


Biochemical and Biological Properties of Soil from Murundus Wetlands Converted into Agricultural Systems

Luciene Nunes Barcelos Martins⁽¹⁾, Flávia Louzeiro de Aguiar Santiago⁽²⁾, Marcela Susana Montecchia⁽³⁾, Olga Susana Correa⁽³⁾, Orivaldo José Saggin Junior⁽⁴⁾, Edicarlos Damacena de Souza⁽⁵⁾, Helder Barbosa Paulino⁽⁶⁾ and Marco Aurelio Carbone Carneiro^{(2)*} 

⁽¹⁾ Universidade Federal de Goiás, Jataí Regional, Departamento de Agronomia, Programa de Pós-Graduação em Agronomia, Jataí, Goiás, Brasil.

⁽²⁾ Universidade Federal de Lavras, Departamento de Ciência do Solo, Setor de Biologia e Processos Bioquímicos do Solo, Lavras, Minas Gerais, Brasil.

⁽³⁾ Universidade de Buenos Aires, Faculdade de Agronomia, Departamento de Biologia Aplicada e Alimentos, Buenos Aires, Buenos Aires, Argentina.

⁽⁴⁾ Empresa Brasileira de Pesquisa Agropecuária, Embrapa Agrobiologia, Seropédica, Rio de Janeiro, Brasil.

⁽⁵⁾ Universidade Federal do Mato Grosso, *Campus* de Rondonópolis, Departamento de Zootecnia, Rondonópolis, Mato Grosso, Brasil.

⁽⁶⁾ Universidade Federal do Triângulo Mineiro, *Campus* Iturama, Departamento de Agronomia, Iturama, Minas Gerais, Brasil.

* **Corresponding author:**
E-mail: marcocarbone@ufla.br

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ABSTRACT: The implementation of conservationist systems that improve soil properties and reduce the impacts of the conversion of native areas is fundamental for feasible agricultural exploitation. This study aimed to evaluate the impact on soil biological properties caused by the conversion of murundus fields into agricultural systems and verify the ability of the no-tillage conservation system to recover these properties over the years. Treatments consisted of three agricultural areas subjected to the same management (no-tillage), in a chronosequence (7, 11, and 14 years of conversion) and a reference area (murundus field). To evaluate soil quality, we analyzed total soil organic carbon, microbial biomass carbon, soil basal respiration, metabolic and microbial quotients, and acid phosphatase activities, as well as the potential functionality of soil bacterial communities and the modifications in their genetic structure. The conversion of murundus field into agricultural systems negatively impacted soil biological properties, with expressive reduction in soil organic carbon content and microbial biomass carbon. The periods of adoption of the conservationist system (no-tillage) were not enough to recover the biological properties and/or to reverse the changes observed in the genetic structure of the soil bacterial communities of the managed areas, although stabilization trends were observed in the agricultural systems over the years.

Keywords: anthropic interference, agricultural production, management, Cerrado, soil quality.



INTRODUCTION

The Cerrado (Brazilian Savanna) demonstrates great potential for agribusiness due to good soil and climatic conditions for agricultural development (Gibbs et al., 2015; Arantes et al., 2016). However, owing to the advancement of agricultural frontiers and the need for greater food production, several Cerrado areas with low land suitability have been converted into productive systems, such as murundus phytophysionomies (Paulino et al., 2015), which have been protected by the Law of the state of Goiás (Law No. 16,153) since 2007. Murundus fields are mainly found in the plain regions of Central Brazil (Furley, 1985), located in the so-called headwaters, which are flatter and higher topographic regions than Cerrado wetlands (Rosolen et al., 2015). These areas were neglected by the Agricultural expansion policy, environmental legislation, and scientific research for a long time. However, several hectares had already been converted, indicating the need for studies that assess the impacts caused by the conversion and monitor the management of these soils, aiming to maintain the sustainability of the agricultural system.

Anthropogenic interference in natural ecosystems, together with inadequate soil management have been the major cause of soil sustainability reduction, compromising its structure (Cunha et al., 2012; Wei et al., 2013; Sales et al., 2016), reducing carbon stock (Cardoso et al., 2010; Marques et al., 2016), and limiting its biological activity (Carneiro et al., 2009). The changes caused by the conversion of native areas into agricultural systems affect soil functionality and hinder the re-establishment of a new equilibrium in the soil system.

No-tillage stands out among the sustainable management systems. This is because soil mobilization and straw deposition provide greater physical protection to the soil surface layer; increase water retention (Tormena et al., 2007; Marouelli et al., 2010; Vilela et al., 2014; Carneiro et al., 2015), and soil carbon stock (Albuquerque et al., 2015; Sá et al., 2015; Ferreira et al., 2016; Souza et al., 2016); promote greater biological diversity (Campos et al., 2016) and the continuity of the ecological functions of the soil; and directly increase crop yield (Carneiro et al., 2009). Soils under no-tillage system are more sustainable for the soil biological (Calegari, 1998); however, in tropical regions, the consolidation and efficiency of the system may take longer due to the higher rate of decomposition of organic residues, which implies long-term benefits (Pragana et al., 2012). The quality of the organic residues also hinders the efficiency of the no-tillage system, as it is directly related to the adaptation of the soil microbial communities. In addition, in areas with low resilience, such as murundus phytophysionomies, the negative impact of conversion on agricultural areas may be so severe that even consolidated management systems such as no-tillage need to be improved (Souza et al., 2016).

Microorganisms are the main mediators of biological and biochemical processes in the soil, which are very sensitive to changes in the ecosystem and excellent indicators of agricultural sustainability (Doran and Parkin, 1994). In previous studies, some of these biochemical properties and processes, such as total organic carbon, microbial biomass carbon, metabolic quotient, and enzymatic activities of the soil, have shown sensitivity to the management adopted, being potential to indicate impacts suffered by the conversion of natural environments to agriculture (Pragana et al., 2012; Lacerda et al., 2013; Souza et al., 2016).

Thus, this study aimed to evaluate the impact of the conversion of murundus fields into agricultural systems on the biochemical and biological properties of the soil and to verify the ability of no-tillage system to recover these properties over the years.

MATERIALS AND METHODS

Site description and field sampling

The study was carried out in areas belonging to Fazenda Boa Vista (lat. 17° 57' 59" S; long. 52° 04' 35" W), located in the Rio Claro watershed, between the municipalities of

Jataí and Mineiros, in the state of Goiás, Brazil. The climate of the region is classified as type Aw (Köppen classification system), with rainy summer and dry winter. The annual precipitation is approximately 1,700 mm, and the temperature ranges from 18 to 32°C.

The experiment consisted of a completely randomized design in four areas, three with anthropic interference, varying the time of conversion into agricultural systems (7, 11, and 14 years, in relation to the year 2011), and one without anthropic interference. The agricultural areas consisted of the same type of soil management (no-tillage), with the same crop sequence (soybean/corn). The only difference was the conversion time, as can be observed in history of the areas described in table 1. The soil of the study areas was classified as Plinthosol (IUSS, 2015), which corresponds to a *Plintossolo Háplico* (Santos et al., 2013). Chemical and physical properties are described in table 2.

Table 1. Physical-chemical properties of Plinthosol of the study areas

Area	pH(H ₂ O)	cmol _c dm ⁻³			mg dm ⁻³		g kg ⁻¹		
		Al ³⁺	Ca ²⁺	Mg ²⁺	K	P	Sand	Silt	Clay
RF	5.4	0.82	0.04	0.22	24.9	0.40			
NT7	6.1	0.06	2.49	0.90	40.8	3.09	530	25	445
NT11	5.8	0.07	2.76	1.22	30.5	3.86			
NT14	6.3	0.05	3.43	1.34	41.2	2.31			

pH in water at a soil:solution ratio of 1:2 (v/v). K and P extracted with Mehlich I; Ca²⁺, Mg²⁺, and Al³⁺ extracted with KCl 1 mol L⁻¹; sand, silt, and clay were determined according to the methodology presented by GEE and Bauder (1986). RF = reference area (murundus field); NT7 = area converted into no-tillage system for 7 years; NT11 = area converted into no-tillage system for 11 years; NT14 = area converted into no-tillage system for 14 years.

Table 2. Identification and history of management and use of the study areas

Identification	History
RF (Murundus fields)	The area has not undergone anthropic intervention. Murundus present 6 m mean diameter and approximately 1 to 2 m height. The top of the murundus (TM) presents typical vegetation of Cerrado <i>stricto sensu</i> , with high diversity of shrub, trees and creeping plants, and constant presence of termites; the soil was collected from the upper third of the murundus. This reference area has approximately 148 ha and 33 murundus.
NT14	The area has undergone anthropic intervention since 1996/1997. In 1996, 3 Mg ha ⁻¹ of dolomitic limestone were applied with the incorporation, using plow and leveling grid. At the initial planting, 1 Mg ha ⁻¹ of reactive phosphate (33 % P ₂ O ₅) and 2 Mg ha ⁻¹ of gypsum were applied. From 1998, no soil rotation was performed, that is, no-tillage system was used. In 2005/06, 1.5 Mg ha ⁻¹ of dolomite limestones were applied on top. In this area, crop succession was performed with soybean (season) and corn (off-season), with approximately 3.4 and 6 Mg ha ⁻¹ yield, respectively.
NT11	The area has undergone anthropic intervention since 1999/2000. Initially, it presented native areas and native pasture, to which 6 Mg ha ⁻¹ of dolomitic limestone were applied with the incorporation, using plow and leveling grid. At the initial planting, 0.6 Mg ha ⁻¹ of reactive phosphate (33 % P ₂ O ₅) was applied. From 2000, no soil rotation was performed, that is, no-tillage system was used. In this area, crop succession was performed with soybean (season) and corn (off-season), with approximately 3.4 and 6 Mg ha ⁻¹ yield, respectively, in the first years. The year of 2006 consisted of soybean/fallow. In the years of 2002/2003 and 2007/2008, 2.5 Mg ha ⁻¹ of dolomitic limestones were applied on top.
NT7	The area has undergone anthropic intervention since 2003/2004. Initially, it presented native pasture, to which 5 Mg ha ⁻¹ of dolomitic limestone was applied in 2003 with the incorporation, using plow and leveling grid. At initial planting, 0.6 Mg ha ⁻¹ of reactive phosphate (33 % P ₂ O ₅) and 2 Mg ha ⁻¹ of agricultural gypsum were applied. From 2004, no soil rotation was performed, that is, no-tillage system was used. In this area, crop succession was performed with soybean (season) and corn (millet or sorghum) (off-season), with approximately 3.1 and 4.5 Mg ha ⁻¹ yield, respectively, in the first years. From 2007, crop succession consisted of soybean and corn rotation (season) and fallow (off-season). In 2005/2006 and 2008/2009, 1.5 Mg ha ⁻¹ of dolomitic limestone was applied on top.

RF = reference area (murundus field); NT7 = area converted into no-tillage system for 7 years; NT11 = area converted into no-tillage system for 11 years; NT14 = area converted into no-tillage system for 14 years.

In each area, 100 × 100 m polygons were marked, of which ten were randomly taken, considering the replications. Ten soil subsamples were taken from each polygon to form a composite sample of 2 kg of the 0.00-0.10 m layer. The area without anthropic alterations consisted of 33 murundus per hectare, of which ten murundus per hectare were selected for soil collection. Soil samples were sieved in a 2 mm mesh, a portion of this material was stored in sterile plastic bags in a cold room at 4 °C for biochemical analyzes and another portion was stored at -80 °C for extraction of DNA.

Laboratory analyses and analytic methods

Total organic carbon (TOC) was determined by titration with a solution of ferrous ammonium sulfate after carbon oxidation in potassium dichromate (Walkley and Black, 1934). Microbial biomass carbon (MBC) was obtained by the fumigation-extraction method (Vance et al., 1987), and microbial respiration (CO₂) was estimated by the CO₂ evolved in soil samples incubated with NaOH 0.05 mol L⁻¹ (Alef and Nannipieri, 1995).

The metabolic quotient (qCO₂) was obtained by the ratio between basal respiration and microbial biomass carbon. The microbial quotient (qMic) was determined using the ratio of the microbial biomass carbon and the total organic carbon content of the soil (Anderson and Domsch, 1993). Acid phosphatase activity was estimated based on the methodology proposed by Dick et al. (1996) and quantified by spectrophotometry at 490 nm.

The analysis of the physiological profiles, which aims to verify the decomposition capacity of carbon substrates by the bacterial communities, was performed in 96 well microplates. The carbon substrates selected for analysis were L-lysine, L-arginine, L-asparagine, L-tryptophan, glucose, glucose-P, β-glycerol-P, fructose, D (+)-mannose, sucrose, erythritol, D-glutaric acid, itaconic acid, D(-) quininic acid, DL-malic acid, glycogen, 2-aminobenzoic acid, D (+) cellobiose, soy peptone, carboxymethyl cellulose, and tween 80, all from Sigma-Aldrich Inc. Stock solutions (3 g L⁻¹) of each substrate were prepared in deionized water, sterilized by filtration, and stored at 4 °C. Initially, 60 μl of a saline solution (21 g K₂HPO₄; 9 g KH₂PO₄; 0.3 g MgSO₄; 1.5 g (NH₄)₂SO₄; 0.03 g CaCl₂; 0.015 g FeSO₄; 0.0075 g MnSO₄; 0.0075 g NaMoO₄) and Tetrazolium violet solution (0.0075 %) were added to the wells. Afterward, 60 μL of each stock solution of the carbon substrates were separately added to each well.

Suspensions of 2 g of soil (seven replications of each randomly chosen soil) were prepared in 50 mL polypropylene tubes with 10 mL of deionized sterile water. Sterile glass beads were added to the soil suspensions; tubes were shaken by hand for 1 min and centrifuged at 2,600 g for 10 min. After this procedure, 60 μL of the supernatant from each soil suspension were immediately placed in the wells, together with the previously added solution. Initial absorbance readings at 590 nm were performed using the Multiskan Ex (Thermo) equipment. Microplates were incubated at 30 °C for three days, and absorbance readings were obtained every 24 h. The average color development of each well (AWCD) was calculated for the sources with the equation 1 proposed by Gryta et al. (2014):

$$AWCD = \sum ODi/n \quad \text{Eq. 1}$$

in which ODi is the corrected OD value of each substrate; n is the number of substrates, in this case n = 31. Correction is done by subtracting the blank from the absorbance readings of each well in order to remove the effects of inoculum density.

Soil bacterial community structure was evaluated by the DGGE technique for the analysis of 16S ribosomal RNA genes (16S rRNA) (Muyzer et al., 1993). Total DNA was extracted from 0.25 g soil samples using the Power Soil DNA isolation kit (Mo Bio Laboratories, Inc.), following the manufacturer's recommendations. The universal bacterial primers GC-F984 and R1378 (Heuer et al., 1997) were used for 16S rDNA amplification. The PCR and DGGE analyses were performed as previously described (Montecchia et al., 2011).

The analysis of variance was performed for the biological and biochemical properties evaluated, including the average color development of each well (AWCD). Significant differences between means were assessed by Tukey test with $p < 0.05$. Then, the graphs of total organic carbon and carbon of the microbial biomass were made with the aid of SigmaPlot Software. The DGGE bands patterns (amplicon profiles), representing the structure of the bacterial community were analyzed in discrete data (presence or absence of bands with the same mobility in the gel, in relation area of reference) with the software GelCompar II v.6.6 (Applied Maths NV, Belgium), using the Pearson correlation coefficient and the non-classified working group method with arithmetic mean (UPGMA).

RESULTS

For TOC, the reference area (murundus field) presented higher content in relation to the no-tillage chronosequence (NT) areas, which, in turn, did not present differences between each other (Figure 1a). However, during the years of NT, absolute values indicated an increase in the TOC content in the agricultural areas. Microbial biomass carbon content (MBC) presented the same trend as that of TOC, differing between the areas of NT, with an increase in function of the conversion time (Figure 1b).

The CO_2 was lower in the area converted into agriculture for a shorter time (7 years - NT7). The other areas of no-tillage system did not differ from each other, or from the reference area, with basal respiration almost five times greater than that recorded in the NT7 area (Table 3). The metabolic quotient ($q\text{CO}_2$) presented higher values in the agricultural areas in relation to the reference area (Table 3). However, the NT7 area had demonstrated smaller $q\text{CO}_2$ when compared with the areas of 11 and 14 years of conversion.

As for the microbial quotient ($q\text{Mic}$), there was a greater relation in the reference area, not being observed effects of the conversion time in the no-tillage chronosequence (Table 3). The acid phosphatase activity in the areas of 7, 11, and 14 years of no-tillage was 60, 33, and 38 %, respectively, in relation to the enzyme activity in the reference area (Table 3).

From the 21 organic substrates used in the evaluation of the physiological profiles, only in nine were verified differences between the studied areas. Bacterial community from soil

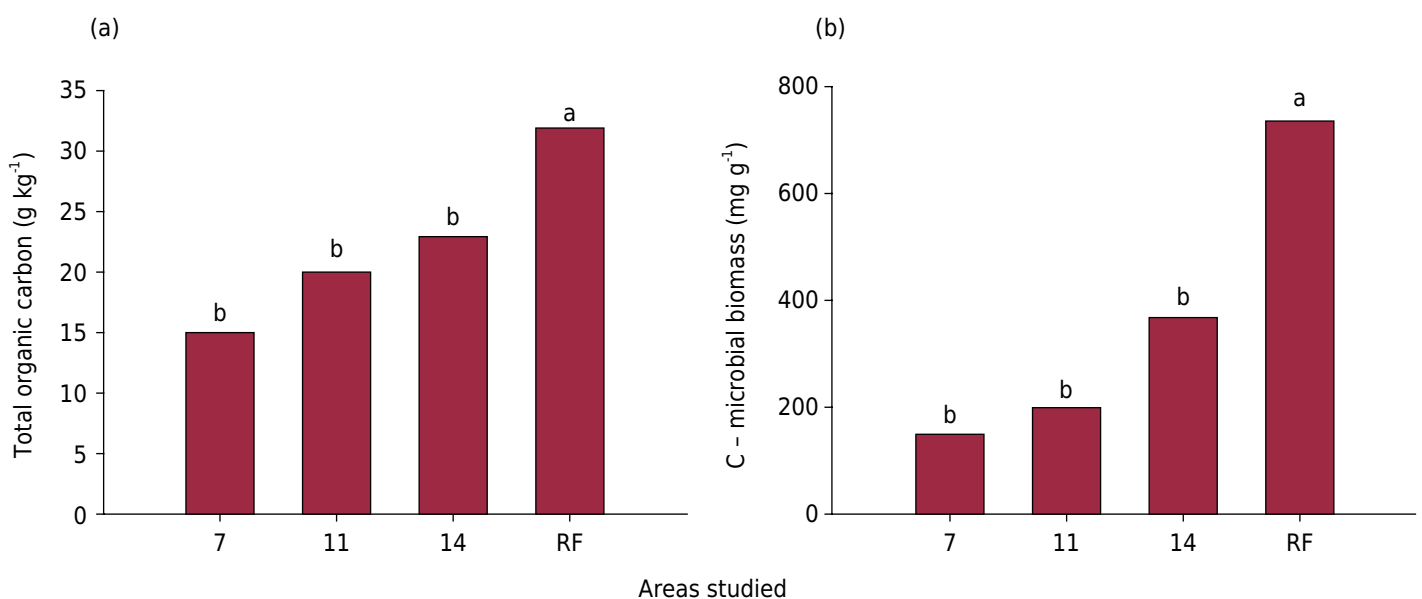


Figure 1. Content of the total organic carbon of the soil and microbial biomass carbon in the study areas. RF = reference area (murundus field); NT7 = area converted into no-tillage system for 7 years; NT11 = area converted into no-tillage system for 11 years; NT14 = area converted into no-tillage system for 14 years. Means followed by the same letter do not significantly differ from each other by the Tukey's test at 5 %.

without anthropic intervention showed higher activity in most of the carbon substrates, except for glucose-P. In the clustering analysis, the physiological profiles revealed the area with the shortest conversion time (NT7) was the most distinct from the other areas. Conversely, results showed that the area with the longest conversion time (NT14) was the closest to the natural ecosystem (Figure 2).

Table 3. Basal soil respiration (CO₂), metabolic quotient (qCO₂), microbial quotient (qMic), acid phosphatase, and urease in no-tillage chronosequence areas and in Murundus field (reference)

Areas	C-CO ₂ mg C-CO ₂	qCO ₂ mg C-CO ₂ mg MB-C ⁻¹	qMic %	Acid Phosphatase mmol PNP kg ⁻¹ h ⁻¹	Urease μg g ⁻¹ h ⁻¹
RF	17.0 a	26 c	2.3 a	116 a	305 a
NT7	3.5 b	56 b	1.0 b	70 b	55 b
NT11	15.3 a	82 a	1.0 b	39 c	143 b
NT14	17.7 a	72 a	1.6 b	44 c	79 b
CV (%)	29	35	56	23	67

CO₂ according to Alef and Nannipieri (1995); qCO₂ and qMic according to Anderson and Domsch (1993); acid phosphatase determined according to Dick et al. (1996). RF = reference area (murundus field); Microbial biomass carbon (MB-C); p-nitrophenol (PNP); NT7 = area converted into no-tillage system for 7 years; NT11 = area converted into no-tillage system for 11 years; NT14 = area converted into no-tillage system for 14 years. Means followed by the same letter do not significantly differ from each other by the Tukey's test at 5 %

Table 4. Overall rate of color development in different substrates used by the soil microbiological communities from chronosequence areas of no-tillage and murundus field area

Areas	Carbon substrates used by microbiological communities								
	VAL	MAL	TRYP	ASP	GLUC	SUC	TWE	GLYC-P	β-GLI
RF	0.14 a	0.43 a	0.64 a	0.55 a	0.41 a	0.57 a	0.43 a	0.14 b	0.14 a
NT7	0.06 b	0.27 b	0.53 b	0.41 b	0.32 b	0.40 b	0.26 b	0.33 a	0.05 b
NT11	0.07 b	0.36 a	0.55 b	0.40 b	0.33 b	0.43 b	0.36 a	0.39 a	0.06 b
NT14	0.08 b	0.30 b	0.46 b	0.38 b	0.30 b	0.42 b	0.36 a	0.35 a	0.09 b
F	3.962*	6.287*	3.764*	4.528*	5.408*	4.016*	4.106*	10.671*	5.903*
CV%	66.63	30.86	24.81	29.35	22.68	29.35	36.17	39.89	66.97

RF = reference area (murundus field); NT7 = area converted into no-tillage system for 7 years; NT11 = area converted into no-tillage system for 11 years; NT14 = area converted into no-tillage system for 14 years. Means followed by the same letter do not differ by the Tukey's test at 5 % probability. VAL = Valeric acid; MAL = DL-malic acid; TRYP = L-tryptophan; ASP = L-asparagine; GLUC = glucose; SUC = sucrose; TWE = tween 80; GLUC-P = glucose-P; β-GLYC = β-glycerol-P.

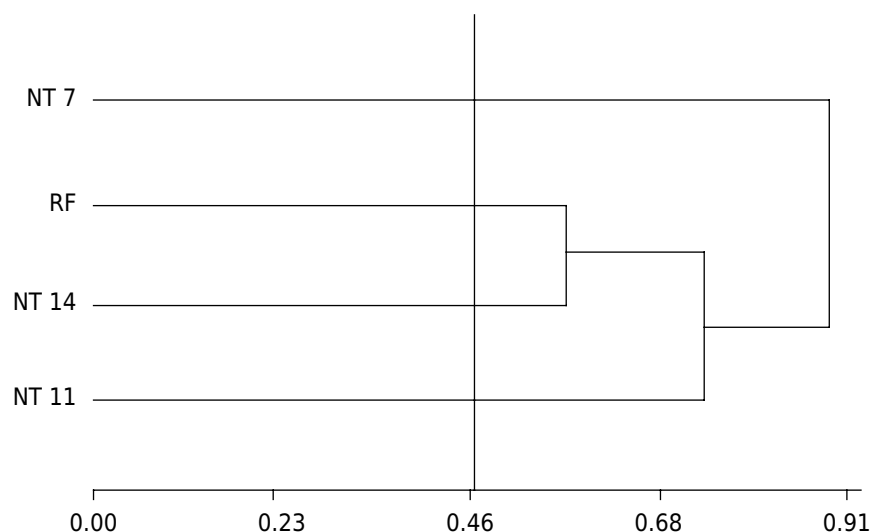


Figure 2. Clustering analysis of bacterial communities physiological profiles. Correlation = 0.87**. RF = reference area (murundus field); NT7 = area converted into no-tillage system for 7 years; NT11 = area converted into no-tillage system for 11 years; NT14 = area converted into no-tillage system for 14 years.

Soil bacterial community DGGE fingerprints revealed complex and distinctive banding profiles for each area, being very similar among replications (Figure 3). Cluster analysis of fingerprints showed differences in the bacterial community structure of soils from the chronosequence of agricultural use (groups II to IV), and also low similarity (less than 10 %) with the bacterial communities in the reference area (group I). Bacterial communities from the areas converted into no-tillage systems were more similar to each other than those from murundus field reference area (Figure 3).

DISCUSSION

The conversion of native areas into agricultural systems causes sudden changes in soil conditions, especially in soil microbial communities, since the agricultural practices and the intensive management initially adopted in these areas negatively affect soil physical properties. Due to the breakdown of aggregates and the destruction of microhabitats, the protected organic matter is exposed. The use of limestone to alter soil pH and fertilizers increases the decomposition activity that degrades native organic carbon (TOC), reducing its levels in the first cultivation years (Souza et al., 2016).

Several studies have shown that the reduction of TOC is mainly related to the degradation of the biological and biochemical properties of the soil caused by the conversion of native areas into agriculture (Viana et al., 2011; Carneiro et al., 2015). This fact occurs due to the low carbon input in the system via organic residues (Beheshti et al., 2012; Marques et al., 2016; Souza et al., 2016). In summary, the results obtained in the present study for TOC can be interpreted as indicative of the conversion impact, which is observed in the area of 7 years of conversion, and of the efficiency of no-tillage system as a conservationist system in the area with 14 years of conversion, revealing the need for management improvements for greater carbon entry into the system in a shorter time.

Microbial biomass carbon (MBC) in the area with 14 years of conversion into no-tillage (NT) presented 50 and 67 % higher content when compared with the areas of 7 and 11 years of conversion, respectively (Figure 1b). However, the area of 14 years presented 48 % of the MBC when compared with the reference area. This is justified because the

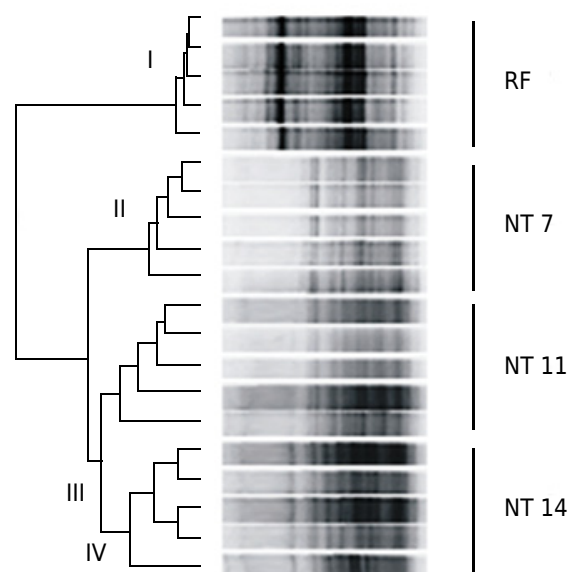


Figure 3. Dendrogram (UPGMA) of 16S rRNA gel DGGE profiles of the soil bacterial communities analyzed in the experiment (five replications per area). Clusters were defined at 50 % similarity level. RF = reference area (murundus field); NT7 = area converted into no-tillage system for 7 years; NT11 = area converted into no-tillage system for 11 years; NT14 = area converted into no-tillage system for 14 years.

native area presents a greater diversity of compounds added by rhizosphere, besides the accumulation of leaf litter on the soil surface, which helps maintain temperature and humidity at adequate levels, and constant entries of different organic residues (Matsuoka et al., 2003; Rosa et al., 2003).

In the present study, the results observed in the MBC between the NT chronosequence demonstrated the negative effect on the native microbiota in the area with 7 years of NT and the improvement of this property with the increase of the NT conduction time. These results are consistent with several other studies (Silva et al., 2010; Lacerda et al., 2013; Raiesi and Beheshti, 2015), where higher MBC was observed in native areas in relation to agricultural systems. Even in the area with 14 years of implantation, the system no-tillage been not efficient in reestablishing the microbial biomass when compared with the reference area. In addition, the reduction of microbial biomass is directly associated with the decrease of the labile fraction of organic matter (Wei et al., 2013; Raiesi and Beheshti, 2015). Results obtained for basal respiration (CO_2) are in agreement with several reports in the literature (Fialho et al., 2006; Carneiro et al., 2009; Lacerda et al., 2013), which show a trend of higher respiratory rates in areas with higher carbon content in the system (TOC and MBC). Thus, it justifies the area with 7 years of conversion have presented lower basal respiration.

The metabolic quotient ($q\text{CO}_2$) obtained in the present study is not consistent with Pragna et al. (2012), who verified, in absolute values, a reduction of $q\text{CO}_2$ in function of the time of NT adoption. The $q\text{CO}_2$ values are lower in a more stable ecosystem, or in environments that are closer to equilibrium (Anderson 1982; Souza et al., 2006, 2010), as observed in the reference area. However, in non-consolidated areas with anthropic alteration, microbial biomass increases its metabolism by using little labile carbon sources to guarantee the maintenance of the population, even in the presence of environmental stress (Cunha et al., 2012). This behavior occurred in areas with 7 and 11 years of no-tillage system, with greater increases in CO_2 emission and lower efficiency in the incorporation of carbon into the soil, via microbial biomass, when compared with the reference treatment.

Reduction of $q\text{Mic}$ in the agricultural areas is related to the loss of the decomposition capacity of organic residues by the bacterial communities. This fact interferes directly with the functionality of the system since it compromises, among other factors, the cycling of nutrients and the direct benefits of the soil-plant relationship. However, in the long term, this period may be responsible for the accumulation of soil organic matter. The fact that the reference area presents higher $q\text{Mic}$ indicates better quality of the organic matter, i.e., it explains that the diversity native area provides a greater of added compounds. This information has been proven by the results of the physiological profiles.

Phosphatase activity is common in areas with high TOC content and great litter accumulation (Massensini et al., 2015; Saha et al., 2016), especially in Cerrado soils, where P availability is very low (Rotta et al., 2015). This information justifies the results obtained in the present study since the reference area, which not receive phosphate fertilization at the time of NT implantation, presented both highest acid phosphatase activity. The practice phosphate fertilization, may have inhibited the enzyme activity in NT chronosequence. The use of chemical products, mainly fungicides (Baćmaga et al., 2015) and herbicides (Majumdar et al., 2010), also influence the reduction of acid phosphatase activity, which may have contributed to the low enzyme activity in agricultural soils. This fact happens because soybean cultivation demands several applications of these products.

The diversity of decomposition activity of soil bacterial communities was affected by the conversion of native areas to agricultural areas. In this conversion process, among other factors, we can say plant composition influences a lot the metabolism of the microorganisms (Chen et al., 2013). The uniformity of use of the organic substrates between the areas converted to no-tillage is related to the similarity of the soybean/corn cover in

the areas, in addition there is also the effect of exudates released into the rhizosphere that directly influences (Maloney et al., 1997) and favors to have the same metabolic behavior and the same structure, as presented in the analysis of molecular DGGE. In the cluster analysis, the physiological profiles revealed the effect of time, where the area with the shortest conversion time (TN7) was the most distinct of the other areas, while the area with the longest conversion time (TN14) was the nearest natural ecosystem.

The structure of the bacterial community evaluated by the DGGE was different in the agricultural and native areas, with radical changes at the beginning of the chronosequence and more abundant and diverse ribotypes in the latter. This behavior regarding the negative impact on the microbial structure is justified by a combination of factors such as the impact of anthropic interference, quantity and quality of plant residues and consolidation of the adopted agricultural system. In addition, it reflects the negative effect of conversion on soil microbial diversity as well as verified in other studies (Verbruggen et al., 2013; French et al., 2017).

The present results are associated with the establishment of new communities in the agricultural areas that presented higher similarity between each other. These findings are consistent with the homogenization of soil bacterial communities over time, together with the stabilization of the NT. By the molecular analysis, the adopted conservationist system proved to establish biological relations, although it strongly influences the selection of soil bacterial communities and the ecosystem functionality.

CONCLUSIONS

The conversion of the murundus field into agricultural systems negatively impacts biological and biochemical soil properties, with significant reductions in soil total organic carbon and microbial biomass carbon content and changes in the structure of soil bacterial communities. Soil quality indicators, except for CO₂, were sensitive to distinguish the converted areas from the natural ecosystem. Areas with 11 and 14 years of no-till management were at least sufficient to recover soil carbon content; nevertheless, they were not efficient in recovering the soil biological properties. However, a trend of stabilization in agricultural systems has been observed over the years.

AUTHOR CONTRIBUTIONS

Field work: Luciene Nunes Barcelos Martins and Marco Aurelio Carbone Carneiro.

Laboratory analysis: Luciene Nunes Barcelos Martins and Marco Aurelio Carbone Carneiro.

Writing: Luciene Nunes Barcelos Martins, Flávia Louzeiro de Aguiar Santiago, Marcela Susana Montecchia, Olga Susana Correa, Orivaldo José Saggin Junior, Edicarlo Damacena de Souza, Helder Barbosa Paulino, and Marco Aurelio Carbone Carneiro.

Statistical analysis: Flávia Louzeiro de Aguiar Santiago, Marcela Susana Montecchia, Olga Susana Correa, Orivaldo José Saggin Junior, Edicarlo Damacena de Souza, Helder Barbosa Paulino, and Marco Aurelio Carbone Carneiro.

Molecular analysis: Marcela Susana Montecchia, Olga Susana Correa, Orivaldo José Saggin Junior, Edicarlo Damacena de Souza, and Helder Barbosa Paulino.

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