the pathogen (Rodríguez-Kábana et al., 1975).

Isolation of aflatoxigenic fungi from field trials: Isolation of aflatoxigenic fungi from pegs and pods was performed every other week throughout the peanut growing season in plots containing peanuts during the third year of the study. Five plants were randomly selected throughout the two rows adjacent to harvest rows in each plot for fungal isolations. Pegs and developing pods were removed from plants, surface-sterilized, moistened with sterile saline solution, and incubated at 32 °C for 3 days. *Aspergillus flavus*-type fungi were identified by their conidial morphology and colony color. The area under the curve (AUC), used to quantify pod invasion over the entire growing season, was estimated as

$$\mathrm{AUC} = \sum_{i}^{n-1} \left(\frac{y_i + y_{i+1}}{2} \right) (t_{i+1} - t_i)$$

in which y = the proportion of pegs and pods infected with *A. flavus*-type fungi at sampling date t, and n = number of sampling dates (Shaner and Finney, 1977).

Microbial isolation and identification from field trials: Peanut roots and pods were collected three times during the growing season during the third year of the study in plots planted to peanut (60, 90, and 120 days after planting (DAP)). Samples were collected arbitrarily from two rows adjacent to the harvest rows in each treatment containing peanut. Roots and pods with attached soil were placed in plastic bags and transported in a cooler for processing. Samples were processed within 24 hours. The samples were manually separated into rhizosphere soil (removed from the roots) and geocarposphere soil (removed from the pods), and 2 g of each soil type was weighed from each plot containing

peanut. Switchgrass roots were collected randomly throughout the plots at each sampling time and processed for isolation of rhizosphere bacteria as described for peanut roots.

Populations of bacteria were determined by dilution plating with a Model D spiral plater (Spiral Systems, Bethesda, MD) onto 5% trypticase soy agar (TSA) to allow detection of oligotrophs. Plates were incubated for 48 hours at 28 °C prior to counting. Random samples of 35 bacterial colonies, as determined by rarefraction analysis (Hurlbert, 1971), were taken from 5% TSA plates of root and pod samples. Each isolate was purified prior to extraction of fatty acids (Sasser, 1990). The extracts were analyzed with a Hewlett-Packard gas chromatograph (Model 5860) and the Sherlock Microbial Identification System Software (MIDI) using the aerobe method and environmental library version 3.8 (MIDI, Newark, DE). The isolates were identified to the genus level, and isolates with a similarity index below 0.200 were grouped as ''no match'' to known genera.

Richness, diversity, and similarity indices were used to compare aerobic-heterotroph bacterial rhizosphere communities and geocarposphere communities at the genus level among crop rotations over time. Richness was defined as the number of genera identified in each sample. Diversity was estimated using Hill's diversity number, *N2* (Hill, 1973; Ludwig and Reynolds, 1988). *N2* $(1/\lambda)$ is a modification of Simpson's index, $\lambda = -\sum[n_i(n_i - n)]/[n(n-1)]$, where n_i is the number of individuals of the i^{th} genus and n is the total number of individuals in the sample (Hill, 1973).

Community similarity was calculated using the coefficient of biotic similarity (*B*) (Pearson and Pinkham, 1992; Pinkham and Pearson, 1976) and the computer program BIOSIM1 (obtained from J. G. Pearson, EPA Environmental Monitoring Systems Laboratory, Las Vegas, NV).

Interpretation of community structure from indices

Because each of the employed indices is one dimensional in the information it relays about a community, at least two complementing indices (i.e., ones that measure different characteristics, such as richness and diversity) are needed to assess changes in community structure (Ludwig and Reynolds, 1988; Washington, 1984). For example, when richness and *N2* are statistically identical but *B* is different, this indicates that the total number of genera and distribution of isolates within these genera are equal but that the present and (or) dominant genera in each community are different. This is confirmed by examining the number of genera isolated from each environment. In this study, we used richness, *N2* and *B*, in combination with the actual genera identified to determine if communities differed (Mahaffee and Kloepper, 1997).

This interpretation likely results in subjective conclusions, regardless of whether differences between individual indices were significant. To reduce this subjec-

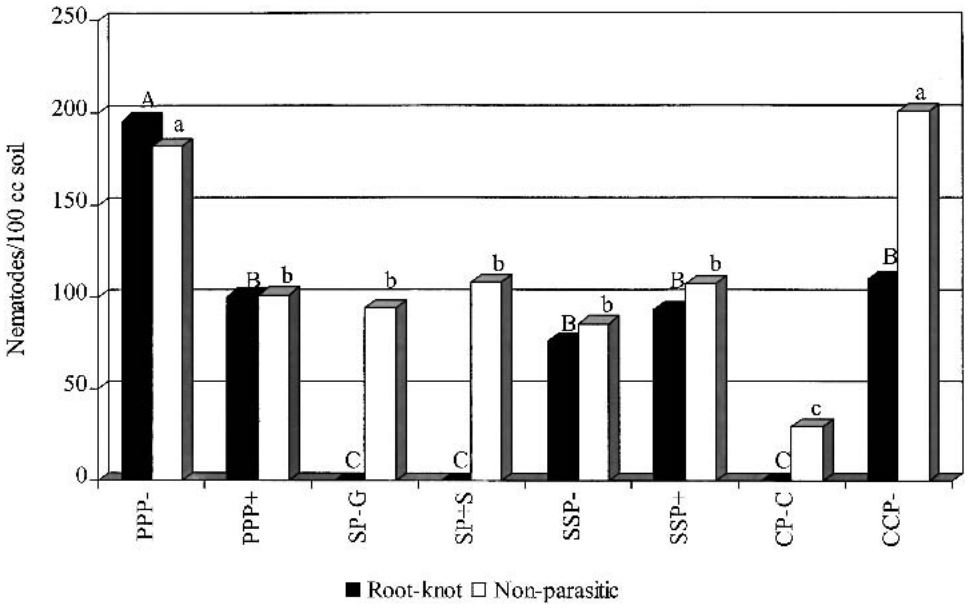

FIG. 1. Effects of switchgrass (S) and cotton (C) rotations on populations of root-knot nematode in nematicide treated (+) and nontreated (–) peanuts (P). PPP– denotes 3 years of peanut without nematicide, PPP+ denotes 3 years of peanut with nematicide, SP–S denotes 1 year of switchgrass followed by 1 year of peanut without nematicide followed by 1 year of switchgrass, SP+S denotes 1 year of switchgrass followed by 1 year of peanut with nematicide followed by 1 year of switchgrass, SSP– denotes 2 years of switchgrass followed by 1 year of peanut without nematicide, SSP+ denotes 2 years of switchgrass followed by 1 year of peanut with nematicide, CP–C denotes 1 year of cotton followed by 1 year of peanut without nematicide followed by 1 year of cotton, and CCP– denotes 2 years of cotton followed by 1 year of peanut without nematicide. Bars designated by either uppercase or lowercase letters are comparable. Means labeled with the same letters are not significantly different ($P \leq 0.05$).

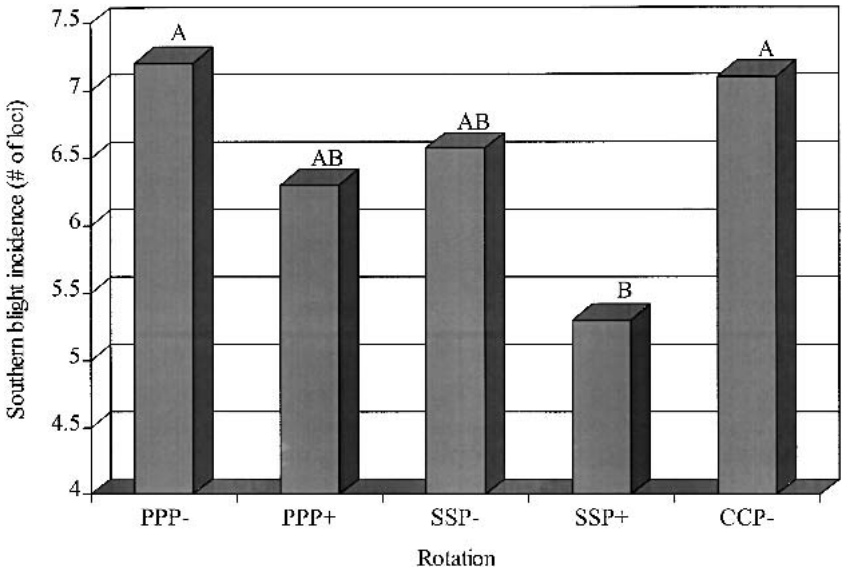

FIG. 2. Effects of peanut (P), switchgrass (S), and cotton (C) rotation on incidence of southern blight in peanut with (+) or without nematicide (–) application. PPP– denotes 3 years of peanut without nematicide, PPP+ denotes 3 years of peanut with nematicide, SSP– denotes 2 years of switchgrass followed by 1 year of peanut without nematicide, SSP+ denotes 2 years of switchgrass followed by 1 year of peanut with nematicide, and CCP– denotes 2 years of cotton followed by 1 year of peanut without nematicide. Bars with the same letters are not significantly different at $P \leq 0.05$.

tiveness, all interpretations of indices were blind with respect to treatment.

Statistical analysis: Disease data were analyzed following standard procedures for analysis of variance (SAS Institute, Cary, NC). Unless otherwise stated, differences were significant at the $P \leq 0.05$. Bacterial population data were converted to log cfu/g fresh weight of root tissue, and populations below the detection limits were registered as zero for calculation of means (Kloepper and Beauchamp, 1992). Analysis of variance for population and community structure estimates was accomplished using the GLM procedure in PC-SAS (SAS Institute, Cary, NC). Significant differences were determined using single degree of freedom contrasts. Interpretation of community structure was done as described by Mahaffee and Kloepper (1997).

RESULTS

Effects of rotations with switchgrass on infection by root-knot nematodes, Sclerotium rolfsii, *and aflatoxigenic fungi*: Neither switchgrass nor cotton following peanut supported populations of root-knot nematode (Fig. 1). Switchgrass after peanut supported higher populations of nonparasitic (non-stylet-bearing, microbivorous) nematodes than did cotton after peanut. Peanut with no nematicide following 2 years of switchgrass supported the same parasitic and nonparasitic nematode populations as continuous peanut plus nematicide (Fig. 1).

Peanut planted with nematicide following 2 years of switchgrass had significantly lower incidence of southern blight than continuous peanut without nematicide and peanut with no nematicide following 2 years of cotton (Fig. 2). Continuous peanut with nematicide and peanut both with and without nematicide following 2 years of switchgrass had similar levels of southern blight. Peanut yields did not differ significantly among rotations.

Previous crop and nematicide treatment did not have a consistent effect on the incidence of pegs infected with *A. flavus*. One exception was with pegs collected on 5 September from plots treated with nematicide,

TABLE 1. Area under the curve (AUC) that describes peanut seed invasion by aflatoxigenic fungi over a growing season.

Treatment	Previous crop	AUC
P(–)[a]	Peanut	390.2
P(+)[b]	Peanut	22.2
P(–)	Switchgrass	121.2
P(+)	Switchgrass	34.6
P(–)	Cotton	0.0

[a] P(–) = Peanut without nematicide.
[b] P(+) = Peanut with nematicide.

TABLE 2. Total aerobic-heterotrophic bacterial populations (log10 cfu/g fresh weight) isolated from the rhizosphere and geocarposphere of peanut.[a]

	Rhizosphere			Geocarposphere		
Treatment	60[b]	90	120	60	90	120
Switchgrass	5.79 a[c]	6.17 a	5.40 a	–[d]	–	–
Switchgrass/peanut	4.86 b	6.12 a	5.68 a	–	4.57 a	4.83 a
Continuous peanut	3.91 c	5.96 a	6.06 a	–	5.09 a	4.74 a

[a] Isolations were made on 5% TSB agar.
[b] Days after planting.
[c] Means followed by the same letter within the same column are not significantly different ($P \geq 0.05$).
[d] No sample.

which had significantly more ($P = 0.06$) *A. flavus* incidence than those from plots not treated with nematicide. Previous crop and nematicide treatment did not have a significant effect on the incidence of pods infected with *A. flavus*, except pods collected on 24 August from peanut-peanut rotations without nematicide had significantly more ($P = 0.06$) *A. flavus* infection than those from other rotations. In collections made on 5 September, *A. flavus* was detected only in developing pods from plots not treated with nematicide. Area under the curve describing pod invasion by *A. flavus* was highest from plots previously planted to peanut and to which nematicide had not been applied (Table 1).

Bacterial populations of peanut rhizosphere and geocarposphere: Total bacterial populations from the switchgrass rhizosphere did not vary over time, while populations in peanut rhizosphere and geocarposphere samples increased from 60 DAP to 90 DAP (Table 2). Bacterial

TABLE 3. The number of isolates per bacterial genus from the rhizosphere and geocarposphere of peanut and the rhizosphere of switchgrass over a growing season.

	Number of isolates[a]												
	Rhizosphere									Geocarposphere			
	Peanut/peanut[b] DAP[c]			Switchgrass[d] DAP			Switchgrass/peanut[e] DAP			Peanut/peanut DAP		Switchgrass/peanut DAP	
Genus[f]	60	90	120	60	90	120	60	90	120	90	120	90	120
Acidovorax		1				1							
Acinetobacillus	1	9	2	8	1	1	2						
Actinobacter	2			4	5			3			11	9	1
Agrobacterium	2	1	7		10	20			1			2	2
Alcaligenes			4					6	4			1	
Arthrobacter	4	4	5	17	5	12	8	1	1	6	7	6	8
Aureobacterium	1				6	3		1	5	6	1	1	1
Bacillus	100	16	24	68	26	32	129	11	12	2	12	20	2
Bergeyella				16	2		5			1	1		
Burkholderia	36	78	59		20	2	14	48	123	38	58	17	90
Cellulomonas				1							1		
Citrobacter									1				
Clavibacter		6	9	2	10	25		7	2	7	20	19	39
Comamonas	1	1	2		1	2		2	2			2	
Corynebacterium	1	1	1		2	3	2	7		4	15	6	12
Curtobacter	1			13	10	15					2	1	
Cytophaga		2					1		2			2	
Enterobacter	8		3	1	1	3	1	1	1	24	4	1	1
Escherichia	1		1			1		6	6		7		8
Flavobacterium			1		1	2			2	2			
Hydrogenophaga				1				3			1		
Klebsiella		3	2		3	1		2	3		1		1
Kluyvera								5	1	8		3	
Microbacterium	1	3	2		5	11			1	3			2
Micrococcus	3		1		8		4		1	35	5	4	2
Ochrobacter	2				2			3	1				1
Paenibacillus	2	1					9						
Pantoea	2	3	1	5	4	9	1	4	5		1	1	
Phyllobacterium		23	9		2			20		10	9	19	4
Pseudomonas	5	9	2	3	20	10	1	34	6	3	4	12	
Rathayibacter	2	2	2	1	1	3	1			6	2	6	1
Rhodococcus			2								1		
Salmonella	2		1				4			2	12	14	
Serratia									1			6	
Spingobacterium						1			1				
Sphingomonas										10		7	
Staphylococcus			2						1				
Stentrophomonas	8			17									
Variovorax					2							3	
Xanthobacter		1	6		4			2				1	
Xanthomonas		3		1	4	10		2		2	2	4	14
No match	21	39	58	48	51	39	24	38	23	37	29	39	17
Total number of isolates	206	206	206	206	206	206	206	206	206	206	206	206	206

[a] The number of isolates identified for each sampling time pooled over six replications.
[b] Rotation treatment of continuous peanut.
[c] Days after planting.
[d] Rotation treatment of switchgrass following peanut the previous year.
[e] Rotation treatment of peanut following peanut the previous year.
[f] Bacterial isolates identified to genus based on fatty acid methyl ester analysis and Microbial ID software and TSBA library 3.8.

populations from the rhizospheres of switchgrass and peanut following switchgrass were greater ($P \leq 0.05$) than those from the rhizosphere of continuous peanut at 60 DAP but not at 90 and 120 DAP. Rhizosphere populations of switchgrass were greater ($P \leq 0.05$) than those of peanut following switchgrass at 60 DAP. Geocarposphere populations were not significantly different among treatments at any sampling time (Table 2).

In total, 2,678 isolates were identified (Table 3). The most frequent genera in the rhizosphere samples were *Bacillus* (comprising 23% of the isolated bacteria) and *Burkholderia* (21%), while the most frequently isolated genera in the geocarposphere were *Burkholderia* (25%) and *Clavibacter* (10%). In all samples, a relatively high proportion of the isolates were classified as ''no match'' (17%), and when the ''no match'' isolates were compared to each other using the unweighted 2-D dendogram technique (Sherlock Software, MIDI, Newark, NJ), 85% of the isolates formed a single group at less than a Euclidean distance of 10 (data not shown), indicating the ''no match'' isolates were probably a single genus (Sasser, 1990) that is not represented in the MIDI library. All ''no match'' isolates were considered as a single genus for subsequent analysis.

Effects of switchgrass on the indigenous microbial community structure of the rhizosphere and the geocarposphere: Genus richness and *N2* of the peanut following switchgrass rhizosphere community were never significantly different ($P < 0.05$) from the continuous peanut rhizosphere community (Table 4). However, they were significantly $P < 0.05$) lower than the switchgrass rhizosphere community at 90 and 120 DAP but not at 60 DAP. The geocarposphere communities of peanuts following switchgrass were significantly ($P < 0.05$) greater than continuous peanuts at 90 DAP and not at 120 DAP.

Cluster analysis of the bacterial community structure using the coefficient of similarity (*B*) indicated that there were two main clusters (26% similar) corresponding to the rhizosphere and geocarposphere samples (Fig. 3). All geocarposphere environments were dissimilar from each other. However, the geocarposphere samples at 90 and 120 DAP from continuous peanut were more closely related (56%) to each other than to the geocarposphere at 90 and 120 DAP from peanut following switchgrass (50% and 37%, respectively). The rhizosphere communities from all sampling times were dissimilar from each other except for the rhizosphere communities of continuous peanut at 90 and 120 DAP.

The microbial communities of the peanut rhizosphere and geocarposphere were both quantitatively and qualitatively altered by rotation with switchgrass. Switchgrass following peanut, peanut following switchgrass, and continuous peanut supported different aerobic-heterotrophic bacterial rhizosphere communities as reflected by genera richness, diversity (*N2*), and similarity (*B*), even though these indices did not always differ at statistically significant levels. For instance, at 60 DAP, richness and *N2* for each treatment were not statistically different, while the total population and *B* values were significantly varied.

TABLE 4. Changes in the community structure of aerobic-heterotrophic bacteria over time as measured by the richness and diversity of genera.

Richness[a]	Rhizosphere			Geocarposphere		
Treatment	60[b]	90	120	60	90	120
Switchgrass	9.3 a[c]	12.2 a	10.2 a	–[d]	–	–
Switchgrass/peanut	7.8 a	8.3 b	7.2 b	–	11.3 a	7.9 a
Continuous peanut	8.7 a	9.2 b	8.3 b	–	7.3 b	8.3 a
N2[e]						
Switchgrass	5.2 a	9.3 a	7.1 a	–	–	–
Switchgrass/peanut	2.7 b	5.7 b	3.8 b	–	8.3 a	4.5 a
Continuous peanut	3.7 ab	4.2 ab	4.0 b	–	4.2 b	5.8 a

[a] Actual number of genera present.
[b] Days after planting.
[c] Mean of six replications. Means followed by the same letter within the same column and representing the same index are not significantly different ($P \geq 0.05$).
[d] No sample.
[e] Hill's modification of Simpson's diversity index.

Discussion

Use of switchgrass in a peanut rotation has beneficial effects on soil. Rotation of peanut with switchgrass reduced parasitic nematode populations and increased numbers of free-living nematodes. Crop rotation also caused shifts in rhizosphere and geocarposphere microbial ecology. The geocarposphere community that developed following a 1-year rotation with switchgrass is structurally different from the geocarposphere community that developed in a continuous peanut rotation. In addition, the differences in bacterial community structure between the geocarposphere and rhizosphere agree with previous reports (Katznelson, 1946; Kloepper and Bowen, 1991; Rao et al., 1972) that these two environments are distinct habitats that support different microbial communities. These results indicate that these communities had similar numbers of genera with a comparable distribution (i.e., number of dominant genera) but differed as to which genera were present or composed the dominant portion of the community.

In the complex soil ecosystem, it is difficult to show cause and effect with microbial communities. Therefore, we cannot say definitively that reductions in root-knot nematode populations resulted from shifts in microbial populations. The diversity and composition of the rhizosphere bacterial assemblage lead us to the theory that switchgrass rotation affected the rhizosphere carrying capacity early in peanut crop growth, possibly due to alteration of physical and chemical properties of the soil (e.g., fertility and porosity) (Roder et al., 1988; Workneh et al., 1993).

The reduction of root-knot nematode populations by the switchgrass rotation could have resulted from an

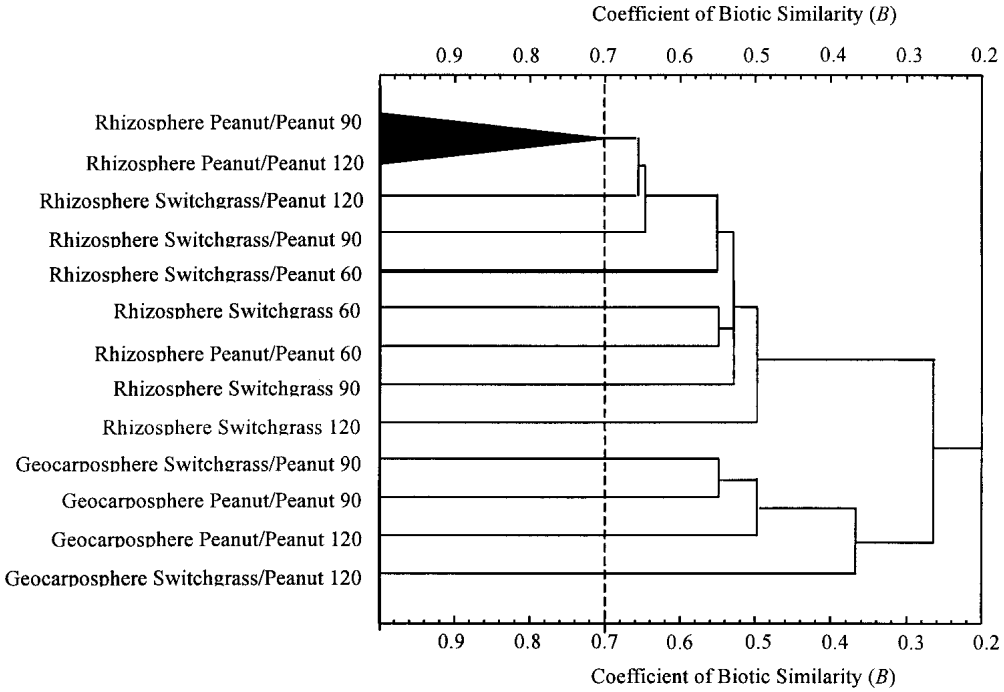

FIG. 3. A 2-D dendogram of habitat/rotation/sampling time similarity (*B*) based on the distribution of genera among each habitat/rotation 60, 90, and 120 days after planting (DAP). Clusters were derived from a matrix of *B* values based on comparisons of all possible pairs, where all matches were considered and the weighted cluster method was used. Cophenetic correlation was 0.96 with 95% confidence limits of 1.00 to 0.92. Dotted vertical line indicates the *B* value where the sample with the most dissimilarity among replications became one cluster.

increase in the microorganisms antagonistic to nematode feeding or reproduction. The number of *Burkholderia* species and other pseudomonads were three times greater from plots where peanuts followed switchgrass than from plots with continuous peanuts at all three sampling times. Kloepper et al. (1992) observed that more *Burkholderia* species were antagonistic to root-knot and soybean cyst nematodes than any other genus of bacteria isolated from plants.

These results do not lead to any firm conclusion that switchgrass rotations can minimize *A. flavus* activity and fungal invasion of peanut seed. However, these data do support the hypothesis that particular rotation sequences can contribute to reducing seed invasion by aflatoxigenic fungi, and subsequently reduce aflatoxin contamination of the peanut crop.

Effects of crop rotation with switchgrass on species diversity and richness, and identification of specific microbial taxa that predominate in the presence of switchgrass could lead to their use in integrated efforts to enhance plant growth and control diseases. A more complete understanding of soil microbial ecology with regard to crop rotation will enable researchers to develop production systems that incorporate crops beneficial to soil. These rotation practices could ultimately lead to more sustainable crop production and reduced dependence on chemical pesticides and fertilizers.

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