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COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

CLIMATE CHANGE AND MICRO-ORGANISM GENETIC RESOURCES FOR FOOD AND AGRICULTURE: STATE OF KNOWLEDGE, RISKS AND OPPORTUNITIES

by

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This document has been prepared at the request of the Secretariat of the FAO Commission on Genetic Resources for Food and Agriculture, as a contribution to the crosssectoral theme, *Consideration of scoping study on climate change and genetic resources for food and agriculture*, which the Commission will consider at its Thirteenth Regular Session.

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EXECUTIVE SUMMARY

This technical study focuses on the role of micro-organism genetic resources for food and agriculture under a changing climate. Micro-organisms form the basis of most ecosystems on which agriculture and food production depend. Put simply, agriculture and food production would not exist without this “hidden” but critically important biodiversity. Micro-organisms play essential roles that in this study are separated into five interlinked functional domains: soil inhabitants, plant and rhizosphere inhabitants, plant pathogens, biological control agents and food production micro-organisms. The scope of this study is vast as a consequence of the unrivalled diversity of micro-organism genetic resources for food and agriculture, and the correspondingly huge variety of functions they confer – largely beneficial, but also some harmful to agriculture. By virtue of this diversity, large hitherto untapped opportunities exist for using micro-organisms to improve the efficiency of food and agriculture, including buffering, adapting to and mitigating climate change effects. Micro-organism genetic resources for food and agriculture control ecosystem functions and services and therefore crop productivity and quality. Some can cause crop diseases leading to severe food shortages and famines. However, micro-organisms that cause disease on weeds and insect pests have a positive influence on agriculture and can be used as biopesticides. Many beneficial micro-organisms are linked with plants in the soil, where they induce resistance or perform biological control functions. Free-living soil-borne micro-organisms contribute to the formation and structure of soil, the storage of nutrients and carbon sequestration. Those acting in association with crop plants further regulate soil fertility and the accessibility of nutrients. Soil micro-organisms are also responsible for bioremediation of polluted sites by restoring soil fertility. Once food is produced, micro-organisms are relied upon for its conservation and transformation. However, a constraint to realizing the potential of micro-organism genetic resources for agriculture is the urgent need for fundamental advances to better characterize their taxonomy, function and interactions.

Demand for food is set to increase by 70 percent as the world population increases to a predicted 9 billion by 2050. Meeting this demand requires drastic changes to the manner in which agriculture is managed. These changes will be particularly important in developing countries, where population increases are expected to be the greatest and where crop yields are still far below attainable yields. It is logical and important to focus on organisms, such as micro-organisms, that are critical to the performance of food and agriculture and to achieving the required changes in agricultural production. Climate change will act as an additional driver of change in agricultural systems as environmental conditions are altered drastically. As a consequence of the vital functions that micro-organism genetic resources for food and agriculture confer, they can be considered as pivotal to sustainable agriculture when challenged by such drivers of change. Because the performance of plants is directly linked to interactions with micro-organisms, future strategies to counteract negative effects of climate change will need to involve more than simply deploying crop plants in environments to which they are well adapted. Rather, synergy between crop germplasm and micro-organism genetic resources must be sought and exploited to ensure that ecosystem services – such as nutrient cycling, supporting the soil food web, imparting ecosystem resilience, transforming food and protecting it from spoilage, and controlling pests, diseases and weeds – are achieved.

Climate change will drive changes in the distribution and performance of micro-organism genetic resources for agriculture. Although the precise effect of climate change on micro-organism genetic resources for agriculture is unpredictable and complex as a consequence of the array of ecological interactions that exist and the influence of the environment on each, a working knowledge can be readily generated through targeted research, which can highlight gaps and opportunities and thus influence policy, strategy and tactical interventions. Novel methods are now available to characterize micro-organism strains, species, communities and interactions, based on genetic and functional analyses. These powerful techniques, when combined with appropriate experimental procedures, benchmark sites and

metadata approaches, can improve significantly our understanding of the essential role of micro-organisms as indicators of soil health, in ecosystem resilience and in enhancing adaptive capacity of production and post-harvest agriculture to a changing climate. Similarly, micro-organisms that threaten sustainable production can be prioritized based on their potential impact. Contingency plans can then be made to promote the survival and distribution of those micro-organisms that are beneficial for any given crop or cropping system. Conversely, for those micro-organisms that act antagonistically, systems could be deployed to facilitate their rapid and precise detection as a means of preventing their introduction, establishment or spread. The scale of micro-organism diversity, and hence the multitude of ecosystem functions they perform, dictates that steps must be taken to better characterize this diversity in a targeted manner with focus on key crops, thereby permitting the deployment of crop and micro-organism species that act in synergy.

Climate change, agriculture and energy production are inextricably linked. For example, around 80 percent of deforestation can be attributed to the demand for agricultural land. Deforestation increases greenhouse gas emissions. Micro-organism genetic resources for agriculture can be used to produce energy directly, facilitate adaptation to climate change and mitigate climate change. As agricultural systems are intensified, due to the demand for more food, and modified, due to climate change, risks from new and emerging diseases increase. This requires careful monitoring and deployment of management strategies. Novel biological control agents can be used to limit the harmful impact of pathogens and pests, obviating the need for energy-expensive pesticides. Other micro-organisms could also be used to improve the efficiency of intensified agriculture, such as those that store carbon in the soil, and hence prevent the emission of greenhouse gases. The fertility of the soil for any particular cropping system could be enhanced naturally, either by creating conducive conditions for the proliferation of beneficial micro-organisms or by introducing them directly into targeted environments. Soil-regulating micro-organisms can be used to manage soil health and ecosystem resilience and to obviate the need for producing and transporting energy-expensive fertilizers. Reducing the application of synthetic fertilizers soils would reduce the generation of greenhouse gases. Micro-organisms also have an important role in the protection and transformation of agricultural produce, post-harvest. They can be used selectively to increase the shelf-life of food, protect foodstuffs from spoilage by other micro-organisms, and minimize the risk of mycotoxin contamination. This in turn would save energy and reduce greenhouse gas emissions associated with cold packaging, storage and transportation.

Strategies for using micro-organisms for agriculture will require access to and knowledge of micro-organism biodiversity. This will need to be facilitated through national, regional and international coordination to pool the existing, limited, human and infrastructural capacities, especially for developing countries. Optimal conservation techniques that preserve organism characteristics would need to be implemented. Accessions of micro-organisms could then be used for research, training and active deployment to optimize biotic and abiotic interactions for any given cropping system and location. A major advance would be to establish a global inventory of micro-organism genetic resources for agriculture and the interactive links between the various communities. This would promote better understanding and conservation of processes and groups of micro-organisms responsible for the delivery of ecosystem services. To link the inventory of micro-organisms to their function in the field, a network of practitioners is needed to monitor their performance and the influence of factors such as crop, climate, soil type and market. State-of-the-art scientific technologies and benchmark experimental sites could be used to generate empirical data to inform policy makers, quantify risks and optimize prediction models. Coordinated efforts employing research, capability development and communication, backed by a robust policy framework are essential for this to happen. International cooperation and coordination between farmers, government institutions, research agencies and living reference collections will be critical in order to characterize and share micro-organism genetic resources for agriculture to support crop production patterns as they move due to climate change. Leadership is needed from policy-makers and researchers to inform the farming community of the importance of micro-organism genetic resources for agriculture and to empower them to utilize these resources. Empowerment at this grassroots level will

deliver direct benefits through the use of participatory approaches to the development of farm management techniques that conserve beneficial micro-organism resources.

I. INTRODUCTION

1.1. Scope

This technical study focuses on the role of micro-organism genetic resources for agriculture and the influence of a changing climate. Agriculture is defined as crop-based food production for yield and quality. It excludes micro-organism genetic resources associated with livestock, fish and non-food-borne human pathogens. The study encompasses micro-organisms in five functional domains: soil inhabitants, plant and rhizosphere inhabitants, plant pathogens, biological control agents and food production systems. The scope of this study is vast as a consequence of the unrivalled diversity of micro-organism genetic resources for agriculture and the correspondingly huge variety of functions they perform, largely beneficial but also some harmful to agriculture. The study summarizes the role of micro-organism genetic resources for agriculture, provides examples demonstrating the potential influence of changes in climate on their performance, and describes their potential role in adapting agriculture to climate change and in mitigating changes in climate. While this study can only take preliminary steps towards detailing the complexity of the subject, the authors greatly appreciate the opportunity to increase awareness of micro-organism genetic resources for agriculture among the global community of decision-makers.

1.2. Micro-organism genetic resources for food and agriculture

Micro-organisms have been largely ignored despite their key role in ecosystem functions and services. When they have been put in the spotlight, the emphasis has mainly been on the negative role micro-organisms can play in agriculture and food production. Micro-organisms can infect and colonize plants as pathogens, causing diseases that reduce growth, general vigour, yield and quality of food and feed. Some pathogens are responsible for epidemics that cause severe food shortages and famines. While pathogens mostly have a negative impact on agriculture and natural ecosystems, their ability to devastate plant communities has been harnessed as a means to control agricultural and environmental weeds, and hence they also provide a positive contribution to agriculture. These pathogens are the active ingredients of biopesticides. The role of micro-organisms in biological control is only now beginning to be fully understood and exploited. It extends far beyond their use in commercial biopesticides. For example, *Drechslera anthonia* was isolated from leaves and found to use special hyphal structures to trap nematode pathogens. Some micro-organisms produce secondary metabolites that are toxic to an extremely wide range of crop pests. For instance, the bacterium *Bacillus thuringiensis*, produces proteins called Bt toxins, which are now the most widely used natural pesticides in agriculture.

Interactions among micro-organisms associated with roots help to determine the productivity of crops. Especially in agricultural systems with low external inputs, micro-organisms can help crops to make optimal use of available nutrients such as nitrogen and phosphorus. They confer soil fertility and the acquisition of these nutrients by plants through the establishment of mutually beneficial symbioses with crop roots, i.e. nodulating bacteria that enable nitrogen fixation in legumes and mycorrhizal fungi that increase the efficiency of nutrient uptake. Mycorrhizal fungi and nitrogen-fixing bacteria are estimated to be responsible for 5–20 percent of nitrogen acquired by plants in grassland/savannah and 80 percent in temperate or boreal forests, and for up to 75 percent of phosphorus acquired (Van Der Heijden *et al.*, 2008). New types of association continue to be discovered: for example, a micro-organism association with roots supports heat tolerance in plants in a three-way symbiosis involving a fungus and a virus. Other micro-organisms, such as *Neotyphodium lolii*, live inside grasses and render them resistant to insect attack and drought. Soil micro-organisms may directly interfere with plant pathogens by competing for

nutrients, producing antibiotics, or parasitizing plant pathogens. Soil micro-organisms may also condition plants to be more resistant to pathogens above or below ground.

Free-living micro-organisms are responsible for the formation and fertility of soil. Fertility is enhanced through the activity of, for example, *Azobacter* that supply nitrogen and through other micro-organisms that decompose organic matter and transform mineral nutrients in the soil. These are the primary agents of soil structure, mitigation of greenhouse gas emissions, and nutrient recycling and acquisition by plants. The soil organic carbon pool is the second largest carbon pool of the planet. Micro-organisms are able to fix carbon into proteins bound within their cells and convert labile pools of organic matter into humus. Soil biodiversity can also indirectly affect water and air infiltration and retention by influencing the decomposition and structure of organic matter. Soil micro-organisms are also responsible for bioremediation of polluted sites by restoring biological soil fertility.

Many of the functions performed by micro-organisms provide essential services to human society. Micro-organisms form the basis of the ecosystems on which agriculture and food production depends. Put simply, agriculture and food production would not exist without this “hidden” biodiversity. While this study categorizes micro-organisms into five main functional groups, it is important to note that they are highly interlinked, with many micro-organism taxa fulfilling roles across all functional groups. For example, soil- and rhizosphere-inhabiting micro-organisms play a primary role in nutrient formation, storage and cycling, and therefore as soil-health regulators/indicators. Further, soil-, rhizosphere- and plant-inhabiting micro-organism and biological control agents interact to confer ecosystem resilience. Finally, the security and safety of food derived from crop-based agriculture is directly influenced by interactions between micro-organisms that are active as plant pathogens and involved in food production systems.

II. IMPORTANCE OF MICRO-ORGANISM GENETIC RESOURCES IN SUSTAINABLE AGRICULTURE AND FOOD SECURITY

2.1. Links between functional groups and subgroups of micro-organisms

Annex 1 consists of a table summarizing the functional groups and subgroups of micro-organisms, and provides examples of each and of overlaps between groups and subgroups in relation to crop-based agriculture. These groups and subgroups are discussed in further detail in the following sections.

The flow diagram presented in Figure 1 demonstrates the many and complex linkages between groups and subgroups of micro-organisms related to soil, plants, biological control and food production. As such, the importance of an ecosystem approach when discussing the roles of micro-organism genetic resources in agriculture becomes clear. In contrast, but also by way of complementing the functional groups shown in Figure 1, Figure 2 illustrates the natural linkages between groups and subgroups of micro-organisms and their roles in agricultural production.

Grouping micro-organisms into functional domains is challenging because many perform more than one function. Plant growth regulators can be biological control agents through indirect antagonistic effects on pests and diseases. For example, *Trichoderma* spp., the most common fungus used for biological control, confers disease suppressiveness of soil, resistance to abiotic stresses and promotes plant growth (Harman *et al.*, 2004b). Its beneficial effects extend beyond the plant ecosystem, because it aids in the maturation of compost for natural fertilizer production. The use of *Trichoderma* extends even beyond agriculture into cellulase production (Kubicek *et al.*, 2009), the food industry, paper and pulp treatment, and bioremediation (Harman *et al.*, 2004a; Lynch and Moffat, 2005). On the other hand, plant symbionts that enhance plant nutrition can indirectly enhance resistance to some diseases, partly by boosting the plant’s “immune system”. However, under certain conditions, symbionts, such as mycorrhizal fungi, can be mildly pathogenic and incur a cost to the plant. Some soil micro-organisms produce phytohormones that influence plant productivity and resistance to pests and diseases. Some fungal pathogens produce toxins

that contaminate food and feed, causing human and animal health concerns. Toxin-producing fungi can also out-compete other micro-organisms, including biological control agents such as *Trichoderma atroviride*, due to their sensitivity to the toxin.

2.1.1. Soil inhabitants

Soil micro-organisms can be divided into the following categories: bacteria, Archaea, Actinomycetes, fungi and algae. They perform several vital functions: soil formation, carbon (C) fixing and cycling, nutrient cycling, water regulation, acting as indicators of soil health, and imparting resilience to soil and ecosystems. Micro-organisms provide continuous inputs, ranging from soil genesis to long-term soil development and maintenance. Their presence distinguishes soils from non-soils. The initial colonization of new parent material by soil organisms with simple energy flows and basic material-cycling pathways marks the start of soil formation. Soil organisms physically modify, maintain or create new habitats for other organisms, which may in turn lead to increased species diversity. Soil micro-organisms are “ecosystem chemical engineers”, mediating changes to inorganic and organic substrates through secretory and excretory activities. Micro-organisms interact with and progressively modify other soil-forming factors, such as climate, type of parent material and topography, in developing soil.

Soil micro-organisms are vital in the global carbon cycle, playing a role in the sequestration of carbon in soil organic matter (SOM) and also the release of carbon as carbon dioxide (CO₂) from the decomposition of SOM. The soil carbon pool is in a dynamic equilibrium of inputs and outputs. With an estimated 2 500 gigatonnes of carbon up to 1 metre depth, soil is the second largest global carbon pool and, together with plant biomass, contains 2.7 times more carbon than the atmosphere. CO₂ – released from SOM decomposition by soil micro-organisms – is one of the major greenhouse gases (GHG) contributing to global warming. In addition to CO₂, soil micro-organisms can also control fluxes of other GHGs, such as methane (CH₄), which is produced during the carbon cycle, and nitrous oxide (N₂O), which is produced as part of nitrogen cycling. While these gases represent much smaller fluxes than those of CO₂, they are much more potent than CO₂ as a GHG. Through their capacity to store carbon, soils act as a buffer offering a low-cost tool for climate-change mitigation. Appropriate farming practices, such as no-till, are necessary to maintain soil carbon stocks (Schils, 2008). Moreover, the soil carbon pool is itself susceptible to warming. Rising temperature rise creates a “carbon cycle feedback”, whereby the uptake and storage of carbon by land and oceans is reduced, enhancing carbon loss to the atmosphere (Joos *et al.*, 2001; Lal, 2004).

Micro-organisms play a key role in nutrient cycling processes in soil. Organic nutrients and some inorganic compounds are supplied through animal excreta, the death of plants and animals, and exudation by plant roots. In agricultural ecosystems, nutrient input is also provided by the application of inorganic fertilizers. Nutrient-cycling micro-organisms possess enormous metabolic diversity and versatility. All naturally produced compounds and most anthropogenic compounds are substrates for micro-organism growth. Micro-organism degradation processes themselves generate chemically complex compounds, such as humic material, which are important for the maintenance of soil structure. When conditions are favourable, micro-organisms grow rapidly to assimilate substrates present at very low concentrations.

Micro-organisms also play an essential role in soil structure and water regulation. Soil structure is the spatial distribution and composition of soil particles, their aggregates and pores, and is mediated by physiochemical processes and biological activity from bacteria, fungi, meso- and macrofauna, and plant roots. Soil micro-organisms excrete chemicals during the decomposition of organic material, which act as binding agents between soil particles, facilitating aggregate formation. The organic material becomes encrusted with soil particles, which slows down decomposition and improves SOM formation.

Soil micro-organisms can be used as indicators of soil health based on their nitrogen fixation, organic-matter mineralization, nitrification and other functions. “Soil health” is a relative term and its meaning

varies according to the functional and spatial context in which it is used. Existing indicators comprise long lists of potentially relevant variables, but no general agreement has been reached on their interpretation (Doran and Zeiss, 2000) and, as yet, no comprehensive index is available that combines all aspects of soil health (Bloem *et al.*, 2006). For instance, soil fertility can be described by physical, chemical and biological fertility, where physical fertility relates to soil texture, structure, porosity, water retention capacity, etc.; chemical fertility is due to SOM content, pH, cationic exchange capacity, availability of key nutrients N, P and K, presence of pollutants, etc.; and biological fertility is the carbon content and activity of micro-organism biomass, micro-organism community structure, presence of pathogens, etc.

Many studies have shown that the relative abundance of soil organisms responds to changes in soil health. However, the exact biodiversity of any given soil is affected by the manner in which the land is used. More natural, undisturbed, soils contain higher levels of biodiversity than those that are actively managed by humans, and the most commonly cited explanation for loss of biodiversity is human intervention. Change in land use affects soil communities by altering the quantity and quality of inputs available to soil microbiota (Bardgett and Cook, 1998). Conversion of natural habitats to agricultural land involves practices that destroy mycorrhizal networks and the whole micro-organism soil community (mechanical soil tillage, flood-irrigation, agrochemicals, fertilization, monoculture, land clearance through fire, etc.). It is of grave concern that the loss of biodiversity is much faster today than at any time in the past. In fact, the majority of human activity results in soil degradation, which negatively affects the services provided through soil biodiversity. The decline in micro-organism taxa richness that accompanies habitat loss is a non-linear process across soil types, but what is certain is that more species are becoming extinct as more habitats are destroyed.

Micro-organisms contribute to soil resilience, which is the capacity of the soil ecosystem to withstand negative impacts without falling into a qualitatively different state that is controlled by a different set of processes (Griffiths, 2000). To be resilient, a soil needs to have (a) repertoire: the presence of organisms to carry out the biologically-mediated processes; (b) diversity: a broad range covering all necessary functions; and (c) redundancy: more than one set of organisms to carry out the same function. A resilient system will persist in providing the range of ecosystem services needed from agriculture (Cheatham *et al.*, 2009). Soil resilience assures that soil functions are maintained and nutrients are made available when other factors vary.

Another example of the potential of the soil micro-organism community to promote soil resilience is its role in the creation and maintenance of disease suppressive soil (i.e. soil that reduces the risk of plant disease) (Borneman and Becker, 2007). In fact, all soils tend to be disease suppressive to some extent; if soil-borne plant pathogens are introduced to sterilized soil, they often have greater negative effects on plants than they do in normal soils. In agricultural soils, crops may select particular sets of micro-organism taxa by producing exudates that induce suppressiveness. Disease suppression may be more resilient if micro-organism taxa are in some ways redundant in function. For example, multiple taxa may produce antibiotics that inhibit a pathogen, yet the optimal temperature for the metabolism of these taxa may vary. This type of system redundancy in function can help to maintain system function for disease suppression even if some taxa become less active, for example because of a change in climate. Maintaining higher diversity will tend to maintain higher redundancy. Micro-organisms can also make ecosystem services more resilient if specific taxa are highly plastic in being able to adapt to new circumstances while maintaining the same function.

2.1.2. *Plant and rhizosphere inhabitants*

Rhizosphere describes the whole volume of soil that is directly influenced by roots, and includes all the biological, chemical and physical processes associated with soil functioning. The rhizosphere is the site of a range of complex interactions between the living and dead soil components, which may be grouped into the following three main processes: (a) extraction of nutrients from the soil solutions, organic reserves

and from the general and soil atmospheres; (b) the production of modifier substances that promote plant growth; and (c) the formation and maintenance of soil macro- and microstructure.

Mutualism is a biological interaction between two different species where each individual derives a fitness benefit such as food resources or protection from predators. Micro-organisms are involved in any mutualistic interactions in soil ecosystems. Two characteristic examples are rhizobia and mycorrhizae. Root exudates stimulate multiplication of the free-living rhizobia bacteria. Their colonies typically develop on a root hair and the plant cell is penetrated by the bacteria. The plant then encloses the multiplying bacteria by laying down a cell wall, forming an infection thread that may develop into a nodule. In this association, rhizobia produce ammonium, thereby allowing plants to absorb nitrogen by the easiest route possible (compared to nitrate), as ammonium can be directly incorporated into proteins without the need for any further chemical reactions. Importantly, rhizobia cannot fix nitrogen without the plant, and the plant cannot absorb atmospheric nitrogen without the rhizobia, so these organisms need each other to thrive. A similar type of mutualism occurs in the roots of higher plants (gymnosperms, angiosperms) that form mycorrhizae with fungi. The mycorrhizal fungi gain constant and direct access to the carbohydrates produced by the plants and, in turn, the fungi form a network of filaments that grow in and around the plant root, thereby enabling the plants to use the larger area to improve their mineral absorption capacity (especially for phosphorus).

It is relatively well known that these associations benefit plants, and they have been well characterized in terms of the mechanisms through which they provide the plant with nutrients. Addition of the respective micro-organisms to the soil is a common practice in some cropping systems, and the practice may be amenable to improvement through the development of improved strains or methods of introduction. The endophyte *Neotyphodium* spp. lives inside its grass host *Lolium* spp. and protects it from insect attack, drought, cold and fire by producing alkaloids. However, these alkaloids are also harmful to sheep and cattle grazing on the grass. Strains of the bacterium *Pseudomonas syringae* living in association with plant leaves create a less-favourable environment for ice formation and thereby protect plants from frost damage. Heat tolerance in a tropical grass is conferred by association with the endophytic fungus *Curvularia protuberata* only when the fungus is infected by a virus (Márquez *et al.*, 2007). There are many other types of association between micro-organisms and plants that are only just beginning to be understood.

An open area of study is the management of soils to support beneficial micro-organisms. The System of Rice Intensification (SRI) is an example of efforts to develop cropping-system management that simultaneously intensifies production and maintains sustainable production (Anas *et al.*, 2011; Kassam *et al.*, 2011). SRI can include cropping system modifications to provide greater soil aeration and thus support root growth and microbial activity. SRI can support higher populations of micro-organisms that support plant growth, including nitrogen-fixing bacteria such as *Azospirillum* and *Azobacter*.

Micro-organism communities in the rhizosphere and soil can change the soil environment to make it less-favourable or suppressive to fungal, bacterial or nematode pathogens. The micro-organisms that produce disease suppressive soils are an important, but little-understood, resource. Suppressive soils offer a form of naturally occurring biological control that reduces losses from plant disease. For example, the effects of wheat take-all – a disease caused by the soil-borne pathogen *Gaeumannomyces graminis* var. *tritici* – decline over time as other micro-organisms in the soil community, such as *Pseudomonas* spp. and *Trichoderma* spp., proliferate to reduce the abundance of the take-all pathogen.

2.1.3. Plant pathogens

A large variety of micro-organisms – including fungi, bacteria, viruses and phytoplasmas – are harmful to agriculture as they cause crop diseases which reduce production and quality of food, fibre and animal feed. *Phytophthora infestans*, the infamous Irish potato famine pathogen and *Cochliobolus miyabeanus*, a

fungus that causes brown spot disease in rice, which was the causal agent of the Bengal famine, have altered the course of society and political history. The population of Ireland fell from 8 million before the famine to 5 million as people died or emigrated to countries such as Australia, Britain and the United States of America. Many pathogens cannot be easily controlled, and therefore routinely cause severe losses to crop yields. Such losses are particularly high in developing countries, where demand for food is greatest, because capacity to diagnose plant pathogens is weak and because the cost of pesticide application is prohibitive. An estimated 10–16 percent of global harvest is lost to plant pathogens each year, which translates to over US\$ 200 billion (Oerke, 2006). Infection in the field by aerial plant pathogens can lead to decreased quality or spoilage of food after harvest, and these losses are again particularly severe in developing countries as they lack appropriate infrastructures for safe storage and transport. Certain pathogens, such as *Ralstonia solanacearum* race 3 biovar 2, are considered a select agent by the United States of America, under the Agricultural Bioterrorism Protection Act, because of the threat they pose to agricultural production. Others, such as the causal agent of karnal bunt of wheat (*Tilletia indica*), have restricted international trade and are subject to strict quarantine regulations.

The way plant pathogens obtain their nutrition often determines the nature and severity of crop losses. Biotrophic pathogens derive nutrients only from living host cells, and include all viruses, phytoplasmas and some fungi. A resistant host plant reacts through “programmed cell death”, which starves the pathogen of nutrients. Biotrophic rusts and smuts produce massive quantities of spores that are carried by wind currents over great distances between countries and continents. Their massive population size, rapid generation time and well-developed host specialization allow these pathogens to adapt quickly to overcome the resistance of host plants. In agriculture, new races continuously evolve, colonize resistant crop varieties and can reach near-extinction in what is popularly known as “boom and bust cycles”, prompting the need for continuous deployment of new resistant varieties. Pathogens can rapidly spread and devastate large areas of cereal crops. For example, a new race of stem rust of wheat (*Puccinia graminis* f. sp. *tritici*) known as Ug99, which originated in Uganda, is now travelling towards Asia where it is predicted to cause a 10 percent yield loss, amounting to US\$ 1–2 billion per year (Globaltrust, 2010).

Necrotrophic pathogens derive nutrients from dead host cells and include bacteria and the vast majority of fungal pathogens, many of which produce toxins to kill host cells and hijack host defence mechanisms to initiate programmed cell death. Necrotrophic pathogens survive long periods outside living crop hosts by colonizing organic matter (and acquiring nutrients in a saprophytic manner). In contrast to biotrophic pathogens, their populations can easily bounce back after resistant crop varieties temporarily restrict their growth and reproduction. Commonly, such micro-organisms will have a broad host range, which also helps to maintain their biodiversity. Many necrotrophs cause chronic production losses as there is little or no host resistance or other effective means of control. Their impact on crop production is often magnified when crops experience physical or abiotic stress, for example due to drought, excessive heat or limited nutrient availability – factors which are set to increase with climate change.

Some necrotrophs produce toxins in grains, fruits and crop residues that are harmful to human and animal health, and that are prohibited in traded products through international trade agreements. High levels of mycotoxins produced by the fungal pathogen *Fusarium graminearum* in grains during head blight infection of wheat and barley makes them unsuitable as food and feed. These mycotoxins persist through most kinds of food processing, including brewing, malting and extrusion-based processes, and as a result end up in breakfast cereals, biscuits, noodles and beer. One estimate suggests that US\$ 2.7 billion was lost during 1998–2000 in northern and central parts of the United States of America because of price discounts, or even destroyed harvests, caused by lowered or unsafe grain quality. The production of toxins by necrotrophs confers a competitive ecological advantage against other micro-organisms during the saprophytic phase and can actively reduce the effectiveness of biological control agents. For example, the toxin deoxynivalenol suppresses the expression of chitinase genes for the biological control agent *Trichoderma atroviride*.

Weed pathogens can be either biotrophic or necrotrophic, and are used for biological control of weeds, providing they have a high degree of specificity to particular weeds so as not to harm crops and other plants of economic or environmental value. For example, the fungus *Phytophthora palmivora* has been registered for biological control of milkweed vine.

While plant pathogens may not appear to be an important genetic resource at first consideration, there are many reasons to ensure that their biodiversity is maintained under controlled conditions. For example, certain necrotrophs are critical to sustainable crop production. By switching on host defence mechanisms without causing severe damage, a weakly pathogenic strain can make the host plant more resistant to subsequent invasion by a more virulent strain of the same species. Some of these beneficial effects stem from the use of pathogens as biological control agents, which is summarized in the following section. While here we emphasize agricultural species, it is also of interest to note that plant pathogens in natural plant systems generally contribute to increased plant intra- and inter-specific diversity through selection pressure for plant diversification through co-evolution. Similarly, pathogens in *in situ* reserves of wild crop relatives continue to select for new resistance genes that will be a resource for agriculture in the future.

2.1.4. Biological control agents

Micro-organisms are used for biological control of pests (pathogens, insect pest and weeds), while many perform this function naturally as part of the micro-organism community in disease suppressive soils. There are three types of biological control: classical (where natural enemies are introduced to control an exotic, invasive pest); augmentative (where a large number of a previously mass-reared natural enemy is released in the environment); and conservation biological control (where the environment is manipulated to increase the fitness of natural enemies). Augmentative biological control can be inoculative (where the released natural enemy persists by self-replication for a certain time span) or inundative (where immediate action is expected within the life span of the released natural enemy). In some augmentative application, the control micro-organism is applied to as many of the niches that may maintain the pest as possible. The success of augmentative control is generally a function of how thoroughly and quickly the biological control micro-organisms can spread through the relevant niches, and how well they are maintained over time. Insect pathogens are the most researched and commercially used micro-organisms for augmentative biological control. Parasitoids, such as *Neozygites fresenii* used to control the cotton pest *Aphis gossypii* in California, are the most common classical biological control agents. Only very few micro-organisms are used; examples include the rust fungus *Maravalia cryptostegiae*, which is used in Australia to control the weed rubber vine. Viruses, bacteria and fungi are the active ingredients of numerous biopesticides applied in an augmentative way. The bacterium *Bacillus thuringiensis*, which produces crystalline toxins that kill Lepidoptera and Diptera larvae, has been used on a large commercial scale. Micro-organisms are also being researched for commercial use against plant pathogens. *Puccinia romagnoliana* is a rust fungus that controls the weed purple nutsedge (*Cyperus rotundus*). The fungus *Trichoderma* is one of the most economically successful biological control agents developed for commercial sales (Lorito *et al.*, 2010).

Micro-organisms used for augmentative biological control comprise a small, yet growing, market. Worldwide, there are 195 strains of micro-organisms registered as active ingredients of biopesticides, which are commercialized into 780 different commercial products. Most of these strains belong to only a few species of bacteria (especially *Bacillus thuringiensis* and *Pseudomonas* spp.) and a few species of fungi (especially *Beauveria* spp., *Metarhizium* spp., *Verticillium lecanii*, *Paecilomyces* spp. and *Trichoderma* spp.). Products based on viruses are far less common, and are solely based on strains of baculoviruses, especially nuclear polyhydrosis virus. Micro-organism biopesticides are biased towards a small selection of easily cultured taxa, such as spore-forming bacteria and asexual fungi. The worldwide market for pesticides is ~US\$ 45 billion per year, of which micro-organism biopesticides capture less than

1 percent (~US\$ 400 million per year). However, whereas the worldwide market for pesticides grows at a rate of 3 percent per year, that for micro-organism biopesticides grows more than five times as fast.

Interestingly, many naturally occurring soil micro-organisms, active in conservation biological control, are now being harnessed and turned into commercial biopesticides. For example, aflatoxin is a major food contaminant worldwide, produced by some strains of *Aspergillus* spp. that occur in the soil, on plants and on stored products. These strains are sometimes out competed by naturally occurring a-toxigenic *Aspergillus* spp. strains, reducing aflatoxin contamination. However, these a-toxigenic *Aspergillus* spp. strains have been isolated and are currently commercialized as micro-organism biopesticides in Kenya, Nigeria and the United States of America.

Recently, micro-organisms are also being investigated as potential biological control agents of animal and human pests, diseases and disease vectors, which are difficult to control using conventional means and which are increasing in incidence partly due to climate change. For example, researchers are currently investigating the use of *Metarhizium anisopliae* against the tick *Ixodes scapularis*, the vector of Lyme disease (Benjamin *et al.*, 2002), and *Anopheles* spp., the vector of the malaria parasite *Plasmodium* spp. (Scholte *et al.*, 2006).

2.1.5. Food production

This section considers the usefulness of micro-organisms in post-harvest control, in food transformation and in prolonging food durability.

For the six most important cultivated crops, post harvest losses caused by insects and rodents amount to about 7 percent, whereas those caused by fungi and bacteria range from 5 to 30 percent (Rajendran, 2002). Some fungi cause qualitative changes in the foodstuffs they affect – inducing changes in the appearance of the foodstuffs or contaminating them with mycotoxin that can be harmful to human and animal health.

Biological control using micro-organisms offers an alternative means of protecting foodstuffs that does not require the use of chemical pesticides which can leave harmful residues especially on the surface of the product. Micro-organisms, such as the yeasts *Meyerozyma guilliermondii* and *Whickerhamomyces anomalus*, can reduce the presence and activity of post-harvest contaminants (Petersson and Schnurer, 1995; Droby *et al.*, 1997; Liu *et al.*, 2010; Zhang *et al.*, 2010; Melin *et al.*, 2011; Olstorpe and Passoth, 2011).

Micro-organisms themselves, especially fungal fruiting bodies, are consumed worldwide. The fruiting bodies of some *Agaricus* spp. are cultivated in mushroom farms and are the most popular edible mushrooms, but other mushrooms (e.g. *Lentinula* spp. and *Pleurotus* spp.) are now also routinely found in supermarkets around the world. Other examples include diseased plant organs such as boil smut of maize, which is considered a delicacy and is commercially cultivated in parts of Mexico.

Micro-organisms – including bacteria, yeast and other fungi – transform many agricultural products, including grains, milk and meat, into specialty food such as bread, cheese and beer. Many bread and bakery products are obtained thanks to the leavening activity of the yeast *Saccharomyces cerevisiae*, alone or in combination with lactic bacteria and sometimes other yeast species. Although there are few species involved, a multitude of strains and mixed cultures are available throughout the world, especially where the introduction of industrial starter cultures has not yet erased the original autochthonous biodiversity.

Since ancient times, milk has been transformed by micro-organisms into a huge variety of beverages and food products. Many populations (e.g. Tibetan and some Caucasian) live fundamentally on milk-derived foodstuffs. Various types of cheese are common and important in the diet of almost every human population. The vast majority of dairy fermentations are carried out by several species of diverse bacterial genera, among which *Lactobacillus* and *Streptococcus* spp. predominate. Some yeast are regularly

present in many types of cheese. Their functions not yet well understood, although it seems that they play a role in reducing the presence of spoiling micro-organisms. Blue cheese is normally produced with the introduction of innocuous moulds such as *Penicillium roqueforti*. Micro-organisms are used extensively to produce salami and salt-conserved meat. Drying and salting have been practised since antiquity. As is the case in cheese and other dairy products, many bacterial and a few yeast species intervene to mature and preserve the foodstuffs.

The most ancient food industry, beverage fermentation, dates back 6 000 years. In spite of the widespread and enormously popular diffusion of beverage fermentation, its fundamental microbiological processes were not known until 150 years ago when Louis Pasteur's seminal work showed that alcoholic fermentation is carried out by yeast. Only during the last century did people learn how to isolate, select and reintroduce yeast cultures to manage beverage fermentations correctly. A few bacterial species contribute to beverage maturation, whereas many yeast, bacteria and moulds can spoil fermented beverages.

Micro-organisms also play an essential role in the pre-roasting fermentation of coffee and cocoa beans. The fermentation is carried out by a succession of yeasts, lactic acid bacteria and acetic acid bacteria (Cleenwerck *et al.*, 2008; Leal *et al.*, 2008; Daniel *et al.*, 2009; De Bruyne *et al.*, 2010; Nielsen *et al.*, 2010).

Some micro-organisms are considered to be "probiotic", i.e. they confer a health benefit when administered in adequate amounts as live micro-organisms. A rather innovative way of using micro-organisms (mainly yeast, such as *Rhodotorula* spp. and *Lipomyces* spp.) is to grow them on low-quality carbon and nitrogen sources to produce high-quality proteins and, in some instances, lipids. Several micro-organisms are used for food conservation. For example, some yeast – such as *Meyerozyma guilliermondii* which is used to extend the shelf-life of apples – can be used to contain pathogens during the post harvest period. The search for micro-organisms that are able to contain the diffusion and growth of spoiling bacteria and moulds is a growing line of research, potentially applicable to most foodstuffs, among which cheese and bread (Daniel *et al.*, 2011). The possibility of lengthening shelf-life without the addition of chemicals or the extensive use of refrigeration is a key aspect of producing environmentally and economically sustainable foods (Di Cagno *et al.*, 2008; Di Cagno *et al.*, 2009).

Some micro-organisms are used as additives in agro-industry. Through fermentation, micro-organisms can produce bioenergy, mainly methane (methanogenic bacteria) and bioethanol (*Saccharomyces cerevisiae*). Other micro-organisms are being used as cell lines for research and the production of various compounds.

2.2. Differences of micro-organism genetic resources from other genetic resources

Micro-organisms are often perceived to have a negative connotation because they are best known as human pathogens. However, as the preceding section underscores, micro-organisms play absolutely essential, beneficial roles in support of agricultural eco- and production systems. Further, micro-organism genetic resources offer huge potential over other taxa as a result of their large biodiversity, rapid adaptability and because of their small size.

2.2.1 Biodiversity of micro-organisms is huge

There are an estimated 5–30 million micro-organism species globally – some 2 million have been formally described, while the remainder are either unknown or unnamed. Of the 1 billion bacteria found in one gram of soil, fewer than 5 percent have been discovered and named. For fungi alone, there are at least 1.5 million species, with only 5 percent described. This number compares with 4.9 million arthropod species and about 420 000 seed plants (Hawksworth, 2001, 2002). Knowledge of biodiversity is uneven, with strong biases towards the species level, large animals, temperate systems, and the components of

biodiversity used by people. Although biodiversity underlies all ecosystem processes, modern agriculture is based on a very limited genetic pool of crops and even more limited exploitation of micro-organism genetic resources for agriculture (Beed, 2009).

Between 55–98 percent of the total biodiversity on earth is found in the soil. The bulk is due to several thousand species and genotypes of micro-organisms. In terms of living biomass, agricultural soil contains in the order of 3 000 kg (fresh weight) of micro-organisms per hectare.

Within-species diversity is often critically important for micro-organisms. This is, for example, one rationale for maintaining diversity of plant pathogens. Genotypes of plant pathogenic species that have low pathogenicity have the potential to serve as biological control agents. The less virulent strains can colonize plant surfaces and thus reduce colonization by more virulent genotypes of the same species (Johnson, 2010). However, micro-organism taxonomy is often more complicated than the taxonomy of higher organisms, such that the definition of a “species” is often not simple, especially when micro-organism taxa can exchange genetic material through multiple means. For this reason, the diversity of micro-organism systems may not be best described by the diversity of taxonomic groups. Functional diversity may be more important for many taxa, such as *Fusarium oxysporum*. When enough is understood about micro-organism functions and the genetic basis for function, it may be possible to identify particularly useful genetic diversity in particular micro-organism genes and gene families. Much scientific work remains to be done to understand micro-organism diversity and its role in agricultural productivity and resilience, particularly for non-culturable micro-organism species. Related to micro-organism biodiversity, is the associated biodiversity in plant species. Plants may select for particular rhizosphere or epiphytic micro-organisms through the production of exudates or through more specific gene-for-gene relationships, where the plant “identifies” particular micro-organisms and responds to them.

In summary, it is perhaps interesting to reflect on conclusions drawn from a position paper developed by the CGIAR’s Inter-Centre Working Group on Genetic Resources for Agriculture, which recognized the diversity of micro-organism genetic resources for agriculture and the relatively small proportion that are represented in *ex situ* collections: “*Micro-organism biodiversity constitutes by far the most diverse yet least studied component of agricultural ecosystems, with an untapped economic potential that could and should be harnessed. Yet the capacity and infrastructure to study micro-organisms is lacking, especially in the developing world. Micro-organism collections are few, disjointed, often without long-term commitments for their maintenance, and legal guidelines and policies for sharing micro-organism germplasm are lacking. As a result, concerted and long-term efforts to study the functionality of this important group, especially in relation to their interactions in the ecosystem, are virtually non-existent*” (SGRP 2009).

2.2.2. *Micro-organisms are invisible*

Micro-organisms are the smallest living beings on the Earth. Their size ranges from a few tenths to some tens of micrometres ($1\mu\text{m} = 1$ millionth of metre). To visualize their size, we could say that if a bacterium were as large as a pea, then a man would be twice as tall as Mount Everest. This small size implies that they can reach very high cell densities. For instance a litre of fermenting grape juice contains up to 600 billion cells, equivalent to one hundred times the current human population on the whole Earth. However, the most impressive aspect of micro-organisms is their unparalleled rate of reproduction, which is due to their short generation time which can be as little as every 20 min. If bacterial growth were not nutrient limited, a single cell would produce a mass as heavy as the Earth (6×10^{24} kg) in about 120 generations, i.e. in some 40 hours.

In summary, environmental micro-organisms form the richest diversity on Earth and yet the most underestimated. Micro-organisms colonize virtually every available niche, including those that are too extreme for other organisms such as submarine vents where temperatures exceed 100°C and pressures

exceed 40 MPa. One of the most impressive aspects of this huge activity is the production of fossil forms of energy: coal, oil and natural gas. Algae photosynthesize approximately 50 billion tonnes of carbon per year, equivalent to the total net production by all the plants on the planet. Even more importantly, they contribute half of the oxygen available in biosphere.

2.2.3. *Micro-organisms can adapt rapidly*

Micro-organisms may reproduce sexually or asexually. Sexuality is normally very rudimentary in the micro-organism world and is often reduced to the presence of two mating types of opposite polarity. Mating types consist of near identical cells but with small biochemical differences allowing one type to be compatible with another. During sexual reproduction, segregation and recombination events occur, yielding different gene associations and therefore causing some degree of variability within the population.

Some fungal species have one form that can reproduce sexually (the “teleomorph”) and another that does not (the “anamorph”). Asexual reproduction resembles that of the cells of our bodies, which are constantly renewed throughout life. When reproducing asexually, cells increase their volume and then divide the entire cell body, including the genetic material, into two equal parts. This phenomenon provides a very quick way of increasing the cellular biomass with a high degree of fidelity; in fact, the cells may be different only due to random mutations. The set of identical cells all deriving from the same mother cell by asexual reproduction is called a pure culture or clone. The two means of reproduction constitute so-called “vertical gene transfer” (VGT), i.e. the transmission of the genetic material from one generation to the next. However, very importantly, DNA (and sometimes RNA) can also be transferred among micro-organisms through “horizontal gene transfer” (HGT), which consists of a movement of DNA from one cell to another (somatogamy and bacterial conjugation), from the environment to the cells (transformation) or from one cell to another via a virus (transfection). HGT produces a high degree of variability and can easily cross species boundaries. This mechanism ensures that micro-organisms have a huge ability to vary their genetic arrangement in a short time – without the need to wait for another generation – because the HGT is borne by the individual receiving the DNA and does not rely on the reproductive process.

The ability of micro-organisms to adapt to the environment is strictly bound to their genetic and reproductive mechanisms, which produce a huge amount of variability. Furthermore, the specificity of selection gives micro-organisms an extra advantage. In plants and animals, mutations or recombinations are normally temporally distant from the potential selective event. In other words, if an animal undergoes a mutation in its seminal cells and the mutation flows vertically to the descendants, it will only become selectable after a specific arrangement of the “locus” in which the mutation occurred. Conversely, in all prokaryotes and in haploid eukaryotes, the mutation is readily selectable because the cell undergoing the mutation is immediately selected within the environment in which the mutation occurred. The two events (mutation and selection) are so close that they are, in some cases, indistinguishable and lead some authors to call them “mutation-adaptive”, as if the environment could somehow direct the mutation event. The reality appears to be much simpler: stressful environmental conditions increase the mutation rate and then select for the fittest cell lines. The increased mutation rate can probably be ascribed to a reduction of the ability of the cell to repair mutations when under stress (Foster, 2000; Foster, 2005; Foster, 2006; Foster, 2007).

The complex of VGT (with sexual and asexual variants), HGT and the specific mechanism of mutation, combined with the huge number of micro-organism cells, creates unparalleled ability to adapt to a wide range of environments. This facilitates two quite different outputs. On the one hand, micro-organisms are able to exploit certain unchanging environments, and on the other are able to overcome plant and animal resistance mechanisms and to adapt quickly to modern biocides and other mechanisms used to defend crops and livestock.

Figure 1. Links between functional groups and subgroups of micro-organisms

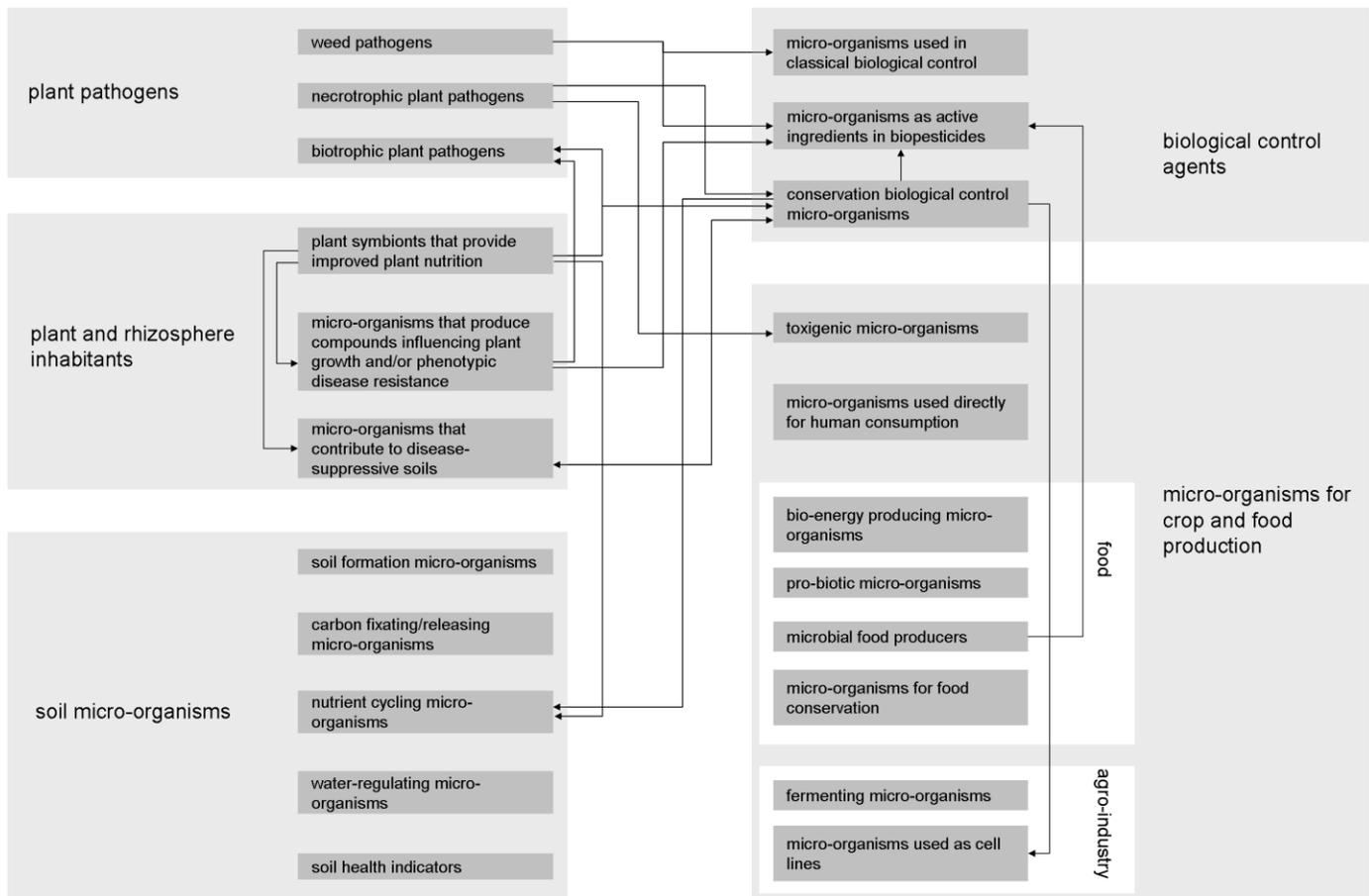
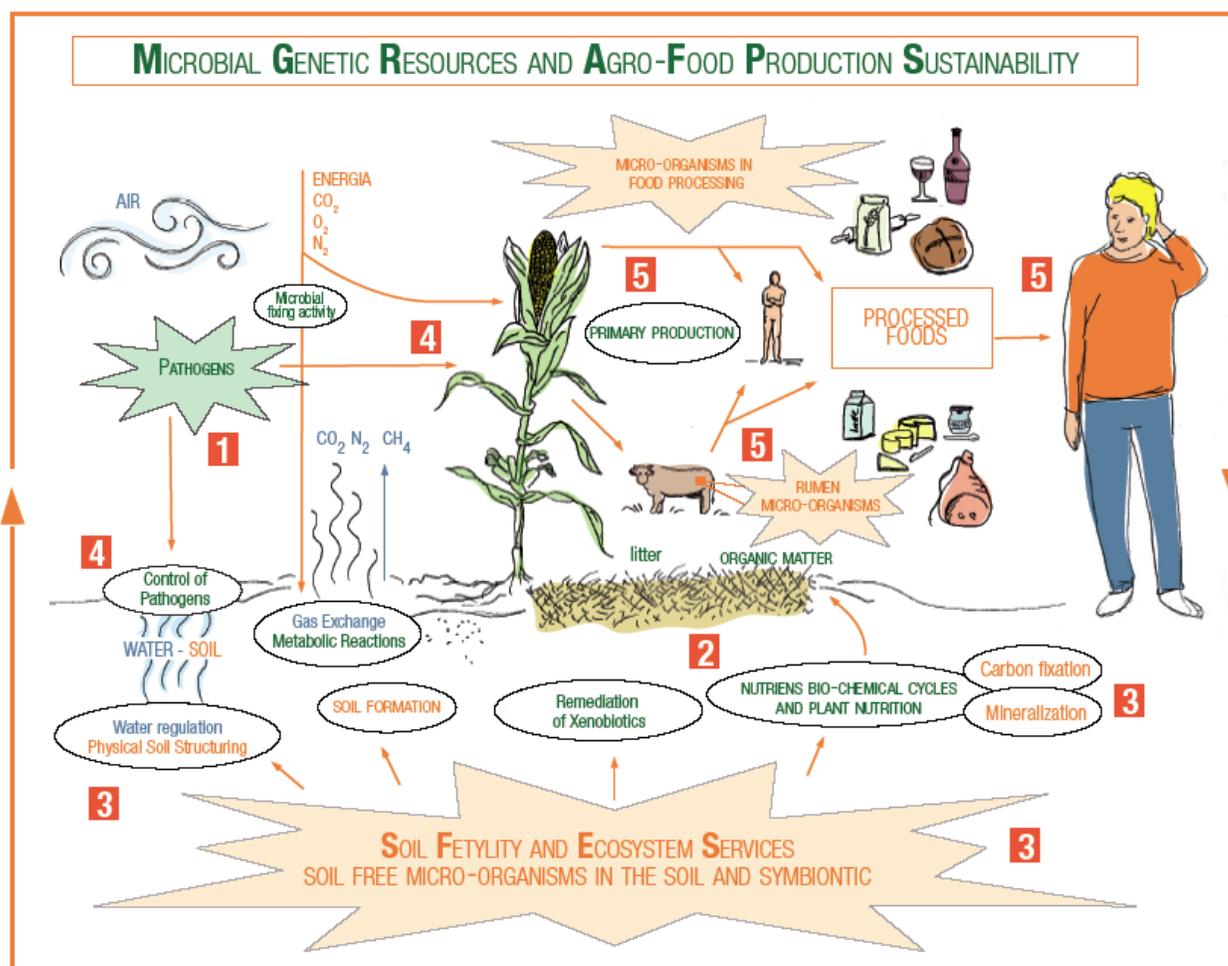


Figure 2. Natural linkages between micro-organism genetic resources and their roles in agricultural production



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Functional groups of micro-organism genetic resources for agriculture: (1) plant pathogens, (2) plant and rhizosphere inhabitants, (3) soil inhabitants, (4) biological control agents, (5) food production.

2.3. New tools highlight increased importance of micro-organism genetic resources

In recent years, metagenomics has allowed the study of the entire genome of soil biota, better assessment of the diversity of complex micro-organism communities, and access to a number of new species or genes (Van Elsas and Speksnijder, 2008), without first isolating micro-organisms. The use of metagenomics and other approaches have identified novel genes associated with biomolecules (esterase/lipase, oxidative coupling enzymes, biotin producing enzymes, etc.), genes for pest control (biopesticides), biofertilization and to degrade pollutants across a range of environmental conditions and new antibiotics from soil micro-organisms. Newly identified Rhizobia species associated with *Medicago sativa* have the potential to operate under various abiotic conditions such as low or high temperature or pH, or low levels of organic matter in the soil (Mocali *et al.*, 2010). These studies clearly point to an enormous unexplored reservoir of genetic and metabolic diversity among micro-organisms.

Similar opportunities to explore micro-organism genetic resources exist in "conservation agriculture", where tillage is reduced and plant material (crop residue or cover crops) is retained in fields for longer so

as not to disrupt biodiversity, community structure and the functions of micro-organisms (Hobbs *et al.*, 2008). Enzyme-encoding genes from *Trichoderma* spp. are being explored as means of improving plant resistance to pathogens (Lorito *et al.*, 1998) and salt stress (Montero-Barrientos, 2010). Improved knowledge of genetic and metabolic diversity within functional groups, genera or species of well-known micro-organisms will help to enable fuller exploitation of their specific characteristics to the benefit of agriculture and other industries.

III. EFFECTS OF CLIMATE CHANGE ON MICRO-ORGANISM GENETIC RESOURCES FOR FOOD AND AGRICULTURE

3.1. Some words on accepted definitions/scenarios

Global climate change has been observed over the past decades and is anticipated to continue in the future (IPCC, 2007). Temperature and CO₂ levels are likely to increase in many areas of the world, though not evenly throughout the year. Precipitation patterns cannot be predicted with as much confidence, and are likely to be more variable, with precipitation increasing in some regions and seasons, and decreasing in others. Extreme events such as droughts and floods may become more common. Predictions of future climate scenarios depend on assumptions about greenhouse gas emissions. In turn, levels of greenhouse gas emissions will depend on which paths of economic and technological development are followed. The uncertainty involved in making predictions about the climate is one source of uncertainty in predicting the role of micro-organisms in future cropping systems. Important aspects of these changes, as they influence the contributions of micro-organisms to system resilience, include the following:

- Changes in “average” conditions will influence cropping systems, for example allowing some systems to move into regions that were previously too cold, and restricting others through drought. Micro-organisms may need to be introduced with cropping systems as they move, and may be used to support drought tolerance.
- Changes in the “variability” of conditions may have important impacts on micro-organism communities. Their short generation times allow micro-organisms to respond more quickly than most plants or animals to new environmental conditions. Thus, when extreme conditions occur, beneficial or detrimental micro-organisms may respond rapidly.

Simultaneously with global climate factors, other global change factors will influence cropping and food systems. Perhaps most importantly, increased transportation and exchange of plant materials will speed the homogenization of micro-organism communities. This process will include more rapid introduction of new plant pathogens. The introduction of other types of plant-associated micro-organisms may go unnoticed for some time because of a lack of baseline inventories of micro-organisms against which to compare any new introductions.

3.2. Effects are mediated through crop plants

Terrestrial vegetation supplies the majority of the energy needed to establish, maintain, enrich and change communities of micro-organisms in the soil and to drive ecosystem functions. As primary producers, plants assimilate solar energy and the inorganic elements carbon, hydrogen and oxygen into organic compounds through photosynthesis. When plants die, canopy litter and root biomass supply further nutrients. The efficiency of carbon assimilation from photosynthesis depends on the biochemical pathway used in assimilating atmospheric CO₂. The majority of plants have a C₃ pathway, in which the first product of photosynthesis contains 3 carbon atoms. C₃ plants, which include major agricultural crop species such as rice, wheat and potato, have poor water-use efficiency (WUE) as much of the water they take up is lost through transpiration. About 3 percent of all terrestrial plant species, including important crops such as maize, sugarcane, millet and sorghum, have a C₄ pathway, with four carbon atoms in the first assimilate they synthesize. C₄ plants are prevalent in tropical climates and have better WUE than C₃

plants, which are more common in temperate climates. High WUE offers a competitive advantage to C₄ plants in high-temperature environments and under water- and nitrogen-limiting conditions.

Climate change will influence the form and function of plants, and there is extensive literature on the influence of high CO₂ on morphology, anatomy, physiology and phenology (Ainsworth and Long, 2007). While C₃ plants will typically respond better than C₄ plants to rising CO₂ levels, the magnitude of this response will depend on water and nutrient availability in the soil, CO₂ concentration, and the WUE of individual crop species and their responses to changing temperature. Higher CO₂ concentration will likely improve WUE and growth in C₃ plants in water-limited environments. C₄ plants are unlikely to be directly affected by changes in CO₂ concentration, but will grow well as temperatures increase. These changes will modify the yield and quality of crops.

With plant-derived organic matter driving “hot spots” of soil micro-organism activity such as the rhizosphere and detritosphere (environment surrounding decomposing litter), climatic changes will influence the dynamics of above- and below-ground communities including those of micro-organisms.

3.3. Climate change effects on functional groups of micro-organisms

3.3.1. Soil, plant and rhizosphere inhabitants

Climate change will affect micro-organism communities and functional groups in the soil, and influence trophic interactions among functional groups. This will lead to changes in the processes and mechanisms that drive soil and ecosystem functions such as nutrient cycling and the formation and decomposition of SOM. Direct and indirect effects of climate change will also change soil structure and thereby influence soil health and the retention of water, air and nutrients (Dijkstra and Chen, 2007).

The main climate-related factors affecting the sustainability of life in the soil are temperature, humidity and nutrient availability. Changes in these physical factors due to climate change will directly influence soil micro-organisms. The effect of rising CO₂ will primarily be indirect and mediated through changes in the above- and below-ground parts of vegetation, because the magnitude of projected atmospheric increases are dwarfed by CO₂ concentration that exists in pore spaces of most soils.

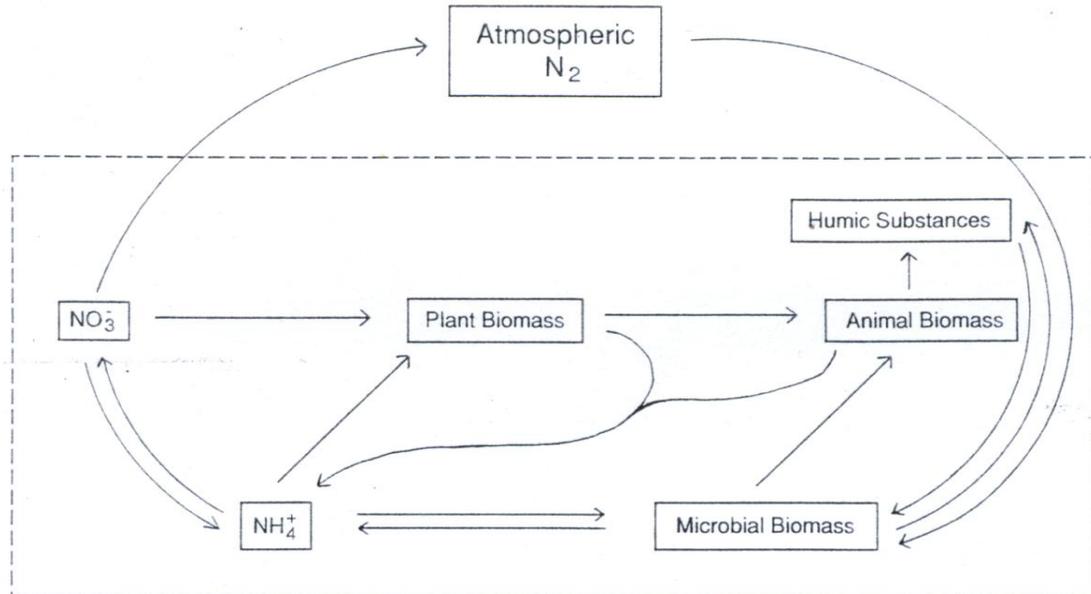
As under current climate, plants will continue to be the main driver controlling the dynamics and functions of soil micro-organism communities under climate change, but quantitative and qualitative changes in above- and below-ground plant tissues will modify these interactions. Rising levels of atmospheric CO₂ will increase C allocation below ground, resulting in increased root growth and root to shoot ratio. Carbon input into the soil generally increases in response to elevated atmospheric CO₂ concentrations even when there is no significant CO₂ stimulation of above-ground growth. These changes, coupled with increased root turnover and root exudation rates will provide greater quantities of substrate for the soil micro-organism community to act upon. In addition to its influence on root biomass, an increase in the level of atmospheric CO₂ affects the quality of below-ground tissue and plant litter, including by raising the C:N ratio, increasing lignification, and giving rise to higher concentrations of tannins and total phenolic compounds (Drigo *et al.*, 2008). Many of these changes will influence the activities of soil micro-organisms that determine soil properties and functions.

The accumulation of SOM depends on physical, chemical and biological processes, many of which are influenced by climate. For example, the extent of mineralization through biological oxidation is determined by climate, certain soil properties (type and amount of clay, pH) and biological activities (especially of larger organisms) (Lavelle and Spain, 2001). The quality of below-ground biomass and plant litter influences the capacity of soil-organism communities to utilize the litter, which in turn determines SOM turnover. Litter quality also determines the rate of SOM decomposition, which is essential for the release of nutrients. The issue of how changes to organic matter turnover influence N and P availability to plants and how this is affected by climate and CO₂ levels is not well understood and

needs further research. However, as the key processes are temperature- and moisture-dependent, climate change will lead to changes in N retention and loss from ecosystems. The nitrogen cycle is illustrated in Figure 3. Warming will generally stimulate soil microbial activity, rates of nitrification, P and N mineralization and soil respiration, but microbial responses to warming may be transient. Many interacting factors influence the intrinsic temperature sensitivity of various soil organic compounds, and despite much research, the temperature sensitivity of SOM decomposition is not well understood.

In addition to influencing nutrient availability, the effects of elevated atmospheric CO₂ concentrations on SOM dynamics may influence soil structure in the long term by altering processes that control soil aggregation, for instance by affecting the concentration of binding agents in the soil. Agricultural soils under intensive farming, growing a limited range of crops, may be less resilient and more vulnerable to these changes than soils under natural ecosystems where the extensive diversity of micro-organisms may allow more rapid adaptation (Mocali *et al.*, 2008).

Figure 3. Conceptual model of the nitrogen cycle. Nitrogen reservoirs enclosed within the dashed lines reside in the soil, whereas dinitrogen is replenished from atmospheric sources (Tate 1995)



The effects of climate change on plant-associated beneficial micro-organisms are difficult to predict (Pritchard, 2011). Plant interactions with rhizobia and mycorrhizal fungi can be altered by small changes in the plant physiological processes that influence allocation to roots. Enrichment with CO₂ may make mycorrhizal associations more beneficial to plants, but N deposition may make mycorrhizal associations less beneficial (Hoeksema *et al.*, 2010). The magnitude of these effects is likely to differ among plant species. The plant and micro-organism signalling that results in rhizobial endosymbiosis is another interaction that may be sensitive to climate. The physiology of the fine roots that form symbiotic relationships with rhizobia and mycorrhizal fungi may be sensitive to climatic shifts, in terms of fine-root “life spans” and turn over. While higher CO₂ levels may be expected to increase root longevity, at least for some plant species, the effects of factors such as temperature and precipitation are less clear. Warming may support increased mycorrhizal associations. Another possible response to a higher C:N ratio is a shift toward greater dominance of soil communities by fungi as compared to bacteria. Changes to the structure and dynamics of soil micro-organism communities will translate into changes in soil processes and functions. Improved understanding of mutualistic association between plants and soil micro-organisms

under climate change will support the development of ways to improve plant nutrition, reducing dependency on chemical fertilizers in the face of rising energy prices and global greenhouse gas emissions.

Little is known about the influence of climate change on micro-organisms or processes that enhance soil and plant health, including the development and functioning of disease suppressive soils. Some rhizosphere micro-organisms offer other benefits, such as buffering plants from drought stress. For example, plant growth-promoting rhizobacteria, such as some *Pseudomonas* spp., may support drought tolerance. Plant phyllosphere communities (leaf surface communities) and their potential responses to climate change are another source of uncertainty. Phyllosphere microbial communities can directly influence plant health in the same way as soil microbial communities can, for example by producing plant hormones that affect plant development and through biological control functions against plant pathogens. Thus, as phyllosphere communities change in response to climate change, there may be shifts in susceptibility to plant diseases. Leaf-surface wetness – often difficult to predict based on common weather measures – has important effects on leaf-surface communities.

Another potentially important effect of rising temperatures is a change in the rate of horizontal gene transfer among plant-associated bacteria (Pritchard, 2011). Warming can accelerate this process, with the potential to speed the evolution of better-adapted beneficial or detrimental micro-organisms.

3.3.2. *Plant pathogens*

The agricultural sector has to wage a continuous battle against plant pathogens. Many control measures – which have included the use of pesticides, surveillance and field-based eradication programmes – have been successful and have contributed to a doubling of food production over the last 40 years. However, the precarious balance between disease and crop is likely to be further complicated under a changing climate, with increasing concerns for global food security (Chakraborty and Newton, 2011). This partly stems from uncertainties regarding how climate change will influence complex interactions between pathogens and their biological and physical environments. Many crop pathogens, viruses in particular, are disseminated and infect plants via insect vectors.

Complex interactions between pathogens, their host plants, ambient weather conditions, and changing agricultural technology make it difficult to predict the effects of climate change on pathogens. Predictions are further confounded by a general lack of specific case studies on plant pathogens. Technological advances, and farmers' and consumers' perceptions of them (e.g. acceptance of GM crops) will also affect the management of pathogens but cannot be predicted accurately. Although the effect of climate change on individual pathogens may be negative, positive or neutral (Chakraborty *et al.*, 2008; Garret *et al.*, 2006), it is certain that climate change and associated changes in atmospheric composition will further complicate the management of plant pathogens. Adapting to gradual rises in temperature or CO₂ may be relatively easy for high-input agriculture. Achieving food security in the face of more frequent catastrophic events such as drought, cyclones and floods will be a greater challenge. Links between severe rust and head blight epidemics and El Niño are already known. Other long-term and well-documented examples of the influence of climate change on pathogens include a link between fluctuations in wheat pathogens (*Phaeosphaeria nodorum* and *Mycosphaerella graminicola*) and changes in spring rainfall, summer temperature and SO₂ emissions (identified using 160 years of data) (Bearchell *et al.*, 2005); early occurrence and increased frequency of potato late blight epidemics in Finland (identified using 69 years of data) (Hannukkala *et al.*, 2007); and links between increased summer rainfall and needle blight (caused by *Dothistroma septosporum*) in pine trees (identified using 40–50-years of data) (Woods *et al.*, 2005). All these studies indicate that climate change will increase uncertainty in plant-pathogen risk predictions.

- Suitability for changed climate

Already, crops are grown in environments that are very different from those in their centres of origin, and where they are exposed to new plant pathogens. For example, viruses such as cassava mosaic (CMV) and brown streak (CBSV) have seriously affected cassava yields in Africa following the crop's introduction from South America. Similarly, a new strain of stem rust (Ug99) of wheat that has arisen in Uganda threatens worldwide production. At the same time, modifications to increase yield – for example to produce larger fruits or grain sizes – have made the development phase during which assimilate reserves are remobilized from storage organs to grains and fruits more vulnerable to pathogen attack (Newton *et al.*, 2010). Urbanization, land degradation and desertification have pushed agriculture to marginal environments. By 2050, global cropping area is predicted to shrink by 8–20 percent due to conversion of croplands to non-food production activities (Nellemann *et al.*, 2009).

As global temperatures increase, some areas where crop growth has been limited, such as those situated at high latitudes and high altitudes, will become conducive to crop production, while some environments where crops have previously been cultivated will become hostile. Global wheat-growing areas are classified into mega-environments based on yield potential as affected by soil fertility, climate, etc. Mega-environment 1 comprising 32 million hectares of highly productive areas in northwestern Mexico, the Indo-Gangetic Plains and the Nile Valley, for example, has high yield potential. By coupling crop simulation and climate-change models, Ortiz *et al.* (2008) have shown that by 2050, the area under mega-environment 1 will be reduced by 51 percent, as areas where the climate is suitable will not have the required soil fertility. As crop species and varieties are reassigned to new environments based on climatic compatibility, plant pathogen populations will be affected. Some plant pathogens will migrate with their hosts from old to new environments, while others that are indigenous to the newer environments may cause disease on crops for the first time. When crops are introduced to new environments where soil or physical conditions are not suitable and plants are stressed, it is predicted that necrotrophs may be more damaging than biotrophs. As potential new disease complexes arise from the interaction of migrating pathogens with endemic micro-organisms that may become pathogenic, targets in crop breeding programmes will need to change.

Climate change will also affect the distribution and impacts of plant pathogens through its influence on the geographical distribution of insect vectors and on the survival of plant pathogens in the environment during transient phases between susceptible hosts. Changes in rainfall and ultraviolet radiation will be important factors affecting vector and pathogen prevalence in addition to regional temperature means. While plant pathogens that are vectored (e.g. by insects) may be limited in their geographical spread, new vectors may arise and move pathogens between crops and other hosts. Often the relationship between plant pathogen and vector is not linked to any critical life-cycle stage of the pathogen in the vector, and therefore different vectors could be employed.

- Elevated temperature

The importance of interactions between micro-organisms and temperature was demonstrated as early as 1932. When wheat was grown in sterilized soil and inoculated with the take-all fungal pathogen (*Gaeumannomyces graminis*), the disease increased with temperature from 13 to 27°C. In natural, unsterile soil, however, the disease declined when the temperature exceeded 18°C because higher temperatures promote other micro-organisms (such as *Pseudomonas* spp.) that are antagonistic to the take-all fungus (Henry, 1932). This example demonstrates the need to study plant pathogens in association not only with their crop hosts but also with their natural environments where other organisms act to increase or reduce their abundance.

Temperature is probably the single most important environmental factor influencing insect behaviour, distribution, development, survival and reproduction (Bale *et al.*, 2002). With a 2°C temperature increase, insects will achieve an estimated one to five additional life cycles per season (Yamamura and Kiritani, 1998). Changes in the physiology, behaviour and population of insects that act as vectors of plant

pathogens will directly influence the epidemiology of the respective pathogens. For example, Stewart's wilt (*Erwinia stewartii*), a bacterial disease of sporadic importance in maize in the northeastern United States of America, is vectored by the corn flea beetle. Survival of the vector through the winter is pivotal to the severity of Stewart's wilt the following year (Castor *et al.*, 1975).

Milder winters associated with climate change would allow larger populations of flea beetles to survive and could extend the growing period for maize with the result that more maize crops are grown each year. The combination of extended maize production and increased vector densities would result in more severe occurrence of Stewart's wilt, ultimately requiring additional insecticide sprays during the winter or deployment of resistant cultivars. Further, at higher temperatures the flea beetle vectors may pass through vulnerable life stages more quickly, reducing the window of opportunity for parasitism. In other instances, such as in the case of barley yellow dwarf virus (BYDV) vectored by aphids, although it might be expected that increased insect survival during the winter months would increase crop losses caused by the disease during the subsequent year, losses due to BYDV are least severe following warmer winters because the resistance of barley to BYDV is enhanced by increased temperatures.

Changes in host-plant resistance to pathogens due to temperature changes are well known but variable. It is difficult to generalize about what the effect of temperature will be in different plant pathogens and their crop hosts. For example, cereal crops such as wheat and oats become more susceptible to rust diseases with increased temperature, while some forages become more resistant to fungi with increased temperature (Coakley *et al.*, 1999). Temperature sensitivity of resistance genes against leaf rust, stripe rust and stem rust in wheat will mean that some genes are less effective at high temperature. Thus, the risks posed by plant pathogens to agriculture will be influenced by various direct and indirect effects of climate change on the complex interactions that exist among plant pathogens, their environments, vectors and hosts.

Some cases in which the effect of rising temperatures has shifted population structures in favour of toxin-producing fungi have already been identified. The necrotrophic toxin producer *Aspergillus flavus* is the most xerophilic of all *Aspergillus* spp. As such, it competes poorly in cool areas (temperatures below 20°C) and is therefore less abundant in cold regions than in warmer regions (temperatures above 25°C) (Cotty and Jaime-Garcia, 2007). Since 2003, frequent hot and dry summers in Italy have resulted in the increased occurrence of *A. flavus*, with consequent unexpected and serious outbreaks of aflatoxin contamination. Serious outbreaks of *A. flavus* in the United States of America have been reported for similar reasons (Leslie *et al.*, 2008). *Fusarium culmorum* and *Microdochium nivale* are the prevalent head blight pathogens in cooler temperate climates of Europe, but in the last decade *F. graminearum* with its higher temperature optima has become the dominant species in the Netherlands, England, Wales and northern Germany (Miedaner *et al.*, 2008). As *M. nivale* is non-toxicogenic and *F. culmorum* produces less mycotoxin than *F. graminearum*, mycotoxin concentrations have risen.

Climate change could drastically increase pathogen severity and result in a pesticide treadmill, as demonstrated by Wallin *et al.* (1950) in a case study of potato and tomato late blight (caused by the fungus *Phytophthora infestans*). Late blight is most severe during periods of high moisture when temperatures are between 7.2 and 26.8 °C (Wallin *et al.*, 1950). For each 1 °C warming, late blight occurs four to seven days earlier, and the susceptibility period extends by 10 to 20 days. An earlier onset of warm temperatures would result in an earlier threat from late blight, with the potential for more severe epidemics and increases in fungicide applications. Increased exposure of the pathogen to a fungicide within a crop season could lead to increased selection for resistance to the fungicide. The duration of each cropping season for potato or tomato may be reduced under elevated temperatures, potentially resulting in more crop cycles per year and allowing increased fungal inoculum to build up. Faster crop development would also result in reduced phyllochrons (the time between the emergence of one leaf and that of the subsequent leaf) with the result that the frequency of fungicide applications would need to be increased.

The overall result would be an increase in amount of fungicides applied per year (Georghiou and Taylor, 1986).

- Increased CO₂

Much of the effect of rising CO₂ and temperature on plant pathogens will be mediated through changes in the host plant. The mode of pathogen nutrition will be an important determinant of this pathogen–plant interaction. Changes in physiology, morphology and nutritional quality of the host plants will influence their susceptibility to plant pathogens. Models predict that crop canopy will be enlarged by rising levels of CO₂, and, when combined with an extended growing season due to rising temperature, pathogens will have increased supply of susceptible tissue if water and nutrients are not limiting. However, different plant pathogens might respond differentially to increased nutrient availability (Walters and Bingham, 2007) and changes in the plant's carbon–nitrogen ratio at high CO₂ levels will influence both biotrophs and necrotrophs. This is because a biotroph often favours higher N:C in plant tissue while a necrotroph will favour lower N:C, although there are exceptions. Nitrogen-use efficiency in plants varies across species and varieties, and depends on their genetic constitution and the prevailing environmental conditions including availability of CO₂ (Hirel *et al.*, 2001). In turn, this influences the C:N ratio in plant tissues and their susceptibility to invasion by, and reproduction of, plant pathogens (Baligar *et al.*, 2001). Also, an enlarged plant canopy might indirectly result in a modified microclimate that is conducive to the development of plant diseases (Pangga *et al.*, 2011).

Other changes in plant physiology and morphology at high CO₂ levels directly influence each development stage of the plant-pathogen life cycle. Fungal spore germination and other development stages that occur before the invasion of host tissue by the necrotrophic *Colletotrichum gloeosporioides*, which infects a type of legume (*Stylosanthes scabra*) to cause Anthracnose disease, are delayed or reduced. A similar reduction in the rate of infection occurs for barley powdery mildew disease (caused by *Erysiphe graminis*) due to increased host resistance through the mobilization of assimilates into defence structures and the accumulation of silicon at sites of fungal penetration (Hibberd *et al.*, 1996). However, following penetration, established colonies of *E. graminis* and *C. gloeosporioides* grow faster under elevated CO₂ due to a reduction in the time taken to produce spores on infected tissue and an up to seven-fold increase in sporulation in infected tissue. Similarly, increases in biomass of the necrotrophic *Fusarium pseudograminearum* at elevated CO₂ (Melloy *et al.*, 2010) leads to increased pathogen biomass in wheat stubbles. It is evident that disease severity at high CO₂ levels is influenced by opposing effects: enhanced host resistance on the one hand, and more plant pathogen infections on the other (Pangga *et al.*, 2011). Furthermore, in *C. gloeosporioides*, increased fecundity at high CO₂ levels, combined with increased trapping of pathogen spores by the enlarged plant canopy, increases the number of infection cycles and this, in turn, accelerates the rate of evolution of the plant pathogen (Chakraborty and Datta, 2003). Fecundity of some rust pathogens also increases at high CO₂, and with increased mutation it seems plausible that new rust races such as Ug99 may appear faster (Chakraborty *et al.*, 2011).

- Water: relative humidity and extreme rain events

The influence of climate change on crop growth has indirect effects on the morphology of the crop that in turn influence relative humidity within the crop. A crop that has high growth that is not limited by nutrient availability, and in particular nitrogen, will form a denser canopy. A denser canopy increases relative humidity on plant surfaces, such as stems and especially leaves, within the canopy and favours dew deposition as temperatures drop during the day. The presence and duration of leaf wetness is a key factor influencing foliar infection by most plant pathogens.

Bacteria are better able to respond to moisture pulses regardless of temperature, while fungi only respond to moisture pulses during cooler periods. In general, dry periods tend to encourage insect and virus outbreaks, while wet periods encourage fungal and bacterial diseases. However, great care has to be taken in such generalizations, as pathogens such as powdery mildew thrive in conditions of relatively low moisture.

The impact of droughts or flooding on the host crop will indirectly influence the impact of a crop pathogen. On the other hand, in the case of aflatoxin-producing fungi, which are common throughout soils, air, and on crop surfaces, grain colonization is significantly increased when host crops are drought stressed prior to harvest (Cotty and Jaime-Garcia, 2007).

Elevated rainfall in short bursts can lead to water-logging of soils, which encourages root diseases by reducing the oxygen supply to roots and enhancing soil-borne plant pathogens. Some of the most destructive of these (e.g. *Phytophthora* and *Pythium* spp.) belong to the oomycetes group and cause devastating diseases in several dicotyledonous crops. Compacted, poorly drained soil is not only an important factor affecting many soil-borne diseases, it also increases canopy humidity and thereby affects leaf infection as described above. To complicate matters further, certain oomycetes are indispensable in nutrient cycling and exchange.

- Wind

Biotrophic plant pathogens often pass through several stages to complete their life cycles. Some, such as rusts and smuts, produce minute specialized spores such as urediniospores in high abundance, which are specifically developed for wind dispersal. Hurricanes can facilitate transcontinental invasion of these fungi. For example, Asian soybean rust (*Phakopsora pachyrhizi*) has spread rapidly in the Americas. Similarly, Ug99, the new virulent strain of wheat stem rust, has moved from Uganda to the Middle East and is in transit to India because of transcontinental winds (Nazari *et al.*, 2009).

3.3.3. *Biological control*

It is impossible to generalize the effect of climate change on micro-organisms used for biological control as they are taxonomically and functionally very diverse, and range from weed pathogens to microbial antagonists of animal and human pests. Therefore, the discussion below will focus mainly on the impact of climate change on micro-organisms used in augmentative insect control. Nevertheless, some generalized principles can be suggested, based on the lifecycle and population dynamics that are specific to any given micro-organism. Viruses and bacteria enter the insect host orally, whereas fungi invade through the cuticle. Once inside the insect, they proliferate and kill it when resources are depleted. The final stage of the micro-organism's infection path results in the release of infectious propagules (Roy *et al.*, 2009). The infectious propagules remain in the environment until the infection process repeats itself. During their stay outside the host, some insect pathogens can grow and multiply in/on dead organic matter. Some insect pathogens can exploit many different hosts, while others are host specific. The reproductive rate of biological control micro-organisms is among the most important parameters, especially for inundative biological control. Insect pathogen fitness is defined as the basic reproductive rate (R_0), which is the number of new infections generated by one original infection when invading a clean, susceptible population. Both transmission efficiency and survival within and outside the host are components of R_0 and are modulated by the biotic and abiotic environment.

There is currently no information on changes in the population dynamics of biological control micro-organisms as a function of the combined effects of climate change. However, several studies have looked at the effect of individual climatic factors on biological control micro-organisms. Although most of these studies have been deterministic and static, and have been based on simple laboratory and greenhouse trials, some comprehensive field studies of the effect of single climatic factors have been undertaken. The following sections discuss the impact of the three most-cited climate parameters: increase in temperature, increase in humidity and increase in CO₂ concentration.

- Temperature

Biological control micro-organisms are physiologically sensitive to temperature, with growth rates highly dependent on temperature. Coupled with short life cycles, high mobility and high reproductive potential,

even modest changes in the climate are expected to have a rapid impact on their distribution and abundance (Ayres and Lombardero, 2000). The most likely consequences of increased temperature are shifts in the geographical distribution of biological control micro-organisms and therefore shifts in patterns of crop loss. The IPCC predicts that infectious diseases will in general increase in prevalence in temperate zones where the climate is predicted to become warmer and wetter. Numerous studies have calculated the temperature growth thresholds for specific micro-organism biological control agents *in vitro*. For example, *B. bassiana*, among the most studied and used pathogenic fungi, partly because its different strains attack many insect hosts, grows at a wide temperature range (8 to 37°C) but has optimal growth at elevated temperatures (25 to 35°C). Scientists have speculated that a plausible direct effect of climate change will be that, due to warmer temperatures, biological control micro-organisms will exploit geographic locations further to the North and South, and in the tropics at higher altitudes. Indeed, performance of *Metarhizium anisopliae*-based biopesticides has been found to vary dramatically across even small spatial scales, in response to relatively small changes in temperature (Klass *et al.*, 2007b).

Within species, biological control micro-organisms vary widely in their thermo-tolerance. For example, individual *B. bassiana* isolates exhibit optimal temperatures as a function of the habitat they colonize: isolates from the Arctic and forested habitats were found to grow at lower temperatures than those from tropical agricultural habitats, which grew at temperatures in excess of 37°C (Bidochka *et al.*, 2002). Hence, shifts among populations of biological control micro-organisms within the same species are expected to occur.

However, insect pest populations are also highly responsive to temperature increases because they also have short life cycles, high mobility and high reproduction potential. Insects are ectothermic, meaning that they do not self-regulate to keep their body temperatures constant, but adjust to ambient temperature. This makes them very sensitive to temperature changes and prevents them from surviving below and above certain thresholds. As such, temperature is probably the single most important climate change factor for insects. Insect hosts are set to expand their geographic ranges as a result of climate change, but how these expansions will interact with those of pathogens and how the insects and the pathogens will affect each other's fitness is less clear and will depend on specific circumstances. For example, the incubation period of *Plasmodium* within the *Anopheles* mosquito is a key determinant of the rate of malaria transmission to humans. This incubation period largely depends on temperature, with increasing temperatures leading to decreasing incubation periods and increasing densities of infectious malaria mosquitoes, ultimately leading to more malaria in the human population. Fungal biopesticides, such as those based on *Metarhizium anisopliae*, are capable of reducing infectious mosquito density considerably, provided they kill mosquitoes within the incubation period before they become infectious. As climate change is set to shorten the incubation period of mosquitoes carrying the malaria parasite, more virulent strains of *M. anisopliae* will be needed to maintain the same effect on the density of infectious mosquitoes.

Many insects survive the cold of winter by spending extended periods of their lifecycles in the soil as larvae or pupae. With increasing winter temperatures, this strategy may enable insect taxa to expand their geographical ranges. Larvae and pupae are known to be much more susceptible than adult insects to micro-organism attack, and this could facilitate the use of biological control micro-organisms even at low population densities. In particular, biological control micro-organisms that can persist in the soil, such as baculoviruses and fungi, are able to take advantage of the presence of more-sensitive host stages at expanded geographical ranges. On the other hand, within their original geographical ranges, increased temperature could result in shorter over-wintering periods for the insect hosts, increasing their ability to withstand the effects of biological control micro-organisms.

Deductions from the effect of linear temperature changes on mostly pure micro-organism cultures in highly controlled laboratory and screen house studies must be treated with caution for a variety of reasons. Diurnal temperature oscillations (regular temperature fluctuations between day and night) strongly affect processes governed by micro-organisms. Entomophthoralean fungi, a specialized group of

insect pathogenic fungi, exhibit an adaptive diurnal pattern of host death and sporulation (Neilson and Hajek, 2006). Host death occurs in the late afternoon or early evening and the fungus releases infective conidia during the night when relative humidity is high, a pattern which benefits transmission of the fungus between hosts. Host death and sporulation are highly synchronized based on a specific diurnal pattern of temperature and moisture, and the effect of an increase in temperature in such a host–pathogen system is difficult to predict. In models of the interactions between insect hosts and parasitoids, divergences between the thermal preferences of the host and those of the parasitoid lead to disruption of temporal or geographical synchronization, decoupling the host–parasitoid system, and ultimately increasing the risk of host outbreaks (Hance *et al.*, 2007). Although biological control micro-organisms are generally considered more robust and adaptable than parasitoids, the same scenario could happen with micro-organisms, especially those that are highly synchronized with their insect hosts.

Insect pathogens predominantly live inside the host body and may therefore be less affected by external climatic changes, as they basically follow the development of their hosts. The effect of temperature on biological control organisms may be mainly manifested indirectly through changes in the body temperature of insect hosts, rendering the effect more complex. Research has shown that some insect pathogens, indeed, depend less on ambient temperature than on the temperature of their insect hosts. Work on the use of *Metarhizium* spp. for biological control of locusts and grasshoppers has shown that the ability of a pathogen to kill the host depends crucially on host body temperature and therefore on changes in host body temperature as influenced by external environmental conditions (Klass *et al.*, 2007).

Temperature can affect host–pathogen dynamics in a variety of other, subtle, ways such as alterations to the latent period of infection, host and pathogen mortality, pathogen virulence and host resistance, and host defence mechanisms such as the innate immune system and melanin production (Roy *et al.*, 2009). For example, the fungus *Entomophaga grylli* can be a major mortality factor of the variegated grasshopper *Zonocerus variegatus*. However, an increase in environmental temperature of 2°C enables infected individuals to recover better from the pathogen by raising body temperature through behaviour such as basking which confers protection to the insect via elevated melanin levels (Blanford *et al.*, 2003).

- Humidity

Infection of insects by fungal pathogens is favoured by high humidity. Hence, their use would be facilitated in areas with extended periods of high humidity and reduced in areas with drier conditions. During the normally wet Northern California winter, the fungal pathogen *Pandora neoaphidis* causes catastrophic mortality to the pea aphid, but during hot dry periods, the impact of the pathogen declines to virtually non-existent levels (Gutierrez *et al.*, 2008). However, humidity not only influences pathogens but also the insect host, and, therefore, many of the more complex effects of temperature on the interactions between insect hosts and pathogens also apply in the case of humidity.

Changes in humidity may have subtle and hitherto unexplored effects on biological control micro-organisms in the soil, such as those used for conservation biological control. Potato common scab, caused by *Streptomyces scabies*, causes virtually no reduction in overall crop yield, but drastically decreases marketability and cooking quality. *Streptomyces* spp., *Bacillus* spp. and *Pseudomonas* spp. produce secondary metabolites antagonistic to potato common scab. These antagonists are better at controlling potato common scab in cold and wet conditions. In hot and dry conditions, the soil micro-organism community would produce these secondary metabolites as gases, which are much more prone to volatilization. In contrast, wet soils reduce the loss of volatile metabolites to the atmosphere by trapping a larger proportion of the gases (Sturz *et al.*, 2004).

- CO₂

The impact of increasing levels of CO₂ on biological control micro-organisms is relatively less studied than temperature and humidity. In general, direct exposure to high CO₂ concentrations often inhibits the

growth of culturable bacteria and fungi, which are used as active ingredients in biopesticides. Because all micro-organisms currently used in augmentative biological control are aerobic, it is plausible that the direct effect of increased CO₂ levels will be reduced growth caused by decreased respiration, and therefore reduced efficacy against insect pests.

However, just as is the case for temperature and humidity, the effect of increasing levels of CO₂ on biological control micro-organisms becomes more difficult to predict when host–pathogen interactions are considered in unison; arms races between pathogens and insects lead to much more complex outcomes than simple changes in reproduction rates.

3.3.4. *Post harvest and food transformation*

Micro-organisms are important in protecting crops after harvest and in transforming and maintaining food. Many micro-organisms affect product quality through post-harvest spoilage and some produce toxins that are harmful to human and animals that consume the affected products. The impact of climate change on micro-organisms that produce toxins causing post-harvest spoilage has recently been reviewed by Paterson and Lima (2010). This section mainly deals with beneficial micro-organisms that protect produce post-harvest and transform agricultural produce into food products. The potential effect of climate change on micro-organism genetic resources can be examined by considering three possible scenarios frequently mentioned by the International Panel on Climate Change (IPCC): global warming, increased precipitation in some areas and catastrophic events (especially at low latitudes) (IPCC, 2007).

- Global warming

Increased temperature is likely to interfere with the ripening of fruits and vegetables, causing a shift in the life cycles of micro-organisms naturally resident on their surfaces. These micro-organisms will also be influenced by any metabolic changes that climate change may bring about in the produce (e.g. changes in pH or sugar content). Many of these organisms can potentially provide protection (Ippolito and Nigro, 2000) or competition to micro-organisms that are harmful to the quality of the produce. Some are used by the industry as post harvest biological control agents. Examples include soaking fruits in suspensions of yeast (e.g. *Meyerozyma guilliermondii*) to reduce the presence and activity of spoiling micro-organisms, particularly moulds of the genera *Botrytis*, *Alternaria* and *Penicillium* (Zhao *et al.*, 2009; 2010). However, very little is known about the composition and dynamics of micro-organisms living on the surface of agricultural produce. Global warming is expected to select naturally occurring species or strains that prefer or can tolerate high temperatures. Although it is obvious that such selection would affect microbial biodiversity and that synergistic and competitive relationships including new biological control options may develop, the magnitude and direction of these changes can not be predicted.

Another aspect to consider is that while average global warming may be no more than a few degrees Celsius over several years, local changes of temperature may be much more severe. This may lead to a state of stress in populations of beneficial micro-organisms, which would in turn increase mutation rates with consequent selection of strains quite different from those originally present (Foster, 2007). Once the dynamic equilibrium between spoilers and controllers is broken, intense pesticide treatments will be needed to maintain quality and food security. This can lead to negative consequences in terms of residues, higher costs and potential dangers to human health, as demonstrated in apples, where bacteria and moulds start to predominate when the presence of yeast declines (Doores, 1983).

- Increased precipitation

An increase in overall humidity is expected to boost the growth of moulds on plants, especially if this is coupled with rises in temperature. Increased precipitation events can lead to large increases in pesticide usage and systemic pesticides may prove more reliable than contact pesticides, which may be washed off by intense or more regular rainfall. Intensive use of systemic pesticides can have significant influence on

some surface-borne micro-organisms such as yeasts leading to changes in the genetic structure of the population (Cubillos *et al.*, 2009).

- Catastrophic events

Drought and flood are the two major types of catastrophes predicted at lower latitudes under climate change. The effect of these extreme events on micro-organisms may be direct or indirect. Severe drought or flood can directly wipe out entire populations of micro-organisms associated with agricultural production. However, genetic resources of micro-organism associated with food processing, transformation and protection are unlikely to disappear entirely, as the most important genetic resources may be conserved in various laboratories and factories and any catastrophic event caused by climate change is unlikely to affect all areas of the globe. Catastrophic events such as droughts can lead to the migration of large human populations, often carrying stocks of useful micro-organisms.

Indirect effects of catastrophic events would arise from the destruction of habitats and hosts that normally support beneficial micro-organisms. The effects of losing beneficial micro-organism genetic resources may extend far beyond their immediate spheres of influence. Such losses may affect human health, wellbeing, food safety and food security in the wake of catastrophic events that limit the availability of safe and nutritious food due by disrupting supply and distribution networks. The “take home” message from this discussion is that these micro-organisms are not mere food additives, but are integral parts of complex and dynamic interactive systems that include micro-organisms, pathogens, plants, animals and humans within physical environments affected by anthropogenic factors. They affect post-harvest processing, storage, transportation and distribution. Even an apparently small and insignificant event can have system-wide effects and lead to serious consequences (Mazzocchi, 2008).

3.4. Lessons learnt and limitations

3.4.1. *A lot of complexity and noise*

The current limits to our understanding of how micro-organism communities respond to environmental conditions makes it challenging to anticipate how climate change will influence these communities. Uncertainty affects future predictions at every level: the climate itself, micro-organism responses to climate, and micro-organism impacts on crop productivity. The complexity of these interactions can be demonstrated through the example of a predictive model for *Botrytis cinerea* and *Trichoderma* spp.: respectively, a plant pathogen and a biological control organism used to control it. Model results showed interactions to be highly dynamic and unpredictable (Jeger *et al.*, 2009). Even very small changes in parameter values used in the model resulted in large changes in interactions. For some of these changes, it was predicted that equilibrium would not be reached until 10 years after the change occurred.

3.4.2. *Other important factors (e.g. ultraviolet radiation, sea level, drought, salinity) are excluded*

A factor that will have an especially big impact on micro-organisms for biological control, particularly those used in inundative control, is ultraviolet-B radiation (UV-B), which according to some climate change models is set to increase due to depletion of the ozone layer. Fungi and bacteria are generally more sensitive to damage by UV-B radiation than weeds and insects are. However, micro-organism species differ in their UV-B sensitivity. Unfortunately, entomopathogenic fungal taxa currently being used in augmentative biological control have poor survival rates when exposed to UV-B, and some biological control products are now formulated with UV-B protectants. In the case of conservation biological control, the consequences of increased UV-B can also be significant and unexpected. Increased UV-B irradiation can have indirect negative effects on the species composition of micro-organism communities deep under the ground, including noteworthy biological control organisms living in the

rhizosphere such as endophytes and mycorrhizae, by altering the quality and quantity of plant root exudates. In one study, populations of rhizosphere inhabitants decreased by 20 percent because of UV-B. This reduction even coincided with an increase in root biomass, which is counterintuitive, as an increase in root biomass normally enhances micro-organism populations in the rhizosphere (Caldwell *et al.*, 2007).

3.4.3. *Importance of the ecosystem approach*

The ecosystem approach is particularly important for understanding the role of micro-organisms in agricultural systems because of the multiple interactions that occur among micro-organisms and with the other components of the system, including plants. Micro-organisms link cropping systems across space and time, as micro-organisms selected for by one cropping system may have effects on other cropping systems. Building our understanding of micro-organism communities will be important for understanding climatic effects on agriculture. An approach that incorporates ecosystems will make it possible to evaluate climate effects more realistically, and will facilitate estimates of error in predictions. Historically, the study of soil biodiversity began with the study of food webs. Studies of food webs illustrated the fact that each process is interlinked and that the organisms involved exist together and are bound ecologically. The soil food web is fuelled by a variety of micro-organisms – mainly bacteria and fungi, protists, nematodes and predaceous Acari – that interact with plants, animals and physical components of the air and soil to convert nutrients from organic to inorganic (Jenkinson and Ladd, 1981; van Elsas *et al.*, 2008). Soil food webs are characterized by several levels of complexity, as they include grazers, predators and superpredators. Fungi and bacteria perform distinct functions and often colonize quite separate microsites. Mycorrhizal fungi have roles that are critical to the success of the plants with which they are associated.

The interactions between any two organisms are strongly influenced by environmental conditions (and thus will be affected by climate change) and the level of variability is further increased by orders of magnitude as more and more organisms within the ecosystem interact. In the case of mycorrhizal fungi, environmental conditions will determine whether fungus and plant form a relationship, and how much benefit the plant gains from the mycorrhizal fungi (under some environmental conditions the relationship may be slightly detrimental to the plant). Environmental conditions are the key in determining how much damage pathogens cause to plants, and thus in determining how much benefit plants may gain from micro-organisms that act as biological control agents for the pathogens.

In the case of biological control, the ecological processes determining the outcome (e.g. success or failure) for each biological control agent and its target host are complex and therefore often poorly understood. It is also difficult to generalize about biological control processes because of the wide variety of types of biological control (augmentative or conservation), types of targets (insect pests, plant pathogens or plants) and biological control agents (fungal, bacterial or viral). Most models aimed at understanding the dynamics or even predicting the outcome of the use of a biological control agents have focused on small temporal and spatial scales, while higher hierarchical levels remain – partly due to complexity – unexplored. Yet, it is at such higher levels that the effects of climate change are taking place.

Investigations have focused largely on micro-organisms that are used commercially. Even for micro-organisms used in augmentative biological control, basic characteristics, such as host range, are still debated. For example, host ranges established from laboratory or confined screen-house tests seem larger than actual host ranges observed in the field. This is presumably related to a lack of spatial or temporal synchronicity with the hosts. Factors influencing the spatial distribution of pathogens and their hosts are fundamental to disease dynamics, especially when vertically transmitted, with the probability of pathogen transmission decreasing with increasing distance between susceptible hosts. Unfortunately, spatial dynamics of insect pathogens have not been studied on a large landscape level. Ecological interactions of biological control micro-organisms might be much more complex than currently thought. For example, naturally occurring strains of the same micro-organisms that are used for augmentative control are responsible for natural epizootics among non-target insects. Such interactions, poorly investigated and

often ignored, are important drivers of population densities in insect hosts, non-target hosts and the micro-organisms themselves (Roy *et al.*, 2002), especially in the face of climate change. Populations of biological control micro-organisms could maintain themselves on new non-target hosts or, alternatively, be reduced if non-target hosts disappear because of climate change.

3.4.4. *Combinations of factors have to be taken into account*

Incorporating changes in single environmental parameters will rarely be adequate for understanding climate change effects. For example, the structure and function of soil and rhizosphere micro-organism communities are influenced by combinations of atmospheric CO₂, soil temperature, moisture and nutrient levels, and predicting their performance based on a limited number or combination of factors will give erroneous predictions. Additionally, soil heterogeneity, buffering and functional redundancy can obscure, mask or compensate localized effects of environmental influences. Temperature has important effects on many plant pathogens, and changes in temperature to more closely match pathogen optima may increase risk, all else being equal. However, if the change in temperature is associated with a decrease in available moisture on plant surfaces, the net effect may be to reduce disease risk, as free moisture supports the reproduction of many pathogens.

Research on impacts of climate change on biological control micro-organisms has been virtually non-existent, with most work concentrating on the effects of a single atmospheric or meteorological parameter on the host, micro-organism or their interaction. Deductions from single parameter-based effects on mostly pure micro-organism cultures in highly controlled laboratory and screen-house studies must be treated with caution. Temperature, humidity and CO₂ will not change individually but in unison because of climate change. In addition, changes in these parameters will be accompanied by changes in other, less often investigated parameters. Also, micro-organisms can tolerate one suboptimal factor if all others are near optimal. Very few studies/models have looked at the combined effects of climate change parameters. Unless a comprehensive holistic multi-parameter approach is used, the predictive power of existing models is limited.

There may be feedback loops for some types of environmental effects (Garrett *et al.*, 2011). For example, disease management strategies that work under lower pathogen pressure may have reduced efficacy when abiotic environments are more conducive to disease and so become “saturated” with pathogens. Biological control may be subject to this type of constraint. Likewise, forms of disease management such as sanitation (removing infected plant materials from in and near a field) may have reduced efficacy if abundant regional inoculum sources make within-field inoculum sources irrelevant. Because of these types of feedbacks, small increases in climatic favourability (or unfavourability) to disease may be magnified.

Research on the effect of climate change on plant responses has been extensive, but work on herbivore responses has been less complete and work on higher trophic levels nearly non-existent. Weed pathogens, and pest and disease pathogens, used for biological control are at the second and third trophic levels, respectively. Predicting the effect of climate change on members of a third trophic level is very difficult, because many direct effects of climate change on the two lower levels trickle up to the third level as indirect effects, and vice versa, creating feedback loops. Only for aphids have researchers begun to investigate responses at a third trophic level, including aphid predators and parasitoids. From these studies, it has become clear that the tri-trophic interaction involving insect predators and parasitoids is very complex and therefore often unpredictable, and this must hold also for the less-studied tri-trophic interaction involving insect pathogens. To further complicate the situation, interactions within the third trophic level, namely between predators/parasitoids and insect pathogens, are even less well known (Hoover and Newman, 2004).

The abundance of a target insect pest regulates the population dynamics of its biological control micro-organisms. For example, in the absence of its nematode pest, the endophyte *Fusarium oxysporum*, a potential biological control agent, remains dormant rather than growing inside banana plants. Its population only increases when triggered by the presence of nematode pests, a process called priming.

An interesting example of the effect of climate change on the tri-trophic interaction between insect pathogen, insect pest and plant is provided by Neumeister (2010). In temperate regions, many insect species have broad thermal tolerance but are living below their temperature optima. Climate change might allow them to increase their population growth rates. The combined effect of elevated CO₂ concentrations and increased temperatures might also lead to increased biomass production – especially in C₃ plants – but with lower protein content. As a result, C₃ plants might be able to support insect populations that are larger but have lower overall fitness, because the insects have access to more plant material but of lower quality. Insect pathogen populations could take advantage of the larger, yet weaker, insect host populations, because they are more pathogenic if their host is weakened. They are also more deadly when insects are overwintering, especially as larvae. On the other hand, increasing insect pathogen populations could cause the target insect populations to crash with the consequent loss/extinction of the insect host that the pathogen depends upon for its survival.

3.4.5. *Lack of essential information for decision making*

It is important to develop a more complete understanding of many micro-organisms in order to determine how to prioritize micro-organism conservation. The role of many types of non-culturable micro-organisms, such as the Archaea, is little understood although they are common in many agricultural soils (Roesch *et al.*, 2007). Lack of understanding of ecological roles is generally associated with a lack of understanding of how to increase or reduce the abundance of these micro-organism taxa. Even for relatively well-studied micro-organisms, environmental effects on functionality may only be understood for some weather variables. If climate change results in unusual weather scenarios, we may lack information about how even well-studied micro-organisms will respond and interact with other species.

Drivers such as globalization, agricultural intensification and climate change will influence the predominance of different plant pathogens in a manner that is difficult to predict.

The risk to agriculture posed by this uncertainty can be limited by greater knowledge of, and access to, crop and microbial materials. For example, the characterization and selection of resistant or tolerant crop germplasm can be used to mitigate the effect of prevalent plant pathogens. Furthermore, this crop germplasm can be deployed in combination with micro-organisms that are known either to be antagonistic to those that cause plant disease or to enhance ecosystem resilience and hence crop performance through enhancing ability to tolerate the impact of plant pathogens. Finally, characterizing different variants of given plant pathogens would facilitate the development of diagnostic tools that encompass all known variability. This would facilitate the rapid and precise detection of specific plant pathogens that are known to reduce yields for targeted cropping systems. Surveillance systems would furnish real data on the presence of specific plant pathogens and hence the risk they are posing. This in turn could be used for contingency planning that may include the deployment of crop germplasm with resistance to the recently found forms of plant pathogen.

For many biological control micro-organisms, especially those that play a role in conservation biological control and are less known, the impact of basic climate-change parameters other than temperature on their growth rate and survival is unknown. Even less information is available on the impact of climate-change parameters on interactions between biological control micro-organisms and their hosts. Fundamental aspects of biological control micro-organisms, such as reproduction and infection pathways, which are essential for predictive modelling, are not always known. Until recently it was assumed that the transmission of baculoviruses, a specialized group of insect pathogenic viruses with commercial potential, was primarily horizontal, resulting in overt and lethal infection. However, recent studies have revealed

some vertical transmission of these viruses (Graham *et al.*, 2004). Such information, relatively basic compared to what is known in non-micro-organism systems, is essential in order to model the micro-organism/host systems and ultimately the impact of climate change on this relationship. Vertical transmission, which is more widespread than previously thought, allows for sublethal effects on host fitness, and renders the baculovirus populations much less density-dependent, with big implications for population models.

Other fundamental aspects of micro-organism/host systems that are not well understood include host range and environmental persistence. Together, vertical transmission, extended host ranges and prolonged environmental persistence result in more robust and less density-dependent micro-organism populations, especially in view of changing climatic factors that affect the host populations. Modelling the impact of micro-organism biological control organisms has mainly focused on two parameters: efficacy of and mechanism used by the biological control micro-organism. Sometimes, other parameters are found to be more important. Using *Trichoderma* spp./*Botrytis cinerea* as a model for quantifying the interaction between a biological control organism and a plant pathogen, respectively, Jeger *et al.* (2009) actually found that colonization of healthy plant tissues by the biological control organism is among the most important yet overlooked parameters.

IV. ROLE OF MICRO-ORGANISM GENETIC RESOURCES IN CLIMATE CHANGE BUFFERING, ADAPTATION AND MITIGATION

4.1. Role of micro-organism genetic resources in climate change buffering

4.1.1. Definition

Micro-organisms play a key role in climate change buffering, which we define as lessening of the impact of climate change. The most important role micro-organisms play in buffering climate change is in the soil, where they fulfil a key role in breaking SOM down and making it available to crops while, at the same time, contributing to the rate of production and consumption of CO₂, CH₄ and nitrogen. Worldwide, an estimated 70–140 million tonnes of nitrogen are fixed by micro-organisms annually. Soil micro-organisms provide opportunities to rely on biological processes rather than external, climate change-inducing, inputs such as synthetic fertilizer. Increased biodiversity confers increased ecosystem resilience, which can buffer and stabilize climate change impacts. Micro-organisms other than those fulfilling soil functions can also play a key role in climate change buffering. For example, biological control micro-organisms can stabilize population levels of plants and herbivores, making them more resilient to climate change (Hoover and Newman, 2004).

4.1.2. Resilience and sustainability of the ecosystem

Resilience, the tendency of a system to return to its “original” state after a perturbation, is a common goal for crop-based agricultural systems. Sustainability, the tendency of a system not to degrade from an “original” state, is another common goal. As an example, an agricultural system may include disease-suppressive soils. If the system is resilient, the soils will maintain or return to disease suppressiveness after a perturbation such as a change in temperature or precipitation. Similarly, if the system is sustainable, it will not suffer a decrease in disease suppressiveness. If a system is resilient and sustainable, the original “status quo” of the system will not be diminished if the environment changes, either because of changed land-use practices or climate change. However, it cannot be assumed that natural resilience and sustainability is inherent in every ecosystem. For example, some soils have become degraded by the actions of humankind and there is therefore no benefit in sustaining them in their current form; rather, changes in management practices, and potentially amendments to micro-organism communities, are needed in order to produce a preferred state.

4.1.3. *Micro-organism biodiversity leads to ecosystem resilience and sustainability*

Microbial biodiversity contributes to ecosystem resilience and sustainability, although understanding of this relationship is still just developing. For example, overly simplified agricultural systems such as large-scale monocultures of similar crop varieties may be less resilient and sustainable, because such systems may support the build-up of very large pathogen populations, and exert strong selection pressure for pathogens to overcome crop disease resistance. This is illustrated by the concept of “portfolio stability” which refers to the number of crops grown on a farm and their degree of risk from plant pathogens (Robison and Brake, 1979). If a farmer’s portfolio includes more crop species, a severe problem with one species will have less impact on the farmer. In many ecosystems, functional diversity is observed to be more important than taxonomic diversity, and the same is likely also to be true for micro-organisms contributing to resilience. This provides further incentive to develop a clear understanding of micro-organism functions. New tools are now available to elucidate micro-organism functions without the need to establish their identity. Some of these are listed in Table 2. However, until the contributions of micro-organisms are completely understood, maintaining biodiversity, *per se*, is a good strategy for a number of reasons. Among these: first, maintaining biodiversity will tend to maintain the micro-organisms particularly valuable for ecosystem services; and second, maintaining biodiversity will tend to maintain micro-organisms that are either highly plastic, such that the same species can provide services regardless of the abiotic environment, and/or maintain a wide enough range of micro-organisms to provide services regardless of the abiotic environment through functional redundancy.

The concept of “complex adaptive systems” can be applied to micro-organism communities (Levin, 2005) based on the following characteristics: a) “sustained diversity and individuality of components” – micro-organism communities meet this criterion by exhibiting high diversity, as well as individuality in the sense of more-or-less distinct species; b) “localized interactions among those components” – a large number of micro-organisms generally interact only with other micro-organisms that are close enough in space to compete for resources and experience the same chemical environment; c) “an autonomous system that selects from among those components, based on the results of local interactions, a subset for replication or enhancement” – those micro-organisms that can reproduce most successfully in a small local environment (such as a leaf or root) will become more abundant there and may then successfully disperse to other environments.

A complex adaptive system may be resilient and sustainable – and thereby buffering the effects of climate change – if it tends to maintain its higher-level traits despite changes at lower levels. That is, a micro-organism community may be resilient if it maintains functions (such as disease regulation or nutrient cycling) despite changes in the structure of the micro-organism community (such as changes in abundance of particular taxa or strains). It is reasonable to think that maintaining micro-organism biodiversity systems will support resilience in complex adaptive systems. In practice, maintaining particular strains or taxa may often be most important for maintaining ecosystem services.

4.1.4. *Adaptability of micro-organism genetic resources to a changing ecosystem*

The precise impact of climate change on micro-organism genetic resources for agriculture is uncertain because some changes will favour some organisms and inhibit others. Caution is required against a simple approach to predicting the effects of individual environmental factors on single micro-organisms without adopting an ecological approach. It is the combined interactions among micro-organisms and their relationship with crops in an ecosystem that will dictate the impact of changes in climate. Climate change must be considered as a selection pressure that is additional to existing selection pressures, such as changes in agricultural practices and land use, and adds further complexity and uncertainty to the sustainability of farming systems. As such, climate change must not be studied in isolation but rather as an intrinsic part within a holistic ecosystem.

Recently, technologies have been developed that allow studies not only of single micro-organism species but also of density, diversity and activity of micro-organism populations isolated across a wide range of natural environments (Van Elsas, 2006). This has enabled improved characterization of micro-organism community structure and diversity across multiple situations, and allowed the identification of populations preferentially associated with various habitats under different environmental scenarios. It is clear that micro-organisms are highly adaptable to different ecosystems. This can be partly explained by their short reproduction time (from hours to days), which allows them to respond to introduced selection pressures very quickly. Micro-organisms live in all environments ranging from thermophilic to halophilic conditions, illustrating the highly dynamic response of micro-organism genetic resources to different human or climatic impacts (Averhoff and Muller, 2010). The adaptability of micro-organisms to different pressures is clear in the behaviour of extremophilic prokaryotes. They are able to live in environments characterized by extremely high or low pH, temperature, salinity, pressure and various combinations thereof. Ever since extremophiles were discovered, their physiology and their adaptation to the hostile environment have attracted much interest, and led to their exploitation in novel biotechnological tools (e.g. thermo-active enzymes) (Moreno *et al.*, 2005).

Ecologists studying plants and animals have long recognized that genetic diversity across a landscape is central to understanding the impact of environmental factors. Micro-organisms offer valuable insights into relative influence of dispersal limitations and environmental heterogeneity, as well as environmental and evolutionary changes, in shaping the structure of ecological communities. In some cases, the functional adaptability of micro-organisms to environmental changes hides changes in the community structure.

4.2. Role of micro-organism genetic resources in adapting to the effects of climate change

4.2.1. Definition

Micro-organisms can play a key role in assisting humankind to adapt to the effects of climate change. For example, crop exposure to abiotic stressors will shift under climate change. Plant-associated micro-organisms that contribute to traits such as drought tolerance may help in adapting to these effects. Much work needs to be done to better understand how micro-organisms may contribute to drought tolerance, and the extent to which micro-organisms from one plant species may be adapted for use in other plant species. Micro-organisms that have the potential to support crop adaptation to challenging environments are one priority for conservation. Further studies are needed to help overcome the limitations to current understanding of the interactions among environment, plants and micro-organisms in this context.

4.2.2. Conservation biological control

Micro-organisms are essential components of soil ecosystems but have been under-utilized in conservation biological control. Climate change will influence the importance of particular pest and diseases at any given location. To some degree, natural biological control agents, such as those in disease-suppressive soils, can help adapt to the effects of climate change. Conservation biological control is inherently based on local knowledge and management practices, and principled on the buffering capacity of ecosystems. It is especially local communities in developing countries that have practised conservation biological control, and their ecosystem approaches are only now becoming mainstream in large-scale commercial agriculture in developed countries. On the other hand, these same local communities in developing countries are most at risk from the direct effects of climate change. They also often lack the modern tools (e.g. fertilizers, pesticides and the availability of genetically modified crops) the developed world has available to combat the effects of climate change. Therefore, conservation biological control is ideally suited as a means for such communities to adapt to the effects of climate change, which will hit them the hardest. Because of their presumed buffering capacity against pests and diseases, biological

control micro-organisms have an essential role to play in helping smallholder farmers of the developing world to mitigate risk.

Biological control micro-organisms will also help humankind adapt to the effects of climate change through the adoption of technologies that preserve or even increase biodiversity, such as crop rotation and preservation of soil through no tillage. Preserved and increased biodiversity will increase the effects of conservation biological control, and therefore keep population levels of damaging pest and diseases below economic injury levels. It is possible that many other, hitherto unknown, roles of biological control micro-organisms exist and can be utilized in adapting to the effects of climate change. For example, research has shown that rice, a C4 plant, can cope with elevated CO₂ levels when combined with the right strains of mycorrhizal fungi (Tang *et al.*, 2009).

4.2.3. *Biomonitoring and diagnosis*

Any strategy to manage micro-organism biodiversity cannot be separated from the need for effective biomonitoring, collection and diagnosis. With climate change, this need is set to increase. For example, increasingly, plant pathogens that did not previously pose a problem at any given locations will begin to do so. Climate change is just one among several drivers of change that include increased human mobility, globalization of agriculture and trade, and intensification of land-use management to meet the food demands of the rising population. Constant evolution of emerging, re-emerging and endemic plant pathogens will challenge our capacity to produce crop-based foodstuffs. The first critical step towards managing a plant disease is to correctly and rapidly diagnose the causal agent. Early and accurate diagnoses, combined with pathogen surveillance (4.1.2) on local, regional and global scales, are necessary to predict outbreaks and allow time for development and application of mitigation strategies (Miler *et al.*, 2009). The need for coordinated surveillance systems aided by robust diagnostic networks is recognized by CABI International through its Global Plant Clinic (www.cabi.org).

Biomonitoring, collections and diagnosis are particularly critical for micro-organisms due to the intrinsic invisibility of these organisms. Whereas the botanist can “see” plant biodiversity and then possibly collect and study it, the microbiologist has to sample randomly and then study the sample in order eventually to realize the type and extent of micro-organism biodiversity. Biomonitoring can be accomplished through microbiological and/or molecular approaches. The microbiological approach consists of growing sampled micro-organisms on appropriate media and obtaining colonies (clusters of micro-organism cells all identical to their mother cell), which are subsequently used for further manipulations and studies. The advantage of this system is that, once mother cells form a colony, the microbiologist maintains the cells and can carry out every type of study, including a rather accurate estimate of the cell density in the substrate. However, most micro-organisms are not culturable and are not suitable for the microbiological approach. The molecular (genomic) procedure is based on sequencing and analysing DNA with bioinformatic tools in order to identify the species of micro-organisms present in the sample. This approach can be used for a sample in which several species are present and is therefore called “metagenomic”. The molecular approach does not provide cells to work with, but overcomes the problem of viable but not cultivable (VNC) micro-organisms, which represent some 95 percent of micro-organism taxa.

Micro-organisms will be among the very first to manifest signs of climate change because of their rapid adaptation to changing conditions. They offer a unique tool to monitor changes in atmospheric composition and biophysical changes resulting from a changing climate. Populations of micro-organisms from specific habitats spanning geological times can be used to decipher signatures of climate change.

Plant-pathogenic micro-organisms, by virtue of their size, similarity in disease symptoms and closely related morphologies, are notoriously difficult to diagnose and detect. Diagnosis gives proof as to the causal agent of disease and permits the deployment of appropriate control measures. Often a strain will have a very distinct pathogenicity or host range that cannot be diagnosed from its morphology and may

require the use of serological or molecular tools. Such diagnostics are essential for border security, quarantine and trade.

Accurate diagnoses of a pathogen can be facilitated through the development and use of diagnostic kits that encompass all known genetic variation of any given plant pathogen. This will also allow for increased awareness and characterization of closely related new variants as they arise. Biomonitoring is also very useful for conservation because it can help guide the decision as to where biodiversity should be sampled for *ex situ* conservation. Alternatively, it is the only tool available for studying biodiversity conserved *in situ*.

New molecular approaches promise to improve the speed and accuracy of disease diagnostics and pathogen detection both in the laboratory, through high-throughput and technologically advanced methods (RT-PCR and even micro-arrays), and in the field through practical and robust technologies (i.e. immunological lateral flow devices – akin to human pregnancy test kits). Although technology such as DNA barcoding is reliant on the use of PCR, it is relatively simple and cheap, and unlike traditional molecular methods, can be used to diagnose unknown samples to the species level and even enhance the discovery of new species (Miller, 2007). In addition, widespread adoption of standard operating procedures and diagnostic laboratory accreditation serve to build trust and confidence among institutions.

4.2.4. Soil micro-organism amendments

Soils are complex systems in which micro-organisms are fundamental to the preservation of quality and capacity to deliver ecosystem functions and services. Soil micro-organisms are involved in soil formation, regulate its characteristics, sustain its fertility, break down toxic compounds, and enhance sustainable production, ultimately promoting ecosystem resilience and sustainability. As such, to adapt to the effects of climate change, farming practices that increase soil biodiversity – crop rotation, green fertilization, organic manure fertilization and biological control, etc. – must be encouraged. Furthermore, micro-organisms can be introduced to farming systems as biofertilizers alongside the crops they benefit: e.g. arbuscular mycorrhizal fungi (*Glomus* spp.) to increase nutrient acquisition, and root-nodulating bacteria (*Rhizobium* spp.) or free-living nitrogen-fixing bacteria (*Azospirillum* spp.) to fix nitrogen. Other soil micro-organisms can be deployed as natural antagonists to manage plant pathogens. A large number of soil amendments containing micro-organisms are commercialized as biopesticides. Some include bacteria belonging to the genera *Streptomyces* and *Pseudomonas* for control of pests. These products are applied in various ways, as soil inoculants or soil drenches. The commercial products often present a mixture of dried micro-organism biomass that is activated by rewetting. However, these enrichment approaches designed to modify the soil ecosystem will only work if applications are based on a clear understanding of the ecological niche, mode of action and the interactivity of the applied micro-organisms with communities of resident soil micro-organisms.

Climate change and the burgeoning global human population will create demand for more land to be used in crop-based agriculture, including land that is currently considered to be marginal. Some of this land is marginal because it is polluted. Because micro-organisms are capable of breaking down a range of organic substances to gain energy and recycle carbon and nitrogen, they are suitable for bioremediation processes, i.e. to turn land contaminated by different pollutants, chemicals and organic substances into land suitable for agriculture. Bioremediation occurs in three different ways which have different demands for human intervention. (a) “Intrinsic bioremediation” occurs when the contaminated area is restored naturally over time by indigenous micro-organisms. Human intervention is needed to improve the efficiency of this process through mechanical procedures that, for example, increase soil aeration. (b) “Biostimulating bioremediation” occurs when indigenous micro-organisms are stimulated by the artificial addition of specific nutrients to increase the rate of pollutant decomposition. (c) “Bioaugmentation” relies on the artificial introduction of specific micro-organisms with the capacity to degrade specific pollutants into the polluted environment.

4.2.5. *Improvement of the conservation and production of food by micro-organisms*

Prolonged drought or sudden catastrophic events are expected to increase in frequency because of climate change. Such events create an urgent need to nourish the affected populations in a sustainable and correct way. The first step is normally a huge international effort, which may lead to the accumulation of more or less perishable foodstuffs in places where conservation is extremely difficult because of a lack of proper storage facilities and energy. Because local food production is halted for weeks or even decades, the international community may bring in large quantities of food. In the case of drought, it may be that “broken systems” cannot be fixed, at least for several decades. In the case of fresh water floods, the system may be broken for a few weeks or months. Seawater floods are much more complex because salt deposits on the soil make future cultivation extremely challenging. Prolonged campaigns of food transportation are costly, especially in terms of energy, due to three major factors: transportation energy, temperature conditioning, and loss during delivery. Micro-organisms may be able to play a role in protecting food during transportation and temporary storage in conditions that favour the proliferation of micro-organisms that cause spoilage. Further, there are novel technological methods, such as the production of myco-protein in fermenter cultures, that might be used at sites dislocated from the food supply chain. However, it has been predicted that drought and catastrophic events causing loss of farmland will predominantly occur at low latitudes, in countries with minimal capacity for the use of such technologies (IPCC, 2007).

Micro-organisms (*Penicillium* spp., *Alternaria* spp., *Botrytis* spp., *Fusarium* spp., *Erwinia* spp., etc.) causing spoilage are responsible for food deterioration and contamination with toxins. Toxins are not easily detectable in the final food product, although they are harmful to human and animal health especially after chronic exposure. Even in non-catastrophic situations, a large part of agricultural production is lost because of spoilage by fungi and bacteria. Preventing and reducing spoilage by micro-organisms is always essential, but especially when the normal food production and supply chain is broken. Micro-organisms and microbiological techniques can be employed to extend the shelf-life of food, maintaining its intrinsic quality and nutritional properties. Throughout the food chain, micro-organisms can add value, especially as biological control agents. Some aspects, including their role in post-harvest quality control of fruits and vegetables, are discussed above in Section 3.3.4.

Grain harvests contaminated by mycotoxins from micro-organisms generally transfer to food and beverage produced from these grains. The problem is acute for maize in many developing countries due to lack of proper storage facilities (Chulze, 2010). As much as half of all the grains produced in some countries are contaminated by mycotoxins, especially in wet years (Bhat and Miller, 1991). Because of climate change, this situation is likely to worsen in some areas that will experience more humid conditions (Paterson and Lima, 2010). Introduction of biological control micro-organisms that restrict the growth of mycotoxin-producing micro-organisms, will be an ecologically sustainable approach to manage this problem. Currently, field research is ongoing in Kenya and Nigeria to test this technology on a large scale.

Currently, food processing is heavily dependent on refrigeration, freezing and cold-chain supply, which require huge amounts of energy and are therefore likely to worsen the problem of global warming (see Section 3.3.4). Recent research, based on the introduction of particular micro-organisms or combinations of micro-organism species during the production of various foods, suggests that significant prolongation of food shelf-life is possible with reduction or even elimination of antibiotics and preservation chemicals.

The use of strong biocides, surfactants and other hygienic practices has helped to reduce food safety problems, but has also selected for resistant species and strains of micro-organisms. However, a stringent aseptic environment is probably inhibitory or lethal to species that are active as natural biological control agents of pathogenic and food-spoilage micro-organisms. An ecological approach to industrial food environments and investigation of these unknown beneficial micro-organisms may lead to the discovery of more sustainable ways to produce and maintain foodstuffs.

Micro-organisms themselves can be used as a food source. In the years before 1973 it was suggested that paraffin be used as a source for the production of "single cell proteins" (SCP), which are proteins extracted from yeast cultures. The oil crisis following the Yom Kippur war ended these attempts, although huge amounts of money had been invested. Still, the basic idea of SCP remains interesting because yeast can grow quickly on poor media, use several non-expensive compounds as source material, and provide large amounts of proteins and vitamins. Therefore, yeast SCP might be a resource that could be used to improve the nutritional quality of feed and food. The process can be summarized as follows: (a) complex polysaccharides, particularly common even in poor lands, are subject to procedures that yield simple sugars (e.g. steam explosion); (b) the simple sugars are integrated with a low-cost nitrogen source; (c) yeasts are cultured; and (d) the resultant biomass is treated to extract proteins and vitamins, eliminating nucleic acids which are dangerous to humans in large amounts. This procedure is not intended to provide food, but rather to produce high-quality/cost ratio products that can be integrated into feed and food (mainly consisting of carbohydrates) that is already available. Moreover, the system can be used to delocalize food production and allow the use of portable stations that can be moved quickly to areas hit by catastrophic events. Of course, such solutions still need to be extensively studied and carefully designed, but could help in climate change adaptation, especially because SCP technology itself will not be affected by climate conditions.

4.2.6. Biodiversity conservation and micro-organism collections

Conservation of micro-organisms is an open scientific field. It is not yet known what processes lead to the extinction of micro-organism taxa or significant loss of genetic variability. It has sometimes been assumed that in the case of micro-organisms "everything is everywhere". Obviously this cannot be true for more specialized micro-organisms that depend on interactions with, for example, endangered plant species.

Because plant pathogens are so difficult to diagnose in the first place, a systematic approach to the characterization of biodiversity is required. However, the ever-shrinking human and technical capacity in this area means that work needs to be concentrated at key reference collection sites for the benefit of the global community. Micro-organism collections preserve "type strains" that represent key genetic entities by serving as living references for each functional group. Live reference collections at centralized and open-access facilities are needed in order to characterize the taxonomy and function of micro-organisms as a prerequisite to the development of tools for diagnosis and detection (Barba *et al.*, 2010). Such collections can also be used to increase awareness of the available living material through databases and web-based portals, and to provide access for research and capacity building. If submission of strains becomes a condition of acceptance for scientific publications, a system similar to the GenBank (www.ncbi.nlm.nih.gov/genbank/) could be created to ensure the completeness of collections. Also, the conservation of all variants of any particular micro-organism is necessary to permit the development of a diagnostic tool that encompasses all the known variants. This is critical as micro-organism pathogens adapt rapidly in the face of selection pressure such as the mass deployment of "resistant" crop germplasm, and this evolution must be captured in tools used to monitor the presence or spread of pathogen species. All data accrued on the variance of micro-organism pathogens could also be sourced via centralized collections under the auspices of the World Federation for Culture Collections (www.wfcc.info/).

The importance of conserving food-related micro-organisms is underlined by the fact that most of the foods currently eaten derive from different types of micro-organism processes, which give food its specificity and unique taste. *Ex situ* conservation of cultures from these micro-organisms is instrumental in maintaining specific food production systems, as they are potentially altered by climate change or even wiped out by catastrophic events induced by climate change. Biodiversity conservation of food-borne micro-organisms also has a cultural function and is particularly important for maintaining traditional food production.

In situ conservation also has an important role to play. For example, *ex situ* conservation of wild crop relatives depends on maintenance of “appropriate” micro-organism communities, so that co-evolution among plants and micro-organisms can continue. Determining what micro-organism communities are most appropriate is challenging because of our limited knowledge of these interactions. Furthermore, because micro-organisms are highly adaptive to new scenarios, such as those likely to be induced by climate change, *ex situ* collections of micro-organisms may become outdated. Efforts are therefore required to advance *in situ* conservation methods for micro-organisms.

In summary, important milestones related to appropriate conservation of MOGFRA include the following: characterization of biodiversity at the ecosystem level using biochemical and molecular techniques; characterization of key drivers of resilient and sustainable ecosystems for use in research; prioritization of key species for enhanced use based on socio-economic assessment and evaluated against major biotic and abiotic stresses; consolidation of “biobanks” for micro-organism genetic resources for agriculture, with greater diversity captured, including DNA, BAC libraries and genetic stocks; development and implementation of methods and strategies for conserving micro-organism genetic resources for agriculture in natural ecosystems and protected areas; and participatory research to sustain production in the face of climate change and other threats.

4.3. Role of micro-organism genetic resources in mitigating climate change

4.3.1. Definition

Micro-organisms can play a key role in mitigating the contribution of humankind to climate change. For example, agriculture itself contributes to climate change, indirectly through the use of fossil fuels and land use, and directly through greenhouse gas emissions from agricultural practices. Greenhouse gas emissions are especially related to methane releases from ruminant livestock and rice cultivation, but also to nitrous oxide releases from fertilizer application, which accounts for 80 percent of worldwide nitrous oxide emissions. Increased land use for agriculture results in CO₂ releases linked to deforestation and due to the increased exposure of soil. It also leads to increased CO₂ concentrations in the air due to reduced carbon re-uptake, and, especially in the developing world, increased greenhouse gas release due to slash and burn practices.

4.3.2. Carbon budget

The carbon sink capacity of the soil, which is mediated by micro-organisms, has important implications for climatic change. As soil is such a large store of global carbon, one of the major roles of micro-organisms in climate change lies in their sequestration of carbon in SOM and their role in releasing carbon as CO₂ from the decomposition of SOM. Climate change alters soil carbon storage through increasing mineralization of SOM, altering the deposition of SOM, and influencing soil erosion and respiration. The quantity of CO₂ released from the respiration of soil organisms is dependent on how efficient their respiration processes are, which depends on local environmental conditions and the profile of micro-organisms present. Hence, global optimal conditions for soil respiration by micro-organisms cannot be defined.

Agronomic management practices that improve the soil carbon sink will mitigate global climatic changes. Such practices include amendment of soil with organic fertilizers (manure, compost, slurries, etc.), proper crop-residue management (type and mix, C/N ratio, lignin content, etc.), no-tillage, maintenance of cover crops on the soil surface, avoidance of flood irrigation, and use of mineral fertilizers according to absolute uptake by crops and of types that are environmentally friendly (slow-release, coated, precision agriculture, etc.). Some inorganic nitrogenous fertilizers provide micro-organisms with easy-to-use nitrogen, thereby boosting the activity of these “chemical engineers”. This increases the rate of decomposition of low-quality organic inputs and SOM, resulting in continuing decline of SOM content. This in turn causes a loss in the structure of soil, and with it the ability of soil to retain water, air and

nutrients. Conversely, high levels of SOM amendments stimulate the immobilization of carbon and nitrogen in micro-organism biomass, leading to high turnover of SOM into humic substances.

4.3.3. Energy budget and greenhouse gas budget

In addition to their role in carbon sequestration, micro-organisms contribute to the “greenhouse gas budget” of agricultural systems in other ways. The greenhouse gas budget for an agricultural system can be evaluated directly in terms of the greenhouse gases released per unit of food produced, or less directly in terms of the amount of land required per unit of food produced. All the ways in which micro-organisms influence crop productivity can influence the greenhouse gas budget. For example, if management results in an increase in food produced per greenhouse gas “investment”, this is a form of climate change mitigation (Mahmuti *et al.*, 2009). Further, beneficial micro-organisms can increase food production through many mechanisms, such as increasing nutrient uptake and drought tolerance, and reducing the effects of pathogens. In some cases there may be a greenhouse gas “cost” associated with some of these benefits. For example, if a biological control micro-organism needs to be added to a field and is applied using a tractor, the resulting greenhouse gas cost of the tractor use must be factored into the budget. If the benefit in increased productivity is greater than the cost of the tractor use, then the biological control micro-organism contributes to climate change mitigation.

One of the positive features of many beneficial micro-organisms is that their performance relies less on high greenhouse gas costs than the manufacture of synthetic pesticides does. For example, naturally occurring biological control micro-organisms will not incur the costs associated with the production, transport and application of synthetic products. If the micro-organisms can be maintained or enhanced without fossil fuel use, they may provide climate change mitigation. Because the role of many micro-organisms is not understood, we probably currently underestimate this role in climate change mitigation. Especially micro-organisms that contribute to plant nutrition, such as mycorrhizal fungi and rhizobia, can make very important contributions of this kind in systems with low external inputs. Not only do they generally increase plant productivity per unit of land, but the greenhouse gas emissions associated with their use are lower than those associated with fertilizer production and transport. Interest in developing complete greenhouse gas budgets for agricultural systems is increasing, with the United Kingdom one leader in the field (Mahmuti *et al.*, 2009). It will be important to develop our understanding of micro-organisms’ contributions to greenhouse gas budgets to ensure that the budgets are correct and that important micro-organisms are conserved accordingly.

Micro-organisms can also be used to produce bio-energy. An analysis of the energy and CO₂ balance in bioethanol production from crops is required in order to avoid worsening the effects on climate change (Börjesson, 2009). Some gross calculations have estimated that to replace petroleum with bioethanol from cereals would require the use of the whole terrestrial surface of the world (Rittmann, 2008). As it becomes increasingly clear that biomass for biofuel production should not be produced on conventional arable lands where it would reduce the area available for food production, improvement and development of appropriate technologies to produce biomass on lands not used for conventional agriculture, e.g. drought-afflicted areas, is warranted. An intriguing possibility is offered by “micro-organism fuel cells”, which can permit the production of energy directly from special bioreactors that contain biomass and particular micro-organisms (Du *et al.*, 2007). The three types of fuels (methane, bioethanol and biodiesel) and the electricity produced directly by micro-organisms represent great potential for obtaining energy without increasing the greenhouse gas budget. However, all of them require relatively large amounts of biomass as input. Several types of biomass, including molasses and processed cellulose, can be fermented by the yeast *Saccharomyces cerevisiae* to produce bioethanol. Especially the use of cellulose as a substrate by yeast holds great promise as it is plentiful and currently underutilized, but the technology required to do this is still lacking. Methanogenic Archea (prokaryotic cells similar to bacteria) produce methane from various sources including waste water, and animal and municipal waste (Thauer *et al.*,

2008). Algae can be used to produce biodiesel directly from sunlight, but this technology also is still not fully developed (Scott *et al.*, 2010; Krohn *et al.*, 2011; Patil *et al.*, 2011; Pfromm *et al.*, 2011).

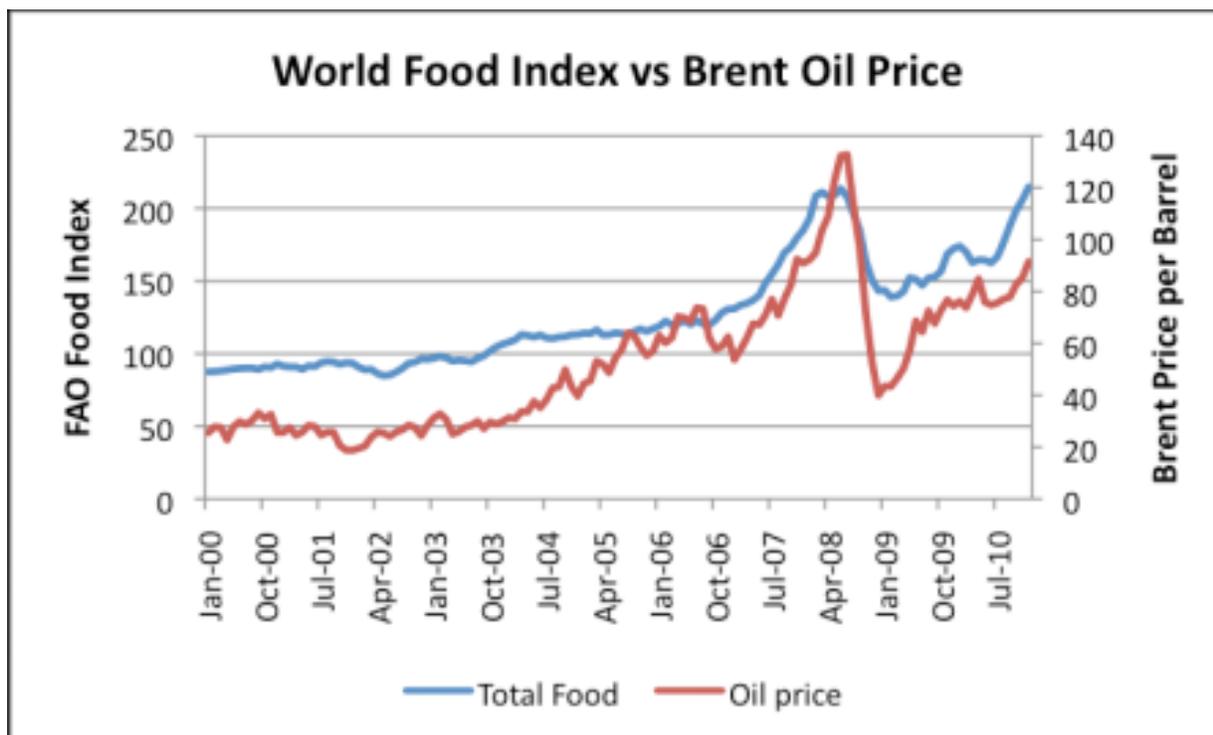
4.3.4. Reducing food transportation and energy production

Transportation is one of the human activities contributing most to the CO₂ budget, and reducing transport costs can therefore be considered a major goal in climate change mitigation. Food-transportation costs comprise the energy costs of the transportation itself and costs related to temperature conditioning. The efficiency of the food chain can be evaluated by the ratio between the energy contained in the food and the energy required to produce and transport it. In traditional, pre-industrial agricultural systems the energy ratio was around 100, whereas it is currently below 1 and can even reach values of 0.01 when food is transported by air (Church, 2005). In fact, food production is currently so dependent on oil consumption, that it has become one of the major sources of energy consumption and greenhouse gas production (Whiffen and Bobroff, 1993; Bachman, 2010). Many products are transported frozen or refrigerated, which further aggravates energy requirements. The energy needed for freezing vegetables and fruits is three times greater than that needed for canning. Although frozen food is richer than canned food because thermolabile components are retained, the average cost of freezing and cold-chain food production is likely not to be sustainable in the future if energy becomes more expensive. Micro-organisms could become essential in increasing the shelf-life of food without consuming energy.

Food transportation becomes particularly important when humanitarian aid is required, because food needs to be transferred from producers to areas affected by catastrophes and droughts. Because of climate change, catastrophic events and prolonged droughts, and therefore emergency food aid, are expected to increase. Because an expansion of emergency food aid might not be sustainable in the long run, alternative means of *in situ* food production have to be found, and micro-organisms could be essential in this.

Between 2003 and 2008, energy prices increased 230 percent, those of fertilizers fourfold, and food prices increased by 200 percent (European Parliament, 2011). Food prices reflect energy prices, particularly oil prices (see Figure 4). This association risks starting a vicious circle: large amounts of energy are needed to produce food; more food is required because of growing populations; more land is required to sustain energy production (for solar energy, biofuels, etc.); available arable land is decreased; and food prices rise even more. The food production system is thus responsible for a large greenhouse gas budget and thereby increases climate change.

Producing low-cost energy and low-cost food are, therefore, essential means of mitigating climate change. Micro-organisms could contribute to this, and several examples have been highlighted above. Micro-organisms could extract energy from relatively cheap biomasses that are not obtained from arable land. Algae, especially, could prove to be essential in energy extraction in the sea. Large research efforts will be required to achieve these objectives. Priorities include expanding our knowledge of biomass and production, increasing our knowledge of industrial manipulation of micro-organisms, improving the micro-organisms involved, and promoting multidisciplinary projects and research centres for micro-organism energy production.

Figure 4. World food index versus oil price (Tverberg, 2011)

4.3.5. Reducing pesticide use

Because of agriculture's contribution to climate change, a drive for alternative technologies is needed in order to feed the fast-growing world population while reducing the quantity of chemical pesticides and fertilizers entering our food chain and the environment. Biological control micro-organisms can help agriculture reduce its contribution to climate change and environmental degradation. They will play an important role in the search for new knowledge and technologies, to replace older control strategies that are less effective. Because of their selectivity and minimal environmental impact, micro-organism control agents will be ideal components of integrated pest management programmes in the early twenty-first century and beyond.

It is widely documented how energy-demanding the production and transport of agricultural pesticides is. Climate-related changes that increase crop disease pressures could lead to reliance on broad-spectrum pesticides and the elimination of natural antagonists to disease-causing agents. Excessive rains in Brazil in 2004 favoured the development of soybean rust, which led to an alarming increase in fungicide use (Rosenzweig *et al.*, 2005). However, the reverse could also be true, and the selection and deployment of biological control agents could be preferred? Use of biological control agents would avoid the development of pesticide resistance as a consequence of the over application of synthetic chemicals and would preserve those natural enemies that would otherwise be destroyed by broad-spectrum pesticides (Langewald *et al.*, 2003).

V. GAPS

5.1. Knowledge

5.1.1. Monitoring and surveillance

Our current lack of knowledge makes it impossible to predict precisely how climate change will affect the outcomes of interactions between crops, micro-organisms and other components of the ecosystem. Therefore, integrated systems for routinely monitoring the influence of climate change, alongside other drivers such as land-use management practices, are required. Based on the knowledge accrued from practical scenarios, better-informed decisions can be made on how to adapt to climate change and ensure that crop-based sustainable agriculture thrives.

A few soil monitoring initiatives have been established, and include France's "Soil Quality Measurement Network", Germany's network of 800 soil-monitoring sites, the Netherlands' "Soil Quality Network", and the soil section of the European Commission's Joint Research Centre. While these discrete activities recognize the importance of soil, there is no global system to evaluate and share genetic and functional information on soil biodiversity. An optimal system would be to select key sites based on climate (continental, Mediterranean, arid, temperate; etc.), soil type, podogenetics and cropping system. The sites would be selected strategically so that they represent larger areas, allowing interpolation of the results to scale.

For plant pathogens, monitoring programmes have been established as a means to ensure that genetic resistance of crop plants or control through pesticides are not overcome. When crop resistance is overcome or pesticide resistance occurs, efforts are made to screen for new forms of resistance or develop new pesticides with different modes of action. However, plant-pathogen monitoring programmes, such as the National Plant Diagnostic Network in the United States of America (Miller *et al.*, 2009), are limited to large scale agricultural production in technologically advanced countries.

As crop deployment responds to climate change, it is likely that many crops, often with a narrow genetic base, will be grown far from their centres of origin and apart from the pathogens that have co-evolved with them. In such circumstances, it will be even more critical to have monitoring and surveillance systems that share global knowledge on how to diagnose causal agents of disease and to monitor their global distribution, spread and hence the risk that they will become established in surrounding areas. To provide a historical example: cassava mosaic disease (CMD) does not exist in cassava's centre of origin (South America) but when germplasm was introduced to East Africa the disease appeared. Breeding programmes targeted the development and resistant varieties were mass produced and distributed. This created selection pressure for a new CMD variant, "EACMV-Ug", which was a more virulent form of the disease. EACMV-Ug first appeared in Uganda by 1999, from where it spread to Burundi, the Democratic Republic of the Congo, Gabon, Kenya, Rwanda, Sudan and the United Republic of Tanzania (Bigirmana *et al.*, 2004). Further, the dynamic nature of crop and plant pathogens (and the need for surveillance) was demonstrated by the appearance of even more virulent variants of CMD and sudden appearance of cassava brown streak disease (CBSD), another devastating viral disease (Legg, 2006). Both CMD and CBSD are vectored by whiteflies and changes in whitefly populations (genetics and abundance) have been linked to the spread of these plant pathogens, illustrating the need for a holistic ecosystem approach based on sound understanding of strategies that support sustainable crop-based agriculture. While it appears unrealistic to create global surveillance systems to monitor the spread and impact of plant pathogens, a step forward would be to better link existing initiatives through networking and to develop and implement standardized methodologies (Miller *et al.*, 2009).

Despite all the tiers of likely interactions at any one site, the aim of monitoring and surveillance is to help clarify which micro-organism species could be used as indicators for key ecosystem roles (nutrient

acquisition, biological control, disease, food spoilage, etc.) for a given crop system, ultimately leading to ecosystem resilience and therefore sustainability of the agricultural system.

5.1.2. *Methods for characterizing micro-organism species, communities and their functions*

Rapid advances in genomic and other “omic” techniques provide exciting new ways both to detect micro-organisms and to interpret their function. This is of particular importance as so few species can be cultured artificially for study through traditional microbiological means. Studies of micro-organism community metagenomes can provide profiles of the genetic potential of full communities, while studies of proteomes and lipidomes provide profiles of the proteins and lipids produced by the communities and thus more insights into community function. Table 2 summarizes methods used to characterize micro-organism species, communities and their function.

5.1.3. *Experimentation methods*

Where data from monitoring exercises and “omics” studies can demonstrate the presence and even potential function of a micro-organism community, the critical causal role of a species often needs to be clarified. Experiments under controlled conditions in the laboratory offer the opportunity to alter single parameters while the others remain constant, thereby permitting an improved understanding of specific relationships without the complexity of ecosystems. This approach is useful when there is no prior knowledge, and produces results that can help construct hypotheses that can then be tested *in vivo* or through models.

Efforts are now being made to test climate change effects in a simplified manner. For example, “free air CO₂ enrichment” (FACE) is a method used to experimentally enrich the atmosphere enveloping portions of a terrestrial ecosystem with controlled amounts of CO₂ (and in some cases, other gases), without using chambers or walls. As such, FACE enables the study of interactions between micro-organisms and other organisms in an open environment. Many published studies have used discrete levels of CO₂, temperature or other factors, mostly in isolation, and have yielded substantial data. However, oversimplifying relationships from such single-factor studies may be misleading. Similarly, climate change is a gradual process and realistic experiments should mimic gradual increases and not shock organisms by applying levels of CO₂ drastically different from those to which the organisms have previously been exposed. Only a gradual increase in treatment levels can point to thresholds beyond which known rules and relationships will no longer apply. Facilities with CO₂ and temperature gradients will be one way to achieve this.

In a “classical” microbiological approach, micro-organisms are isolated, cultured and studied *in vitro* on artificial media, in isolation from their normal environments. Although such studies allow for functional analyses under controlled conditions, they can investigate only 1–2 percent of all micro-organism biodiversity. Methods are needed to investigate micro-organisms *in situ*, and the advent of new molecular methods such as metagenomics clearly opens new, exciting, possibilities (see 5.1.3.). However, methods to manipulate the composition of soil micro-organism communities experimentally without introducing artefacts (that confound results) would be an extremely important contribution to micro-organism ecology. Current methods for soil sterilization, for example, tend to modify the abiotic (i.e. structural) properties of soils such that effects of introduced micro-organisms are difficult to interpret.

In summary, a combination of both field and laboratory-based observations are required to piece together an improved knowledge of key interactions between micro-organisms and the influence of their environment. Data generated in the laboratory must be verified under field conditions and vice versa before it is accepted as being worthy of influencing future recommendations.

5.1.4. Standardized methods and metadata

The standardization of methods used to characterize designated parameters is critical if data from different locations, collected by different individuals, are to be compared. The need to compare data is especially important as the climate changes and lessons learned in one location need to be applied elsewhere. Because assumptions and recommendations will be made based on analysis of the data collected, it is imperative that the data are of the utmost quality. Data about data are called “metadata” and are used to describe data sets in order to support their synthesis. For example, publication of microarray data needs to follow “MIAME” (minimum information about a microarray experiment) standards, to enable the interpretation of the results of the experiment unambiguously and potentially to reproduce the experiment (Brazma *et al.*, 2001).

There are particularly stringent requirements for metadata that define micro-organism within ecosystems. Micro-organism data will include observations that may not be of immediate interest to experimenters collecting the data, but are important for synthetic analyses across data sets. Examples of this type of data include time of day of data collection, slope, cropping system, land-use patterns, recent weather and aspect of location. Other types of metadata will include, for instance, information about experimental methods and potential changes in methods from one data set to another. One example of a tool for systematizing ecological metadata is the “Ecological Metadata Language” (EML, software published by the Knowledge Network for Biocomplexity). Currently, efforts are being made to accumulate large metagenomic data sets. These data sets are available for a broad range of environments. A next phase of analysis will be data synthesis for evaluation of hypotheses across environments, providing metagenomic metadata are complete.

Table 2. Methods used to characterize micro-organism species, communities and their function

| Method | Information generated | Applications |
|--|--|---|
| Phospholipidic fatty acid (PLFA) | Total biomass and community composition of the soil microbiota | Comparative analysis of community structure, monitoring changes in community composition |
| Community-level physiological profiling (Biolog) | Functional diversity (high resolution) | Metabolic diversity of culturable community members |
| DNA re-association Rate | Total genetic diversity, theoretical “species” number, community “genome size” (low resolution) | Global analysis of the genetic potential of communities, comparative analysis of the overall biodiversity |
| Mole (% G+C) composition | Genetic community profile, overall community composition (low resolution) | Comparative analysis of overall changes in community composition |
| PCR-DGGE/TGGE sequencing of individual bands | Genetic fingerprinting of communities, affiliation of predominant community members (intermediate resolution) | Comparative analysis of community structure, spatial and temporal changes in community composition |
| PCR-SSCP sequencing of individual bands | Genetic fingerprinting of communities, affiliation of predominant community members (intermediate resolution) | Comparative analysis of community structure, spatial and temporal changes in community composition |
| PCR-T-RFLP | Community composition, relative abundance of numerically dominant community members (intermediate resolution) | Comparative analysis of distribution of micro-organism populations, monitoring changes in community composition |
| PCR-ARDRA | Genetic fingerprinting of simple communities, populations or phylogenetic groups, discrimination at lower taxonomic (species) levels (high resolution) | Comparative analysis of micro-organism population dynamics, diversity within phylogenetic or functional groups of micro-organisms |

| | | |
|--|--|---|
| PCR-RISA | Genetic fingerprinting of populations or phylogenetic groups, simultaneous analysis of different micro-organism groups, discrimination at species or group level | Comparative analysis of micro-organism population dynamics, diversity within phylogenetic or functional groups of micro-organisms |
| PCR of rDNA (cloning and sequencing) | Phylogenetic diversity, identification of community members (high resolution) | Phylogenetic diversity of community members |
| PCR of functional genes (cloning and Sequencing) | Functional diversity (high resolution) | Comparative analysis of the functional potential of communities |
| RNA dot/slot blot hybridisation | Phylogenetic identification of metabolic active community members (intermediate resolution) | Qualitative and quantitative analysis of metabolic active populations in communities, phylogenetic information on active community members |
| FISH | Detection and specific counting of metabolic active micro-organisms (intermediate resolution) | Comparative analysis of community structure, detection and identification of active cells, direct phylogenetic information on community members |

5.1.5. Modelling

Models allow examination of complex interactions from different perspectives by using combinations of factors based on available data and considered assumptions. Micro-organism community function is so varied that models can be used to simplify a range of interactions and to focus only on those that are critical to crop-based agriculture. Modelling offers the opportunity to test hypotheses developed based on controlled environment studies or field-based observations, and to determine whether specific relationships are robust when ecosystem complexity is increased. Modelling also offers the opportunity to test whether inferences made from field studies are correct when other factors are varied. However, the predictive power of a model is dependent on the quality of the data it is based upon and recognition of which factors and interactions play the strongest role when assessing any outcome. Unfortunately, models for micro-organism function are limited because of the lack of baseline studies to generate data. Steps need to be taken to better characterize micro-organism function. To this goal, modelling is a logical approach to improve understanding and eventually our capacity to predict the likely outcomes of climate change.

In the case of plant pathogens, models are commonly developed to support farmers in predicting plant disease responses to weather variables, across sites and seasons. An important research challenge for the use of these models is the development of approaches for spatial and temporal scaling that can be used in the context of climate change scenario analysis. In fact, this is a challenge for use of many types of knowledge about environmental effects on plant-associated micro-organisms: how to scale-up information from necessarily small experiments to support our understanding of national and global effects and thus needs for adaptation strategies (Garrett *et al.*, 2006).

If we consider biological control micro-organisms and their interaction with the environment and target pests, there have been surprisingly few models developed. Those that do exist are mathematical, and investigate the analytical (qualitative) and less often numerical (quantitative) outputs of the parameterized micro-organism–host–environment system. They range from simple dose-response relationships (e.g. Cabrefiga and Montesinos, 2005) to complex simulation models (e.g. Kesselet *et al.*, 2005). Often the models focused on single aspects of the complex: for example, Jeger *et al.* (2009) concentrated on modes of action to build their model, while Stolk *et al.* (1998) focused on the energy requirements of biological control micro-organisms. Even though most models are deterministic (i.e. without randomness or probability), some stochastic epidemiological models do exist (e.g. Gibson *et al.*, 2004) but such models are limited in making qualitative, let alone semi-quantitative, predictions.

While there is always a risk of over-simplifying our examination of interactions and making imprecise recommendations, models can be optimized based on site-level observational effects. This is necessary because a simple parameter such as temperature can vary greatly between an observation at a weather station and an observation at the micro-level of a plant or insect. Klass *et al.* (2007a, b) predicted the effects of temperature on performance of a *Metarhizium anisopliae*-based biopesticide for controlling locusts and grasshoppers at site-specific locations. The model uses site-specific environmental temperature data to predict a locust body temperature model, which in turn drives a biological control performance model. Testing showed that weather-station estimates of temperature had to be recalibrated for individual locust/grasshopper species to be valid. They enhanced the utility of the model by linking it with meteorological station data in a geographic information system (GIS) framework. As such, they could investigate the spatial variation in the performance of the biopesticide by providing maps that define spatial variation in pathogen performance across different regions. The GIS-based model was validated using actual field-based biopesticide performance data against four economically important pest species. The model provided good estimates of biopesticide performance in >75 percent of the cases, but could not predict biopesticide performance when extreme temperatures occurred (Klass *et al.*, 2007b).

5.1.6 Biological control

Huge potential exists to exploit biological control micro-organisms to buffer, adapt to and mitigate climate change if our knowledge is improved. While it is clear is that biological control applications are fast expanding, there are still fundamental gaps in our understanding of how to implement this widely across cropping systems and locations. Twenty years ago, farmers sprayed the living bacterium *B. thuringiensis* in fields to control insects. Subsequently, toxins were harvested from this bacterium through fermenter culture and applied directly to combat insect pests. Now, genes coding for *B. thuringiensis* toxins are used to modify crops genetically so that they produce this active ingredient in the absence of the bacterium and its metabolites. Biological control of plant pathogens has also made strides forward recently. The principal mechanisms involved in biological control of plant pathogens include mycoparasitism, antibiosis, competition for space and/or nutrients, and induced crop resistance (Punja and Utkhede, 2003). Advances in genomic and gene expression analyses offer novel approaches to triggering crop defence mechanisms through the identification and use of weakly plant-pathogenic strains. Identifying weakly pathogenic strains with high saprophytic fitness that can reduce saprophytic colonization of stubble and other substrates by highly virulent strains is another option. For example, the use of non-toxic strains of *Aspergillus* spp. out-competing aflatoxin-producing ones in maize and peanut fields has been commercialized in the United States of America and is undergoing registration trials in Africa.

A central problem in biological control is inconsistency of performance. Micro-organisms for plant disease management may vary in their effects as a function of environmental conditions and may also be sensitive to timing of introduction. Greater understanding of the interactions among members of micro-organism communities may lead to improvements in biological control agents, as more information is available about how to effectively reduce pathogen escape from the biological control agents. Fundamental advances have been made towards overcoming environmental limiting factors through novel biopesticide formulations (e.g. through the addition of UV protectants and oil emulsions).

Potentially, the biggest revolution in biological control will arise from genetic engineering. Recently, researchers modified *Metarhizium anisopliae*, one of the most common entomopathogens and considered a model organism, to increase its pathogenicity to the point where fewer than five spores can represent a lethal dose to an insect, using genes coding for a scorpion toxin (Wang and St Leger, 2007). Such developments would drastically reduce the doses that need to be applied in the field and make biopesticides highly competitive with conventional chemical pesticides.

5.1.7. *Deployment of micro-organisms in synergy with crop germplasm*

Altered climatic conditions will mean that currently adapted crop landraces and varieties will most likely become maladapted, requiring new crop materials with novel abiotic and biotic traits. While crop function and varietal traits are largely understood and can therefore be matched according to their adaptive capacity to new environments, the success of their performance is dependent on interactions with beneficial and antagonistic micro-organism genetic resources. Therefore, it is logical that the deployment of crop germplasm to adapt to or mitigate potential impacts of climate change is performed in unison with the deployment of beneficial micro-organism germplasm. As illustrated in previous sections, beneficial associations confer ecological resilience through biodiversity enhancement, regulate plant nutrients, manage pests and diseases through biological control, and facilitate food preservation and processing. In contrast, antagonistic micro-organisms include those that cause crop disease or produce toxins that render agricultural produce unsaleable to international markets and not safe for local consumption.

Therefore, as cropping patterns change to adapt to climate change there needs to be an evaluation, for each environment, of which micro-organism should be distributed with crop germplasm and which micro-organisms should be excluded. When beneficial micro-organisms are identified they can be mass produced and distributed with crop planting material. Further, marker-assisted selection is known for its use in crop improvement, but can also be used for beneficial micro-organisms such as biological control agents and to select for types better suited for productive crop–micro-organism interactions. There is also the potential to engineer plants to select for communities of particularly beneficial rhizosphere and phyllosphere micro-organisms. This might be through the production of exudates of related types of plant–micro-organism interactions. It may also be possible to engineer plants to form optimal symbiotic relationships with micro-organisms. Conversely, it may be possible to engineer beneficial plant-associated micro-organisms for improved performance in agricultural systems. One of the paradoxes here is that until these micro-organisms have been engineered it will be impossible to predict their likely impact. For antagonistic micro-organisms identified as posing a risk to crop performance in new environments, landraces and varieties can be screened for resistance prior to deployment. As climate change influences the geography of crops, plans can be developed to create the correct ecological equilibrium to maximize crop performance. The major constraint to this approach is the lack of knowledge of micro-organism distribution and function and of methods for their characterization, storage and distribution.

5.2. **Increased capacity through networks and coordination**

5.2.1. *Technical capacity, knowledge sharing and infrastructure*

As a consequence of the fact that micro-organism genetic resources for agriculture have been largely ignored, fundamental changes are required to increase awareness of their importance. This requires a concerted effort to develop active networks and to pool technical and human resources. Taking the example of plant pathogens, it was recognized by NATO in the “Tools for Crop Biosecurity” project that networking was required to develop a broad multinational diagnostic consortium across the United States, the European Union, Israel and others (Gullino, 2008). Such consortia have value in bringing like-minded scientists and policy-makers together to promote dialogue and information exchange. For plant pathogens, threats are many and resources are few, leading Miller (*et al.*, 2009) to conclude that the only solution was to create synergy through networks that link capacities across the field to basic and advanced laboratories. In addition to the development of appropriate methods to diagnose plant pathogen species and variants, it was recognized that data storage and mechanisms for rapid and secure communications were of critical importance to sharing and interpreting results. To adapt to and mitigate climate change, countries will need to access micro-organism genetic resources and associated data on their genetic and functional characteristics. By nature of the way climate change will impact upon the globe, these

materials will need to be accessed from beyond the borders of individual countries. Increasingly, as the movement of micro-organism genetic resources is driven by climate change, national and regional systems for monitoring the impact of their utilization will need to be integrated to enhance collective learning. One of the best ground-truthing methods to verify model predictions or hypotheses is to monitor impacts following introduction of, for example, a micro-organism symbiont of crop plants or a biological control agent, or following control of a plant pathogen. Similarly, if a new variant of a plant pathogen arises, it needs to be characterized as precisely and rapidly as possible; using pooled global resources, and the risk it poses to crop-based agriculture reported. Coordination across countries and continents will need to be boosted significantly – particularly in the developing world – to meet the challenges associated with climate changes. These efforts will need to be supported by international pooling of representative samples of micro-organism diversity – species and strains (and hence functions) – for comparative taxonomy, research, and training.

5.2.2. *Culture collections and international coordination*

Obviously, culture collections have an important role to play in internationally coordinated efforts. There are currently 589 culture collections listed under the World Data Centre for Micro-organisms (WDCM). The vast majority of these collections are hosted by public and semi-public organizations and universities (WDCM, 2011). Altogether, it is estimated that these collections hold 1.75 million strains. Each year, these listed collections distribute approximately 500 000 isolates. It is estimated that a considerably higher number of isolates are exchanged each year informally via peer-to-peer exchanges based on informal networks (Dedeurwaerdere, 2010). While some of the collections listed under WDCM are specifically focused on micro-organism genetic resources for agriculture, most collections are established to service a broader range of sectoral interests and users, including, for example, pharmaceutical and industrial research.

Most collections are located in developed countries, largely because of the high cost of collection, characterization and conservation, and because there is still less demand for strains as inputs for research in countries where there is less scientific capacity to use them. The situation is changing however, with increasing levels of investment by countries such as India and Brazil. Brazil now has 59 collections with 142 000 strains and India has 24 collections with 60 000 strains (WDCM, 2011). One example demonstrating the value of a southern-based collection concerns cocoyam in Cameroon. Cocoyam is a tuber crop used to feed more than 200 million people living in the tropics and subtropics. Cocoyam production in Cameroon is, however, seriously impaired by the cocoyam root rot disease, against which biological control was sought. The bacterium *Pseudomonas aeruginosa*, isolated from the chickpea rhizosphere in India, and conserved at ICRISAT in India, has been shown to efficiently suppress cocoyam root rot by the production of antibiotics and biosurfactants. Based on this prior knowledge, and by using the ICRISAT strain for comparison, a screening programme was set up in Cameroon using local Cameroonian strains. These efforts ultimately led to the adoption of new farming practices in Cameroon, such as the use of a compost of oil palm containing local pseudomonas bacteria and joint cultivation of white and red cocoyam.

Less than half of the WDCM-listed collections distribute materials. Moreover, there is very little harmonization of the conditions under which access is provided, with very different costs and limitations and placed on the uses recipients can make of materials. Within Europe, and through the OECD, there have been attempts to harmonize material transfer agreements, with some degree of success. Similarly, there have been attempts to create internationally accessible information systems that bring together data on strains, and facilitate locating and requesting them. These efforts too, are far from reaching their full potential (Dedeurwaerdere, 2010).

Ultimately, therefore, several factors constrain the ability of researchers to pool micro-organism genetic resources for agriculture and information related to them. These constraints include the following: only a minute percentage of predicted diversity has actually been identified; a very small percentage of that

diversity is amenable to culturing; and the cultured strains that do exist are dispersed widely around the world in hundreds of collections, all subject to wildly different access policies and practices. Less than half of the collections publish catalogues of their holdings (WDCM, 2011). As a result such factors, possibly the majority of micro-organism strains are transferred through peer networks or clubs, with the result that non-club members are unable to obtain access to potentially important materials. While it is impossible to quantify these missed opportunities, it is not unreasonable to expect that it is scientists from poorer developing countries that are “left out” most frequently.

There is clearly a need for considerably higher levels of technical and policy coordination and harmonization at international levels to support countries in pooling resources, information and know-how in ways that are accessible and to the advantage of *all* potential users. Opportunities to promote requisite harmonization exist at various levels and in various fora.

In the context of biodiversity, it is essential that industrialized nations conserve micro-organism germplasm. In the near future it will be of crucial importance to further promote the setting up of resource centres in developing countries. Micro-organism collections will act as depositories of live micro-organism diversity, particularly in tropical and subtropical areas which are the widest repositories of micro-organism biodiversity on Earth. They represent a resource that has both local and global impact. One area where there is clearly a need for policy development to support the virtual pooling and use of micro-organism genetic resources for agriculture is in the area of access and benefit sharing. Internationally endorsed access and benefit sharing standards for depositing, distributing and sharing benefits associated with using micro-organism genetic resources for agriculture would help to overcome some of the barriers to international cooperation that have been highlighted above.

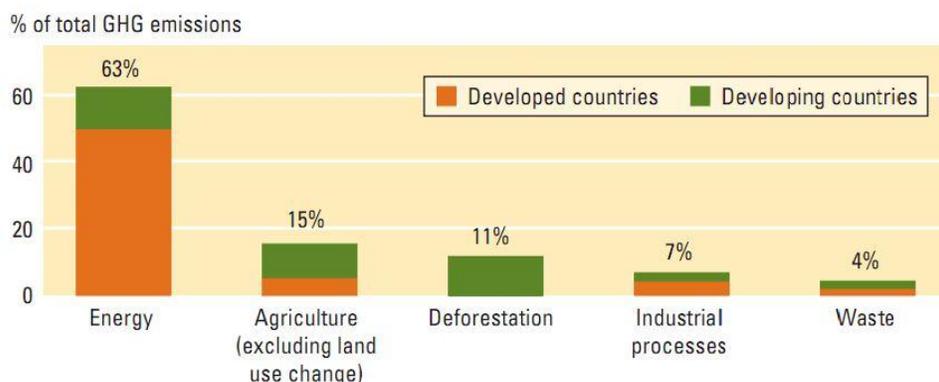
In relation to global coordination to minimize the impact of plant pathogens, great strides have been made through the IPPC (International Plant Protection Convention). The IPPC is a global international agreement on plant health with 177 signatories that aims to protect cultivated and wild plants by preventing the introduction and spread of pests; its secretariat is provided by FAO. The IPPC recognizes that the overall diversity of plant pathogens can be tiered at continental, regional and local spatial scales, and this forms the basis for exclusion-based measures such as quarantine to keep particular pathogens or races out of countries or regions. Characterization efforts to identify which pathogens pose the greatest risk to different localities must recognize that this risk is dynamic as a consequence of the globalization of agriculture and trade combined with the extensive biodiversity of plant pathogens and the numerous mechanisms that generate this variation. Further, plant pathogens are well-known for their rapid adaptation to changes in their environments, such as the use of chemicals or resistant varieties to control them. All of these factors point to the need for a global body, such as the IPPC, to coordinate knowledge sharing, awareness raising and development of recognized detection methods and monitoring techniques. Where there are concerns is at the national and regional level of plant protection organizations (NPPOs, RPPOs) where capacities and linkages differ significantly. Whereas the European regional authority (EPPO) is extremely well organized, this cannot be said of their counterparts across the world (Miller *et al.*, 2009).

VI. CONCLUSIONS

- Micro-organism genetic resources for agriculture carry out many of the vital functions that underpin the ecosystem services that sustain life. Their role is vital to nutrient cycling, supporting the soil food web, imparting resilience, transforming and protecting food from spoilage, and controlling pests, diseases and weeds.
- Micro-organism genetic resources that affect agriculture negatively include species responsible for crop diseases that inflict severe losses in production and quality.

- There will be changes in the distribution and performance of micro-organism genetic resources for agriculture due to climate change. The precise effect of climate change on micro-organism genetic resources for agriculture is unpredictable and complex as a consequence of the wide array of relevant ecological interactions and the influence of environment on each. However, a working knowledge can be readily generated through targeted research and development, and this can be used to inform policy, strategy and tactical measures.
- Climate change, agriculture and energy production are inextricably linked (Figure 5). Micro-organism genetic resources for agriculture can be used to produce energy, facilitate adaptation to climate change and mitigate climate change.
- In the light of emerging challenges, including climate change, the efficient management of micro-organism genetic resources can contribute to the sustainable intensification of agriculture that is needed to meet the predicted increase in food demand.
- To adapt to the effects of climate change, farming practices that increase soil biodiversity, such as crop rotation, green fertilization, organic manure fertilization and biological control, must be encouraged. Selected micro-organisms can be introduced to farming systems as biofertilizers to increase nutrient acquisition and transformation. This will reduce reliance on chemical fertilizers and thereby reduce energy consumption and emission of greenhouse gases.
- Soil-regulating organisms can be managed to increase soil health, ecosystem resilience and obviate the need for energy-expensive inorganic fertilizer.
- Novel biological control agents can be used to limit the harmful impact of pathogens and pests, obviating the need for energy-expensive pesticides.
- Micro-organisms have an important role in the protection and transformation of agricultural produce post-harvest. Use of micro-organisms can increase shelf-life of food, protect food from spoilage by other micro-organisms and minimize the risk of mycotoxin contamination, while saving on energy and greenhouse gas emissions by reducing the need for cold packaging, storage and transportation.

Figure 5. Factors contributing to greenhouse gas emissions and hence climate change



Source: WDR 2008 team, based on data from the United Nations Framework Convention on Climate Change, www.unfccc.int.

- The scale of micro-organism diversity and hence function is without parallel. Therefore, steps must be taken to better characterize this diversity in a targeted manner with focus on key crops to permit the distribution of crop and micro-organism species that act in synergy.

- There is an urgent need to establish an inventory of micro-organism genetic resources for agriculture and to create interactive links between user communities. This is necessary to better understand the functional processes and to conserve those micro-organisms responsible. Critically, results from monitoring exercises can be used to refine these activities towards the delivery of ecosystem services.
- Currently, the capacity and infrastructure to study micro-organism taxonomy and function is limiting, especially in the developing world. State-of-the-art scientific technologies, benchmark experimental sites and living collections of micro-organism genetic resources for agriculture can be used to generate empirical data that can be out-scaled to inform policy-makers, quantify risks and optimize prediction models. Coordinated efforts employing research, capability development and communication backed by a robust policy framework are essential for this to happen.
- International cooperation/coordination between farmers, government institutions, research agencies and living reference collections will be critical in characterizing and sharing micro-organism genetic resources for agriculture to support crop production patterns as they move due to climate change.
- Leadership is needed from policy-makers and researchers to inform the farming community and build capacity on the importance of micro-organism genetic resources for agriculture. Empowerment at farm level will enhance the development of sustainable farm management techniques to conserve and use beneficial micro-organism resources.

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Annex 1. Table (for Section 1.3): Functional groups of micro-organisms in relation to food and agriculture

| Group | Subgroups | Description / definition | Service | Example |
|-----------------------------------|--|---|--|---|
| Soil inhabitants | Soil formation micro-organisms | Micro-organisms that play a key role in pedogenic processes | Beneficial in agriculture: physical stability, organo-mineral aggregate formation, chemical property regulation, water and air regulation (through soil porosity) | Lichens and other photoautotrophic micro-organisms: organic acid production involved in the decomposition of organic matter, but also in the bioweathering of rock and sediments in soils |
| | Carbon-fixing/releasing micro-organisms | Micro-organisms that play a key role in carbon sequestration and/or release | Detrimental/beneficial in agriculture: organic matter decomposition, primary enzymatic decomposition, carbon organisation (humus formation and microbial fixation) | <i>Bacillus macerans</i> : involved in mineralization of soil organic matter |
| | Nutrient-cycling micro-organisms | | Beneficial in agriculture: nutrient recycling, xenobiotic compound degradation | <i>Nitrobacter</i> spp.: ammonification processes; <i>Azospirillum</i> spp.: N-fixation |
| | Water-regulating micro-organisms | | Beneficial in agriculture: water retention | Bacteria and fungi: by production of mucilage, soil structuring and water retention |
| | Soil health indicators | Micro-organisms that act as indicators for soil health | Beneficial in agriculture and food: used to measure impact of man-made changes such as climate change, pollutants, soil biological fertility | Bacteria and fungi: used as soil health indicators |
| Plant and rhizosphere inhabitants | Plant symbionts that provide improved plant nutrition | Micro-organisms that enhance plant nutrition through facilitating uptake of nutrients, fixing of nutrients | Beneficial in agriculture: increase plant access to nutrients and stress tolerance | <i>Glomus</i> spp.: the largest genus of the arbuscular mycorrhizal fungi, which, when they mycose plant roots, enhance nutrient uptake |
| | Micro-organisms that produce compounds influencing plant growth and/or phenotypic disease resistance | | Beneficial in agriculture: probably most typical effect is to enhance plant productivity | <i>Pseudomonas</i> spp: some strains produce phytohormones that increase plant growth |
| | Micro-organisms that contribute to disease suppressive soils | Micro-organisms that compete with, produce compounds detrimental to, and/or parasitize pests and/or pathogens; Micro-organisms that increase plant resistance and/or tolerance to pests and/or pathogens | Beneficial in agriculture: decrease crop losses to pests and diseases | <i>Trichoderma</i> spp.: one of the most successful commercial biological control agent, and probably naturally occurring strains routinely provide benefits to crops |

| | | | | |
|---------------------------|---|--|--|--|
| Plant pathogens | Biotrophic pathogens | Micro-organisms that are pathogens of crops and can survive on living plant material | Harmful in agriculture: reduce crop yield and some life cycle stages can cause rapid adaptation and wide spore dispersal | <i>Puccinia graminis</i> f. sp. <i>tritici</i> : causes wheat stem rust; a new variant (Ug99) threatens wheat production across the world due to overcoming host resistance and vast spread through prevailing winds |
| | Necrotrophic pathogens | Micro-organisms that are pathogens of crops and can survive on dead plant material | Harmful in agriculture: reduce yields of crops, reduce food safety and/or are quarantine pests | <i>Apergillus flavus</i> : produces mycotoxins in maize and groundnut; <i>Ralstonia solanacearum</i> : causes devastating bacterial wilt on potato and other Solanaceae |
| | Weed pathogens | Micro-organisms that are pathogens of weeds, can be either necrotrophic or biotrophic | Beneficial in agriculture: weed management | <i>Phytophthora palmivora</i> : attacks milkweed vine |
| Biological control agents | Micro-organisms used in classical biological control | Introduction of natural enemies to control an exotic, invasive pest species | Beneficial in agriculture: antagonistic against weeds, and plant pests and pathogens | <i>Neozygites fresenii</i> : control of the cotton pest <i>Aphis gossypii</i> in California |
| | Micro-organisms as active ingredients in bio-pesticides | Release of a previously mass-reared natural enemy in the environment, either inoculative or inundative | Beneficial in agriculture: antagonistic against plant pests and pathogens, or against weeds | <i>Bacillus thuringiensis</i> : its endotoxins kill Lepidoptera and Diptera larvae; <i>Puccinia romagnoliana</i> : this rust controls the weed purple nutsedge (<i>Cyperus rotundus</i>) |
| | Conservation biological control micro-organisms | Micro-organisms naturally residing in soil that are indirectly manipulated | Beneficial in agriculture: antagonistic against weeds, and plant pests and pathogens | Entomophthorales: fungal order of highly specialized entomopathogens |
| Food production | Food processing micro-organisms | Fermenting micro-organisms | Beneficial in food: used to increase quality of food | <i>Lactobacillus bulgaricus</i> : (yoghurt fermentation), <i>Saccharomyces cerevisiae</i> (wine, beer and bread) |
| | | Pro-biotic micro-organisms that reside in human body | Beneficial in food: reside in human body, where they are beneficial | <i>Bifidobacterium bifidum</i> : favourably alter intestinal microflora balance in humans |
| | | Micro-organism food producers that transform low-quality carbon and nitrogen sources into food for human consumption | Beneficial in food: produce high-quality proteins and lipids | <i>Phodotorula</i> : used for production of high-quality proteins |
| | | Micro-organisms used in post-harvest technologies to preserve food (as opposed to food sterilization) | Beneficial in food: extend shelf-life of food without the need for sterilization | <i>Meyerozyma guilliermondii</i> : used to extend shelf-life of apples |
| | | | | |

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|--|--|------------------------------------|---|--|
| | Agro-industry processing micro-organisms | Fermentating micro-organisms | Beneficial in agriculture: facilitated production of substances | <i>Saccharomyces cerevisiae</i> : facilitates bio-ethanol production from sugarcane |
| | | Micro-organisms used as cell lines | | <i>Escherichia coli</i> , <i>Saccharomyces cerevisiae</i> and <i>Kluyveromyces lactis</i> : cell line for recombinant production of e.g. ethanol |