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# COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

## THE CONSERVATION AND USE OF MICRO-ORGANISMS AND INVERTEBRATES IN ROOT CROP-BASED SYSTEMS: STATE OF KNOWLEDGE, TRENDS AND FUTURE PROSPECTS

By

Peter Okoth<sup>1</sup>, Sheila Okoth<sup>2</sup>, and Joyce Mnyazi Jefwd<sup>3</sup>

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<sup>1</sup> International Centre for Tropical Agriculture (CIAT), c/o ICIPE Duduville Complex, Off Kasarani Road, P.O. Box 823-00621, Nairobi, Kenya

<sup>2</sup> University of Nairobi, School of Biological Sciences, P.O. Box 30197, Nairobi, Kenya

<sup>3</sup> International Centre for Tropical Agriculture (CIAT), c/o ICIPE Duduville Complex, Off Kasarani Road, P.O. Box 823-00621, Nairobi, Kenya



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## EXECUTIVE SUMMARY

This report was compiled by the Tropical Soil Biology and Fertility Institute of the International Center for Tropical Agriculture (CIAT-TSBF) at the request of the Food and Agriculture Organization of the United Nations (FAO) Commission on Genetic Resources for Food and Agriculture. It is focusing on the state of knowledge and trends in the conservation and use of micro-organisms and invertebrates in cropping systems based on roots and tubers -, including cassava, potatoes, sweet potatoes, yams, cocoyam and aroids. The main emphasis is to understand the status and trends of micro-organism and invertebrate diversity in root crop-based production systems and to review the current and potential contribution of such organisms to these systems. Areas for future research and gaps in knowledge are also identified and highlighted.

The soil is “alive”, harboring organisms whose diversity and abundance is largely unknown. Specific information is still lacking on the importance of species that are key to specific functions and their role in maintaining below and above-ground biodiversity. It is this information gap that this report addresses. Most of what is presented deals with the integration of the root and tuber crops with soil organisms and their functions.

When soil organisms eat, grow, and move, they contribute to the delivery of ecosystem services that are essential for human society. Among the key ecosystem services mediated by soil biota are: the transport, storage, and provision of clean ground water; the storage of carbon and the prevention of trace gas emissions crucial for climate control; the provision of nutrients; pest and pathogen regulation; and supporting plant growth and above-ground biodiversity. Most of the structure and functioning of the above-ground individuals and communities are regulated directly or indirectly by altering the dynamics of nutrients that are available to plants.

As production of the root and tuber crops expands, it is important to use production technologies which secure a safe and clean environment that minimizes use of synthetic chemicals. Research is needed on how best to integrate soil organisms in the production of the crops both as bio-fertilizers as well as use as bio-control agents (BCAs). Mechanisms of co-existence of soil organisms in mutualistic, proto-cooperation, commensalism, neutralism, antagonism, predation and parasitic relationships can be used to explore further how best to integrate these associations with the root and tuber crops. Biological control methods have provided alternative safer methods to pesticides and herbicides for pathogen, insect pest and weed control. However developing BCAs is labor intensive but this may lead to localized niche businesses that provide jobs and create wealth. Benefits might also accrue to the growers who use BCAs because of the premium price for pesticide-free and organic produce. This may not yet be happening but the major benefit from BCAs may be in preserving root and tuber crops from postharvest breakdown because of the perishable nature of root and tuber crops that can inhibit large scale exports apart from cassava which are first dried before chips are exported.

Emerging technologies in biological sciences allow the study of these soil microorganisms beyond the microscope. *Gene marking, DNA finger printing, PCR amplification, genomics, proteomics and metabolomics* and associated microarray technologies have enhanced opportunities for throughput in bio-prospecting and understanding mechanisms of soil organism action that can lead to discovery of novel properties and products especially from microorganisms. More research is needed to ensure food security and to increase food production levels in developing countries in part by a better understanding of how to manage soil biological processes. In order for this to be realized, there will be need for budgets, reference databases, North-South collaborations as well as championing.

The main recommendations fall under the following headings.

***Policies interventions***

- An inventory and a spatial distribution map of below and above ground soil micro-organisms will be required to inform on the kind of associations root and tuber crops are associated with.
- An elaborated sector with a gene bank and microorganisms collection may be needed in order to take full advantage of the science involved in invertebrate biodiversity and soil micro-organisms with emphasis on root and tuber production systems.

***Capacity strengthening***

- Promote root and tuber farming approaches and practices that sustain soil micro-organisms, biological control agents and pathogens, such as reduced tillage, the use of cover crops and mulches, and mixed cropping.
- Promote integrated pest management, which draws on resistant cultivars, biological control agents, bio-pesticides and habitat management to protect root and tuber crops.
- Provide growers the opportunity for better understanding the ecosystem services in the root and tuber crop production systems, the importance of soil health and related soil micro-organism and biodiversity, and provide growers the capacity to develop strategies to manage pest and disease problems more effectively.

***Investment in research for development for***

- Bridging the gaps in the knowledge of soil micro-organism and invertebrate biodiversity under root and tuber production systems.
- Increasing the knowledge on inoculants ecology for the control of soil-borne diseases, determination of nutrient availability to plants and soil structure formation.
- Taxonomic identification of the non-culturable species in order to determine if the large numbers of naturally-occurring, non-culturable cells are unknown species, or whether they are representatives of known species.
- Identification of organisms that occur in symbiosis with the root and tuber crops and which ones assist and support them in fighting pests and diseases.
- Improvement and development of human capacity and laboratory infrastructure for determining invertebrate and soil micro-organism diversity and their contribution to ecosystem services in the root and tuber production systems.



## I. INTRODUCTION

### **Scope of the study**

The aim of the study was to have a global synthesis on the status and trends of the conservation and use of soil micro-organisms, biological control agents and pathogens in root and tuber crop production systems.

The main emphasis is on the use and application of soil biota (organisms) in the root and tuber crop production systems where a mechanism is established between the crops and the soil organisms as the basis for increasing yields which may be used in disease and insect pest control as well as their contribution to a “healthy” and productive soil.

Areas for future research and gaps in knowledge are also identified. This report is limited to discussing the major root and tuber crops: cassava, potatoes, sweet potatoes, yams, cocoyam and the aroids.

### **Root and tuber crops in integrated production systems and the role of soil biota**

#### ***Farming systems***

Sustainable intensification of root and tuber farming systems are founded on three key best practices. First, the practice should aim at protecting soil structure, soil organic matter and overall soil health by limiting mechanical disturbance of the soil.

Along with conservation tillage, the second should aim at maintaining a protective organic cover on the soil surface, i.e. using crops (intercropping, alley cropping and green manuring) and mulches (crop residues and cover crops) to reduce soil erosion, conserve soil water and nutrients, and suppress weeds. Organic soil cover not only improves soil's physical properties; it also encourages the proliferation of soil biota – including earthworms and beneficial protozoa, fungi and bacteria – that are beneficial to soil health and crop performance.

Third practice is about the cultivation of a wider range of plant species in associations, sequences and rotations that may include trees, shrubs and pasture. Mixed cropping diversifies production, which helps farmers to reduce risk, respond to changes in market demand and adapt to external shocks, including climate change.

Rotating or associating nutrient-demanding crops with soil-enriching legumes and shallow-rooting crops with deep-rooting ones maintains soil fertility and crop productivity and interrupts the transmission of crop-specific pests and diseases.

By improving levels of soil organic matter and biotic activity, reducing pest and disease pressure, reducing erosion and increasing the availability of crop water and nutrients, those three practices enhance the presence and function of soil biota and increase yields sustainably.

#### ***Mixed cropping***

Root and tuber crops are grown as a monoculture or as an intercrop with a wide range of other crops, either in a regular pattern or in irregular mixture of various crops, or as relay crops.

Intercropping with grain legumes, which fix atmospheric nitrogen, makes nitrogen (N) available to the cassava crop. Although biological fixation cannot meet all of cassava's nitrogen needs, it has some benefits. Alley cropping with deep-rooting and fast-growing leguminous trees may be an effective means of improving soil fertility and yields, where mineral fertilizer is not available.

There are pests and diseases that are endemic to the specific root or tuber. Nutrition and agronomic management also varies between the species. Temperature, rainfall and day-light hours or photoperiodicity also affect the quality as well as the productivity of the specific root or tuber.

### ***Soil organisms***

They play major roles in several ecosystem functions including:

- enhancing plant productivity;
- regulating water movement processes by the action of altering soil physical structure with the bacteria producing polysaccharides that act as adhesives for soil particles and the fungi producing thread like hyphae that bind soil particles into stable aggregates and thereby reducing potential soil losses by erosion;
- controlling diseases and insect pests; regulating nutrient mobilization; driving decomposition and mineralization of soil organic matter;
- and acting as environmental buffers. (Neher, *et al.*, 2012; Neher, 2010; Neher, 1999; Beare, *et al.*, 1997; Chotte, *et al.*, 1993; Blanchard, 1992; Gupta and Germida, 1988; Eash *et al.*, 1994).

These ecosystem functions performed by soil biota are beneficial to all crops and some occur through a symbiotic co-existence. These interactions have been little explored for root and tuber crops (see Chapters 3 and 4). When the root or tuber crop is planted as an intercrop specific pests and diseases and beneficial soil organisms adhering to the planting propagule may be transmitted to a new field and likewise the intercrop may attract pests that also attack the tuber crop. It is important to understand the interactions between the crops and soil organisms in order to assist the development of a healthy soil environment with fertile soils that are disease free.

Though not currently used in many farming systems, crop combinations (intercrops) may reduce diseases and pests of either crop. A recent review by Watt *et al* (2006) outline ways in which plant exudates can affect the microbial populations in the rhizosphere and to thereby benefit crop growth. The opportunities for similar interactions in root and tuber crops are outlined in the following chapters.

### ***Symbiotic relationship***

Recent research is exploring the ways that rhizosphere microbial populations communicate with plants. In this process the plant 'communicates' with the bacteria by releasing certain compounds such as flavonoids. When the bacteria recognize the flavonoid, they respond by releasing a specific signal molecule, which is only recognized by the appropriate host plant. Such an interaction occurs between the nitrogen fixing bacterium *Rhizobium* and the host legume and this leads to the infection of the plant and the establishment of the symbiosis and formation of the nodules on the root. Such a specific chemical response might not be a general phenomenon in the microbe-plant interaction, but the existence of other less specific forms of communication between plants and microbes exist. This provides excellent opportunities for developing so-called biased rhizospheres, by rhizosphere 'breeding'. This involves the breeding of cultivars, either by traditional or molecular biological methods, which are conducive to the development of beneficial microbial populations in the rhizosphere as a result of the excretion of specific plant compounds.

Though most of the current knowledge on this symbiotic relationship is limited to legumes and bacteria, further research is required to establish if such relationships exist with root and tuber crops and how this opportunity can be harnessed and used to increase the productivity of the root and tuber crops using natural processes and plant-organisms communication.

New developments have also been reported in the field of mycorrhizal associations of specific beneficial fungi with plant roots that support plant nutrition particularly of elements such as phosphorus and zinc that are relatively immobile in the soil. Cassava forms a symbiotic relationship with mycorrhizal fungi. Mycorrhizal associations are widespread throughout the plant kingdom and are found on most agricultural crops where they are important for sustainable crop production in many different climates, soils and types of agricultural practice. Arbuscular mycorrhizal (AM) fungi form a tree like haustoria within the plant cell that is the interface for exchange of materials between fungus and plant (Bago *et al.*, 2000).

Molecular techniques have led to greater knowledge of genetic variations within the arbuscular mycorrhiza. Carbon transport within the plant-fungus association, and into the relationship between fitness and mycorrhiza association (Bago *et al.*, 2000). AM fungi derive most, if not all, of

their carbon from the host plant (Jennings, 1995). Attempts to grow the AM fungus axenically (without host plants) have not been successful to date (Bago *et al.*, 2000).

The AM symbiosis usually increases plant biomass and photosynthesis and directs the flow of a significant fraction of the host plant's photoassimilate. The AM symbiosis therefore determines the flow of huge quantities of carbon worldwide and according to (Bago *et al.*, 2000) the estimate to be as much as 5 billion tons annually. The AM symbiosis usually enhances crop productivity through increasing nutrient and water uptake (Bago *et al.*, 2000).

### ***Interaction between crop management and soil biology***

Integrated Pest Management (IPM) practices for the root and tuber crops should also be used to control some of the pests and diseases that attack the root and tuber crops. This will essentially involve the use of invertebrates, and to a lesser extent the use of micro-organisms above and below-ground.

Soil fumigation experiments suggest that there may be ways to capitalize on interactions between crop management and soil biology (Meliani *et al.*, 2012; Bever 2003; Molofsky *et al.*, 2002; Mills, 1998). Agronomic responses that implicate influential changes in soil biology are those associated with conservation farming practices. Such practices invariably improve many attributes of the soil that are associated with high fertility; structural stability, infiltration rates, faunal and microbiological activity, soil organic matter, are all typically increased. Yet farmers' evaluations of the crop performance in conservation farming, worldwide, have been highly variable (Wall *et al.*, 1999; Van Veen *et al.*, 1985; O'Donnell *et al.*, 2001).

What is clear is that the apparently major improvements in soil properties do not always translate reliably into better crop yields. The range of possible contributory factors includes: increased pests and diseases; toxic chemicals arising from retained stubble; greater residual effects of herbicides; growth-inhibitory bacteria in the rhizosphere; inhibited root growth in the harder unploughed seed bed; inhibitory signals passing from roots to leaves when the roots are experiencing less than ideal soil conditions; and concentration of nutrients in the surface soil. Unraveling the underlying causes of crop response to changed agronomic practice such as these is difficult, but processes occurring within the rhizosphere are central.

## **II. HISTORICAL PERSPECTIVE**

### **Important milestones on the role of soil organisms and their use in crop production systems**

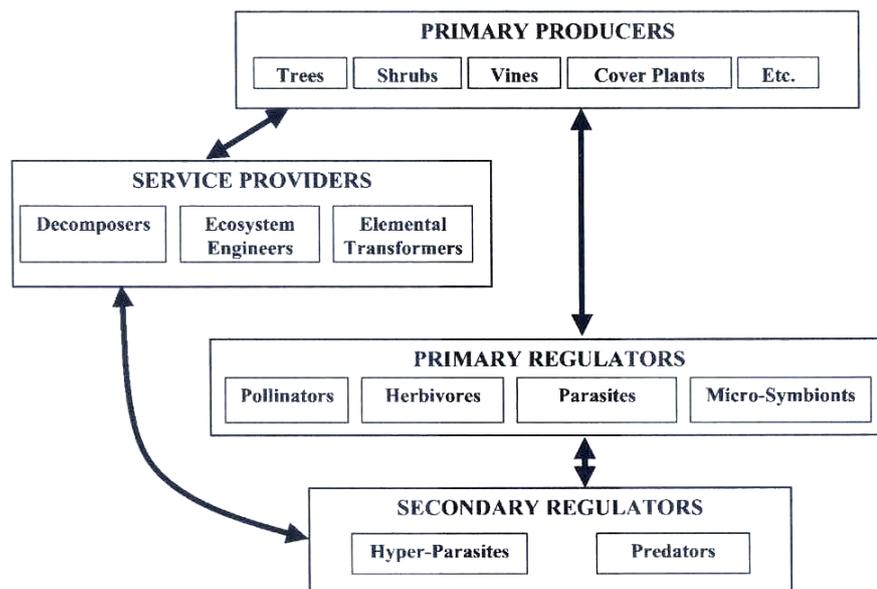
The early concepts of the soil and life-forms living in it were based on ideas developed by a German Chemist, [Justus von Liebig \(1803-1873\)](#) that soil contained different nutrients necessary for plant growth. The soils were rarely examined below the depth of normal tillage. These chemists held the "balance-sheet" theory of plant nutrition. Soil was considered a more or less static storage bin for plant nutrients—the soils could be used and nutrients replaced. This gave soil chemistry the central role in soil science for most of the 19<sup>th</sup> century.

Today we view the soil as a dynamic resource that plays an important role not only in the food production, but in the provisioning of other environmental services, like for example carbon sequestration and the provision of fresh water (regulation of the hydrological cycle). From the perspective of soil biology, soil embodies mineral and organic matter with organisms that thrive and depend on it. Assemblages of soil organisms are responsible for ecosystem processes such as nutrient cycling, control of soil borne crop diseases, and soil structure development that sustain these environmental services including primary production.

The soil teems with life but the diversity of soil organisms is largely uncharted terrain with probably only a small percentage of the total number of species that populate the soil environment known (Figure 1). Specific information is still lacking on the importance of species that are key to

specific functions, or to the importance of maintaining above and below-ground biodiversity to maintain particular soil functions (GLIDE Project, Ayuke, et al., 2003).

The Scientific Committee on Problems of the Environment (SCOPE) sub Committee on Soil and Sediment Biodiversity and Ecosystem Functioning (SSBEF) synthesized knowledge of soils in a series of international workshops (Wall, 2004). Their findings suggest that most steps in soil ecosystem processes are performed by groups of species from many phyla, resulting in high species redundancy (different species performing same ecosystem functions) particularly in the microbial component. Swift *et al.*, (2004) proposed a hierarchy of key categories of functional groups in order to harmonize approaches to defining functional groups (Figure 1).



**Figure 1.** Hierarchy of categories of functional groups

Until the recent advent of molecular genetics the smaller the size of the organism the smaller the number of species that had been described for that group of organisms. The more ‘visible’ organisms had received relatively more attention. However, advances in molecular biology and technology for DNA, PCR and RNA finger-printing and sequencing, have facilitated a break-through in understanding soil communities of micro-fauna and micro-flora making possible a more effective study of the diversity of micro and macro-organisms and their functional properties. Box 1 illustrates some of the available techniques for identifying and characterizing micro-fauna and flora that are currently rapidly advancing the study of soil micro-organisms.

These new developments in soil biology can now be applied to Iroot and tuber crops production. Use of molecular techniques to identify soil and rhizosphere microflora and trace the fate of microbial inoculants used for plant growth promotion, disease and pest control are such applications. More recently these techniques have been applied to the study of nematodes. Nematophagous fungi are specialized in trapping and digesting [nematodes](#) (Hertz, 2004; Dowe, 1987). However formulations of these fungi have not been effective in reducing nematode galls on root and tuber crops and other plants in the field or glasshouse to date.

Box 1.

**Advances in molecular technology benefiting work on biological nitrogen fixation**

A widely used exploration technique in microbiology is rDNA sequencing of the 16S ribosomal DNA, an indicator gene for bacterial biodiversity (Horner-Devine 2004). Other identification techniques include polymerase chain reaction (PCR) sequencing, ribonucleic acid (RNA) sequencing among others.

According to Haq (2000) microbiological studies were able to show differences between several groups of the soil bacteria such as the *rhizobia* and *bradyrhizobia* species, but the full extent to which they differ only became clear with the application of molecular techniques. Molecular comparisons of the Deoxyribonucleic acid (DNA) in *rhizobia* and *bradyrhizobia* showed the large genetic difference between them.

By DNA fingerprinting it was shown that the inoculants strain of clover *rhizobia* transferred some of its DNA to other strains even during one growing season. This exchange of DNA leads to greater diversity of *rhizobia* which might also correspond with differences in the capacity of the *rhizobia* to survive in the soil or to fix nitrogen.

Identification and detection methods are facilitated by the increasing knowledge of ribosomal (particularly 16S, 18S and 23S) sequences. New methods are often based on DNA extraction followed by PCR-amplification. DNA analyses using direct denaturing gradient gel electrophoresis (DGGE) are particularly interesting for assessing the microbial diversity of soil/plant systems. Molecular biological methodology may also increase effectiveness and hence the general application of inoculants for several important purposes such as the control of soil-borne diseases, nutrient availability to plants and soil structure formation, etc. However, effective inoculants can only be found and applied if there is adequate knowledge of inoculants ecology. This is largely lacking. However, genetic markers facilitate the study of the fate of inoculants in soil and molecular biological techniques are useful in studying the genetic potential in microbial cells for adapting to the prevailing conditions in bulk soil and rhizosphere.

One of the most intriguing questions in soil ecology relates to the existence and formation of so-called 'non-culturable' cells. Upon inoculation large proportions of the microbial cells are transformed into small, non-culturable cells. Yet the question remains whether the large numbers of naturally-occurring, non-culturable cells are unknown species, or whether they are representatives of known species. Basically this means more work in identification and taxonomy of the non-culturable species.

Other interesting new developments in methodology relate to improvements of existing techniques for the use of tracers in nutrient cycling studies, and for mathematical modeling of population dynamics and (bio) chemical processes in the heterogeneous soil system.

The rhizosphere has been identified as the main hot-spot for biological activity in soil, this being due to the availability of energy-rich substrates released by roots. Quantification of the release process still presents problems. However, it is necessary to improve our knowledge of spatial and temporal dynamics in soil life occurring in response to the release of root products. The theory that microbe activity in the rhizosphere is related to the cell density of colonies and bio-film is of particular interest here.

### **What are the drivers of change?**

#### **Market demands of the root crops**

Root and tuber crops have traditionally been used as food crops and in some cultures in Africa as hunger crops that become handy during the periods of drought and when grain is in short supply. As global eating habits changed and with the advent of the potato chips, the root and tuber crops developed new commercial values. They are fried in the fast food restaurants as well as packaged as

fried chips that are easy to carry around in small packs. Many snack-packs in Supermarkets are currently mainly packages of the root and tuber crops.

One marketing advantage of root crops is that they can typically be stored for relatively long periods until ready to market. In 1995–97, the major root and tuber crops of cassava, potato, sweet potato, and yam occupied nearly 50 million hectares worldwide with an annual average production of 643 million metric tons (mt), 70% of which was harvested in developing countries (FAO, 1998; Scott *et al.*, 2000). By the mid-1990s, an estimated 250 million mt of these crops were consumed in Asia, Africa, and Latin America, contributing to the diet of over two billion consumers in these regions (FAO, 1998). At the same time, over a billion people in industrialized countries consumed nearly 100 million mt of root and tuber crops (almost entirely potato). The bulk of the remainder was utilized for feed, planting material, and processed products for food or industry. According to recent estimates, the annual economic value of root and tuber crops produced in developing countries is roughly US\$40 billion, or one quarter that of the major cereals.

Marketing of the root and tuber crops will largely depend on the dynamics of the eating habits of the community concerned and the rate at which the middle class population grows in countries and regions of the world. Scott *et al.* (2000) project that slightly over half (53%) of the total absolute increase in utilization of root and tuber crops in developing countries of about 123 million mt is expected to occur in Sub-Saharan Africa. According to the authors, the overwhelming bulk of that increase will consist of cassava (80 million mt). Further, utilization of yams will increase rapidly, particularly in West Africa. The remainder will be split between sweet potato and potato, with the increases for these commodities concentrated in East and parts of Southern Africa, e.g. Uganda and Malawi (Minde *et al.*, 1999) and in Asia, e.g. China and India (Scott *et al.*, 1999). Apart from potatoes which already have a high market share, it will require more effort to process and package the root and tuber crops and especially the sweet potatoes, and cassava for up-market marketing. The common notion in Africa, is that these are rural crops and not anymore fashionable in the Cities. This notion could be limited to some parts of Africa but is something to contend with. Best economic opportunity presented for root and tuber crops is likely an increased utilization in industry for manufacturing of starch.

The market expansion will mostly be realized in response to the ever expanding populations and will mostly be for domestic rather than an export oriented market. This does not in any way mean that there will be no growth in production. While there are increasing trends in production, due to the bulky nature of the root and tuber crops it will not be easy to export them to high transport costs. However, their demand as sources of starch and as food will continue to grow. This growth needs to be supported by local institutions that are strong in soil biology to take advantage of the gains. For example, CIP's multi-stakeholder partnership programme, Sweet potato for Profit and Health has set a goal of reaching 10 million households across 17 Sub-Saharan Africa countries over the next 10 years to achieve a widespread uptake of sweet potato that will significantly reduce malnutrition among children under the age of five. On the other hand, cassava's starchy roots are the basis of many food and industrial products. The roots can be eaten in various forms: raw, roasted, boiled, baked, fried, granules, pastes and flour. In many of the cassava-growing countries in Africa, as well as a few other countries of the world, the leaves are also consumed as a green vegetable, which provide protein and vitamins A and B. Cassava starch is used in a wide range of products: for example, in various food products, in pharmaceuticals, as a binding agent, in the production of paper and textiles and as monosodium glutamate, an important flavouring agent in Asian cooking. In Africa, cassava flour is beginning to be used in partial substitution for wheat flour.

### Maintaining good soil health

An important aspect for the future of root and tuber crops is the new awareness of the need to maintain a healthy environment in which the ecosystem functions are balanced. One of the important examples in this is the quest for a healthy soil. The underlying principle in the use of the term “soil health” is that soil is not just a growing medium; rather it is a living, dynamic and ever-so-subtly changing environment. Use can be made of the human health analogy to categorize a healthy soil as one:

- In a state of composite well-being in terms of biological, chemical and physical properties;
- Not diseased or infirm (i.e. not degraded, nor degrading), nor causing negative off-site impacts;
- With each of its qualities cooperatively functioning such that the soil reaches its full potential and resists degradation;
- Providing a full range of functions (especially nutrient, carbon and water cycling) and in such a way that it maintains this capacity into the future.

In its definition and according to the Soil Science Society of America Agronomy (1995), soil is a living system that represents a finite resource vital to life on earth. It forms the thin skin of unconsolidated mineral and organic matter on the earth's surface. It develops slowly from various parent materials and is modified by time, climate, macro- and micro-organisms, vegetation, and topography. Soils by composition are complex mixtures of minerals, organic compounds, and living organisms that interact continuously in response to natural and imposed biological, chemical, and physical forces. Vital functions that soils perform within ecosystems include:

- Sustaining biological activity, diversity, and productivity;
- Regulating and partitioning water and solute flow;
- Filtering, buffering, degrading, immobilizing, and detoxifying organic and inorganic materials, including industrial and municipal by-products and atmospheric depositions;
- Storing and cycling nutrients and other elements within the earth's biosphere; and
- Providing support for socioeconomic structures and protection for archeological treasures associated with human habitation.

Conceptually, the intrinsic quality or health of a soil can be viewed simply as "its capacity to function." The definition encompasses **productivity, environmental quality, and health** as major functions of soil. The definition requires that values be placed on specific soil functions as they relate to the overall sustainability of alternate land-use decisions. Soil quality in its broadest sense is therefore enhanced by land-use decisions that weigh the multiple functions of soil, and is impaired by land-use decisions that focus on single functions. Soil quality can be degraded by using inappropriate tillage and cropping practices; through excessive livestock grazing or poor timber harvesting practices; or by misapplication of animal manures, irrigation water, fertilizers, pesticides, and municipal or industrial by-products.

To enhance soil quality and soil health, everyone concerned must recognize that the soil resource affects the health, functioning, and total productivity of all ecosystems. We must become more and more aware of potential side effects of soil management and land-use decisions. Based on this understanding, and especially that on the knowledge of its functions of enhancing productivity and that of enhancing environmental quality and health; the cultivation of root crops and tubers need

to preserve if not to protect or take advantage of these intricate aspects of the soil. These may best be realized through the use of the natural provisions of nature in the form of soil biota, natural processes and other life-forms on the earth's surface or through artificial introduction and manipulation of organisms such as in inoculation. From this understanding, it is important to point out that adapting crops rapidly to new situations becomes an increasing challenge requiring the intelligent use of the latest advances in the knowledge of plant genetics and soil biota relationships.

In this regard, it is important to mention that most crops have a diverse genetic base that breeders draw from to identify new sources of genes for trait improvement. This diverse base comes in different forms, ranging from traditional varieties and landraces adapted to cultivation methods without modern fertilizers and equipment, to wild relatives collected from the centres of origin of the crop species. These wild relatives contain, for example, genes useful for combating new pathogens or challenging growing environments. To maintain a productive agriculture we need to be drawing on this wealth of genetic resources, and using efficient mechanisms to incorporate the traits they bring into modern varieties to meet the challenges identified.

For example, Scotland looks after one internationally recognized crop and crop wild relatives' genebank, the Commonwealth Potato Collection (CPC). The collection comprises around 1500 accessions of about 80 wild and cultivated potato species. Each accession traces back to a handful of berries or tubers from potato plants in South or Central America, gathered from the wild or obtained from a grower at a market. This collection is maintained to international standards and is Scotland's contribution to the multilateral system regulated by the International Treaty on Plant Genetic Resources for Food and Agriculture.

The importance of the collection to the potato industry is hard to over-emphasize. Genes from the plants held within the collection can be found in most varieties which are grown today. This includes the gene known as *HI* which provides resistance to a major potato pest - Potato Cyst Nematode. Furthermore, new potato varieties such as Mayan Gold, which has unique flavour and texture have been developed from the CPC which provides a major repository of the variation required by breeders to deal with the challenges of sustainable agriculture production in the future. Next generation crops must deal not only with new pests and disease but also with reduced access to declining supplies of water and fertilizers. It is the use of the existing root and tuber crop genebanks complemented with new species discoveries and bioprospecting that will open up the opportunity space of breeding as well as developing symbiotic linkages with soil organisms.

## **Impact on the environment**

### **Greenhouse gas emissions due to fertilizer and other chemicals use**

Global warming is the increase in the average temperature of the Earth's near-surface air and oceans since the mid-20th century and its projected continuation. Global Earth's-near surface temperature increased 0.74 °C and 1.33 °F between the start and the end of the 20th century. Most of the observed temperature increase was caused by increasing concentrations of greenhouse gases resulting from human activity such as fossil fuel burning, use of fertilizers in farmlands and deforestation. The effects of global warming are already being felt in terms of drought, floods and emergence of diseases. Most often, mitigations involve reductions in the concentrations of greenhouse gases, either by reducing their sources or increasing their sinks. The main natural sinks known are the oceans, soil organic matter (SOM) and photosynthetic plants and algae. The activities of soil organisms and their possible role in carbon sequestration are increasingly recognized as mentioned in the Commission's background study papers on micro-organisms, invertebrates and climate change.

Through the soil formation and transformation processes, including nutrient cycling, we see the roles of soil organisms (micro, meso and macro) as those of increasing the productivity of the root and tuber crops as well as supporting more soil carbon storage and therefore contributing to a reduction in the greenhouse gas emission through carbon sequestration. Their roles on pest and disease control and management is also crucial for a clean environment. Based on this knowledge, farmers should be encouraged to include soil organisms in their production methods as a measure of reducing overreliance in chemical interventions for productivity, disease and pest control. This will leave the environment cleaner and in balance with its own natural products. Otherwise as the food demand by the ever increasing human population grows, and the demand for synthetic fertilizers and pesticides also grows, it might get to a situation where an irreversible imbalance is created in the atmospheric composition of the gases that may lead to an environmental disaster driven by global warming and other greenhouse related processes.

### **Effect on soil biodiversity**

#### **Diversification versus crop specific specialization or organisms**

Does root and tuber crops cultivation have any effect on the soil organisms or above ground biodiversity? This debate is still premature, because a lot of research work still needs to be conducted, to identify and establish, which organisms occur in symbiosis with the root and tuber crops and which ones assist and support them in fighting pests and diseases. In this way, we shall know whether the root crops condition selective and specialization of specific soil organisms within the rhizosphere where they live. Previous work done by CIAT-TSBF on below-ground biodiversity did not address the root and tuber crops. The tuber crops encountered during the inventory of soil organisms by the Conservation and Sustainable Management of Below-Ground Biodiversity project was only the lily bulbs in Mexico which are not within the scope of the crops discussed in this report. This therefore leaves a major gap in knowledge that needs to be addressed both in terms of similarity with other soil biota communities and the effect of above ground vegetation. Work needs to be done on kind of root and tuber crop-soil organisms associations and the mechanisms of the interactions.

## **III. THE SOIL MICROBIAL DIVERSITY AND FUNCTIONS**

This chapter describes in-depth the diversity of soil organisms and their interactions with each other as well as their roles in soil process and in disease control. It also discusses the use of bio-control agents in the control and management of pests and diseases that may attack the root and tuber crops. It is in line with the studies prepared for the Commission's 12th Regular Session, in particular to documents CGRFA-12/09/Inf.15 and CGRFA-12/09/Inf.17.

### **Soil components**

The soil ecosystem is dynamic and composed of biotic and abiotic components. Plant roots, microorganisms, and macro-organisms make up the biotic component while abiotic portion is made up of mineral particles, water, gases, nutrients, and nonliving organic matter. Commonly fifty percent of soil volume is solid fraction and is made up of mineral particles (45%) and organic matter (<1% to 10%). The gaseous fraction is 25% of soil volume and is in the form of air filled pores while 25% is liquid fraction in the form of water filled pores.

These proportions however will vary with soil type. Soil organisms constitute 1-5% of the organic fraction by weight, hence only 0.04% of the soil mass. However this fraction is home to a large proportion of the world's genetic diversity that range in size from the tiniest one-celled bacteria,

algae, fungi, and protozoa, to the more complex nematodes and micro-arthropods, to the visible earthworms, insects, small vertebrates, and plants (Table 3). The largest populations of microorganisms are mostly found in the top 10cm soil, in thin water films around soil particles, water filled pores of soil aggregates, decaying plant and animal debris, in the rhizosphere of plants, and on decaying plant and animal debris. However bacteria are found throughout the soil profile.

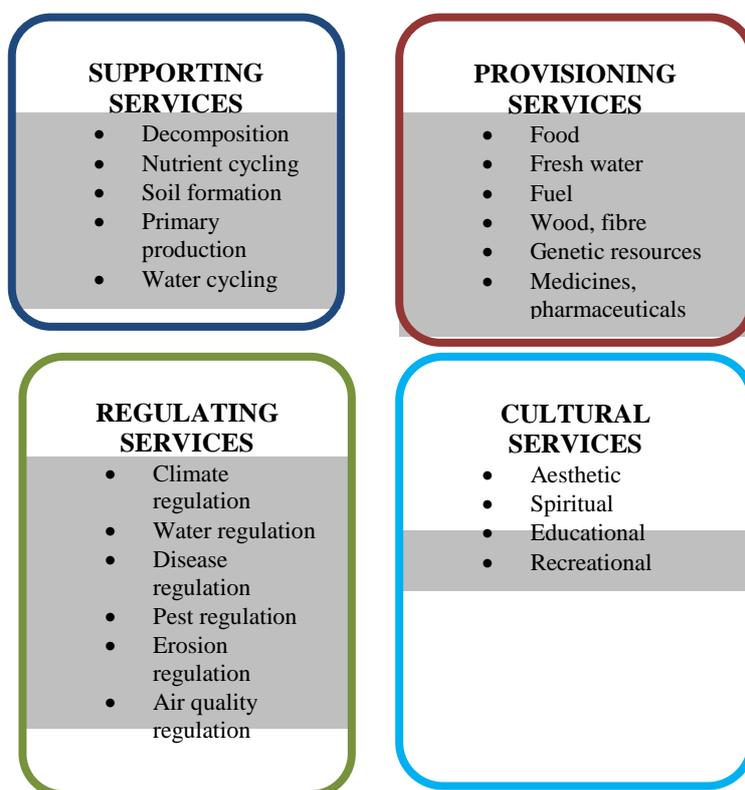
Micro-organisms are the dominating group of organisms, both according to numbers and total biomass. A large number of bacteria exist in the soil, but because of their small size, they have a smaller biomass. Actinomycetes are a factor of 10 times smaller in number but are larger in size so they are similar in biomass to bacteria. Fungus populations are smaller but they dominate the soil biomass when the soil is not disturbed. Bacteria, actinomycetes, and protozoa are hardy and can tolerate more soil disturbance than fungal populations so they dominate in tilled soils while fungal and nematode populations tend to dominate in untilled or no-till soils.

**Table 1: Diversity of soil microorganisms**

Group	Organisms	Body form	Size	Mode of nutrition
Micro-organisms (<0.2mm)	Bacteria	Unicellular Prokaryote	Cell diameter 0.5-8µm	Decomposers, Mutualists, Parasites, some are autotrophic
	Actinomycetes	Unicellular, filamentous Prokaryote	Hyphal diameter 0.5-2 µm	Decomposers, Mutualists, Parasites,
	Fungi	Hyphal Eucaryote	Hyphal diameter 5 µm Hyphal length <1002 µm	Decomposers, Mutualists, Parasites,
	Algae	Eucaryotic thallus ; unicellular, colonial, filamentous, foliuous, tubular, blade-like, leafy	0.5 µm -50m long	Autotrophic Symbiotic
	Protozoa	Unicellular <i>Eukaryote</i>	10 µm to 1000 µm long	Graze on bacteria and algae
	Nematodes,	Multicellular	50 µm diameter, 1mm length	Bacterivores, fungivores, decomposers, herbivores (feed on plant roots), predators (feed on other nematodes)
	Rotifers	Multicellular	200-500 µm long. A few are more than 1mm long	Decomposers, feed on algae
Meso-organisms (0.2-10mm length, 0.1-2mm width)	Collembola	Multicellular	0.2-8mm long	Decomposers, feed on algae, fungi , bacteria, plant roots, nematodes
	Tardigrades	Multicellular	0.05-1.2mm	Feed on organic matter, algae and other microorganisms
	Others are enchytraeids, mites, and smaller arthropods	Multicellular		
Macro-organisms (>10mm)	Earthworms	Multicellular	1cm-6.7m long	Decomposers, eat live seeds and seedlings
	Others are ants, termites, mollusks and larger arthropods.			

### Soil microbial functions

When soil organisms eat, grow, and move, they perform essential services for ecosystems, as well as for human society. Ecosystem services as listed by MEA (2005) are shown in Figure 2. Among the key ecosystem services mediated by soil biota are the transfer, storage, and provision of clean ground water, the storage of carbon and the prevention of trace gas emissions crucial for climate control, as well as the provision of nutrients and pest and pathogen regulation, supporting plant growth and aboveground biodiversity. As shown in the figure, soil biotas are involved in the provision of all the main supporting and regulating ecosystem services. Most of the structure and functioning of the aboveground individuals and communities are regulated directly or indirectly by altering the dynamics of nutrients available to plants. The scenic appearance of plant communities such as woodlands, grasslands and ornamental plants provide aesthetic values, some animals are spiritual in some religions, while microbially driven nutrient cycles play key roles in mediating global climate change, by acting as C sources and sinks and by generation of greenhouse gases such as nitrogen oxides and methane, thus the indirect link to soil regulatory and cultural services not highlighted by MEA (2005). These indirect effects tend to involve less specific interactions and occur over longer durations than the direct regulations (?).



**Figure 2:** Contribution of soil biodiversity to the provision of ecosystem services (highlighted services) (adapted from MEA 2005)

Soil organisms contribute a wide range of essential services to the sustainable functioning of all ecosystems by acting as the primary driving agents of nutrient cycling; regulating the dynamics of soil organic matter, soil carbon sequestration and greenhouse gas emission; modifying soil physical structure and water regime; enhancing the amount and efficiency of nutrient acquisition by vegetation; and enhancing plant health. These services are not only essential to the functioning of natural ecosystems but also constitute an important resource for the sustainable management of agricultural

systems. The precise role of many soil organisms in these cycles and functions is unknown, although the great diversity and abundance of microbial, plant and animal life in soil seems likely to influence ecosystem function in various ways. Quantification of diversity and functional roles of each soil organism is however limited by methodology and is a substantial scientific challenge. A better understanding of the relations between diversity and function requires use of high resolution techniques with which to detect inactive and active microbial cells in the soil matrix. Some of the soil functions of microorganisms are discussed below.

### **Role of microorganisms in soil structure and water dynamics**

The capacity of soil to regulate the terrestrial freshwater supply is a fundamental ecosystem service. Water percolating through soil is filtered, stored for plant utilization, and redistributed across flow paths to groundwater and surface water bodies. The sustainability of water resources, (both quantity and quality), is directly influenced by soil and is a function of soil texture and structure. (O'Geen *et al.*, 2010).

**Soil structure and texture** affect water holding capacity of soil, nutrient retention and supply, drainage, and nutrient leaching. While soil texture is dependent on parent rock, soil structure is influenced by soil organic matter content and soil organic carbon. Soil organic matter influences the formation of soil aggregates. Micro-aggregates are 20–250  $\mu\text{m}$  in size and are composed of clay microstructures, silt-size micro-aggregates, particulate organic matter, plant and fungus debris, and mycorrhizal fungus hyphae: these particles are stable in size, Fig 2. Roots and microbes combine micro-aggregates in the soil to form macro-aggregates. Macro-aggregates are linked mainly by fungi hyphae, roots fibers, and polysaccharides and are less stable than micro-aggregates. Macro-aggregates are greater than 250  $\mu\text{m}$  in size and give soil its structure and allow air and water infiltration. Compacted soils tend to have more micro-aggregates than macro-aggregates.

Glomalin, an amino polysaccharide or glycoprotein created by combining a protein from the mycorrhizal fungus with sugar from plant root exudates initially coats the plant roots and then coats soil particles (Allison, 1968). Glomalin acts like a glue to cement micro-aggregates together to form macro-aggregates and improve soil structure. Glomalin needs to be continually produced because it is readily consumed by bacteria and other microorganisms in the soil. Roots also create other polysaccharide exudates to coat soil particles.

Bacteria are involved in soil aggregation by producing polysaccharides which are more stable than plant polysaccharides. Bacteria develop a small electrostatic charge that attracts the electrostatic charge on clay surfaces, bringing together small aggregates of soil. Oxides also act as glue and join particles together. This aggregation process is very common to many highly weathered tropical soils. Soil particles may also naturally be attracted to one another through electrostatic forces. Stable aggregates increase water holding capacity of the soil and reduce evaporation. Organic matter encourages root development, improves aggregation, preventing erosion and compaction. Compacted soils results in: (a) restricted root growth; (b) poor root zone aeration; and (c) poor drainage that results in less soil aeration, less oxygen in the root zone, and more losses of nitrogen from denitrification.



**Figure 3:** Roots, fungal hyphae and polysaccharides stabilize soil micro-aggregates and promote good soil structure (from Dr. João de Moraes Sá).

**Current application of biological control in root crop systems**

A variety of biological controls are available for use in root crop systems while others require further development and effective adoption (Table 2).

**Table 2: Biocontrol of Pests and Diseases of Root Crops and tubers**

Host	BCA	Target pathogen	Mode of action	Disease	Mode of Application	Where used	Reference
Raddish ( <i>Raphanus sativus</i> )	<i>Trichoderma harmatum</i>	<i>Pythium spp.</i>	Mycoparasitism	Damping off	Seed coat	Experimental level	Harman <i>et. al.</i> , 1980;
		<i>Rhizoctonia solani</i>	Mycoparasitism	Damping off	Seed coat	Experimental level	Henis et al., 1978
	<i>Pseudomonas fluorescens</i>	<i>Fusarium oxysporum f. sp. raphani</i>	Induced resistance	Wilt	Seed coat	Experimental level	Leeman <i>et al.</i> , 1995
Table beet ( <i>Beta vulgaris</i> )	<i>Corticium spp.</i>	<i>Pythium ultimum</i>	Mycoparasitism	Damping off	Seed coat	Experimental level	Liu and Vaughn, 1965
Cassava ( <i>Manihot esculenta</i> )	<i>Pseudomonas spp.</i>	<i>Sclerotium rolfsii</i>	Antagonisms	Tuber rot	Spore suspension	Experimental level	Manjula <i>et al.</i> , 2005
Yam ( <i>Dioscorea spp.</i> )	Xanthomonas spp	<i>Sclerotium rolfsii</i> <i>Fusarium solani</i> <i>Botryodiplodia theobromae</i> <i>Sclerotium rolfsii</i> <i>Sclerotium rolfsii</i>	Competition	Tuber rot		Experimental level	Manjula <i>et al.</i> , 2005
	<i>Bacillus spp.</i>	<i>Botryodiplodia theobromae</i>	Chemotaxis			Experimental level	Manjula <i>et al.</i> , 2005
	<i>Trichoderma harzuanum</i>	<i>Fusarium solani</i>	Inhibition of conidial germination			Experimental level	Manjula <i>et al.</i> , 2005
	<i>Penicillium oxalicum</i>	<i>Fusarium solani</i>	Inhibition of conidial germination			Experimental level	Manjula <i>et al.</i> , 2005
<i>Botryodiplodia theobromae</i>		Inhibition of conidial germination			Experimental level	Manjula <i>et al.</i> , 2005	
Cassava	Wasp Lady bird	Cassava mealybug ( <i>Phenococcus manihoti</i> )	Predation (Classical biological control)			Covers 400,000km <sup>2</sup> in Africa (11 countries e.g. Ghana,	IITA

						Nigeria, Togo) Benin	
	Predatory mite ( <i>Typhlodromalus aripo</i> )	Cassava green mite ( <i>Mononychellus tanajoa</i> )	Predation (Classical biological control)			Covers 400,000km <sup>2</sup> in Africa (11 countries e.g. Ghana, Nigeria, Togo)	IITA
	Lady bird	Aphids ( <i>Aphis gossypii</i> )	Predation			Guyana	Homenauth and DeSouza, 2011
		Cassava Hornmorm ( <i>Erinnyis ello</i> )	Predation			Guyana	Homenauth and DeSouza, 2011
	<i>Bacillus thuringiensis</i> Braconid wasp	Cassava Hornmorm ( <i>Erinnyis ello</i> )	Parasitism			Guyana	
Cassava	<i>Trichoderma viride</i>	<i>Botryodiplodia theobromae</i> <i>Rhizopus oryzae</i> <i>Aspergillus flavus</i> <i>Fusarium solani</i>	Antagonism	Root rot	Culture filtrate	Experiment	Ubalua and Oti, 2007
Yam ( <i>Dioscorea cayennensis</i> )	Actinomycete isolates ( <i>S. thermotolerans</i> , <i>S. griseus</i> subsp. <i>griseus</i> , <i>Streptomyces</i> sp. N0035, <i>S. purpurascens</i> , and two isolates identified as <i>Streptomyces</i> sp.) and their metabolites	<i>Curvularia eragrostides</i>  <i>Colletotrichum gloeosporioides</i>	Parasitic	Leaf spot diseases		Experiment	Soares et al., 2006  Yang et al, 2011
Yam ( <i>Dioscorea alata</i> )	<i>Trichoderma harzianum</i> , <i>Pseudomonas syringae</i> and <i>Pseudomonas chlororaphis</i>	<i>Botryodiplodia theobromae</i> and <i>Fusarium solani</i>		Root rot	Culture filtrate	Experiment	Okigbo and Emeka, 2010
All crops	<i>Metarhizium anisopliae</i> (Green muscle)	Desert locust	Mycoparasite			Commercial product Africa, Australia	FAO, 2007
Sugar beet	<i>Bacillus mycoides</i>	<i>Cercospora beticola</i>	Non-pathogenic, phyllosphere inhabiting			Experiment	
Potato	Foil-sis® ( <i>Solanum sisymbriifolium</i> )  Nemaslug® Xtra ( <i>Phasmarhadtis hermaphrodita</i> )	Potato cyst nematodes  All the most destructive species of slug are completely susceptible, including the keeled slug ( <i>Milax</i> and <i>Tandonia spp.</i> ), the round-backed slug ( <i>Arion spp.</i> ) and the grey field slug ( <i>Deroceras reticulatum</i> ).	Trap crop  Pathogenic nematode		Seeds	Commercial product	UK, www.branston.com
Potato	<i>Verticillium biguttatum</i>	<i>Rhizoctonia solani</i>	Mycoparasite	stem canker and black scurf	spore suspension		Demirci, 2009

Potato	Riyoplan ( <i>Pseudomonas putida</i> ) Bectofit ( <i>Bacillus subtilis</i> ) Immunofit M. biomonas ( <i>Pseudomonas</i> ) TU-20, nikfan and azotovit	<i>Phytophthora infestans</i>	Inhibition	Potato late blight	Culture	Experiment in Russia.	CAO and FORRER, 2001
	<i>Xenorhabdus bovienil</i>	<i>P. infestans</i>	Antibiotics (indoles and dithiopyrrolones)	Potato late blight	Antibiotic preparation	Experiment in Russia.	CAO and FORRER, 2001
	<i>Fusarium sambucinum</i> ( <i>Gibberella pulicaris</i> )	<i>P. infestans</i> and <i>Alternaria solani</i>	Induced resistance	Potato late blight	Mycelial filtrate as spray of tubers before planting or as dip		Cao and Forrer, 2001
Potato	<i>Fusarium sambucinum</i> ( <i>Gibberella pulicaris</i> )	<i>P. infestans</i>	Induced resistance	macrosporangiosis	Mycelial filtrate as spray of tubers before planting or as dip		Cao and Forrer 2001
Potato	BmJ <i>Bacillus mycoides</i> isolate J	PVY virus	Induced resistance	Potato late blight		Commercial (Certis USA)	www.agprofessional.com
Potato	<b>Other Antibiotics</b> Biomonas , TU-20, Azotovit , <b>Mycelial extracts</b> <i>Fusarium sambucinum</i> , <i>F. culmorum</i> , <i>P. infestans</i> , <i>P. capsici</i> , <b>Organism</b> <i>Phytophthora infestans</i> <i>P. cryptogea</i> <i>Penicillium aurantiofriseum</i> , <i>Fusarium equiseti</i> , <b>Culture filters</b> <i>Streptomyces</i> isolates <b>Bacterial antagonism</b> <b>Compost extracts</b>		Induced resistance				Eduardo <i>et al</i> , 2007
Carrot	Contans® ( <i>Coniothyrium minitans</i> )	<i>Sclerotinia sclerotiorum</i>	Suppression	Cottony soft rot	Soil spray	Commercial	Carlifornia (CFCAB, 2005)
	Owls	Pocket gophers ( <i>Thomomys bottae</i> ), rabbits (black tailed jackrabbits, desert cottontails), and ground squirrels ( <i>Spermophilus beecheyi</i> )	Predatory		Natural enemy	Commercial	Carlifornia (CFCAB, 2005)

### **Benefits and Problems in Developing BCAs**

Biological control methods where used have provided an alternative safer mode to pathogen, pests and weed control. Developing BCAs is labor intensive and has thus lead to job and wealth creation because of the numerous niche markets they would have to satisfy if chemicals were phased altogether. The growers may also receive more income because of the premium on pesticide-free and organic produce. However the development of BCAs has met a lot of challenges that can be summarized as follows:

#### **Challenges related to the process of production**

1. There is little investment in the research and development of microorganisms compared with that spent on the discovery of chemical pesticides because BCAs usually have a narrow host range and often give inconsistent and poor control in field trials. Consequently, more attention is being given to the selection of broad-spectrum BCAs and improvements in the production, formulation and application technologies. Efforts are also being made to optimize the impact of these agents by integrating them with other novel crop protection strategies.
2. Determination of successful colonization and expression of bio-control traits.
3. Determining the components and dynamics of plant host defense induction.
4. Mass culture of obligate parasites
5. Determining formulations to be used to enhance activities of known bio-control agents.
6. Determining the crop systems that are appropriate for application of a particular BCA.

#### **Challenges related to application process**

1. Improper timing of the release of the natural enemy.
2. Impatience on the part of the grower can often lead to failure of a biological control program. Such impatience usually results in the resumption of the chemical control program before there is any need to do so. The basic cause of this is probably a lack of appropriate experience with biological control.
3. Lack of adequate pest suppression achieved by the control agent and cultural or chemical practices which adversely affect the natural enemy are some of the problems. Natural enemies may not control their hosts at all times or under all conditions. Many failures can be attributed to improper environmental conditions.
4. Distribution of the beneficial organism uniformly through the soil system.
5. Application of beneficial organisms in controlled greenhouse conditions has proved more effective than with outdoor crops, which cover millions of hectares.
6. Defining environmental conditions under which the beneficial microbe performs best; compatibility with the crop production system and grower inputs; soil pH, temperature, humidity, target plant tissue (root, tuber, etc.) all affect the establishment of beneficial microbes in the soil. Also important are how pesticide inputs, nutrient inputs, irrigation method and frequency, affect beneficial microbe performance or longevity. These have to be considered for the proper use of beneficial microorganisms.

7. Longevity of a beneficial microbe or microbes in the soil.
8. Ultimately all introduced beneficial microbes must be re-introduced to maintain protective levels in soils.

#### **Challenges related to commercialization**

From the commercial perspective specialized niche markets are at present the likely outcome. The full potential of BCAs commercially has not been realized because of the following:

1. Absence of strong incentives to develop these agents and/or discourage chemical pesticides.
2. Appropriate packaging to ensure shelf survival of the organism.
3. Quality control
4. Availability of new, biodegradable chemical pesticides.
5. Absence or breakdown of the infrastructure, which facilitates transfer of new technologies and research knowledge to the end-user (e.g. grower).
6. Absence of a universally acceptable registration procedure.
7. Restrictions in the use of exotic BCAs.
8. Lack of robust and reliable field effects.
9. Very few growers or extension workers know how to use BCAs.
10. Progress is also slow because the main producers of BCAs are often small-medium-size enterprises, which have limited resources for the effective development and marketing of products.

#### **Challenges related to potential hazards and safety concerns**

The following are potential safety issues:

1. competitive displacement of non-target organisms
2. allergenicity
3. toxicity to non-target organisms and
4. pathogenicity to non-target organisms.

In addition, indirect effects, such as those that could come about through the depletion of the target pest host itself, with the altered ecological system becoming a potential safety issue.

## **IV. TRENDS AND INNOVATIONS FOR THE USE OF MICRO-ORGANISMS, BIOLOGICAL CONTROL AGENTS AND PATHOGENS**

### **Trends in diversity and functions**

#### **Land use dynamics**

Land use practices have largely transformed the biosphere (Vitousek et al., 1997; Foley et al., 2005). The magnitude of human transformation culminating from increasing demand for food security has resulted in escalating conversion of natural vegetation/habitats into cropland and pasture (Ramankutty et al., 2008). The changes in land use transcends beyond changes in land cover to virtually all realms of biodiversity and biogeochemical processes. Soil, a living system is a resource largely affected by these changes.

Large scale/industrialized agricultural systems, the main drivers of land use change, are characterized by management practices such as cultivation with heavy machinery, use of fertilizer and pesticides, monocropping, annual crops with limited incorporation of perennial crops and organic materials (Foissner, 1992; Wardle, 1995; Giller et al., 1997). Evidence of the consequences of agricultural practices on soil organisms is still limited for the different cropping systems. Land use

trends, an aspect of crop and management, influences richness of species, structure, abundance and functions. Crop management may cause different gradients of disturbance depending on the crop and soil fertility level.

Disturbance plays a major role in altering diversity with intermediate disturbance promoting macro-faunal diversity and extreme or lack of disturbance reducing diversity relative to undisturbed systems (Petraitis et al., 1989; Hobbs and Huenneke, 1992), the intermediate disturbance hypothesis (Connell, 1978) could explain why some groups of organisms are more abundant in no till (i.e. intermediate disturbance) than either conventionally tilled (i.e. extreme disturbance) or old field (i.e. no disturbance) systems (Wardle, 1995). If disturbance is common or harsh, only few taxa that are resistant to disruption will persist (Petraitis et al., 1989). If the disturbance is mild or rare, soil communities will approach equilibrium and be dominated by few taxa that can out-compete all other taxa.

Reducing the frequency of cultivation (Hedrix et al., 1986) and including perennial crops in agricultural systems (Wasilewska, 1979; Freckman and Ettema, 1993; Neher and Campbell, 1994) are two ways of increasing trophic diversity in arable soils. In contrast, Wardle (1995) reported several cases in which conventional agricultural practices stimulate diversity. Croplands occupy a significant area of the terrestrial biosphere, and play a disproportionate role in global biogeochemistry, and constitute part of the biosphere most essential to well being (Monfreda et al., 2008). Out of the 175 crop types aggregated into major functional types, the annuals and perennials have very different consequences for ecosystem functions (Monfreda et al., 2008).

Crops that live for more than one year are considered perennial and crops like potatoes (root and tubers) are considered annuals because they are harvested within one season even though they could live for more than one year under typical cultivation practices count as perennials (Monfreda et al., 2008). These include crops like banana and plantain that send off shoots but maintain a perennial rhizome. Root and tuber crops: Cassava (*Manihot esculanta* Crantz), Sweet potatoes (*Ipomoea batatas* Lam. L.), potatoes (*Solanum tuberosum*), Yam (*Dioscorea* sp.), Taro (*Colocasia* sp.), Elephant yam (*Amorphophallus paeonifolius*), *Coleus rotundifolius*, Arrowroot (*Maranata arundinaceae*), Tannia (*Xanthosoma sagittifolium*) are usually as annuals because they are harvested within the year of planting.

Biogeochemical processes such as carbon, nitrogen, phosphorus and sulphur cycles are mediated by soil organisms. Soil microorganisms play a key role in the process of bio-geochemical cycling, soil aggregate formation and plant health (Madsen, 2005). Soil microorganisms possess the ability to give an integrated measure of soil health, an aspect that cannot be obtained with physical, chemical measure and/or analyses of diversity of higher organisms (Nielsen and Winding, 2002). They respond to changes in land use more rapidly and may therefore function as excellent indicators of changes in soil health (Kennedy et al., 1995; Pankhurst et al., 1995; Jefwa et al., 2012, Jefwa et al., 2009; Okoth, 2009) reported intense land use (intense agricultural practices) leads to the loss of AM fungi.

### **Dynamics in the rhizosphere**

The rhizosphere is the zone surrounding the root which produces exudates, a food source for microorganisms, and modifies and stimulates the density, structure and functions of microbial communities (Raaijmakers et al., 2009). It is the main zone for plant nutrition, health and quality, microorganism driven carbon sequestration; ecosystem functioning and nutrient cycling processes (Garbrielle Berge and Smalla, 2009). The rhizosphere microbes are composed of bacteria, archaea, viruses and fungi and may interact directly or indirectly with plants, their effects on soil biotic and abiotic parameters affecting plant growth. Rhizosphere microbes can be beneficial and promote plant growth and well being or detrimental, causing plant diseases and death (Buée et al., 2009). Many rhizosphere microbes are beneficial and decompose organic materials, perform mineralization and availability of nutrients and turnover processes.

The organic carbon secreted by plant roots is what forms, sustains and drives the rhizosphere web, a continuum of microbial populations colonizing niches from the plants interior and into the bulk

of the soil, responding to the plant, interacting with each other and impacting upon their environment. Within this continuum, the rhizosphere forms a transition zone between the bulk of soil and the plant root surface. Plant roots exert strong effects on the rhizosphere through rhizodeposition (root exudation, production of mucilage and release of sloughed-off root cells) and by providing suitable ecological niches for microbial growth (Bais et al., 2006).

Microbial communities in the rhizosphere form a subset of the total microbial community present in bulk soils. The quantity and quality of available carbon compounds originating from plants, as well as novel sites for microbial attachment discriminate rhizosphere from bulk soil (Curl and Truelove, 1986). Other parameters intrinsic to the plants' physiology, genetic makeup, life history and ecology, and soil itself, have major influences on the structure of rhizomicrobial communities, impacting on their spatial, temporal and functional components.

Rhizosphere microorganisms play important roles in the growth and ecological fitness of their plant hosts. Important microbial processes that are expected to occur in the rhizosphere include pathogenesis and its counterpart, plant protection, as well as the production of antibiotics, geochemical cycling of minerals and plant colonization (Kent and Triplett, 2002; Fulthorpe et al., 2008). Methods for isolation of microbes range from simple pure petri-dish isolations through spread, streak and exposure followed by enumeration by viable counts, turbid metric and direct microscopic counts to highly advancing molecular techniques (Durbin, 1961; Moreira et al., 2008). Most microbes cannot be recovered through cultivation *in-vitro* and more advanced molecular techniques show that the majority are non culturable (Goodman, et al., 1998; Donadio et al., 2002 and Sessitsch et al., 2012).

Many phytopathogenic organisms, bacteria and fungi, have evolved with plants and show high degree of specificity (Raaijmakers et al., 2009). This is exemplified by the rhizobial community associations with legumes, Frankia symbiosis and Azolla association with rice (Long, 2011; Beijerinck, 1988; van Rhijn and Vanderleyden, 1995; Schwintzer and Tjepkema, 1990; Peters, 1977); to mycorrhizal associations that are specific to non-specific (Brundrett, 2004).

The denaturing gradient gel electrophoresis (DGGE) analysis of 16S rRNA gene amplified from total community DNA of three crops, potato, oilseed rape and strawberry, all hosts of the soil borne pathogen *Verticillium dahlia*, revealed plant-species dependent pattern with the strawberry different from the two crops (Smalla et al., 2001). Alterations of rhizosphere communities have also been reported in cultivars of modern wheat cultivars which was dominated by fast growing Proteobacteria compared to old wheat cultivars dominated by rhizobacteria (Garner et al., 2003).

The structure of bacterial communities is strongly influenced by presence of roots with some microbes more specific and only associating with some specific plant species. Rhizosphere conditions sustain communities which differ from those found in bulk soils hence, these communities exhibit a rhizosphere effect (Curl and Truelove 1986; Lynch and Hobbie, 1988). There is higher bacteria population residing in the rhizosphere than the bulk of soil largely constituted by gram negative cells, more symbionts and strategists (Curl and Truelove, 1986).

The microorganisms have adaptive strategies resulting from selective environments to efficiently enable them utilize resources, time and energy effectively for survival (Atkins, 1980; Mathews and Mathews, 1987; Elzinga, 1977; Price, 1984; Horn, 1976). The two common adaptive strategies are the R strategy, which encompasses organisms that operate to maximize reproductive rates in harsh unstable and unpredictable environments, disturbance and competition. The r strategists have short life span, typically weak, reproduce rapidly and mature quickly, have high productivity, less energy efficient and prone to predation.

Recently few isolates belonging to Acidobacteria group and Verrucomicrobia were obtained from the rhizosphere of *Allium porrum* (Leek) and Potato (*Solanum tuberosum*). Although the knowledge of these two organisms and their roles in biogeochemical cycles is limited, their abundance and diversity suggests their potentially great ecological importance (Sevenson et al., 2004). Both bacterial phyla are underrepresented in microbial culture collections. Evidence with environmental genomics has demonstrated Acidobacteria to form a coherent but highly diverse group with capacity to

utilize organic carbon. Acidobacteria are difficult to culture with only few recovered from the bulk of soils (Janssen et al., 2002).

Similarly, Verrucomicrobia are ubiquitous, have ability to oxidize methane and occur in low frequency. Fast growing opportunists such as *Pseudomonas* dominate in the rhizosphere because of excess availability of nutrients with low nutrient availability in the bulk soil limits strategists (copiotrophs).

Oligotrophs will thrive in root zones exhausted in nutrients like older root parts and abundant under resource limited conditions (e.g. bulk soil) as opposed to Copiotrophs such as  $\beta$  proteobacteria which thrive under conditions of high resource availability (soils with labile rhizodeposited carbon) and high nutrient availability like root hair zones (Semenov et al., 1999; Gardner et al., 2001). Stress caused by nutrient limitations may be a common occurrence in the rhizosphere and it can be held responsible for the presence of a wide variety of physiologically different groups in this habitat. Isolation of bacteria from grass rhizosphere soil on low nutrient agar media (ten times diluted TSB and soil extract media) resulted in a recovery of a large diversity of gram positive and gram negative species, belonging to the Proteobacteria, Actinobacteria and Firmicutes (Nijhuis et al., 1993).

Bacterial communities in the rhizosphere are not static, but will fluctuate over time in different root zones, and bacterial composition will differ between different soil types, plant species, plant growth seasons and local communities (Semenov et al., 1999). Changes induced in the soil by the growing root provide additional niches for soil microbes. Soil types and growth stages are important factors in shaping rhizobacterial community structure (Latour et al., 1996; Marchner et al., 2004; Seldin et al., 1988; Herschkovitz et al., 2005; Lemer et al., 2006) and may be the strongest factor affecting bacterial communities in potato rhizosphere (Van Overbeck and Van Elsas, 2008); plant species (Grayston et al., 1998; Smalla et al., 2001) and even 'cultivar (genotype) within the same species (Van Overbeck and Van Elsas 2008; Andreote et al., 2009). The rhizosphere is a highly dynamic environment for bacterial communities with even small topographical landform changes can alter environmental conditions that may accelerate or retard the activity of organisms (Scowcroft et al., 2000; Barnes, 1998).

### **Dynamics of Rhizosphere Fungal Communities**

Fungi play a major role in the function and dynamics of terrestrial ecosystems, directly influencing the structure of plant, animal and bacterial communities through interactions that span the mutualism-parasitism continuum (Kabir et al., 2003). Fungi account for the bulk of microbial biomass either as saprotrophs or as mycorrhizae (Wain-Wright, 1988; Read and Perez-Morino, 2003). They are important in the carbon cycle and eliminating them results in a significant reduction in both carbon and nitrogen production from litter (Beare et al., 1992). Fungal hyphae account for the greatest fraction of soil biomass (Wardle, 2002; Taylor and Alexander, 2005) and are also major components of terrestrial food web with the mycelia the primary carbon source in a number of soil food webs and fruiting bodies as food source for human (Wardle, 2002).

Some fungi act as predators e.g. nematode-trapping fungi, but also trap, poison, parasitize and feed on other groups of soil invertebrates including targegrades, collembolan, copepods and rotifers (Thorn and Barron, 1984). They express this mainly on nitrogen-poor environments suggesting they seek nitrogen rather than carbon from their predation. Fungi indirectly shape the community dynamics of plants, animals and bacteria through a range of interactions. Particular assemblages (or communities) of mycorrhizal fungi are characteristic of each forest type (Cripps, 2004). They are the most common pathogens, causing serious crop loss and shaping the composition and structure of natural plant communities. Their functional roles in plant communities may be significant but often under-unappreciated pathways.

The nature of some fungi may change depend on the environment in which the interaction occurs (Johnson et al., 1997). The endophytic fungi which are ubiquitous inside the leaves, stems, and roots are good examples (Saikkonen et al., 2004) and for many their ecological roles are unknown (Arnold et al., 2007). These include the effect of different plant genotypes including transgenic

varieties. Plant growth stage affects rhizosphere fungal community and plant genotypes also have specific effects on the soil fungal community (Hannula et al., 2010).

The number of filamentous fungi species and total number of cultivable microorganisms showed tendency to decrease with increasing depth of soil. The total DNA was significantly higher in forest and abandoned land soil than agricultural land (Lelde Grantina et al., 2011). The amounts of *Trichoderma* spp. DNA was similar for all land use groups but its relative amount as % of total fungal DNA was high in meadow and arable land soil. Land use has a significant effect on the diversity of cultivable soil fungi and fungal DNA, soil depth and mosaic. The number of filamentous fungal species and total number of cultivable microorganisms showed tendency to decrease with increasing soil depth (Lelde Grantina et al., 2011 (Jurgensen, 2003) Nussel Tiedje, 199; McCaig et al 2001; Webser et al., 2002.; Clegg et al., 2003; Graystone et al., (2001)).

The mycorrhizal associations are being attributed to adaptation of plant life on land 400 million years ago (Simon et al., 1993). Many plants depend heavily on mycorrhiza for mineral nutrition and absence of appropriate fungi can significantly alter plant community structure (Weber et al., 2005). Although most mycorrhizal interactions are thought to be mutualistic, there are examples of mycorrhizal symbioses in which plants are parasitized by fungi (Johnson et al., 1997) or fungi are parasitized by certain plants e.g. non-photosynthetic plants (Bidartondo 2005). Other symbioses include lichens, some termites; attune ants, wood wasps, ambrosia beetle (Gurrie et al., 2003). Fungi also break down indigestible materials in return for a constant food source and a stable environment that is greatly pathogen free (Curie et al., 2003).

### **Plant-Microorganisms Rhizosphere Interactions**

The interaction between plants and microbes is essential for plant health and growth and important when aiming to combine high yields with farming practices which are environmentally friendly (Kloepper et al., 1992). Interactions with the rhizosphere, the part of soil which is highly influenced by the plant, are important (Soerensen, 1997). Composition, abundance and dynamics of microbial community in the rhizosphere play an important role and may have a positive or negative influence on plant growth, Microbes are essential for the mobilization of plant nutrients and may produce plant growth hormones which are important for plant development (Lynch, 1990), other organisms act as biocontrol agents and protect plants from phytopathogenic bacteria and fungi (Bashan and Holguini, 1998).

Anatoginists such as *Pseudomonas* may lead to natural suppression in soils of take all disease. *Pseudomonads* (*P. putida*) antagonistic to the soil borne fungal pathogen *Verticillium dahlia* were isolated from the rhizosphere of strawberry, potato and oil seed rape (Berge et al., 2002). The potato rhizosphere soil showed that pseudomonas (*P. chlororaphis*, *P. fluorescens*, *P. putida* and *P. syringae*) and serratia (*S. grimesii*, *S. plymuthica*, *S. proteamaculans*) antagonized *Plectobacterium carotovorum* (Formerly *Erwinia carotovorum*) and *Verticillium dahlia* (Lottman et al., 1999).

### **Land management and bacterial dynamics**

Microbial community can play a critical role in ecosystem function (Schimel, 1995; Schimel and Gullede 1998; Cavigelli and Robertson, 1999). Factors affecting shifts in microbial community structure have postulated changes in variables such as pH (Froslegård et al., 1993., Bååth, 1996., Blagodatskaya and Anderson, 1998., Bååth and Anderson, 2003., Steenwerth et al., 2003); nitrogen (Steer and Harris, 2000., Clegg et al., 2003., Gray et al., 2003., Girvan et al., 2004); soil physico-chemical characteristics (physical properties, tilling, pH, Carbon, nitrogen, phosphorus) (Groffman et al., 1996., Latour et al., 1996., Marchner et al., 2003., Schutter et al., 2001., Girvan et al., 2003) and plant community structure (Grayson et al., 1998., 2001; Methling et al, 200; Marchner et al., 2001; Smalla et al., 2001).

Distinct bacterial community compositions are obtained by molecular fingerprints in different root zones (Yang and Crowley, 2000). Based on DGGE analysis, soil bacterial diversity decreases with process of land degradation in Karst (limestone) derived soils (Zhang et al., 2006a; Xiangbi et al., 2012). The composition and diversity of soil bacterial community, based on RFLP and 16S rDNA

sequencing in a cropland, naturally vegetated land with former cultivation disturbance, and primeval forest in the subtropical Karst of Southwest China showed Proteobacteria to account for 44.8% followed by Acidobacteria and Planctinomyces compared to primeval forest, the proportions of Proteobacteria decreased by 30.2% and 37.9% while Acidobacteria increased by 93.9% and 87.9% and the Shannon Weiner diversity indices in physicochemical parameter, declined in cropland and revegetated land respectively.

Low molecular weight (LMW) compounds are released into soil in large quantities through root exudation (rhizodeposition) and via leaching of litter, and the inputs of these compounds have an important influence on both long-term and short-term C dynamics (Lynch and Whipps, 1990; van Hees et al., 2005; Hartman et al., 2009). Major types of low molecular weight (LMW) – compounds released from roots include simple sugars (e.g. glucose, fructose), amino acids (e.g. glycine, alanine) and carboxylic acids (e.g. citric acid and lactic acid) (Lynch and Whipps, 1990; Baudoin et al., 2003; van Hees et al., 2005; Hartman et al., 2009) many of which are readily metabolized by microbes.

The addition of LMW-C substrates to soil simulating root exudates or leaf leachates increased microbial biomass and CO<sub>2</sub> production and also caused distinct shifts in the composition of bacterial communities (Bernard *et al.*, 2007; Cleveland *et al.*, 2007; Peterson *et al.*, 2007 and Chen *et al.*, 2008) added microcosms containing three distinct soils from grassland, hardwood, forest and coniferous forest showed citric acid additions to influence bacterial communities that produce 2-5 fold increase in relative abundance of the  $\beta$ -proteobacteria. Whereas the assessment by molecular approach of fungal automated ribosomal intergenic spacer analysis (FARISA) of fungal biomass by necessary soil ergosterol showed addition of nitrogen (with or without lime) to decrease soil pH, fungal biomass and fungal type number with little corresponding change on fungal community.

The overall plant species composition was more affected through interaction between plant species and chemical treatments as opposed to changes in individual improvement factors. Fertilizer lime applications typically resulted in increased bacterial number and decreased fungal biomass (Lovell *et al.*, 1995; Kennedy *et al.*, 2005).

Fertilizer and lime applications typically result to increased bacterial numbers and decreased fungal biomass (Lovell *et al.*, 1995; Bardget *et al.*, 1999a, b; Brodie *et al.*, 2003). Fatty acid methyl esters (FAME) of soil microbial community under pasture showed a higher fungal: bacterial ratio compared to the soil under lettuce, potato, onion and broccoli. Soil under potato showed higher sum of fungal FAME indicators compared to broccoli, onion and lettuce. Microbial mass C and enzyme activities associated with pasture and potato were higher than other rhizospheres. The lowest activity was found in onion, forest, former agricultural land, meadow and arable land.

Increase of microbiological diversity and activity of soil as a consequence of organic fertilization is widely documented (Shannon *et al.*, 2002; Larkan *et al.*, 2006). Organic fertilization was found to have more determining effect on qualitative composition than number of soil fungi. Total number of fungal colony forming units in the soil fertilized with Biohum organic fertilizer at 10t/ha and 5t/ha showed a positive influence of organic fertilizer on the fungal community structure than with mineral NPK. The number of pathogens was limited to 1.2% in fields fertilized with the farm yard manure while the population of saprotrophic fungi possessing antagonistic properties increased (Ambrozak and Bowszys, 2009). Application of organic manure contributes to limiting some of the soil fungi development, including the pathogens *Pythium*, *Phytophthora* and *Fusarium* (Hoiting and Boehm, 1999).

Agricultural practices affect AM fungi communities both qualitatively and quantitatively (Sieverding, 1990; Miller *et al.*, 1995; Jansa et al., 2002; Oehl *et al.*, 2003). There is an interaction between micro-flora and plant species and also localized species and edaphic factors (Allen *et al.*, 1992; Allen & Allen, 1992). The mycorrhizal composition and diversity of spore communities as well as spore densities were affected by species identity of host plant, whereas the P fertilization and the history of the soil affected diversity of the spore communities (Mathimaran *et al.*, 2007). Introduction of leguminous fallow for a season into a conventional system of continuous maize (*Zea mays* L.) cultivation increased microbial diversity and biomass (Bunemann *et al.*, 2004; Bossio *et al.*, 2005).

## Bio-Prospecting for Beneficial Microorganisms and Biocontrols

There is great value in bio-prospecting for the soil organisms from the existing diversity. Novel traits in these soil organisms can be harnessed for drought tolerance, nutrient uptake, biopesticides, bioremediation, etc. Also the richness in traits can be transferred to root and tuber crops to sustain their production. This will include only the organisms or functional groups that associate or are beneficial to the root crops.

Tapping the potential of microbial diversity to improve tuber production systems is possible through adoption of already existing innovations that have been applied to other crops; based on knowledge of functions of specific groups and knowledge on possible similarities to closely related groups. It is possible to prospect and finally develop novel products and new discoveries of the vast diversity that is still under explored. The effectiveness to control diseases, improve nutrient cycling has been demonstrated under greenhouse conditions and could be further evaluated under field and farmer conditions for scaling up. Studies have been undertaken to bioprospect for microbial diversity that can eventually be used to improve nutrient cycling processes and control of pests and pathogens. The diverse realms of beneficial microorganisms in rhizosphere of tuber crops can be explored for use. Understanding the microbes in the rhizosphere of tuber crops is crucial for development of novel products.

### Microbial communities in rhizosphere of Yam (*Dioscorea spp.*)

Microbial communities are able to co-exist and the proportion of the organisms in the rhizosphere determines whether the relationship is either synergistic or antagonistic. In the rhizosphere of wild yams, *Dioscorea pentaphylla*, *D. wallichii*, *D. tomentosa*, *D. spicata*, *D. oppositifolia*, *D. intermedia*, *D. hispida*, *D. bulbifera* and *D. alata* in India had more bacterial populations compared to fungi and Actinomycetes (Channdrababu and Sobhana Raj. 2009). Distribution of gram (+) bacteria was more in the yam except *D. spicata* and *D. alata* which had the highest population of gram (-) bacteria. Soil physical and chemical factors and vegetation influenced the distribution of fungal and Actinomycetes colonies in the rhizosphere of wild species of yam. Distribution of fungal species in the wild yam showed *Aspergillus niger*, *Aspergillus fumigatus*, *Fusarium oxysporum*, *Mucor sp.*, *Mucor echinulatus*, *Rhizopus oryzae*, *R. stolonifer*, *Penicillium notatum* and *Penicillium sp.* as dominant. The Actinomycetes observed were *Wakesmania sp.* and *Micromonospora sp.*

Amongst the rhizosphere organisms, the fungal isolates *Achyla sp.*, *Aspergillus niger*, *Mucor spp.*, *Aspergillus fumigatus*, *Rhizopus oryzae*, *Memnoniella sp.*, *Cunninghamella spp.* have phosphorus solubilizing capacity. They interact with organic acids which dissolve insoluble phosphorus. *Mucor* had maximum solubilizing capacity. In another observation, Yam leaf spot disease in *Dioscorea cayennensis* Lam caused by *Curvularia eragrostides* (Henn) Meyer and *Colletotrichum geoeosporiodes* (Penz) is controlled by *Streptomyces thermotolerans*, *S. griseus* subsp *griseus* and *Streptomyces sp.*, (Ana Cristina Fermino Soares et al., 2006). The *Streptomyces spp.* produces secondary metabolites that inhibit the mycelia growth and spore germination of *Colletotrichum* and *Curvularia*.

There is a positive interaction between Actinomycetes and pathogenic fungi which is inhibitory to mycelia growth. A rhizobacteria, *Bacillus spp.* at the Yam rhizosphere is inhibitory against *Aspergillus niger*, *Rhizopus stolonifer*, *Curvularia lunata*, and *Fusarium solani* (Akrasi and Awuah, 2012).

In another study, microorganisms that can be used in post harvest storage rot have been studied. The principal organisms associated with rotting yam include: *Botryodiplodia theobromae* pat, *Fusarium oxysporum* Schlecht, *Penicillium oxalicum* Curies and Thom, *Aspergillus niger* van Tiegh and *Aspergillus tamari* Kita (Adeniji). The post harvest storage rot in yam, tubers, was reduced by *Trichoderma viride* pers. Ex. S. Grat and *Bacillus subtilis* (Okgbo and Nwakammah, 2005; Okigbo and Emeka, 2010, 2011). The potential of some bacteria and fungi as biocontrol agents of cassava and yam tuber rot pathogens under lab and greenhouse conditions include bacterial isolates *Pseudomonas sp.* (*Pseudomonas syringae* and *Pseudomonas chlororaphis*) *Xanthomonas sp.*, *Bacillus sp.* and the

fungi *Trichoderma harzianum* and *Penicillium oxalicum* as biocontrol agents of pathogens of cassava and yam tuber rot.

The arbuscular mycorrhizal fungi have also been evaluated for use as potential biofertilizers in micro propagated yam (Tchabi et al., 2010). An evaluation of temperate and tropical AMF on the growth of yam indicated tropical isolates of AM fungi to be more effective than temperate isolates with the temperate only efficient in P concentration. The African isolates *Glomus mosseae*, *G. hoi*, *G. etunicatum* and *Acaulospora scrobiculata* and *A. spinosa* increased *Dioscorea rotundata* tuber growth compared to non-mycorrhizal plants.

Nematodes are major pests of yam (*Scutellonema bradys*), root knot nematodes (*Meloidogyne* spp.) and the lesion nematodes (*Pratylenchus coffea* and *P. sudanensis*) Bridge et al., 2005. The AM fungi symbiosis has long been confirmed to control nematodes in other crops but the proven association of AM fungi with banana under natural conditions where improved growth was realized on inoculation with AMF (Declerck et al., 2002; Elsen et al., 2002., 2003; Lieselot et al., 2008., Tchabi et al., 2010). There is no proven evidence of control of pests in Yam as is the case in cassava yet there are many insects associated with Yam damage under field and storage conditions (Osagie, 1992).

### Microbial communities, opportunities and interventions for Cassava (*Manihot esculenta*)

The genera of fungi isolated from the rhizosphere of cassava include: *Aspergillus*, *Brettanomyces*, *Botrytis*, *Byssochamys*, *Doratomyces*, *Geotrichum*, *Gliocladium*, *Moniliella*, *Mucor*, *Monascus*, *Neurospora*, *Oidiodendron*, *Penicillium*, *Papulospora*, *Piricularia*, *Rhodotorula*, *Rhizopus*, *Saccharomyces*, *Cladosporium*, *Humicola*, *Trichoderma*, *Ustilago*, *Acremonium* and *Trichophyton* (Sule and Oyeyiola, 2012). The most common species associated with the rhizosphere include *Aspergillus flavus*, *Aspergillus fumigatus*, *Aspergillus niger*, *Aspergillus repens*, *Botrytis cinerea*, *Neurospora sitophila* and *Varicosporium elodea*, *Geotrichum candidum* *Byssochamys fulva* and *Papulospora coprophila* (13.1%). Table 6 shows the pathogenic and beneficial organisms and nematodes associated with cassava.

**Table 3: Pathogenic and beneficial microorganism and nematodes associated with Cassava**

Pathogenic fungi	Pathogenic bacteria	Pathogenic nematodes	Other non-pathogenic microbes
<i>Armillaria mellea</i>	<i>Ralstonia solanacearum</i>	<i>Helicotylenchus erythinae</i>	<i>Aspergillus clavatus</i>
<i>Botryodiplodia theobromae</i>	<i>Erwinia carotovora</i> subsp. <i>catotovora</i>	<i>Helicotylenchus dihystera</i>	<i>Aspergillus flavus</i>
<i>Cercospora caribaea</i>	<i>Xanthomonas campestris</i> pv <i>manihotis</i>	<i>Meloidogyne arenaria</i>	<i>Aspergillus niger</i>
<i>Cercospora henningsii</i>	<i>Xanthomonas campestris</i> pv <i>cassavae</i>	<i>Meloidogyne hapla</i>	<i>Aspergillus terreus</i>
<i>Cercospora vicosae</i>		<i>Meloidogyne incoginta</i>	<i>Aspergillus wentii</i>
<i>Colectotrichum gloeosporioides</i> f. <i>sp. manihotis</i>		<i>Pratylenchus brachyurus</i>	<i>Acremonium strictum</i>
<i>Cochliobolus lunatus</i>		<i>Rotylenchus reniformis</i>	<i>Brettanomyces bruxellensis</i>
<i>Elsinoe brasiliensis</i>		<i>Scutellonema bradys</i>	<i>Botrytis cinerea</i>
<i>Erisyphe manihotis</i>			<i>Byssochamys fulva</i>
<i>Fomes lignosus</i>			<i>Doratomyces stemonitis</i>
<i>Fusarium moniliforme</i>			<i>Geotrichum candidum</i>
<i>Fusarium oxysporum</i>			<i>Gliocladium catenulatum</i>

<i>Fusarium semitectum</i>			<i>Moniliella acetoabutans</i>
<i>Fusarium solani</i>			<i>Mucor racemosus</i>
<i>Leptoporus lignosus</i>			<i>Monasais ruber</i>
<i>Phaeolus manihotis</i>			<i>Neurospora sitophila</i>
<i>Phoma sp.</i>			<i>Oidiodendron griseum</i>
<i>Phytophthora drechsleri</i>			<i>Penicillium Chrysogenum</i>
<i>Rhizoctonia solani</i>			<i>Papulospora coprophila</i>
<i>Rosellinia necatrix</i>			<i>Penicillium digitatum</i>
<i>Sclerotium rolfsii</i>			<i>Piricularia oryzae</i>
<i>Corticium rolfsii</i>			<i>Penicillium thomii</i>
<i>Scytalidium lignicola</i>			<i>Rhodotorula glutinis</i>
<i>Sphaerostilbe repens</i>			<i>Rhizopus stolonifer</i>
<i>Uromyces sp.</i>			<i>Saccharomyces cerevisiae</i>

Amongst the insects associated with cassava are pests and the viral vectors: African cassava mosaic and its white fly vector (*Bemisia tabaci*); cassava mealybug (*Phenacoccus manihotis*) and cassava green mite (*Mononychellus progresivus*) and the vectors cassava bacterial blight which is the most important disease in Africa second to cassava Mosaic virus (CMV) disease (CIAT, 1996) and the pathogen *Xanthomonas campestris* pv *manihotis* which causes 13 – 50% loss (Wydra et al., 2001a). The pests, cassava mealybug, *Phenacoccus*; green mealybug, *Phenacoccus madeirensis*; the striped mealybug, *Ferrisia virgata*; Cassava green mite, *Mononychellus tanajoa*; variegated grasshopper, *Zonocerus variegates*; spiraling whitefly, *Aleurodicus disperses*; whitefly, *Bemisia tabaci* and termites may be controlled by the common IPM practices namely biological control, microbial control, and cultural control.

The natural enemies commonly found in cassava fields include several kinds of beetles, predatory mites, and tiny wasps. The tiny wasps are called “parasitoids”. Predatory ladybird beetles can also help to control cassava mealybug or cassava white scale. Predatory beetles are also sometimes seen feeding on cassava green mite, but the most important biological control agents of mite pests are predatory mites called “phytoseiids”. The predatory mites, *Typhlodromalus aripo* is the most effective against the cassava green mite.

Parasitoids such as the wasp *Apoanygyrus (Epidinocarsis) lopezi* are the most effective natural enemy against the cassava mealy bug, and it has controlled the pest in most of Africa. Another tiny wasp, *Encarsia haitiensis*, is a common natural enemy of the spiraling whitefly. The prospect of microbial biopesticides for control of pests is unlimited.

#### **Microbial communities associated with sweet potatoes (*Ipomoea batatas*)**

Plant growth promoting rhizobacteria isolated from the rhizosphere of sweet potatoes are *Pseudomonas corrugata*, *Serratia ficaria*, *Klebsiella terrigena*, *Erwinia cypripedii*, *Acinetobacter terrigena*, *Pseudomonas maculicola*, *Paenibacillus pabui* and *Pseudomonas fuscovaginae* (Yasmin et al., 2009). The genus *Pseudomonas sp.*, *Bacillus sp.*, *Klebsiella sp.*, *Azospirillum sp.* *Enterobacter sp.* *Serratia sp.* are all capable of producing Indole-3 acetic acid (IAA), a plant hormone for growth and development (Martens and Frankenberger, 1991; Frankenberger and Arshad, 1995). *Pseudomonas sp.* *Bacillus sp.* *Enterobacter sp.* and *Erwinia sp.* act as antagonists inhibiting growth of pathogens (Howell et al., 1988; Thomashow and Weller, 1988). *Pseudomonas* inhibited the growth of *Rhizoctonia sp.*, while *Serratia* and *Erwinia* inhibited the growth of *Pythium sp.* (Yasmin et al., 2009).

The major pests of sweet potato are:

1. Sweet potato weevil (*Cylas formicarius*) whose natural enemy is the fungus *Beauveria bassiana*. The disease is controlled by sanitation; flooding to drown weevil; hilling, routine irrigation and mulching to prevent soil cracks.
2. Sweet potato stemborer moth (*Omphisia anastomasalis*) which infests potato throughout the life time has natural enemies are Earwigs, ladybird beetles, ground beetles, rove beetles, ants and spiders. The pest is also controlled through management by the use of healthy planting materials, destruction of infested crop residues, rotation and the use of light traps.

There are still opportunities to explore natural enemies of

3. Leaf folders (*Brachmia convolvuli* and *Herpetogramma hopponalis*),
4. Horn worms (*Agrius convolvuli*)
5. Army worms (*Spodoptera exigua* and *Spodoptera litura*)
6. Tortoiseshell beetles (*Aspidomorpha elevate*).

Sweet potato is grown worldwide and it is a crop of interest to CIP. It has ability to grow on poor soils under drought conditions. Virus diseases of sweet potato have contributed enormously to decline in sweet potato production. The main diseases are transmitted by vectors and successful control of these diseases would be through vectors. The main viral diseases and their vectors are (1) Sweet potato feathery mottle virus (SPFV) (SP virus, SP chlorotic leaf spot, SP russet crack, SP internal cork) transmitted by aphid. (2) Sweet potato vein mosaic virus (SPVMV) (3) White fly transmitted Ipomovirus (Potyviridae) species, Sweet potato mottle virus (SPMMV) and the (4) SP yellow dwarf (SPYDV) (Bennett et al., 1995).

The sweet potato feathery mottle virus (SPFMV) is the most serious disease agent affecting resource poor farmers in sub-Saharan Africa. The current interventions to control SPFMV are heat treatment, meristem-tip treatment, naturally diseased materials removed (infected cuttings). The common diseases of sweet potato are also caused by fungi, bacteria and nematodes (Clark, 2007). The diseases include the Scab disease caused by the fungus *Elsinoe batatas*, the black rot disease caused by the fungus *Ceratocystis fibricata* and the Scurf pathogen *Monilochaetes infuscans*; diseases caused by the root-Knot nematode *Meloidogyne* spp. and reniform nematode *Rotylenchus reniformis*. The nematode diseases are mostly controlled by chemicals including fumigants such as dichloropropene and non-fumigant materials such as ethoprop.

The bacterial pathogen *Streptomyces*, bacterial root and stem rot pathogen *Erwinia chrysanthemi*, and *Fusarium oxysporum* f. sp. *batatas* cause rot disease. Other diseases known to cause post harvest damage are the soft rot pathogens *Rhizopus stolonifer* and *Rhizopus oryzae* and charcoal rot *Macrophomina phaseolina*. There are no biological interventions for these diseases. The pathogens and pests co-exist naturally with other microbes that regulate their populations.

#### **Microbial communities and pests associated with Potato (*Solanum tuberosum*)**

The emergence of new strains of *Phytophthora* and other pathogens and the repeated use of chemicals resulting in fungicide resistance to the pathogen metalaxyl (Daayf et al., 2003; Daayf et al., 2001) has increased the cost of crop production and search for an environmentally friendly pesticide in the market. There is still limited information on microorganisms associated with *Solanum tuberosum*. A recent study of rhizosphere bacteria associated with *Solanum tuberosum* isolated *Massilia* spp. *Chryseobacterium* spp. *Agrobacterium tumefaciens*, *Pseudomonas* spp and *Lysobacter* (Turnbull et al., 2012).

In separate study bacteria isolated from the phylloplane and/or rhizosphere of potato and canola plants were tested for ability to control the pathogen *Phytophthora infestans*. The bacteria *Bacillus*, *Pseudomonas*, *Rahnella*, and *Serratia* were all demonstrated biocontrol activity of *Phytophthora infestans* with the mechanisms of control including those occurring directly, through antibiosis and indirect through induction of plant defense systems. Organisms that induce systemic acquired resistance are also being explored. A pathogen – inducible defense mechanisms in plants is

being explored. Selected non pathogenic, root colonizing bacteria trigger a systemic resistance response as well. Wild plants unable to accumulate salicylic acid (SA) were responsive to *Pseudomonas fluorescens* WCS417 r-mediated induction of resistance (Pieterse et al., 1996).

Other studies associated with control of post harvest rot in potatoes showed *Sclerotium rolfisii* causing typical soft rot on potato tuber in Tunisia (Mejda et al., 2007). The biocontrol of stem rot of groundnuts caused by *Sclerotium rolfisii* occurred with inoculants of *Pseudomonas* cf. *monteilii* and indigenous *Pseudomonas* species (Rakh et al., 2011; Thahir basha et al., 2012) and this can perhaps be applied to control soft rot on potato tuber.

Insect pests associated with potato are the potato tuber moth, *Phythorimmaea opercullele*, the variegated grasshopper, *Zonocerus variegatus*, the noctuid moths, *Agrotis ipsilon* and *Helicoverpa* spp, and the whitefly, *Bemisia tabaci*. There is a transgenic potato cultivar containing a gene expressing toxicity from *Bacillus thuringiensis*, for tuber moth. This has however not been accepted for use.

#### Microbial communities and pests associated with Taro (*Colocassia esculenta*)

Diseases associated with Taro (*Colocassia esculenta*) are threatening the crop and in most places it is being replaced by cassava and sweet potatoes. The most common diseases are Dasheen mosaic virus (DsMV), Taro bacilliform virus (TaBV), Colocasia bobone disease virus (CBDV) and Taro Vein Chlorosis virus (TaVVCV), *Phytophthora colocasiae* which causes Taro leaf blight (TLB), soft rot by *Pythium* spp, Sclerotium rot by *Sclerotium rofsii* and the pests Taro beetle (*Papuana* spp.) and Taro leaf hopper (*Tarophagus prosperina*); Fusarium dry rot (*Fusarium solani*); Rhizopus rot (*Rhizopus stolonifer*), Black rot (*Ceratostyis fimbriata*); Sclerotium blight (*Sclerotium rolfisii*), Bacterial soft rot (*Erwinia* spp) and *Melodogyne* spp.

**Table 4: Pathogens, pests and diseases associated with Taro**

Pathogenic fungi and bacteria	Pathogenic nematodes and other pests (Insects and Snails)
<i>Athelia rolfisii</i> (Corm rot)	<i>Aleurodicus disperses</i> (spiraling whitefly)
<i>Cadosporium colocasiae</i> (brown leaf rot)	<i>Aphis gossypii</i> (Aphids)
<i>Lasiodiplodia theobromae</i> (spongy black rot)	<i>Bemesia tabaci</i> (Tobacco whitefly)
<i>Marasmiellus stenophyllus</i> (corm ad leaf rot)	<i>Hippotion celerio</i> (Hornworm)
<i>Neojohnstonia colocasiae</i> (orange leaf rot)	Family <i>Psedococcidae</i> (Mealybugs)
<i>Phoma</i> spp. (Shot hole)	<i>Papuana</i> spp (Taro beetle)
<i>Phytophthora colocasiae</i> (Taro leaf blight)	<i>Patchiella reaumuri</i> (taro root aphid)
<i>Pseudocercospora colocasiae</i> (Leaf blotch)	<i>Spodoptera litura</i> (Armyworm)
<i>Pythium</i> spp. (Corm soft rot).	<i>Tarophagus</i> spp. (Taro planthoppers)
	<i>Tetranychus</i> spp. (Spider mites)
	<i>Hirschmanniella miticausa</i> (Miti miti nematode disease)
	<i>Meloidogyne</i> spp. (Root knot nematodes)
	<i>Pratylenchus coffeae</i> (Leision nematode.
	Giant African Snail.

Carmichael et al., 2008.

Breeding efforts in Taro have had minimal attention with inception of breeding for disease in 1976. The control of diseases such as the phytophthora blight of yam is still by the use of Borax. Although a gene bank for Taro exists in India, genetic transformation is largely neglected with a few attempts made of *in-vitro* mutation breeding to generate novel plants and cell lines to improve production (Seetohul and Pucooa, 2005).

### Existing innovations

Yield losses in Africa and Brazil occur up to 20% in areas of high rainfall. In these areas, *C. henningsii* and *C. vicosae* cause upto 30% yield losses (Takatsu et al., 1990). Methods for controlling disease are predominantly through cultural methods such as quarantine, crop rotation and screening for resistant varieties. There are numerous microbial innovations for crop management but still few are applied to improve the production of tuber crops. Strategies to devise control exist and include (1) Epidemiological cycle (when the disease starts) (2) the biology of the pathogen (3) search for resistance (host reactions to parasite attack) (4) Epidemiology (5) possible control methods (improvement of crop nutrition, modification of the cropping cycle, improvement of quality of plant material) (6) production and distribution of resistance varieties (7) use of biotechnology and biological control, i.e. to control *Xanthomonas*, introduction into the genome of genes controlling the production of bactericides can be explored.

The biological control of Cassava Bacterial Blight (CBB) by *Pseudomonas* (Lozano, 1986) is one intervention already in practice with the application of *Pseudomonas fluorescens* and *P. putida* reducing the intensity of leaf spotting and leaf blighting. Other control measures that are in place are through (8) sanitation (clean planting material), (9) quarantine (limiting importation), (10) cultural measures to reduce CBB: crop rotation, weed destruction, planting near end of rainy season, pathogen free tissue derived plants, and pruning of infected shoots. (11) Resistant varieties: breeding for resistance - mechanisms appear to involve copious production of latex that contains various enzymes e.g. glucanase and lysozyme and the identification of emerging strains of *Xanthomonas* bacteria (IITA & CIAT).

Post harvest handling and storage of yam is a major challenge. Rotting starts from soil and manifests at storage (Ogawa et al., 1976). Methods of control are through direct application of borax, captan, sodium orthophenylphenate, thiobendazole and benomyl (Ogawa et al., 1976). Fungicides are heavily regulated in use and registration; they are expensive and can cause pollution, and cause resistant bacterial strains to emerge. Alternative methods are control through low temperature, curing, natural plant extracts e.g. *Azadirachta indica* and *Bacillus subtilis* and *Trichoderma* introduced as antagonist on the surface (Okigbo and Osuinde, 2003).

**Table 5: Some commercial arbuscular mycorrhizal products Worldwide**

Company	Country	Products
Agrauxine	France	Endorize standard (1)
Agrauxine	France	Endorize premium (2)
Mycorrhizal Application Inc	USA	Myco Apply Endo (3)
Mycorrhizal Application Inc	USA	Myco Apply Soluble Endo (4)
Mycorrhizal Application Inc	USA	Myco apply Endo Pus (5)
Mycorrhizal Application Inc	USA	Myco Apply Root Dip Gel (6)
Mycorrhizal Application Inc	USA	Myco Apply Maxx (7)
Mycorrhizal Application Inc	USA	Myco Apply Soluble Maxx (8)
Tftech	France	Mycor (9)
Dudutech (K) Ltd	Kenya	Rhizatech (10)
Nutri-Tech Solutions P/L	Australia	Vam- Tech (11)
Zander Middle East LLC	United Arab Emirates	Zander Mycorrhizae (12)

Arbuscular mycorrhizal fungi (AMF) and *Trichoderma* have great potential for use as biofertilizer and biocontrol agents in agriculture (Verkade and Hamilton, 1987; Bi et al., 2003., Cheng and Baumgartner, 2006). Tables 7, 8 and 9 show commercial production of AMF and *Trichoderma* practiced by the private sector worldwide (Gianninazi and Vosatka, 2004). Clean technologies such as the aeroponic production of AMF inoculums for cleaner spore production and physical substrate are an innovation that is currently in use (Shivom Singh, 2012).

### Potential innovations from breeding, production to consumption

There are not too many innovations on microbial and tuber crops such as the emerging innovations with biochar. Biochar can improve soil fertility and mitigate climate change (Lehmann et al., 2011). Biochar is used as a soil amendment for managing pathogens, used as inoculants carrier, manipulation experiment to sorb signaling compounds or toxins. Biochar improved microbial biomass and also resulted in significant change in microbial community composition and enzyme activities. Biochar resulted in decrease in mycorrhizal abundance. This is explained by nutrient availability reducing need for symbionts. There is lack of systematic appreciation of different biochar types and basic manipulative experiments that identify the interactions between biochar and soil biota.

**Table 6: Some Commercial Trichoderma products Worldwide**

Product	Strain	Company. Country
Topshield, Rootsheid	<i>Trichoderma harzianum</i> T-22	Bioworks, Geneva, N.Y.
T-22G, T-22B	<i>Trichoderma harzianum</i> T-22	TGT Inc. New York
T35	<i>Trichoderma harzianum</i>	Makhteshim-Agan Chemical Israel
Harzian 20, Harzian 10	<i>Trichoderma harzianum</i>	Natural Plant Protection, Noguerres, France
F-stop	<i>Trichoderma harzianum</i>	Eastman Kodak Co. United States TGT Inc., New York
Supraavit	<i>Trichoderma harzianum</i>	Bone gaard and Reitzel, Denmark
Solsain, Hors-solsain, Plantsain	<i>Trichoderma</i> spp.	Prestabiol Montpellier, France
ANTI-FUNGUS	<i>Trichoderma</i> spp	Grondontsmettingen De Ceuster, Belgium
Ty	<i>Trichoderma</i> spp	Mycontrol, Israel
GlioGard and SoilGard	<i>Trichoderma virens</i> ( <i>Gliocladium virens</i> )	Grace-Sierra Co. Maryland
Bip T	<i>Trichoderma viride</i>	Poland
Promot Plus WP Promot PlusDD	<i>Trichoderma</i> spp	Tan Quy. Vietnam
	<i>Trichoderma koningii</i>	
	<i>Trichoderma harzianum</i>	
TRiB1	<i>Trichoderma</i> spp.	National Institute of Plant. Vietnam
TRICO-DHCT	<i>Trichoderma</i> spp.	Can Tho University, Vietnam
NLU-Tri	<i>Trichoderma virens</i>	Ho Chi Minh University of Agriculture and Forestry. Vietnam
Biobus 1.00WP	<i>Trichoderma viride</i>	Nam Bac, Vietnam
Bio-Humaxin Sen Vang 6SC	<i>Trichoderma</i> spp.	An Hung Tuong, Vietnam
Fulhumaxin 5.15SC		
Biosaprk Trichoderma	<i>Trichoderma parceramosum</i>	Biospark Corporation, Phillipines
	<i>Trichoderma pseudokoningii</i> , and Ultraviolet	
Trichotech	<i>Trichoderma</i> spp	Finlay International Kenya Ltd. Dudutech, Laboratory
ECO T/T22	<i>Trichoderma harzianum</i> strain Rifai KRL AG2	PHP Ltd., South-Africa

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The potential innovations of microorganisms are enormous and transcend far beyond root and tuber crops. Due to concerns of impacts of synthetic pesticides on the environment and occurrence of herbicide-resistant/tolerant weeds, much interest has developed in exploiting microorganisms for weed management. The potential of deleterious rhizobacteria (DRB), which are non-parasitic rhizosphere bacteria that aggressively colonize plant roots has been shown to biologically control weed seedlings (Kremer and Kennedy 1996). Bacteria from rhizosphere of potato tested for potential to suppress

weeds: *Klebsiella planticola*, *Enterobacter taylorae*, *Pseudomonas paucimobilis*, *Enterobacter* sp., *Flavobacterium* sp.

### Geographic and Habitat Factors Controlling Prevalence and Distribution

In cassava, the angular leaf spot disease, caused by *Xanthomonas campestris* pv. *cassavae* is common in East and South Africa (Onyango & Mukunya, 1982 and Janse & Defranq, 1988). The soft rot of stems and roots is caused by *Erwinia carotovora* ssp. and was common in DR Congo and central Africa (Daniel et al., 1981). Fungal disease of the brown leaf spot (BLS) caused by *Cercosporidium henningsii* Allesch- is a fungus which affects both cassava and sweet potato (Golato, 1963; Powell, 1968, 1972, Golato and Meossi, 1971). In Brazil, brown large spot (BLS) is caused by *Cercospora vicosae* which has a worldwide distribution and occurs in most cassava fields in lower canopy of crops of more than 5 months old.

The White leaf spot (WLS) is caused by *Cercospora caribaea* Cupp & Cifferri which is less common than BLS, and occurs in cooler conditions (all ecozones in West Africa) and at 1% in the dry savanna to 62% of the rainforest zone (Wydra and Msikita, 1998). Diffuse leaf spot (DLS) is caused by *Cercospora vicosae*. It has a worldwide distribution and occurs in warmer and wetter climate areas where BLS is also common like in Brazil and Colombia (Lozano and Booth, 1976) and West Africa (Theberge, 1985). It is the most widely occurring leaf spot disease in west Africa and occurs at 97% in the mountain zones compared to 79% in the lowland rain forest zone.

The ring leaf spot (RLS) causal agent is not known but a number of fungi have been identified such as *Phyllostica* spp. and the now accepted *Phoma* spp. (Lozano and Booth, 1976) more common in Latin America (Viegas, 1943; CIAT, 1972) and reported in India (Ferdinandodo et al., 1968) and Africa (Vincens, 1915) commonly at high altitude. Less serious diseases are the Ash disease caused by *Oidium manihotis* Henn., a powdery mildew disease. It is widespread, with a common occurrence, and is less damaging (Ferdinando et al, 1968; Lozano and booth, 1976).

Fungal diseases of the stem include Anthracnose caused by *Glomerella manihotis* Chev. and *Colletotrichum gloeosporioides* f. s. *manihot.* Henn. (Penz. Sacc. The perfect state occurs worldwide in wetter areas` in Latin America (CIAT, 1972, Lozano et al. 1981) in West Africa (Chevaugeron, 1950, Affran, 1968; IITA, 1972; Akonumbo and Ngeve, 1998). Disease severity is greatest in the lowland rain forest and wet savanna zones and lesser in the drier ecozones (Wydra and Miskita, 1998). Disease facilitated by *Pseudothraupis devastans* insect that punctures the stem (Boher et al., 1983). *Glomerella* stem rot common in cassava cuttings and is caused by *Colletotrichum* sp. and *Glomerella cingulate*; *Botryodiplodia* stem rot also in cassava cuttings and caused by *Botryodiplodia*. It is frequent in Nigeria, Benin and Cameroon (Afouda and Wydra 1996; 1997); rust in Cassava caused by *Uromyces* sp. It is common in Brazil and Colombia and other parts of the world but common in South America (Normanha, 1970; Lozano et al., 1981); Super elongation disease caused by *Elsinoe brasiliensis*, and causes considerable losses. It is prevalent in the wet season.

Fungal diseases of the root caused by *Phytophthora* spp which also occurs with *Pythium* spp. and *Fusarium* spp is a worldwide problem and occurs in the wet season causing root damage such as soft rots of cassava roots. White thread root disease of cassava is common and widespread in Africa and less common in Latin America. It is caused by *Fomes lignosus* (Klot) Bres and is a problem where cassava is planted immediately after forest clearing or near a virgin forest. The fungus has a wide range among the woody species in the humid tropics. *Sclerotium* root rot caused by *Sclerotium rolfsii* Sacc is common in tropical soil in the humid tropics of west Africa. This is the most common disease of roots (Afouda et al., 1995) and affects older plants and also young cuttings (CIAT, 1972; Martin, 1970).

Dry root rot caused by *Rosellinia necatrix* (Hartig) Berl. and *Armillariella mellea* (Vahl) Pat. or by both fungi are more widespread and occur in moist soils high in organic matter. The pathogen has wide host range amongst woody perennials and attacks cassava after forest clearing. It is not regarded as a serious problem though reported to have lost specialization (Mwenge et al., 1998). Other root rot fungi, *Fusarium moniliforme* Sheldon, *Fusarium oxysporum* Schlecht, *Fusarium semitectum*

cause rot of storage in Benin, Nigeria and Cameroon (Osai and Ikotun 1993; Afouda and Wydra, 1996; Msiskita et al., 1996).

Nematodes associated with cassava roots multiply in large populations on cassava and cause insignificant damage (Hogger, 1971, Caveness, 1980; Mcsorley et al., 1983). The nematode species with the greatest effect on cassava production are the root knot nematodes *Melodogyne incognita* (Kofoid and White) Chitwood, *Melodogyne javanica* (Treub.) Chitwood (da Ponte et al., 1980; Nwauzor and Nwanko, 1989); the Lesion nematode *Pratylenchus brachyurus* is the second most important nematode affecting cassava. They are common in most parts of the world and *Helicotylenchus erythrinae* (Zimmerman) Golden.

There is still limited information on the biogeographical distribution of microorganisms, biocontrols and pathogens associated with tuber crops.

An understanding of the vectors that spread CBB, *Bemisia tabaci* and variegated grasshopper (*Zonocerus variegatus*) which spread the bacterial blight is crucial. The biological cycle of the bacterial blight and arthropod pests is related to direct influence of the seasonal climatic factors of temperature, relative humidity, rainfall and wind. There is a correlation between rainfall and development of CBB (Daniel and Boher, 1985), green mites and cassava mealybug as was demonstrated in Congo. Blight epidemics occur in the rainy season and arthropod populations are enhanced by the dry season conditions (Fabers, 1981).

The African mosaic disease epidemics are determined by the interaction between rainfall and temperature (Fargette and Thress, 1994). In Congo, temperature has been shown to influence the biological cycles of cassava mealybug (Le Rü and Fabres, 1987) and associated entomophagous organisms. Intra-specific variability of cassava and crop-pest interaction influence plant physiology as affected by agricultural features. There is a relationship between cassava growth, climatic factors and development of epidemics of African mosaic disease (Fargette and Vié 1994). The effect of varied cultural practices on the biological cycles of bacterial blight guides the (1) design of cultural operations, planting dates and methods, soil cover and irrigation (2) provides assistance to breeders by demonstrating natural plant mechanisms for resistance to the mealy bug (Tertulianor, 1993).

Other interventions emanating from a clear understanding of the biological cycles: Entomophagous organisms (parasitoids and/or predators) of mites, variegated grasshopper, whitefly and mealybug. Studies on mealybugs considered indigenous Coccinellidae predators (Fabres and Kiyindou, 1985) an exotic parasitoid (*Epidinocarsislopezi*) introduced continent wide in an acclimatization campaign by IITA (Biassangama et al., 1988). Each entomophagous organism is potential means of biocontrol of pest populations. The ecological approach to biological regulation enabled integration of exotic entomophagous organisms to become a new regulatory factor and to measure the impact of indigenous beneficial organisms. Understanding the tritrophic plant mealybug-parasitoid relations is crucial (Herbrecht, 1993). This can be translated to understanding of parasites-parasitoid ecological approaches to biological cycles.

Disease and pests impose a severe selection pressure on cassava, as susceptible genotypes are eliminated as a consequence of direct damage by the pests or disease, for which they are propagated compared with resistant cultivars. The scale of genotype turn-over is likely to be highly variable among pests, periods and regions, as it would primarily be dependent of the intensity of the attack, the length of the previous period of co-evolution and the extent and variability of the gene pool available (Nweke, 1994). Climate change introduces new trends in disease and pest epidemics. An understanding of the dynamics of pests and their predators in relation to climate is crucial for sustainability in crop production.

### **Breeding for resistance to pest and nutritional values**

Cassava has many pathogens and pests reducing yield in Africa (Dixon et al., 2003; Oerke, 2006). Cassava breeding started in the 20<sup>th</sup> century as a result of population increase and demands. Breeding concentrated on developing high yielding varieties in marginal and pest prone environments. In Africa breeding has transformed cassava from a poor man's food to urban food and in Asia from subsistence to an industrial crop. Increase in yield of up to 40% has been realized through breeding.

In early days clonal selection was the dominant method for cassava improvement. In Amani, Tanzania, Storey and Nicholas (1938) hybridized the wild species *Manihot glaziovii* with cassava to produce clones resistant to cassava mosaic disease (CMD). The clones were also very productive and drought tolerant (Otim-Nape, 1993) and are still maintained in Amani and used by breeders at IITA Ibadan as a source for resistance to CMD (Phillips and Wolf, 2005). In the 1950's, the Instituto Agronomico de Campinas (IAC, Brazil) identified potential sources of new cultivars which were selected on the basis of their productivity and resistance to disease and insects.

Natural hybridization normally occurs between cultivated cassava clones and wild species in Brazil (Nassar, 1984; 1989). The progeny seedlings of the natural clones grow simultaneously and some of them are selected by farmers and reproduced vegetatively giving rise to new clones. The clones grown in commercial plantations are subject to selfing and inbreeding due to monoculture system of plantations (Nassar and O'Hair, 1985). Emerging homozygous plants have wild genes introgressed to their genomes. This cycle of hybridization is repeated in nature and inbred clones are enriched by highly adaptive genes of wild species brought to cultivation by farmers. These clones were used by IAC in their combining ability trials and are now amongst the most successful clones in Brazil.

Cassava breeding started in CIAT in the 1970's with the aim of extending benefits of the Green Revolution to the less privileged cassava growers in Asia and Latin America (Kawano, 2003). Wild manihot species were collected from South America and Mexico, thoroughly evaluated and hybridized with cultigens in order to incorporate useful genes for high protein content, apomixes, tolerance to drought, resistance to bacterial blight and high yield into cultivars (Nassar, 1999). Hybridization continued by overcoming interspecific barriers and breaking seed dormancy using different methods and techniques (Nassar *et al.*, 2000).

Genetic enhancement produced trisomics as well as triploid and tetraploid hybrid clones (Nassar *et al.*, 1996). This was used by IITA to breed high yielding TMS cultivars which contribute to agricultural food security especially among the poor (Nweke *et al.*, 2002). The highest world yields of cassava were produced by the central tuber crops research institute, India (CTCRI) with productivity of cassava increasing from 7.2t /ha in 1961 to 26.9t/ha in 2000 and South America, it dropped from 13.8t/ha to 12.8t/ha in the same period (FAO, 2003). Knowledge in Integrated Soil Fertility Management (ISFM), associated microorganism, biocontrol agents, biopesticides, and bio-fertilizers in relation to new cultivars is still lacking.

Biological control for cassava was the main research undertaken in the first 15 years of IITA, and resistance breeding was the most frequently used method for combating disease and insect pests. In the 1970's biological control studies were conducted together with breeding – to combat cassava mealybug and cassava green mite (Neuenschwander, 2001). Predator *Anagyrus lopez* was introduced to control mealybug (Norgaard 1988; Zedder *et al.*, 2000; Neuenschwander, 2004). This was followed by research on the control of cassava green mite by Mégevand *et al.*, (1987) who identified predatory mites (*Typhlodromalus aripo* and *T. manihoti*) and later an acaropathogenic fungus (*Neozygites tanajoae*) from Brazil (Nassar and Ortiz, 2006).

Recently studies on the cultivar TMS 30572 have indicated a reduction of fungal population in the soil, other benefits such as improvement in soil pH, water holding capacity, inhibition of some genera which could be pathogenic and stimulation of some fungal species and increase in diversity of fungal species (Sule and Oyeyiola, 2012).

### **Transgenic approaches**

Current cost of crop protection stands at a value of \$31 billion annually (Janier, 2007). The use of insect –resistance transgenic crops for pest management has great potential. Pest associated losses are estimated at 14% of the total agricultural production (Oerke *et al.*, 1994) and may be controlled using transgenic methods. Insect pests, diseases, weeds can cause estimated losses of up to 42%. Crop production losses caused by insects are approximately \$90.4 billion, disease \$76.8 billion and weeds \$64.0 billion. Insects cause direct loss but also act as vectors of various plant pathogens.

Extra cost in the form of insecticides applied for pest control is currently valued at US 10 billion annually.

The application of pesticides has adverse effects on beneficial organisms; leaves pesticide residue in the food chain, causes environmental pollution. Insects develop resistance to insecticides i.e. the green peach/potato aphid. This explains why transgenic plants can play a major role in integrated pest management (Sharma et al., 2002a, Sharma and Crouch 2004).

The Colorado potato beetle is the most destructive chewing pest of potatoes on a worldwide basis and occurs in most parts of the US and has spread to Europe and Asia (Selton et al., 2002). It was only the Monsanto new leaf varieties, which expresses the Cry3 A properties for the control of potato beetle that were registered after being approved in 1995. However, it is limited in production due to market concerns of Genetically Engineered foods and because of foliar insecticide, Imidacloprid which was introduced as an alternative to Bt potatoes. The transgenic Bt potato-expressing proteins from the bacterium, *Bacillus thuringiensis* is no longer in use and Monsanto stopped its marketing. This poses some challenges in the use of transgenic methods in tuber crops.

Plants can influence the composition of microbial rhizosphere community by several mechanisms: Root exudates (rhizodeposition) (Lynch and Whipps, 1991) and release of at least 30 – 60% of carbon dioxide bound photosynthesis to the rhizosphere by roots (Soerensen, 1997). Genetic modification of crops might result in altered root exudation or root morphology or release of antimicrobial substances. Comparing 16S and 18S – rDNA DGGE finger prints from the different bulk soil showed no significant differences between two cultivars of potato and transgenic lines in the microbial community. Similar results were obtained for rhizosphere samples, using eubacterial, and  $\alpha$  and  $\beta$ -proteobacteria and fungal specific primers with the exception of the eubacterial DGGE patterns obtained for the rhizosphere SOLANA. There is still limited information on the effect of transgenic crops on rhizosphere microorganisms.

*Trichoderma* strains induce resistance in plants (Annette Millig et al, 2004). They produce and induce resistance in plants by producing ethylene, hypersensitive response and other defense related reactions. Transgenic plants with the introduction of endochitinase gene from *Trichoderma* into plants such as tobacco and potato plants have increased their resistance to fungal growth. Selected transgenic lines are highly tolerant of foliar pathogens such as *Alternaria alternate*, *A. solani* and *Botrytis cinerea* as well as the soil-borne pathogen *Rhizoctonia* spp.

The transgenic *Trichoderma* spp. has recombinant nucleic acid molecules encoding bioactive molecule. It also relates to methods for controlling plant disease that involve applying a transgenic strain of *Trichoderma* spp. to plant seeds where the transgenic strain of *Trichoderma* spp. has a recombinant nucleic acid molecule encoding bioactive molecule that is capable of controlling plant disease and conferring systemic disease resistance to the plant or plant grown from the plant seed.

Annette Millig et al., (2004) studied the effect of a transgenic potato line (SIBU S1) on composition of bacterial and fungal diversity in the rhizosphere. The transgenic line was modified by RNA antisensing and was compared to non-transgenic parental cultivar (SIBV) and non transgenic cultivar (SOLANA). Using *Pseudomonas* specific primers – differences were found between the rhizosphere patterns of the transgenic line (SIBU S1) and parental cultivar (SIBV). Clear effects of the cultivar SOLANA and SIBU on the structure of *Pseudomonas* community were detected. The use of IPM in complex farming systems and breeding for host plant resistance in IPM is an alternative. The roles of genetic resources in IPM by use of biological control of insect pests on IPM context and host plant-insect parasitoid interactions are proposed as the best option. (Sharama and Francis, 2008).

## V. FUTURE PROSPECTS

### Lessons learned

This report has highlighted many opportunities and challenges that need addressing in order to better integrate root and tuber crops with soil organisms. For example: CIP has a collection of sweet

potato with over 8,000 accessions, potato (over 7,000 accessions), that include native and wild species. The CIP genebank holds over 80% of the world's native potato and sweet potato cultivars and over 80% of the known species of wild potato. It also maintains more than 1,500 accessions of native Andean root and tuber crops (ARTCs). Likewise, there are a number of networks and organizations that focus on cassava research and development, or include cassava among other commodities. This rich resource needs to be exploited by researchers and breeders to produce traits that are disease resistant as well as being highly productive. As has been presented, use of soil organisms to control pests and diseases is an opportunity that needs to be exploited to the fullest. Symbiosis for productivity enhancement needs also to be fully exploited.

In the early 1970s, the International Center for Tropical Agriculture (CIAT) launched a major initiative to collect and conserve cassava landraces. Today, CIAT's collection at Cali, in Colombia, is the world's largest, containing about 5 500 landrace accessions. The collection is maintained in a tissue culture laboratory, and a back-up *in vitro* collection is held at the International Potato Center in Lima. CIAT has created a "core collection" of about 630 accessions that represents the wide genetic diversity found in the main collection and is used for intensive characterization and genetic analysis. A duplicate of the core collection is maintained in Thailand, both *in vitro* and in the field. The International Institute of Tropical Agriculture (IITA) in Ibadan, Nigeria, also has an important cassava genebank of some 2 800 accessions, collected mainly in West Africa. The largest national collection, of 2 900 accessions, is held by the Brazilian Agricultural Research Corporation (EMBRAPA). Other major collections, totalling 7 200 accessions, are held by Benin, India, Indonesia, Malawi, Nigeria, Thailand, Togo and Uganda (Figure 12). Most other cassava-growing countries have established a genebank of local landraces and improved varieties; although little documentation is available on many national collections IITA also has collections of yam (3200 accessions).

As the production of the root and tuber crops is expanding, it is important to use production technologies which secure a safe and clean environment and one that minimizes use of synthetic chemicals in production. Many opportunities exist for research on how best to integrate soil organisms in the production of the crops, both as bio-fertilizers as well use as bio-control agents (BCAs). Transgenic methods can be used to control insect pests by introducing genes into plants that cause resistance to the insect pests. This method is not in use for root and tuber crops at present.

Co-existence of the root and tuber crops with soil organisms in mutualistic, proto-cooperation, commensal, neutral, antagonistic, predatory and parasitic relationships can be used to explore further how best to utilize these associations for the root and tuber crops. Biological methods where used have provided alternative, safer control methods for pathogens, pests and weed control. However developing BCAs is labor intensive and is an opportunity that can lead to job and wealth creation because of the numerous niche markets they would have to satisfy if chemicals were to be phased out

### **Possible Future Research and gaps in scientific knowledge**

This report demonstrates the importance of soil microbes in regulating the Earth System. However, the scope of quantifying the roles of microbes is limited by the following:

1. Inadequate diversity assessment tools and knowledge- most of soil microorganisms cannot be cultivated with conventional methods. Less than 10% of the actual soil microbial biodiversity is usually represented as cultured organisms and molecular gene sequencing techniques are only just becoming available to determine the genes and processes they program in the remainder of the microbial population (Sutherland et al 2010).
2. Lack of clear bio-geographical patterns - while plants and animals show clear taxa-area relationships and biogeography, microorganisms are believed to lack dispersal limitations which ensure a global distribution and that local deterministic factors determine the relative abundance of "latent" and "flourishing" species. These views could also be biased due to inability to assess diversity and abundance. There is need therefore to take an inventory of the relationship between the soil organisms and the root and tuber crops to establish the types and

nature of associations that exist and from that determine the beneficial and how they should be managed.

3. Inability to link diversity to function. Assessing biological ecosystem function relationships requires the connecting of individual microbial species to the biogeochemical processes they catalyze. However, the problems in defining relevant ecological units, the metabolic versatility, the large number of unknown species, the interrelatedness of organisms, makes the objective quite difficult and challenging. The majority of studies have relied on correlating changes in activity to changes in community composition or diversity, and only a few studies actually show a causal relationship (Emmerling *et al.*, 2002).
4. We have discussed in chapter 2 the communication between soil organisms and the host plant. However, the type of communication and how it manifests between the organism and the host plant is still unclear for the root and tuber crops. However new molecular genetics are making it possible to unravel the processes that occur when soil micro-organisms interact with their environment including their host plants and pests and diseases of those plants.

The relatively new disciplines of *genomics*, *proteomics* and *metabolomics* and associated microarray technologies that have enhanced throughput in bio-prospecting geared towards discovering novel properties and products from microorganisms, offer new opportunities for mapping the type of communications and other interactions that exist between the microorganisms and the root and tuber crops. Application of these technologies in developing countries will require support for equipment, operating costs and training.

5. Lack of knowledge of functional redundancy, resistance, and resilience of microbial communities. Many species of microorganisms carry the same function ensuring stability of the process when species populations change or are temporarily inactive.
6. Inability to quantify the activities and presence of microorganisms in soil makes it difficult to use them as indicators of soil health. Agronomic practices may influence soil microorganisms positively or negatively depending on the environmental requirements of the organism. As the good agricultural practices are developed this is usually done without considering the effects on soil microbial biodiversity.

In this regard, there is yet a lot of work ahead to gain a better understanding of the diversity of soil biological components, how they function and how they in turn affect the environment and their host plants. Bio-control can occur when non-pathogens compete with pathogens for nutrients in and around the host plant.

Direct interactions that benefit one population at the expense of another also affect our understanding of biological control. In the process of antibiosis, the antibiotics or metabolites produced by one organism inhibits another organism. For example, *Bacillus* species from soil produce an antifungal agent which inhibits growth of several soil fungi some of which may be beneficial for crop growth. Most of the commercial antibiotics such as streptomycin, chloramphenicol, terramycin and cyclohexamide were produced from the mass culture of *Streptomyces*, a soil bacterium.

### **Strategic partnerships-North-South and South-South cooperation**

1. In the same way flora and fauna are conserved in herbaria and nature reserves respectively, microorganisms apart from being maintained in their natural environment, need to be isolated and kept in their own gene banks and or collection centres as is happening in many developed countries. Those identified should have type cultures in collection centres. This has happened mostly in the developed countries. Access to cultures of microorganisms, cell lines, and genetic material, is an essential requirement for the conduct of microbiology and related disciplines. In developing countries, microbiologists working in industry, quality assurance,

human, animal, and plant health, research, and education are disadvantaged compared with those in most developed countries. Some of the microbial culture collection centres in the world are:

- a. American Type Culture Collection (ATCC), USA
  - b. Bioresources Collection and Research Centre (BCRC), Taiwan
  - c. Collection of Aquatic Important Microorganisms (CAIM), Mexico
  - d. Culture Collection of Algae and Protozoa (CCAP), UK
  - e. Marine Biotechnology Institute Culture Collection (MBIC), Japan
  - f. Microbial Type Culture Collection and Gene Bank (MTCC), India
  - g. National bank for Industrial Microorganism and Cell Cultures (NBIMCC), Bulgaria
  - h. National Collections of Industrial, Food and Marine Bacteria (NCIMB), UK
  - i. Agricultural research Service Culture Collection (NRRL), USA
2. In this regard, there should be the establishment of North-South collaboration to enable the access to microorganisms by scientists in the developing countries along with the information on their functions. Mechanisms for the transfer should be arranged and microorganism transfer agreements (MTAs) signed between the countries and the laboratories. Long-term *ex situ* conservation of microorganisms in microbial gene banks will ensure their availability (a) for future use in screening, genetic improvement, characterization and the production of desirable end-products (b) if their natural environment is destroyed (c) and ensure the integrity of representative cultures derived from bio-prospecting to meet current and future needs. *Ex situ* conservation of cultures will encompass a wealth of knowledge concerning species diversity, metabolism, genetics, epidemiological and evolutionary diversity. National infrastructure funding and legislative protection should be in place to ensure the long-term continuity and security of these microbial diversity collections. The developing countries should also provide budgets to establish such facilities in their own countries to avoid being left behind and to also preserve and conserve their own genetic resources.
  3. Microbiologists in developing countries are often disadvantaged by delays in obtaining cultures from overseas caused by stringent quarantine restrictions. Setting up culture collections of microbial resources within regions will go a long way towards solving the problem. FAO could provide a neutral forum to enable its Member States to discuss such possibility.
  4. Effective and timely use of microbial resources requires quality data and information. Such data enables rational decisions to be made concerning use and conservation of microbial biodiversity. In most developing countries, such information is kept in different forms and often dispersed through different departments within the government, research institutions and universities. Establishment of an electronic access microbial information resource centre, to maintain a database, would provide linkages between users, stakeholders and international partners.
  5. Though most countries are signatories to the Convention on Biological Diversity, it is necessary that each country should have an appropriate legal framework and deliberate policy for the exploitation and sustainable utilization of microbial resources as well as addressing intellectual property rights and safeguarding the nations against potential risks that may be posed by living modified organisms (LMOs) resulting from modern biotechnology. This will set the guidelines and action plans towards the realization of the overall goal of harnessing microbial resources for improving the livelihoods of the people.

6. Creation of partnerships and networks essential in pulling together the required scientific technical and financial resources. Initiatives such as New Partnership for African Development (NEPAD), ASARECA, Africa Bioscience Network, BIOEARN, EU-LAC (European, Latin America and Caribbean) joint initiatives for research, collaboration supported by Gates Foundation are examples. However, more North to South collaborations would overcome such challenges as financial and technology transfer is made possible.
7. Individual governments must take a lead in investing in conservation and utilization of microbial resources. Investment in microbial technology is expensive and so governments should establish partnerships with local and international industry, international funding agencies and NGOs to raise funds.

## VI. THE WAY FORWARD

This report has reviewed current science-based information on the importance of soil biota including micro and macro-organisms, as well as biological control agents and pathogens – and their contributions to ecosystem services/functions that would contribute to sustainable intensification of root and tuber production systems. The biota constitute a significant living community in the soil system offering a wide range of crucial services considered vital for the sustainable functioning of ecosystems and continued root and tuber production and agricultural productivity in general. Because synthetic insecticide, fungicide and herbicide disrupt the natural crop ecosystem balance, it is important to minimize their use to the extent possible. Hence, the first line of defense against root and tuber crop pests and diseases is a healthy agro-ecosystem. It promotes instead integrated pest management, a crop protection strategy that aims at enhancing the biological processes and crop-associated biodiversity that underpin production. In this way, crop losses to insects are kept to an acceptable minimum by deploying resistant varieties, conserving and encouraging biological control agents, and managing crop nutrient levels to reduce insect reproduction. Diseases are controlled through the use of clean planting material, crop rotations to suppress pathogens, and elimination of infected host plants. Effective weed management entails timely manual weeding and the use of surface mulches to suppress weed growth. The development of sustainable agro-ecosystem and the enhancement of root and tuber crop productivity will increasingly depend on the maintenance of below and above ground diversity that provide ecological services such as soil health and fertility enhancement, crop pollination, and biological control of pests.

### **Policies interventions that sustain soil micro-organisms, biological control agents and pathogens**

From this review, it is clear that there is a place for the utilization of soil organisms in the production, yield enhancement, disease control and for establishing a clean environment and a healthy soil in the production systems of root and tuber crops. Mechanisms of symbiotic co-existence of the root and tuber crops with soil organism such as in mutualism, proto-cooperation, commensalism, neutralism, antagonism, predation and parasitism, should be used to explore further how best to tap the benefits of these associations. Biological control methods promise to provide alternative safer methods to the use - instead of synthetic chemicals - for pathogen, pests and weed control.

Sustaining soil micro-organism, biological control agents and pathogens for sustainable intensification of root and tuber production systems calls for political commitment, investment and institutional support.

**Policymakers should begin with an inventory** of the soil micro-organisms and the root and tuber crops that they are associated with. This needs immediate attention as a first step before moving into the next steps of investigating further on the issues presented in section 5.

While there is no “one-size-fits-all” set of recommendations, it is possible to identify the key features of enabling policies and institutions. Interventions for consideration may include the following:

- A spatial distribution map of below and above ground land use will be required to inform the kind of associations related to the root and tuber crop microorganisms.
- Since commercialization of the root and tuber crops is a major game changer driving further the demand for the root and tuber crops for the processing industry, for human food and for animal feed, countries may need an elaborate sector with a gene bank and microorganisms collection in order to take full advantage of the science involved.
- Other game changers are the emerging technologies in biological sciences that currently allow the study of these microorganisms beyond the microscope. *Gene marking, DNA finger printing, PCR amplification, genomics, proteomics and metabolomics* and associated microarray technologies that have enhanced the speed of throughput in bio-prospecting are tools geared towards discovering novel properties and products from microorganisms. All countries those in the North and in the South need such capacity put in place for this to ensure food security in the future. This is a matter that will drive the science of soil organisms and the root and tuber crops far into the future.

In order for this to be realized, there will be need for budgets, reference databases, North-South collaborations as well as championing.

- Promote root and tuber farming approaches and practices that sustain soil micro-organisms, biological control agents and pathogens, such as reduced tillage, the use of cover crops and mulches, and mixed cropping. Extension services will be crucial in building on those practices by ensuring access to relevant external knowledge and linking it to the wealth of knowledge held by smallholders. Root and tuber crops’ growers may require incentives to manage other ecosystem services besides food production, such as soil conservation and protection of biodiversity.

**Incorporating biodiversity and sustainable soil micro-organisms resource management** into root and tuber crop production systems requires a shift in research and extension from “teaching” to “learning”. Root and tuber growers will need to be convinced that ecosystem-based farming practices are better than those they are using already and – very importantly – that they may have economic benefits. Since most technologies have advantages and disadvantages, trade-offs need to be made. Hence growers need to be involved in all stages of technology development, and that they test and validate practices aimed at improving biodiversity and the sustainability of soil micro-organisms.

In section 4, it has been shown that there is a strong relationship between above ground biodiversity and the soils organisms living in the rhizosphere. Vegetation hosts a diverse group of soil organisms and therefore maintaining the above ground biodiversity will also ensure a rich and diverse rhizosphere biodiversity. Maintaining a diverse above ground diversity will depend on how much the land users are sensitized on its importance including roles and functions in ecosystem services. Planting root and tuber crops as intercrops with plants that preserve and conserve above ground biodiversity is crucial if this objective is to be met. Research that supports this management system needs to be conducted and used to guide farmers and other land users. The following recommendations are proposed:

- In controlling pest and disease threats, promote integrated pest management, which draws on resistant cultivars, biological control agents, bio-pesticides and habitat management to protect root and tuber crops – instead of pesticide use that may lead to pesticide resistance and elimination of beneficial predators. Increased international movement of root and tuber germplasm will require improved phytosanitary measures to ensure that planting material is free of pests and diseases. Robust detection and diagnostic methods to prevent the movement of pathogens are essential for improving quarantine security and bringing national phytosanitary regulations into line with international trade conventions and protocols.
- Large-scale deforestation to increase root and tuber growing areas should be prevented to safeguard the native biodiversity and soil micro-organisms.

- Farmer field schools should provide growers the opportunity for better understanding of the ecosystem services in the root and tuber crop production systems and the capacity to develop strategies to manage pest and disease problems more effectively and soil health and related soil micro-organism and related biodiversity, while improving their cassava production practices.

**Investment in research for development** will be needed to support the following:

- Gaps in the knowledge of soil micro-organism and invertebrate biodiversity with investigations targeting root and tuber production systems.
- Work on identification and taxonomy of the non-culturable species in order to determine if the large numbers of naturally-occurring, non-culturable cells are unknown species, or whether they are representatives of known species.
- Research work to identify and establish which organisms occur in symbiosis with the root and tuber crops and which ones assist and support them in fighting pests and diseases.
- Improvement and development of human capacity and laboratory infrastructure for research on invertebrate and soil micro-organism diversity and their contribution to ecosystem services in the root and tuber production systems, as well as to increase knowledge including on inoculants ecology for the control of soil-borne diseases, nutrient availability to plants and soil structure formation, etc.

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