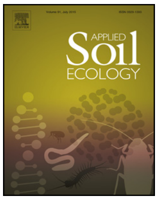
Applied Soil Ecology 110 (2017) 21–33

Contents lists available at ScienceDirect

Applied Soil Ecology

journal homepage: www.elsevier.com/locate/apsoil



Functional diversity and dominant populations of bacteria in banana plantation soils as influenced by long-term organic and conventional farming

Yu-Meng Chou[a], Fo-Ting Shen[a,b,*], Shih-Chao Chiang[c], Chun-Mei Chang[c]

[a] Department of Soil and Environmental Sciences, College of Agriculture and Natural Resources, National Chung Hsing University, Taichung, Taiwan
[b] Agricultural Biotechnology Center, National Chung Hsing University, Taichung, Taiwan
[c] Taiwan Banana Research Institute, Pingtung, Taiwan

ARTICLE INFO

Article history:
Received 14 July 2016
Received in revised form 3 November 2016
Accepted 4 November 2016
Available online 16 November 2016

Keywords:
Functional diversity
Dominant populations of bacteria
Banana plantation soils
Long-term organic and conventional farming

ABSTRACT

A three-year field study (2012–2014) of functional diversity and dominant populations of bacteria in banana plantation soils after long-term organic and conventional farming was conducted. The pH and water content were significantly higher in 17-year and 7-year organic farming soils than that in 39-year conventional farming soils, while organic matter content and viable numbers of four bacterial groups were also slightly higher. Both organic farming soils harbored diverse functional potential and metabolic activity of fast-growing heterotrophs, as can be seen from higher substrate richness, average well color development value and diversity index. Distinct carbon source utilization patterns between organic and conventional farming soils were demonstrated through principal component analysis. A limited number of heterotrophs were isolated during 2012–2013 sampling period to obtain culturable populations, and 16S rDNA sequence analyses assigned them mainly to the phylum Firmicutes. As for 2014-collected samples more diverse uncultured phyla were revealed by clone library-based method, and members belonging to the phylum Proteobacteria were more prevalent in banana plantation soils. The predominance of copiotrophic members affiliated with β-proteobacteria and fewer clones belonging to oligotrophic Acidobacteria and α-Proteobacteria especially in 7-year organic farming soils may contribute to higher functional diversity of fast-growing heterotrophs. The present study addressed functional diversity and dominant populations of bacteria in banana plantation soils and provided insight into the influences caused by long-term organic and conventional farming.

1. Introduction

Almost all arable land that is currently in crop production is highly susceptible to soil degradation, which requires increased fossil energy inputs of fertilizers, pesticides and irrigation in an effort to offset degradation (Kendall and Pimentel, 1994). However, these manipulations have potential to create pollution and health problems, destroy natural habitats, and contribute to high energy consumption and unsustainable agricultural systems (Pimentel et al., 1995). Mäder et al. (2002) reported results from a 21-year study of agronomic and ecological performance of biodynamic, bioorganic, and conventional farming systems in Central Europe. They demonstrated that although crop yields to be 20% lower in the organic systems, input of fertilizer, pesticide and energy were reduced by 34%, 97% and 53%, respectively. Enhanced soil fertility and higher biodiversity found in organic plots may render these systems less dependent on external inputs (Mäder et al., 2002). In the same DOK long-term agricultural field, Hartmann et al. (2006) demonstrated that application of farmyard manure consistently revealed the strongest influence on bacterial community structures and biomass contents. Effects of management and plant protection regimes occurred on an intermediate level, while the two stages in the crop rotation had a marginal influence that was not significant. Esperschütz et al. (2007) also conducted experiments in DOK long-term agricultural field and found higher concentrations of phospholipid fatty acids and phospholipid ether lipids in biodynamic and bioorganic farming systems, indicating a significant influence of organic agriculture on microbial biomass.

---

[*] Corresponding author at: Department of Soil and Environmental Sciences, College of Agriculture and Natural Resources, National Chung Hsing University, Taichung, Taiwan.
E-mail address: ftshen@dragon.nchu.edu.tw (F.-T. Shen).

http://dx.doi.org/10.1016/j.apsoil.2016.11.002

Long-term organic fertilization has been demonstrated to support eutrophic ecosystems, in which copiotrophic taxa increased in relative abundance and have a higher intensity of labile-C-degrading genes (Xun et al., 2016).

While maintenance of soil health is the key to sustainable agriculture (Doran and Parkin, 1994), White and MacNaughton (1997) suggested using diversity of microbial community as a sensitive means to assess soil quality. Previously studies of soil microbial properties have been commonly conducted at the process level, where biomass, respiration, and enzyme activities have been examined (Hill et al., 2000). At that time these provided an important understanding of gross microbial processes but lack qualitative community-level or organism-level responses to changes in soil properties or management. The Biolog redox technology based on sole-carbon-source utilization was evaluated as a rapid, community-level method to characterize and classify heterotrophic microbial communities (Garland and Mills, 1991). The Biolog Ecoplate^{TM} assay was sensitive to changes in the short term due to management practices, which demonstrated that organic amendment significantly increased microbial functional diversity (Gomez et al., 2006). At present community-level physiological profiling (CLPP) using Biolog EcoPlate^{TM} has become a popular method for characterizing and comparing the functional diversity of heterotrophic microbial communities (Button et al., 2016). Traditional approaches to analyze soil microbial communities have relied on culturing techniques. However, it has been estimated that less than 1% of the microorganisms found in natural and perturbed environments are obtained in pure culture (Torsvik et al., 1998). The use of culture-independent techniques provides new ways for assessing soil microbial diversity and ultimately, a more complete understanding of the potential impacts of environmental processes and human activities on responses of soil microorganisms (Hill et al., 2000).

Bananas (*Musa* spp.) which belong to the family Musaceae are the perennial giant herbaceous plants cultivated for their seedless fruits. They have agreeable flavor and high nutritional value in terms of sugars, dietary fiber, vitamins, minerals and antioxidant compounds, which make bananas promising plants grown in tropical and subtropical regions around the world (Arvanitoyannis and Mavromatis, 2009). In Taiwan the main edible cultivars belong to *Musa acuminata* Colla (genome type AAA) Cavendish subgroup (Hwang and Ko, 2004). Organic farming which sustains productivity meanwhile enhances soil quality has also been applied in banana cultivation. Adriano et al. (2012) demonstrated that addition of compost and liquid bioferment not only improve fertility of soil cultivated with banana but stimulates microbial activity and their capacity to metabolize complex organic molecules. Application of bio-organic fertilizer was also confirmed to control Fusarium wilt disease in banana-grown field more effectively by improving soil microbial communities (Shen et al., 2013). Many long-term trials were established primarily to study the impact of fertilizers on crop production; however, an increasing number of scientists are taking advantage of these well documented experiments to study soil microbial communities under different fertilization regimes (Geisseler and Scow, 2014). It will be valuable to monitor the microbial diversity in different farming systems to seek for a more sustainable way in field management. In the present study samples collected over the same season during 2012–2014 were subjected to analyses of soil properties, viable number of four bacterial groups, functional diversity and dominant populations of bacteria under different agricultural management practices.

2. Materials and methods

2.1. Soil site and sampling

The soils used in the present study were taken from the long-term banana plantation field located in Pingtung County, Taiwan (22°43′26.5″N120°30′14.9″E). It was set up in 1973 and is run by the Taiwan Banana Research Institute. Bananas grown on these fields were edible cultivars belong to *Musa acuminata* Colla (genome type AAA) Cavendish subgroup. In Pingtung County the monthly average temperature was the lowest (20.6 °C) in January, and the highest (28.3 °C) in July, and average annual temperature was 25 °C. At three sampling dates (3 April, 2012; 26 April, 2013; 9 April, 2014) the day precipitation was 0, 3, and 0 mm, respectively. Loamy soils under 17-year organic farming (ORG17), 7-year organic farming (ORG7) and 39-year conventional farming (CON39) were sampled to study the influences of different agricultural managements on soil properties and bacterial diversity. In both organic farming systems (ORG17 and ORG7) vegetative meals and palm bunch ash was supplied. Weed control was conducted mechanically and plant extracts were used in disease and pest control. In conventional farming system (CON39) #4 Biotec Organic Compound Fertilizer was provided. As for plant protection, a variety of herbicides, germicides and insecticides were used. The ratoon cropping was conducted under all three farming systems, to

Table 1
Agricultural management regimes in long-term banana plantation field experiment.

Treatment	17-year organic farming (ORG17)	7-year organic farming (ORG7)	39-year conventional farming (CON39)
Fertilization			
Organic fertilizer	Vegetative meals[a] (N-P_2O_5-K_2O: 5–2.5-1.5) (consist of 92% organic matter) + palm bunch ash[b] (N-P_2O_5-K_2O: 0.1-3.4-30, pH 13)		
Complex fertilizer			#4 Biotec Organic Compound Fertilizer[c] (N-P_2O_5-K_2O-MgO: 11–5.5-22-3) (consist of 45% organic matter)
Plant protection			
Weed control	Mechanical		Herbicide Paraquat
Disease control	Deleafing and use of plant extracts from chili, garlic, soapberry or rice vinegar		Germicides Benlate, Mancozeb, Tilt
Pest control	Early bagging and use of plant extracts from chili, garlic, soapberry, neem oil or rice vinegar		Insecticides Carbofuran, Carbaryl, Chlorpyrifos
Others	Ratoon cropping		Ratoon cropping

[a] 3 kg were used per plant per year.
[b] 3 kg were used per plant per year.
[c] 1.5–2.0 kg were used per plant per year.