Multivariate evaluation by microbiological indicators of winter-summer crop rotation and no-tillage system in Oxisol (Brazil)

Clovis Daniel Borges José Eduardo Corá and Ely Nahas

Faculdade de Ciências Agropecuária e Veterinárias, Universidade Estadual Paulista Júlio de Mesquita Filho UNESP, SP, Brazil, Email clovis.borges@posgrad.fcav.unesp.br, cora@fcav.unesp.br, enahas@fcav.unesp.br.

Abstract

Crop rotations have agronomic advantage. Type of crop rotations in combination with no-tillage system has not been evaluated systematically in Brazil. The objective of this work was to evaluate the effect of the crop rotation on the soil microbiological properties (MP) and the effect of winter crops on summer crops in no-tillage systems in a tropical region. This ecosystem management has been carried out annually since 2002. The summer crops are continuous soybean, continuous corn and soybean/corn rotation (SM). The winter crops are: corn, sunflower, radish, millet, pigeon pea, sorghum and sunn hemp. Samples were collected in April 2008 at 0-0,15m depth after summer crops were harvested. Microbial respiratory activity, the activity of the enzymes dehydrogenase, urease and phosphatase, the biomass C, N and P, qMIC, organic matter and organic carbon contents were determined. Data was analyzed by principal components analysis (PCA). Soybean/corn sequence influenced the MP more than continuous corn and continuous soybean. For soybean/corn sequence soil, the main variables selected by PCA were biomass C, N and P, respiratory and phosphatase activities, and qMIC. Pigeon pea, sorghum and sunn hemp strongly affected the soil properties when compared with the other winter crops.

Key Words

Crop sequences, dehydrogenase, urease, phosphatase, bio-indicators

Introduction

Crop rotation improves soil structure and fertility due to growth of dissimilar types of crops in sequential seasons (Balota *et al.* 2003; Govaerts *et al.* 2008). Alternate crops also diminish the incidence of pathogens and pests. The positive effects attributed to the use of no-tillage systems on soil quality have been due to the crop residue that was retained on the soil (Govaerts *et al.* 2008), to soil aggregation (Balota *et al.* 2003), carbon sequestration (Lal 2004), and increased development of microbial biomass (Angers *et al.* 1993; Mercante *et al.* 2008). Principal component analysis is an important tool to discriminate managements, being useful to evaluate the quality of the soil being able to classify the most sensitive indicators of changes in the soil (Benintende *et al.* 2008). The objective of this study was to evaluate the effect of no-tillage associated with crop rotation on soil microbiological attributes.

Methods

The study was conducted in April 2008, after summer crops, at Jaboticabal (Brazil) (21° 25'S, 48° 18'W), with monthly average temperatures ranging from 18 to 32 °C and with a dry winter and rainy summer. The soil is an Oxisol (Rhodic Eutrudox), according to the USDA Soil Taxonomy system. The experimental design consisted of a randomized complete block with three replications. The experiment was conducted since 2002 (six growing season). The treatment consisted of three summer (October to February) crop sequences (continuous soybean, continuous corn, and soybean/corn rotation) combined with seven winter (March to September) crops: corn (*Zea mays L.*), sunflower (*Helianthus anuus L.*), radish (*Raphanus sativus L.*), millet (*Pennisetum americanum (L.) Leeke*), pigeon pea (*Cajanus cajan (L.) Millsp*), sorghum (*Sorghum bicolor (L.) Moench*) and sunn hemp (*Crotalária juncea L*). Basal respiration was determined according to Rezende *et al.* (2004). Microbial biomass C, N and P (respectively, MBC, MBN and MBP) were evaluated by the fumigation-extraction methods proposed by Vance *et al.* (1987), Brookes *et al.* (1985) and Brookes *et al.* (1982), respectively. Metabolic quotient (qCO$_2$) was obtained by the relation between basal respiration and microbial biomass C (Anderson and Domsch 1990) and qMIC by the relation between microbial biomass C and total organic carbon. Dehydrogenase, urease and phosphatase activities were assayed using the methods of Casida (1977), McGarity and Myers (1967), and Tabatabai and Bremner (1969), respectively. Organic carbon (OC) was determined by dichromate oxidation (Sims and Haby 1971). Soil moisture was obtained after drying the soil samples for 24 h at 105°C, and organic matter (OM) after incineration the soil at 550 °C for 24 h. The data set was submitted to principal components analysis (PCA) using StatSoft software.

Results

Analysis of the principal components for summer crop system showed that the first and second components explained 100% of the total variance (Figure 1) 51% of the variability comes from the X-axis and 49% of additional original variability from the Y-axis. The PCA biplot showed three clusters: soybean/corn rotation, continuous soybean and continuous corn. The main variables selected by PCA for continuous soybean summer sequence were MBC, MBN, MBP, phosphatase activity, qMIC, and basal respiration. Continuous soybean influenced urease activity, organic matter, and soil moisture contents, while continuous corn influenced dehydrogenase activity, qCO$_2$, and organic carbon (Figure 1).

The biplot of the PCA for all attributes influenced by winter crops showed that the first and second components explained 78% of the total variance (Figure 2), being 51% of the variability comes from the X-axis and 27% of additional original variability from the Y-axis. The PCA biplot showed two clusters. One cluster included pigeon pea, sorghum, and sunn hemp which was influenced strongly by qCO$_2$, C-CO$_2$, soil moisture, OC, OM, MBP, phosphatase, urease and dehydrogenase activities (Figure 2). The other including radish and millet was affected strongly by MBC, MBN, and qMIC. Sunflower and corn winter crops have a low influence soil microbiological attributes (Figure 2).
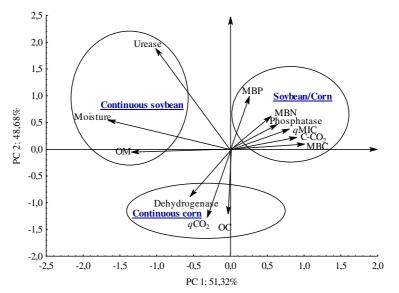

Figure 1. Bi-plot of principal components of the crop summer sequence. Microbial biomass carbon (MBC) (µg *C/g dry soil*), nitrogen (MBN) (µg *N/g dry soil*), and phosphorous (MBP) (µg *P/g dry soil*), microbial quotient (*q*MIC) (%), metabolic quotient (*q*CO$_2$) (µg *C-CO$_2$*/µg *C-MBC/h*), respiratory microbial activity (C-CO$_2$) (µg *C-CO$_2$/100 g dry soil*), dehydrogenase activity (µg *TFF/ g dry soil/ 24 h*), urease activity (µg *NH$_4$-N/g dry soil/ 3 h*), phosphatase activity (µg *pNP/g^1 dry soil/h*), organic carbon (OC) (*mg C/ g dry soil*), and organic matter (OM) (%).
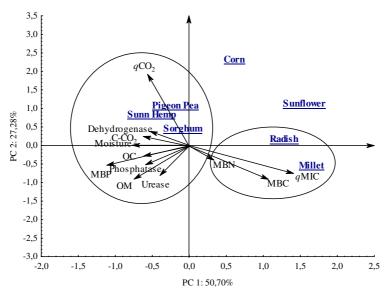

Figure 2. Bi-plot of principal components for winter crops. Abbreviations see Figure 1.

Conclusion

Microbiological attributes were influenced differently by the summer crop sequence and winter crops. The soybean/corn sequence increased soil quality compared to continuous corn and continuous soybean, probably due to greater stimulus of microbial activities. The winter crops pigeon pea, sorghum, and sunn hemp had positive effects on microbial attributes compared to the other winter crops. These effects can be attributed to the crop residue remaining on the soil surface in the no-tillage system and due to the crop rotation ecosystems which probably influenced microbial activity.

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