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Crop rotation and tillage systems as a proactive strategy in the control of peanut fungal soilborne diseases

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Abstract Soil management practices can affect the population dynamics of soil microbial communities. Cultural practices can be adequately combined to benefit natural populations of microorganisms that may have a role in biological control (actinomycetes, *Trichoderma* spp., and *Gliocladium* spp.), thus contributing to the management of peanut fungal soilborne diseases in a sustainable manner within ecological boundaries. During six agricultural cycles, rhizosphere soil samples were taken from a field subjected to crop rotation (soybean, peanut, and maize), peanut being under two tillage systems (no till, reduced tillage) with the aim of quantifying populations of soil microorganisms. The incidence of diseases caused by soilborne fungi in peanut was determined at harvest. The highest amount of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. were recorded when maize was the preceding crop. Regarding tillage systems, the populations of the three groups of microorganisms were higher in peanut under no tillage than under reduced tillage. Under these conditions, the lowest incidence of peanut blight (*Sclerotinia minor*) and root rot (strains of *Fusarium solani*) was observed, suggesting a possible natural control of peanut soilborne pathogens. The quantification of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. was used as a tool to explore the impacts of different management systems on microbial groups that may be involved in the biological control of soilborne diseases, with the aim of combining those practices that improve native populations of possible beneficial microorganisms. This manipulation can provide sustainable management strategies in the control of soilborne diseases, avoiding the use of artificial inoculations of microorganisms, and reducing agrochemical application.

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Introduction

Soil microorganisms are crucial to the sustainment of the biosphere and ecosystem functioning, and consequently can be used for monitoring and predicting environmental changes caused by agronomic impacts on soil (Lupwayi et al. 1998). Many factors affect soil microbial communities, including soil characteristics, environmental conditions, and crop management strategies, plant species and tillage being two of the most important factors (Larkin 2003). Crop rotation has remarkable effects on soil biotic factors (Dick 1992). Plant materials contain a wide range of C and N compounds with different decomposition rates that are affected by many soil factors (Ajwa and Tabatabai 1994), which may influence the development of soil microflora (Van Elsas et al. 2002). Few studies have documented the specific effects of different rotation crops on soil microbial communities within a defined crop production system (Lupwayi et al. 1998).

Tillage also affects soil biota, biotic quality factors in surface soil being inversely related to tillage intensity (Angers et al. 1993; Carpenter-Boggs et al. 2003). Tillage aerates the soil, breaks up plant and microbial cells, mixes biomass-rich top layers with deeper layers, affects the soil temperature regime, and hastens soil drying (Doran 1982). As a consequence, tillage promotes the release and degradation of previously protected organic matter, contributing to long-term reduction in soil microbial biomass and organic matter (de Luca and Keeney 1994).

In Argentina, peanut diseases caused by soilborne fungi have been gradually increasing in the last few decades, blight (*Sclerotinia minor*) and root rot (*Fusarium solani*) being the most important ones (March and Marinelli 2005). Soil health can be defined in terms of its microbiological capacity to counteract (suppress) the activity of plant pathogenic or plant-deleterious microorganisms (Van Bruggen and Semenov 2000). A more stable and reliable cropping system can be obtained by using the broadly based indigenous soil microbial community rather than a single species or strain, since what is pursued is the enhancement of natural biological control already functioning to some extent in soils (Lockwood 1990).

Biological control constitutes a sustainable and environmentally safe component of modern pest management, being a desirable alternative to the use of chemical pesticides (Waage 1991; Partridge et al. 2006). Some strains of the wide group of actinomycetes are known to produce a large and diverse array of bioactive compounds, constituting potential biocontrol agents (Steel et al. 1997; Bressan 2003). For many years, also isolates of *Trichoderma* spp. have been known as potential biocontrol agents of many plant diseases caused by soilborne fungal pathogens (Papavizas 1985). Some *Gliocladium* spp. isolates have the same characteristics as *Trichoderma* spp., and both have been described as destructive mycoparasites by Barnett and Lilly (1962). Because actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. are culturable groups of microorganisms, as indicated by Elmholt and Labouriau (2005), there is general agreement that the majority of fungal colonies are originated from spores or other propagules. Therefore, the dilution plating method is suitable to assess the soil contents on agar medium.

Numerous factors reduce the growth and establishment of introduced biocontrol agents in soil ecosystems and the costs that the increase of target microorganisms would imply to extensive crops is high (Harman 2000). Therefore, knowing the population dynamics of native soil microflora is crucial for the implementation of control strategies for a sustainable crop production system, especially if microorganisms have a role in crop health

and productivity. Accordingly, the objectives of this work were: (i) to evaluate the effects of crop rotation (soybean, peanut, and maize) on soil populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp.; (ii) to evaluate the effects of tillage systems in peanut (no tillage, reduced tillage) on these populations; and (iii) to evaluate the incidence of soilborne fungal diseases on peanut and its relationship with populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp.

Materials and methods

A long-term field experiment was conducted at the Agricultural Experimental Station Manfredi, Instituto Nacional de Tecnología Agropecuaria (INTA) in Córdoba, Argentina. Evaluations were made during six agricultural years (1999/00, 2000/01, 2001/02, 2002/03, 2003/04, and 2004/05). The soil at this site is a typical Argiudol (12.5% sand, 68.3% silt, and 19.2% clay), clease textural (USDA) silt-loam.

The experiment consisted in plots (20 × 70 m) subjected to agricultural rotation including soybean (*Glycine max*), peanut (*Arachis hypogaea*), and maize (*Zea mays*), at two sequences: corn–soybean–peanut and soybean–corn–peanut. Before the start of the experiments in 1999, the site had been planted with soybean. The assay was designed in order that the three crops (maize, soybean, and peanut), were present in each crop year and were rotated annually. Crops were distributed in 15 plots.

Peanut was subjected to no till and reduced tillage (disc harrow). Plots were treated with herbicides appropriate for weed control and fertilizers when necessary. Crops were harvested at full maturity with appropriate equipment.

Six composite soil samples (10 subsamples) (Beare et al. 1992) were randomly taken from each peanut plot. Samples were taken 20 days after peanut planting and 10 days before peanut harvest, totalling 12 samples per treatment for microbiological determination. For soil chemical properties quantification, six of the 12 samples per treatment were employed. Each subsample was taken with a core (3 cm diameter) at a depth of 0–5 cm.

In the laboratory, soil samples were homogenized, spread on paper and cleaned to remove plant material; then they were air dried and sieved through a 2 mm screen and stored at 4°C until processing. For determination of soil moisture, a 5–8 g subsample was weighed before drying at 90°C and 7 days after drying.

Evaluation of disease incidence

The incidence of diseases caused by soilborne fungi in peanut was evaluated at harvest, by establishing 10 sample stations at emergence in each peanut plot, regularly distributed in a V-shaped design (systematic sampling procedure). Each station comprised 50 plants. Incidence was evaluated as percentage of affected plants.

In the field, peanut plants with blight were recognized by the early symptoms, like wilting and stem lesions with white mycelial growth, which occurred on the lower main stem or side branches of the peanut plant. Late symptoms included light tan lesions on stems, stem shredding, and characteristic brown color of the entire plant, signing the death of the plant (Chenault et al. 2006).

Peanut plants with root rot presented light brown lesions along the taproot and on the side roots as early symptoms, while the late ones included the total rot of the roots and the dark brown color of the plants (Burke and Miller 1983).

The causal agents of the symptoms observed were confirmed at laboratory, by plating even pathogen signs or diseased tissue, both previously disinfected, on agar medium.

Plate enumerations

Soil microorganisms were quantified following Vargas Gil et al. (2007). Each composite sample was mixed again and a subsample was taken for dilution plating. For actinomycetes quantification, a soil subsample (1 g) was weighed, transferred into 100 ml of distilled and sterile water, and mixed on rotary shaking machine. Colonies were counted on Küster medium modified by the addition of cycloheximide (0.15 g/l) and sodium propionate (0.4 g/l). *Trichoderma* spp. and *Gliocladium* spp. were quantified following the same procedure, except that the soil suspension was 10 g/100 ml of distilled and sterile water, and that the colonies were counted on PDA supplemented with rose bengal (20 mg/l), streptomycin (100 mg/l), and chloramphenicol (300 mg/l) after 7–10 days at 25°C. Data are expressed as the number of colony forming units (CFU)/g of dry soil, actinomycetes being expressed as $\times 10^4$ and fungi as $\times 10^2$. To simplify data presentation, only sr (square root) CFU/g dry soil is expressed throughout the text.

Soil chemical properties

Organic matter (OM), total N, NO_3, C/N, pH, P, Ca, Mg, Na, and K were measured in the six agricultural cycles. Soil organic C was measured by modification of Walkley–Black method (Walkley and Black 1934), and total N by colorimetry after digestion by Kjeldhal method (Bremner and Mulvaney 1982). Inorganic NO_3–N was measured using the cadmium reduction method, following extraction with 2 M KCl (1:4, w:v) and shaking for 30 min; pH with an electrode in a 1:1 soil:water solution; and available P (with 0.5 M sodium bicarbonate, pH 8.5) was determined by colorimetry, according to Murphy and Riley (1962). Quantification of Ca, Mg, Na, and K was made using a Spectrometer with atomic bulbs specific for the mentioned elements.

Experimental design and data analysis

The experiment was a split plot randomized block design with four replicates. Reduced tillage and no tillage were main treatments, while subplots consisted of rotation between maize, peanut, and soybean. The dependent variables were the soil determination of soil biological (actinomycetes, *Trichoderma* spp., and *Gliocladium* spp.), and chemical parameters. In the statistical analysis, the crop years were considered as blocks, and the sampling times (after sowing and before crop harvest), as repetitions inside the crop year.

Data were subjected to analysis of variance (ANOVA) to test the significance of all factors examined in the experiments. Statistical analyses were conducted using INFOSTAT/Professional 2007 (F.C.A.—Universidad Nacional de Cordoba, Argentina) at $P < 0.05$. Normality of data was tested using the Shapiro–Wilks test. To satisfy the assumptions of homogeneity and normality of error variances in the ANOVA, square-root transformation of CFU was applied to data before the analysis. Other customary transformations were used for normalizing the data, but were not as effective to reach normality as square root. The least significant difference test (LSD) was used to test for differences between treatments (Steel et al. 1997).

A correlation analysis was performed between soil chemical parameters and abundance of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. populations, using Pearson coefficients with a level of significance at $P < 0.05$ (Bulluck et al. 2002).

Results

The ANOVA showed no significant interactive effect of crop rotation and tillage systems on CFU (Table 1).

Rotation crops

Population dynamics of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. was markedly influenced by crop type (Fig. 1). The highest populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. were recorded when maize was the previous crop

Table 1 ANOVA for Actinomycetes, *Trichoderma* spp., *Gliocladium* spp., and the incidence of peanut blight (*Sclerotinia minor*) and root rot (*Fusarium solani*) under different tillage systems and crop rotation, during six agricultural years

Source of variation	Crop cycle	Actinomycetes	*Trichoderma* spp.	*Gliocladium* spp.	*Sclerotinia minor*	*Fusarium solani*
Tillage systems	1999/00	9.4*	2.3*	9.7*	NP	NP
	2000/01	18.3**	4.5*	NS	NP	NP
	2001/02	8.2*	3.9**	6.7**	25.3*	NP
	2002/03	NS	6.5***	5.9 *	NP	4.1**
	2003/04	15.2*	NS	9.2**	21.8*	NP
	2004/05	10.6*	5.1**	7.2**	14.2*	NP
Tillage treatment		*	**	**	*	**
Crop rotation	1999/00	72.3**	NS	20.2***	NP	NP
	2000/01	89.4**	21.2*	25.5**	NP	NP
	2001/02	48.6**	32.2*	27.2 *	20.2*	NP
	2002/03	NS	27.8***	12.2 *	NP	6.6*
	2003/04	64.3*	26.4*	NS	27.1*	NP
	2004/05	54.3	19.3	23.6**	11.7***	NP
Rotation treatment		**	*	**	**	*
Tillage × rotation	1999/00	NS	NS	NS	NP	NP
	2000/01	NS	NS	NS	NP	NP
	2001/02	NS	NS	NS	*	NP
	2002/03	NS	NS	NS	NP	*
	2003/04	NS	NS	NS	*	NP
	2004/05	NS	NS	NS	*	NP

NS (Not significant) at $P > 0.05$; Stars indicate significant at: *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$

NP, not present

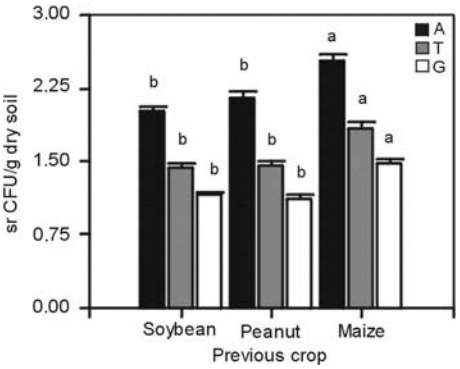

Fig. 1 Effect of previous crop on actinomycetes (A), *Trichoderma* spp. (T) and *Gliocladium* spp. (G) populations (CFU: colony forming units (fungi expressed $\times 10^2$, actinomycetes $\times 10^4$)) in soil under rotation crops (soybean, peanut, and maize), peanut being under different tillage systems (no till and reduced tillage) in EEA INTA Manfredi. Experiments were conducted during six agricultural years (1999/00, 2000/01, 2001/02, 2002/03, 2003/04, and 2004/05). Bars with the same color that have a common letter are not significantly different according to Fisher test at $P < 0.05$. Each bar is the average of samples taken at sowing and harvest ($n = 2$) of each plot ($n = 6$) during six agricultural years ($n = 6$)

(2.54, 1.84, and 1.48 sr CFU/g dry soil, respectively), compared with soybean (2.02, 1.44, and 1.16 sr CFU/g dry soil, respectively) and peanut (2.14, 1.46, and 1.12 sr CFU/g dry soil, respectively).

Soil chemical properties

The ANOVA revealed a statistically significant interaction of rotation-soil chemical parameters and tillage-soil chemical parameters for CFU of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. For this reason, a correlation analysis between the three soil microbial populations and chemical variables was performed (Table 2). A significant positive correlation of actinomycetes with OM (0.15), total N (0.55), C/N (0.29), pH (0.17), and P (0.48) was observed. Also *Trichoderma* spp. had a positive, significant

Table 2 Correlation between soil chemical parameters and potential biocontrol agents

Chemical parameters	Pearson coefficients ($P < 0.05$)		
	Actinomycetes	*Trichoderma* spp.	*Gliocladium* spp.
OM	0.15*	0.15*	0.18*
Total N	0.55*	0.22*	0.15*
C/N	0.29*	0.35*	0.36*
NO_3	0.11	−0.2	−0.24
pH	0.17*	0.18*	0.17*
P	0.48*	0.24*	0.20*
Ca^{2+}	0.15	−0.03	0.12
Mg^{2+}	0.01	0.2	0.11
Na^{+}	−0.01	−0.19	−0.16
K^{+}	0.02	0.1	0.12

* Significant at $P < 0.05$

correlation with OM (0.15), total N (0.22), C/N (0.35), pH (0.18), and P (0.24). Finally, *Gliocladium* spp. had a positive, significant correlation also with OM (0.18), total N (0.15), C/N (0.36), pH (0.17), and P (0.20). Although there was a positive, significant correlation between actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. and several soil chemical parameters, OM had a relevant role in residue decomposition as a source of energy and nutrients (Fig. 2).

Tillage systems

Tillage systems in peanut affected the population dynamics of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. (Fig. 3). Populations of these microorganisms were higher in peanut under no tillage compared with reduced tillage.

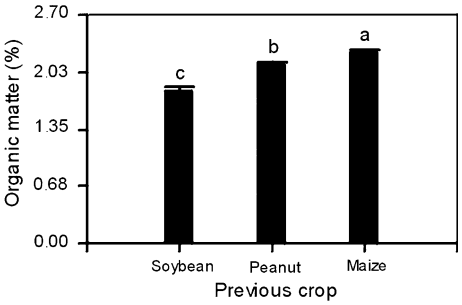

Fig. 2 Influence of previous crop on soil organic matter content, under rotation crops (soybean, peanut, and maize), peanut being under no till and reduced tillage, in EEA INTA Manfredi during six agricultural years (1999/00, 2000/01, 2001/02, 2002/03, 2003/04, and 2004/05). Bars that have a common letter are not significantly different according to Fisher test at $P < 0.05$. The bars are the mean of six measurements per plot, during six agricultural years ($n = 6$)

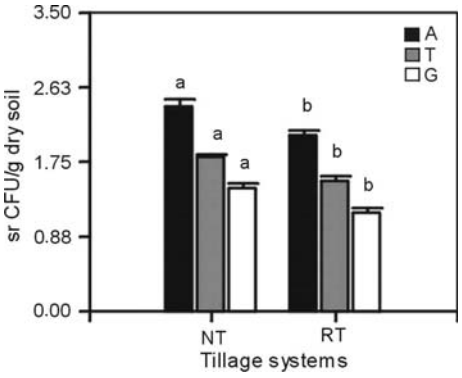

Fig. 3 Influence of tillage systems in peanut on actinomycetes (A), *Trichoderma* spp. (T), and *Gliocladium* spp. (G) populations (CFU: colony-forming units (fungi expressed $\times 10^2$, actinomycetes $\times 10^4$) in soil under rotation crops (soybean, peanut, and maize), peanut being under no till (NT) and reduced tillage (RT) in EEA INTA Manfredi. Experiments were conducted during six agricultural years (1999/00, 2000/01, 2001/02, 2002/03, 2003/04, and 2004/05). Bars with the same color that have a common letter are not significantly different according to Fisher test at $P < 0.05$. Each bar is the average of samples taken at sowing and harvest ($n = 12$) of each plot ($n = 6$) during six agricultural years ($n = 6$)

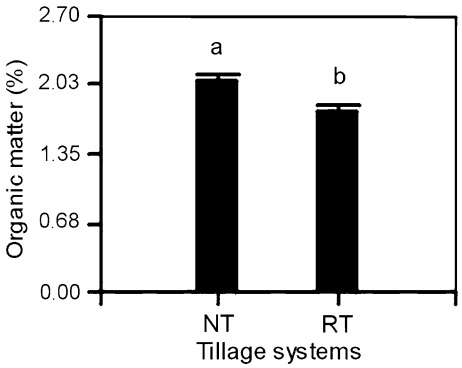

Fig. 4 Influence of tillage systems on soil organic matter content, under rotation crops (soybean, peanut, and maize), peanut being under no till and reduced tillage, in EEA INTA Manfredi during six agricultural years (1999/00, 2000/01, 2001/02, 2002/03, 2003/04, and 2004/05). Bars that have a common letter are not significantly different according to Fisher test at $P < 0.05$. The bars are the mean of six measurements per plot, during six agricultural years ($n = 6$)

Soil chemical properties

Differences in OM content were significant depending on the tillage system employed, with higher OM under no tillage than with reduced tillage (Fig. 4).

Incidence of diseases caused by soilborne fungi

During the six agricultural cycles evaluated, peanut blight (*Sclerotinia minor*) was detected in 2001/02, 2003/04, and 2004/05 and root rot (strains of *Fusarium solani*) was recorded in 2002/03. The relationship of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. and peanut blight with cultural practices are shown in Fig. 5. The ANOVA showed a significant interactive effect of crop rotation and tillage systems on peanut blight and root rot (Table 1).

When soybean was the previous crop and peanut was under no tillage, the highest incidence values of peanut blight were observed (3.81%), associated with the lowest populations of potential biocontrol agents (2.38, 1.70, and 1.26 sr CFU/g dry soil of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp., respectively). With the same previous crop but peanut being under reduced tillage the incidence of blight was lower (2.68%) compared with no tillage, and the lowest populations of actinomycetes, *Trichoderma* spp. and *Gliocladium* spp. (2.08, 1.52, and 1.03 sr CFU/g dry soil, respectively) were recorded. A lower disease incidence was observed with maize as previous crop (2.47%) and peanut under reduced tillage, with records of high populations of soil microorganisms (2.69, 2.06, and 1.66 sr CFU/g dry soil of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp., respectively). The lowest blight incidence values (1.78%) were observed with maize as previous crop and peanut under no tillage, with the highest records of populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. (3.21, 2.41, and 1.99 sr CFU/g dry soil, respectively).

The relationships of the soil microorganisms evaluated and peanut root rot with cultural practices are shown in Fig. 6. The highest incidence of peanut root rot (1.13%) was

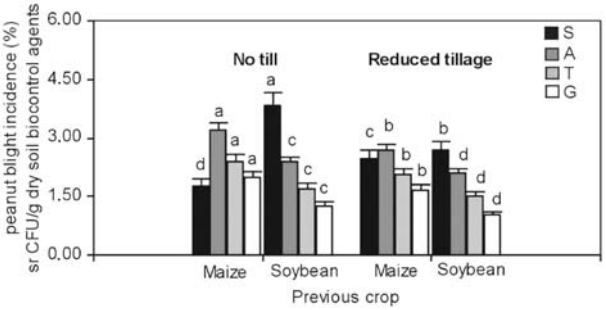

Fig. 5 Effect of previous crop (maize, soybean) and tillage systems (no till, reduced tillage) on the incidence of peanut blight (S: *Sclerotinia minor*) and populations (CFU: colony forming units (fungi expressed × 10^2, actinomycetes × 10^4)) of potential biocontrol agents (A: actinomycetes, T: *Trichoderma* spp., and G: *Gliocladium* spp.) in EEA INTA Manfredi. Experiments were conducted during six agricultural years (1999/00, 2000/01, 2001/02, 2002/03, 2003/04, and 2004/05). Bars with the same color that have a common letter are not significantly different according to Fisher test at $P < 0.05$. For quantification of potential biocontrol agents, each bar is the average of samples taken at sowing and harvest ($n = 12$) of each plot ($n = 6$) during six agricultural years ($n = 6$); for disease incidence evaluation each bar is the average of 50 peanut plants/plot, during 6 years

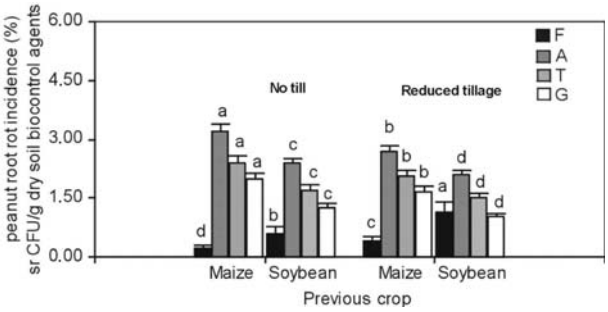

Fig. 6 Effect of previous crop (maize, soybean) and tillage systems (no till, reduced tillage) on the incidence of peanut root rot (F: strains of *Fusarium solani*) and populations (CFU: colony forming units (fungi expressed × 10^2, actinomycetes × 10^4)) of potential biocontrol agents (A: actinomycetes, T: *Trichoderma* spp., and G: *Gliocladium* spp.) in EEA INTA Manfredi. Experiments were conducted during six agricultural years (1999/00, 2000/01, 2001/02, 2002/03, 2003/04, and 2004/05). Bars with the same color that have a common letter are not significantly different according to Fisher test at $P < 0.05$. For quantification of potential biocontrol agents, each bar is the average of samples taken at sowing and harvest ($n = 12$) of each plot ($n = 6$) during six agricultural years ($n = 6$); for disease incidence evaluation, each bar is the average of 50 peanut plants/plot, during 6 years

observed when soybean preceded peanut and peanut was under reduced tillage, with the lowest records of populations of microorganisms (2.08, 1.52, and 1.03 of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp., respectively). With soybean as previous crop but peanut under no tillage, the incidence of root rot decreased (0.60%) with a slight increase of biocontrol populations (2.38, 1.70, and 1.26 of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp., respectively), showing significant differences from the values observed with soybean as a preceding crop and peanut being under reduced tillage. With corn as a previous crop and peanut under reduced tillage a lower incidence was observed (0.42%),

with 2.69, 2.06, and 1.66 sr CFU/g dry soil of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp., respectively. Finally, the lowest incidence of root rot (0.22 %) was recorded with maize as a preceding crop and peanut under no tillage, with the highest records of populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. (3.21, 2.41, and 1.99, respectively).

Discussion

Our results demonstrate that crop rotation and tillage systems influenced native populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp., and that both these microorganisms and crop management had some influence on the incidence of peanut blight and root rot.

Rotation crops

The highest populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. were recorded when maize was the previous crop. Moreover, soil OM content was highest with maize residues; when soybean and peanut were the previous crops, the studied soil microorganisms did not differ significantly. These results show a direct relationship between the type of plant residue, OM content and soil microorganisms evaluated. Bandick and Dick (1999) stated that each residue has unique characteristics that determine the specific activities of those microorganisms directly associated to them.

Dolan et al. (2006) demonstrated that maize and soybean residues influence the abundance of soil C content in different ways. Because maize is a C4 plant, its residues have more proportion of organic C than soybean, thus increasing OM content in soil (Layese et al. 2002), which probably benefited microbial populations in soil in our study.

Maize residues particularly improve soil water content, influencing soil OM content, which is the principal nutrient source for microorganisms (Doran 1980). In agreement with our present work, the author also found that maize as a preceding crop favored the populations of actinomycetes and fungi, being maize residues a source of energy and nutrients. Although Larkin (2003) found similar results, with records of an increase of actinomycetes and *Trichoderma* spp. populations in soil when maize was included in the crop rotation, the author stated that the information about the effects of crop rotation on soil microflora is scarce.

Tillage systems

Actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. populations were higher under no tillage than under reduced tillage. Soil OM content was also affected by tillage systems through the incorporation of crop residues, since it was higher when maize was the previous crop. Tillage determines when and how total C returns to soil and the factors involved in this process, because residues are incorporated in soil strata depending on the tillage system employed (Pankhurst et al. 2002).

Associated with the change in soil chemical parameters, tillage also influences soil microbial populations. Some authors found an increase in soil microorganisms under conservation tillage (Roldan et al. 2005). Our results agree with results found by other

authors (Doran 1980; Linn and Doran 1984), who recorded an increment of actinomycetes populations in no tillage systems. At the same time, Beare et al., (1992) found that fungi were more abundant under conservation tillage systems due to the fewer disturbances that allow the establishment of hyphal nets (Wardle 1995).

Rabeendran (2000) also found a positive and significant correlation of P concentration with microbial populations, whereas K, Ca, and Mg have less influence on crop production or nutrients cycle.

Incidence of diseases by soilborne fungi

Peanut blight

As mentioned by Marinelli et al. (1998), the previous crop had a marked effect on peanut blight, whereas the influence of tillage systems on this disease did not show a clear effect. Populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. followed a clear pattern depending on the preceding crop or the tillage system.

The use of crops that are not hosts to *S. minor* allows the sclerotia to be broken down by various soil microorganisms during periods when there is no host to infect (Phipps et al. 1997). El-Tarabily et al. (2000) mentioned that actinomycetes can produce large quantities of chitinases that are responsible for the hyphal lysis produced on *S. minor*. According to some authors (Doran 1980; El-Tarabily et al. 2000), maize as a preceding crop favors the development of soil microorganisms, actinomycetes being included in these populations. Because several species of actinomycetes are involved in the biological control of soilborne diseases, the probability of finding those species will be higher when maize is the preceding crop, which is one of the causes for finding lower incidence of peanut blight.

The same occurred with *Trichoderma* spp. and *Gliocladium* spp., which were more abundant with maize as a previous crop. The high presence of both fungi could be one of the factors that contributed to a lower incidence of peanut blight, because it is well known that some species of *Trichoderma* have antagonist activity against *S. minor* (Rabeendran 2000). No tillage permits the sclerotia to remain in the upper soil layer, where it is degraded by the soil microflora, *Trichoderma* spp. being one of the most frequently found (Wu and Subbarao 2003), together with actinomycetes (Abawi et al. 1984).

Root rot

When soybean preceded peanut, the highest incidence values of root rot were observed, associated with low populations of potential biocontrol agents. Accordingly, Burke and Miller (1983) found that when some crops like maize, wheat, or sorghum are included in rotation with beans, the large volume of residues that these crops leave prevent soil compaction and also makes the soil rich in suppressive microflora of *F. solani*, including actinomycetes (Steel et al. 1997). Actinomycetes are promising candidates for biological control of soilborne diseases due to their dominance in rhizosphere soil (Sharma et al. 2005). Also *Trichoderma* spp. and *Gliocladium* spp. have been reported as having antagonistic characteristics against *F. solani* (Estevez de Jensen et al. 2002).

Disease incidence was lower under no tillage than under reduced tillage, associated with high populations of actinomycetes, *Trichoderma* spp., and *Gliocladium* spp. According to some authors (Doran 1980; Linn and Doran 1984; Wardle et al. 1999), populations of actinomycetes and fungi increase under no tillage systems due to high humidity content,

more OM content associated to a greater amount of crop residues, and less disturbance that facilitates the establishment and development of microbial communities. This enhanced soil biota associated to no till soils may benefit crop production by releasing available forms of nutrients from organic and inorganic sources and increasing mineral uptake (Carpenter-Boggs et al. 2003). This fact may have partially contributed to the development of more healthy plants and also to the enhancement of pathogen antagonism, which probably have favored the low disease incidence observed.

Disease suppression typically occurs as a result of the activation of the indigenous soil microbial community, which has been much neglected in favor of intensive research on individual antagonistic microorganisms (Lockwood 1990). In fact, field soils typically harbor organisms capable of suppressing a wide range of soilborne diseases through a diversity of mechanisms. The problem is not the lack of biocontrol organisms but the lack of an environment that supports high populations and the activities related to biological control.

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