

SHORT COMMUNICATION

Emergence of Diverse Microbes on Application of Biofilmed Biofertilizers to a Maize Growing Soil

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ABSTRACT

Diverse microbial communities in the rhizosphere perform an amazing role in plant growth and productivity. However, conventional agricultural practices such as the use of chemical fertilizer (CF) and tillage have collapsed the diversity of the microbial communities. Direct application of developed fungal-bacterial communities known as biofilmed biofertilizers (BFBFs) to the soil has been introduced recently, and observed to be multi-functional and more effective than conventional biofertilizers. However, the effect of such biofertilizers on soil microbial diversity has not been studied sufficiently world over. Therefore, the current study was carried out to investigate the effects BFBFs on bacterial, cyanobacterial and fungal species in a maize growing soil. A pot experiment was conducted under greenhouse conditions with different fertilizer treatments; 100% chemical fertilizers (CF) recommended for maize, 50% CF, 50% CF + BFBF, and no fertilizer, as the control. Microbial species richness and abundance of bacteria were evaluated after two months of plant growth. Microbial biomass carbon (MBC) was estimated by using chloroform fumigation-extraction technique. Results showed that the species richness of bacteria, fungi and cyanobacteria, and abundance of bacteria were higher in 50% CF + BFBF, compared to 50% and 100% CF. This implies that the action of BFBFs tends to break dormancy of microbial seeds in the soil, resulting in emergence of a diverse microbial community, which may support natural biocontrol of pathogens. An interesting observation was the stimulation of an additional microflora of cyanobacteria by the application of BFBF. MBC levels did not show a significant difference between any of the treatments. We recommend further testing of the BFBFs for increasing microbial diversity and ecosystem functioning and hence the sustainability of maize cultivating agroecosystems.

Keywords: bacteria, cyanobacteria, fungi, *Zea mays*

INTRODUCTION

Agriculture in Sri Lanka is mainly focused on plantations, cereals, vegetables and field crops. Among cereals, maize is a widely utilized crop for human consumption and as animal feed. Currently in Sri Lanka, 30,000 ha, the highest extent of land next to rice, is cultivated with maize (Department of Agriculture, 2006). Modern farming methods such as the use of machineries, pesticide and chemical fertilizer (CF) *etc.* have achieved increased productivity in the sector. However, the CF application adversely affects natural microbial communities in agricultural ecosystems and thereby affect soil fertility and crop productivity in the long run (Seneviratne, 2009). Particularly, chemical N

fertilizers tend to produce soil microbial communities having reduced N nutrition and hence low biomass (Priha and Smolander, 1995; Cerny *et al.*, 2003; Cruz *et al.*, 2009; Strickland and Rousk, 2010), possibly due to low N supply by suppressed N₂ fixers.

Diverse microflora in soil has been identified for its beneficial functions in the soil-plant system (Kennedy and Smith, 1995). They perform various catabolic activities, and are involved in primary production, nutrient recycling *etc.* In addition, their interactions with plant root system play key roles in several other ecosystem functions, such as decomposition of organic matter and nutrient balancing, rhizoremediation, pathogen suppression and, the maintenance of soil structure and water relationships (Sharma *et*

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al., 2010). Hence, the diversity of soil microorganisms is considered as one of the most important indicators in soil quality (Bastidia *et al.*, 2008; Sharma *et al.*, 2010). Increased microbial biomass with the enrichment of microbial diversity is also an important determinant of quality and productive capacity of soil (Fernandes *et al.*, 1997), since it contributes to beneficial functions such as biosolubilization and mineralization (Brookes, 1995; Pankhurst *et al.*, 1995; Yao *et al.*, 2000).

Generally, research studies pertaining to the application of microbes as biofertilizers in agriculture have been focused to reduce the dependence on CF, due to economic and environmental concerns. Rhizobia and mycorrhizae are the two major candidates of biofertilizers that are used worldwide. In addition, biocontrolling and soil conditioning microbes are also used with a limited application (Milton and Joseph, 1982; Thomas *et al.*, 1984; An *et al.*, 2009). They are generally applied as mono or mixed cultures. Direct application of developed microbial communities known as BFBFs has been introduced recently, and observed to be multi-functional and more effective than conventional biofertilizers (Seneviratne *et al.*, 2011). Application of BFBFs with low levels of CF (*e.g.* 50%) has given yield comparable to 100% CF in tea (Seneviratne *et al.*, 2011), rice (Weeraratne *et al.*, 2012) and in maize (Buddhika *et al.*, 2012a). Further, preliminary studies based on BFBFs for maize showed their positive effects on rhizoremediation, nitrogenase activity, seed germination, seedling growth, photosynthesis and soil N accumulation (Buddhika *et al.*, 2012b & c). Such beneficial biological functions have been reported to be due to diversified microbial communities in the soil (Kennedy and Smith, 1995). However, effect of such biofertilizers on soil microbial diversity has not been studied sufficiently. Therefore, in the current study, the effect of the BFBFs on diversity of microbes, particularly bacteria, cyanobacteria and fungi in a maize growing soil was investigated.

MATERIALS AND METHODS

The study was carried out in a green house at the Institute of Fundamental Studies (IFS), Kandy, Central Province, Sri Lanka. A maize-growing, clay loamy soil collected from a home garden in Kandy was used (pH 6.52, organic C 1.87 %, available $\text{NH}_4^+\text{-N}$ and $\text{NO}_3^-\text{-N}$ 43 $\mu\text{g g}^{-1}$ soil and 15 $\mu\text{g g}^{-1}$ soil, respectively, and available PO_4^{3-} 2.4 $\mu\text{g g}^{-1}$ soil).

Biofilmed biofertilizer inoculum and other treatments

The BFBF that has already been developed (Seneviratne *et al.*, 2011) and tested for maize was used in the study. It contains one fungal species (*Aspergillus* sp.) isolated from maize rhizosphere and seven bacterial species (*Azorhizobium* sp., *Rhizobium* sp., *Acetobacter* sp., *Azotobacter* sp., *Azospirillum* sp. and two unidentified bacteria) derived from various sources including maize rhizosphere. All of them are in the culture collection of the Institute of Fundamental Studies, Kandy, Sri Lanka. These microbes were inoculated into a low cost commercial culture medium (exact composition of the medium and the biofilm development method are not revealed due to intellectual property rights) and incubated at 27-30 °C for 7 days to form fully matured biofilm, and the cell concentration was 10^{10} ml⁻¹. Developed BFBF was used in the study together with a reduced dose (*i.e.* 50 %) of recommended CF for maize, and compared with 50 % CF alone, 100 % CF and no fertilizers as the control. Generally, BFBF alone is not recommended, since fungal counterpart in the BFBF acquires some nutrients from the soil system, thus reducing plant growth (Seneviratne *et al.*, 2011).

Seed material

Zea mays seeds, 'Pacific', a hybrid variety, which is recommended by the Department of Agriculture, Sri Lanka was used in the experiment.

Inoculation, fertilizer application and experimental design

An experiment was conducted in the green house to examine the effect of the BFBFs on microbes that are only in the rhizosphere soil, but not on the root surface, in maize crop. Twelve plastic pots (4 treatments x 3 replicates) were arranged in a completely randomized design (CRD). The pots were filled with 3 kg of a soil mixture (1:1 weight ratio of sand and maize growing soil, < 2 mm), and seeded with maize. Soil and seed inoculations of the BFBF were done after diluting it with water at 1:16. Maize seeds were soaked overnight in tap water and then one half of them were separately soaked in the BFBF, while the other half was continued to be soaked in distilled water for 2 hours, to be placed in CF treatment and no fertilizer control. Seeds were placed at 5 cm depth in all treatments. Remaining suspension of the BFBF was sprayed on to soil at the rate of 10 L ha⁻¹. In 100 % CF treatment, the soil was applied with N, P and K at rates of 200, 100 and 50 kg ha⁻¹ as urea, triple super phosphate and muriate of

potash, respectively. Nitrogen at the rate of 80 kg per hectare was applied at sowing time and the rest at the start of tussling. The crop was managed according to the method recommended by the Department of Agriculture, Sri Lanka (Department of Agriculture, 2006). The pots were watered daily to maintain soil moisture at ca. 60% of water holding capacity. At two months soils from the surface and root zone of each pot were collected (using a hand-held auger) for the isolation of cyanobacteria, and bacteria and fungi.

Isolation of rhizosphere bacteria and fungi

Soil samples of all replicates of each treatment were composited. One gram of the composite soil was serially diluted and 50 μ l from 10^{-3} , 10^{-4} and 10^{-6} dilutions were spread on nutrient agar (NA) and potato dextrose agar (PDA) plates. Thirty six petri plates were incubated at 25 °C for 5 days for fungi, and at 30 °C for 24 hrs for bacteria. After the incubation period, colony forming units (CFU) on NA plates were counted. Morphologically different bacterial colonies were picked from all plates and streaked on another set of new NA plates. Similarly different fungal colonies were also picked from the PDA plates and sub cultured on new PDA plates. This was continued until pure colonies have been achieved.

Identification of isolated bacteria and fungi

Gram's staining was carried out for all isolates of bacteria and morphological characterization was done prior to the biochemical tests. Identification was carried out using standard biochemical tests in the Bergey's Manual of Determinative Bacteriology (Holt *et al.*, 1994). Slide cultures were prepared to identify fungi (Riddell, 1950). Morphological features and sporulating structures of the fungi were used in the identifications.

Identification of cyanobacteria

Cyanobacteria growing on the soil crust in each treatment were carefully scraped without soil by using a sharp needle and were transferred into the BG11 medium (Rippka *et al.*, 1979) with or without NaNO_3 as the N source, in tubes plugged with sterilized cotton plugs. The tubes were incubated at 28 ± 2 °C under a continuous light source from fluorescent tubes at an intensity of 7.5 W m^{-2} for the growth of cyanobacteria. When the medium of the tubes turned green, slides were prepared and observed under an oil immersion lens. Species that grew in different fertilizer treatments were recorded separately.

Determination of microbial biomass carbon in soil

The total microbial C in the soil was measured by

the chloroform fumigation-extraction technique described by Vance *et al.* (1987). Briefly, 10 g of fresh soil from each sample was fumigated with 30 ml alcohol free chloroform and incubated in dark for 24 hrs. It was followed by the soil extraction using 0.5M K_2SO_4 . The extract was titrated using acidified ferrous ammonium sulphate after dichromate digestion. Microbial biomass C (MBC) was calculated using the equation (Vance *et al.*, 1987), $\text{MBC} = 2.64 \times E_C$ where, $E_C = (\text{organic C from fumigated soil}) - (\text{organic C from non-fumigated soil})$, expressed as mg kg^{-1} soil.

Statistical analysis

Data were subjected to one way analysis of variance (ANOVA) and means were compared using Tukey's HSD test at 5% probability level. All statistical analyses were performed using SAS (1998) software. The CFU were expressed as \log_{10} (g^{-1} soil dry weight).

RESULTS AND DISCUSSION

NA was used for the isolation of bacteria, since it is a well-known universal medium that serves the role of supporting many microbes randomly without being selective, whereas other media that are used may be of a selective nature. PDA and BG 11 were used for the isolation of fungi and cyanobacteria, respectively, media generally used for the culture of the relevant groups of microorganisms. The higher species richness of bacteria and the highest number of CFU were observed in 50% CF + BFBF application (Figure 1 and Table 1) compared to control soil. Major species observed were *Azorhizobium*, *Acetobacter*, *Bacillus* and two species of gram positive rods (Table 2). Among those species, *Acetobacter* was more frequently identified in the BFBF treated soil, compared to other treatments. Originally, the BFBF contained 7 bacterial genera, of which only 2 genera were isolated from the BFBF treated soil. This could be due to complexity of the microbial community in succession under the selection pressure which has not been understood yet in the BFBF applied soil-plant system. Other possibilities are the suppression of introduced bacteria, due to the competition of better adapted soil native microbes (van Veen *et al.*, 1997), and also changes in community structure and function of microbes with biofertilizer application (Ge *et al.*, 2003). Gram positive rods were frequent in 100% CF treated soil (ca. 65% of total colonies). Application of 100% CF resulted in significantly

high CFU counts, but an average species number, compared to no fertilizer (Table 1), confirming reduction of species richness and evenness with the CF (Sun *et al.*, 2004). No fertilizer application showed the lowest bacterial richness and CFU count. Therefore, results indicated that the BFBF when applied together with 50% CF supported emergence of new bacteria with their increased abundance in the soil-plant system of maize.

The highest number of fungal species was observed in the 50% CF + BFBF application (Table 2), which was similar to the trend observed with bacteria. *Aspergillus* spp. are natural inhabitants in the maize rhizosphere (Gomes *et al.*, 2003). There were two new *Aspergillus* spp. in addition to the introduced species from the BFBF treatment (Table 2). In 100% CF treatment, only *Fusarium* sp. was observed, which is a common plant pathogen. This may be due to the fact that CF application collapses natural balance of soil microbial communities (Seneviratne, 2009), which may lead to disease transmission (Keesing *et al.*, 2010), possibly due to lack of natural control of pathogens. Interestingly, *Trichoderma* sp. was observed with *Fusarium* sp. only in the BFBF applied soil (Table 2), thus increasing the fungal species richness. Generally, majority of *Trichoderma* species isolated from

tropical soils has been identified as biocontrolling agents (*e.g.* Affokpon *et al.*, 2011), in addition to other eco-friendly effects (Fravel, 2005; Benitez *et al.*, 2004; Zeilinger and Omann, 2007). The above facts are indications of possible effects of the BFBFs along with 50% CF in maintaining microbial balance for natural biocontrol of pathogens.

With regard to cyanobacterial diversity, the highest species number was recorded again in the BFBF application (Table 2). *Anabaena* sp., *Nostoc* sp., and *Oscillatoria* sp. were recorded as dominant species in all treatments whereas *Lyngbya* sp., *Scytonema* sp., *Calothrix* sp., *Fischerella* sp. and *Cylindrospermum* sp. (Table 2), with relatively high visual heterocyst number (U. V. A. Buddhika *et al.*, unpublished data), were present in BFBF applied soils. In general, cyanobacteria are applied in agriculture to gain beneficial effects through their ability to fix atmospheric nitrogen (Nayak *et al.*, 2004; Kaushik, 2004; Ahmad *et al.*, 2008; Prasanna *et al.*, 2010). An interesting observation of this study was that the emergence of additional diverse beneficial cyanobacteria in soil treated with 50% CF + BFBF, this is presumably the first observation of this nature.

Table 1. Number of colony forming units (CFU) of bacteria and microbial biomass carbon (MBC) in maize rhizosphere under different treatments. Values followed by different letters are significantly different at 5% probability level, according to Tukey's HSD test (CV = Coefficient of Variation; MSD = Minimum Significant Difference).

Treatment	Log ₁₀ (CFU g ⁻¹ soil)	MBC (µg g ⁻¹ soil)
100% CF	7.40 ^b ± 0.02	241 ^a ± 26
50% CF	7.30 ^{bc} ± 0.03	202 ^{ab} ± 46
50% CF + BFBF	7.56 ^a ± 0.00	266 ^a ± 21
No fertilizer	7.26 ^c ± 0.05	108 ^b ± 13
F- value	19.28	6.73
MSD (0.05)	0.14	131
CV (%)	0.70	24.8

Table 2. Microbes found in maize rhizosphere under different treatments

Treatment	Bacteria	Fungi	Cyanobacteria
100% CF	<i>Rhizobium</i> sp. <i>Bacillus</i> sp. 1 Gram (+) rod 1	<i>Fusarium</i> sp.	<i>Nostoc</i> sp. <i>Oscillatoria</i> sp. <i>Anabaena</i> sp.
50% CF	<i>Acetobacter</i> sp. <i>Azotobacter</i> sp. Gram (+) rod 2	<i>Aspergillus</i> sp. 1 Unidentified sp. 1	<i>Nostoc</i> sp. <i>Oscillatoria</i> sp. <i>Anabaenas</i> p. <i>Cylindrospermum</i> sp.
50% CF+ BFBF	<i>Azorhizobium</i> sp. <i>Acetobacter</i> sp <i>Bacillus</i> sp. 2 Gram (+) cocci Gram (+) rod 3	<i>Aspergillus</i> sp. 1 <i>Aspergillus</i> sp. 2 <i>Aspergillus</i> sp. 3 <i>Trichoderma</i> sp. <i>Fusarium</i> sp. Unidentified sp. 1	<i>Nostoc</i> sp. <i>Oscillatoria</i> sp. <i>Anabaena</i> sp. <i>Lyngbya</i> sp. <i>Scytonema</i> sp. <i>Calothrix</i> sp. <i>Fischerella</i> sp. <i>Cylindrospermum</i> sp.
No fertilizer	Gram (+) rod 4	Unidentified sp. 2	<i>Nostoc</i> sp. <i>Anabaena</i> sp. <i>Oscillatoria</i> sp.

Soil MBC was not significantly different among treated soils, but it was significantly low in the non-treated soil ($P < 0.05$) (Table 1). Thus, it did not reflect differences of microbial species richness among the treatments. Generally, MBC depends on soil C and nutrient availability. Therefore, higher nutrient availability in the 100% CF resulted in high MBC, as also observed previously (Zhong and Cai, 2007; Lynch and Panting, 1982; Goyal *et al.*, 1992), though there was relatively a low microbial richness. Apparently, higher MBC observed in 50% CF + BFBF than the 50% CF could be due to the introduced microbes and subsequent emergence of cyanobacterial and fungal communities with the application of the BFBF. Cyanobacteria and fungi have been reported to be major contributors to soil MBC (Henrot and Robertson, 1994; Lovell *et al.*, 1995; Prasanna *et al.*, 2009).

Unfavorable environmental conditions and nutrient depletion are some of the many reasons which make microbial cells to become dormant and to incorporate into soil microbial seed bank (Coates, 2003). Adverse conditions created by the 100% CF application collapse microbial communities (Seneviratne, 2009), leading metabolically active cells to become dormant and

hence altering the composition of microbial communities. However, our results suggested that the application of the BFBFs along with 50% CF tends to break dormancy of microbial seeds in the soil, which causes emergence of diverse microbes with a possible indication of pathogen suppression through increased food web interactions.

Generally, dormancy of cysts, spores, akinetes and conidia are broken in the presence of organic compounds in various exudates (*e.g.* low molecular weight sugars and amino acids). Interactions among microbes in the BFBFs have also been observed to release diverse organic compounds including those mentioned above (Herath *et al.*, 2013), as was also observed by Saini *et al.* (1986) and De Boer *et al.* (2005). When such compounds become increasingly available, it resuscitates microbial cells to grow on a broader substrate spectrum (Lennon and Jones, 2011; Teeling *et al.*, 2012). In some cases, cell to cell communication via quorum sensing is reported to resuscitate cells to break dormancy (Lennon and Jones, 2011). In biofilm formation, quorum sensing is a prerequisite, which helps to establish the biofilm. Therefore, the role of BFBFs in breaking dormancy of the microbial

seed bank in this manner could be expected obviously.

It is concluded from the results of this study that the BFBFs allow a diverse community of bacteria, fungi and cyanobacteria to emerge when coupled with 50% of CF inputs. This contributes to strengthen biodiversity-ecosystem functioning relationship (Langenheder *et al.*, 2010), which leads to ecosystem sustainability (Tilman *et al.*, 1996). In order to have a better understanding of the effect of application of the BFBFs and CF on microbial diversity, the use of molecular assisted technologies would be the next step, because culturable microbial community represents less than 1% of the total microbes in some soils.

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