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**COMMISSION ON GENETIC RESOURCES  
FOR FOOD AND AGRICULTURE**

**THE IMPACT OF CLIMATE CHANGE ON COUNTRIES' INTERDEPENDENCE  
ON GENETIC RESOURCES  
FOR FOOD AND AGRICULTURE**

edited by

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This document has been prepared at the request of the Secretariat of the Commission on Genetic Resources for Food and Agriculture by the Consultative Group on International Agricultural Research (CGIAR), coordinated by Bioversity International, as a contribution to the cross-sectoral theme, *Consideration of policies and arrangements for access and benefit-sharing for genetic resources for food and agriculture*, which the Commission will consider at its Twelfth Regular Session.

**The content of this document is entirely the responsibility of the authors, and does not necessarily represent the views of the FAO, or its Members.**

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## ABOUT THIS PUBLICATION

The Commission on Genetic Resources for Food and Agriculture (the Commission), at its Tenth Regular Session, recommended that the Food and Agriculture Organization of the United Nations (FAO) and the Commission contribute to further work on access and benefit-sharing, in order to ensure that it moves in a direction supportive of the special needs of the agricultural sector, in regard to all components of biological diversity of interest to food and agriculture.

At its Eleventh Regular Session, the Commission agreed on the importance of considering access and benefit-sharing in relation to all components of biodiversity for food and agriculture, and decided that work in this field should be an early task within its Multi-Year Programme of Work (MYPOW). Accordingly, the Commission decided to consider arrangements and policies for access and benefit-sharing for genetic resources for food and agriculture at its Twelfth Regular Session (19-23 October 2009). To facilitate discussions and debate on access and benefit-sharing for genetic resources for food and agriculture at the Twelfth Regular Session, the Secretariat of the Commission has commissioned several background study papers on use and exchange patterns of genetic resources in the different sectors of food and agriculture. The studies provide an overview of past, current and possible future use and exchange patterns, as well as a description of terms and modalities for use and exchange of animal, aquatic, forest, micro-organism genetic resources; and of biological control agents. Cross-sectoral studies have been commissioned to analyse use and exchange patterns in light of climate change, subject of the present background study paper, and to review the extent to which policies and arrangements for access and benefit-sharing take into consideration the use and exchange of genetic resources for food and agriculture in particular.

The broad ranges of studies are intended to provide insight, necessary to maintain, establish and advance policies and arrangements for access and benefit-sharing for biodiversity for food and agriculture. The studies may also contribute to the negotiations of an International Regime on Access and Benefit-sharing in the Ad Hoc Open-ended Working Group on Access and Benefit-sharing under the Convention on Biological Diversity.

## CHAPTER I: INTRODUCTION

This paper investigates the impact that climate change will have on countries' interdependence on genetic resources for food and agriculture (GRFA). It has been developed for submission to the twelfth session of the Commission on Genetic Resources for Food and Agriculture on 19–22 October 2009 for consideration under Agenda Item 3, which concerns access and benefit-sharing norms.

The extent of countries' interdependence on categories or sectors of genetic resources is a potentially important consideration when evaluating, and or developing, access and benefit-sharing norms. However, it is beyond the scope of this paper to make policy recommendations to the Commission. Instead, it is our hope that this paper will contribute to a deeper well-source of scientific information from which the Commission can draw when considering access and benefit sharing policy options.

In this introductory section, we describe the degree and kinds of climate change upon which our analysis is based and provide a working definition of 'interdependence on GRFA'. We also describe the method we followed conducting the research in support of this paper, and a summary of our most important findings. An executive summary of this paper is also available online.<sup>2</sup>

### 1. Climate change

With respect to climate change, the most relevant prediction for this paper is that, on average, global temperatures will increase worldwide by 0.2 degrees per decade. There will be both increases and decreases in precipitation. Droughts and floods will increase. (IPCC 2007) The areas with climates that are now suited to a particular suite of crops, forages, livestock, trees, microbes, and aquaculture will shift in ways that are more favourable to a minority of countries and less favourable to the majority.

Climate modelling indicates that growing season temperatures in the tropics and subtropics by 2099 will be greater than the extremes recorded from 1900 to 2006. The hottest season to be recorded in the temperate regions will become the norm in many places. Extreme seasonal heat will severely lower the output of production systems (Battisti and Naylor 2009).

Looking ahead to 2050, the effects of global warming for maize, millet, and sorghum in Africa, for example, will be disastrous and will require concerted responses in crop breeding and the conservation of crop genetic resources:

“The majority of African countries will have novel climates over at least half of their current crop area by 2050. Of these countries, 75 percent will have novel climates with analogs in the current climate of at least five other countries, suggesting that international movement of germplasm will be necessary for adaptation. A more troubling set of countries – largely the hotter Sahelian countries – will have climates with few analogs for any crop ... countries, such as Sudan, Cameroon, and Nigeria, whose current crop areas are analogs to many future climates but that are poorly represented in major gene banks – [provide] promising locations in which to focus future genetic resource conservation efforts (Burke et al. 2009).”

Climate change will be highly variable around the world. According to current models (see Chapter II) some countries/regions will actually benefit as a result of having more, longer growing days as well as increased rainfall. These countries are in the minority. Most countries will experience climate change that work to their disadvantage, with temperature increases, longer droughts, and increasingly frequent, violent storms exacerbating stresses that have already been challenging their agricultural

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<sup>2</sup> [http://agrobiodiversityplatform.org/climatechange/files/2010/12/11\\_WEB.pdf](http://agrobiodiversityplatform.org/climatechange/files/2010/12/11_WEB.pdf)

production systems. Based on existing models, it is reasonable to predict that as all countries' climates change, most countries' climates will become more similar to one another, with only a few countries' climates becoming, relative to the situation today, more different from most other countries' climates. As such, many countries may be headed towards common future conditions, leaving relatively fewer countries that can provide the genetic resources for needed food system adaptation to climate change in the future.

## 2. Countries' interdependence on genetic resources for food and agriculture

For the purposes of this paper, our working definition of "interdependence on GRFA" is, "the extent to which individual countries rely upon GRFA originally collected from other countries in support of their food and agriculture-related research, conservation and production."<sup>3</sup>

The idea that countries are interdependent on GRFA is not new, as the literature reviewed in the following chapters makes clear. Countries' interdependence on plant genetic resources for food and agriculture (PGRFA) is evident in the international pedigrees of most modern crops and forages, which include 'parents' from numerous different countries and continents (Zeven and De Wet 1982, Gollin 1998, Cassaday et al 2001). Countries' interdependence on PGRFA is also evident in the international movements of germplasm facilitated by international genebanks and research stations. In the course of just 12 months, the international agricultural research centres of the Consultative Group on International Agricultural Research (CGIAR) facilitate the international movement of approximately 450,000 samples of PGRFA, 80% of which is sent to developing countries, mostly to public agricultural research programmes (SGRP 2009). Interdependence on PGRFA is also evident in the fact that many major crop staples are now grown around the world, far from their centres of origin. Crops were domesticated over thousands of years in areas of the world that are now "developing" countries or regions. Interestingly, however, the adaptations of diets of people around the world has taken place to such an extent that most countries and regions – including those in centres of diversity – are heavily reliant on non-indigenous, imported germplasm of staple crops from other parts of the world. For example, southern Africa is more than 90 percent dependent on "outside" crops (Palacios 1998). Cassava is a major food source in Africa today (FAO 1997), while African millets and sorghums are major food crops in south Asia and Latin America (Kloppenburger and Kleinman 1987). The extensive cattle pastures of Latin America depend largely on African grasses (Miles et al. 1996; Boonman 1993). Alfalfa from southwestern Asia is now cultivated around the globe (Putnam et al 2009). Forestry has also long benefited from the international movement of tree germplasm (Koskela et al., 2009).

The case is similar for livestock with the private sector heavily involved in the international movement of farm animal genetic resources. Livestock producers have relied on the international exchange of genetic resources throughout human history. Analyses of animal genetic resources trade flows from 1990 to 2005 for 150 countries show that Europe and North America were the primary exporters of genetic resources for the species evaluated. North-South trade had the largest magnitude, followed by South-South, and, finally, South-North. Southern genetic resources are not currently used on a large scale in the North (Gibson and Pullin 2005; FAO 2007).

The management of aquatic resources has always reflected some degree of international collaboration simply because fish are free living and highly mobile, and the water bodies and aquatic ecosystems in which they live do not follow national boundaries. The limited number of major aquaculture species

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<sup>3</sup> The extensive network of *ex situ* collections of genetic resources (not only plant genetic resources for food and agriculture but also sizeable collections of microbial genetic resources and, to a lesser extent, tree, animal, and aquatic genetic resources) means that countries may not need to physically have access to materials located within the borders of a particular country. It may be that material once collected from country X is available from collection Y, which is located in another country. The actual location of the material, once collected, does not affect the extent to which its use in other countries reflects interdependence.

has been associated with considerable movement of genetic resources to areas having suitable ecological conditions around the globe. Over the past 100 centuries, agriculture has been characterized by an increasingly wider movement of crops, forages, farm animals, and, more recently, trees and fish.

In this paper, we do not attempt to quantify baseline levels of interdependence and use this data to calculate quantified increases in that interdependence. Other papers submitted to the Twelfth Regular Session of the Commission under Agenda Item 3 have described patterns of use and the exchange of microbial, tree, crop, and forage, invertebrate, and aquatic genetic resources,<sup>4</sup> including analyses of countries' interdependence on these resources. Our approach in this paper is simply to assess whether climate change will result in countries requiring GRFA from outside their borders as part of their strategies to adapt (and, in some cases, to mitigate) climate change. Assuming all other demands remain equal, an increase in demand for resources from outside countries would result in an overall increase in interdependence. A decrease in demand would lead to a decrease in interdependence.

### 3. Hypothesis and method

When formulating the terms of reference for the paper, our hypothesis was that climate change will indeed lead to an overall increase in countries' levels of interdependence on genetic resources.<sup>5</sup>

Our first step in the process of conducting this research was to identify the subgroups of genetic resources for food and agriculture that could be usefully examined independently from one another. In consultation with the CIAR Inter-centre Working Group on Genetic Resources (ICWG-GR) and the Secretariat of the CGRFA, we identified the following: crop and forage, tree, animal, microbial, and aquatic genetic resources. We contacted experts working in the conservation and use of these genetic resources to conduct the relevant research. Based on their own reviews of existing literature, and their own expert knowledge of the field, these experts were asked to (1) describe and evaluate existing evidence (positive or negative) that climate change has increased or will increase countries' interdependence on the genetic resources concerned; (2) identify whatever gaps may exist in the literature that limit our ability to fully assess the impact of climate change in this way; and (3) summarize their final conclusions. These studies constitute sections 2–6 of this paper.

Our second step was to consider whether there are illuminating differences or similarities between the experts' reports that support or detract from our hypothesis. Our most important findings in this regard are set out below in this chapter, and in the final chapter.

Before proceeding further, it is important to highlight a significant constraint we faced in this research. Numerous interrelated factors affect the way in which GRFA need to be managed and used. It is difficult, and sometimes impossible, to isolate climate change-related influences from those of other variables. The influence of climate change on countries' interdependence on GRFA is embedded in a broader, very complex range of variables. As a result it was often not possible to isolate simple cause and effect relationships between climate change and interdependence.

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<sup>4</sup> Background Study Paper No. 43: The use and exchange of animal genetic resources for food and agriculture; Background Study Paper No. 44: The use and exchange of forest genetic resources for food and agriculture; Background Study Paper No. 45: The use and exchange of aquatic genetic resources for food and agriculture; Background Study Paper No. 46: The use and exchange of microbial genetic resources for food and agriculture; Background Study Paper No. 47: The use and exchange of biological control agents for food and agriculture..

<sup>5</sup> We did not attempt to quantify baseline levels of interdependence or measure quantified increases against them. Our much simpler approach is simply to assess whether climate change will result in countries requiring GRFA as part of their strategies to adapt (and, in some cases, to mitigate) climate change.

#### 4. Main findings

By and large, the balance of evidence supports our hypothesis. The main findings are summarized as follows:

*Crops and forages.* Germplasm interdependence will perhaps be the greatest for crops, augmenting the already high (and well-documented) international movement of plant genetic resources for food and agriculture (PGRFA) that has been taking place for a long time. Interdependence on PGRFA will likely increase in association with adaptive crop improvement achieved through both conventional plant breeding and biotechnological methods. Interdependence will also increase as climate change creates the need to adopt new crops in particularly stressed areas – millets and sorghum in the place of maize, for example. (See chapter II)

*Trees.* Countries' interdependence on tree germplasm will likely increase as a result of the future demands for genetic resources in support of both tree plantation and agroforestry use, both of which will require the adoption of new species and improved, better adapted varieties. Small-scale agroforesters will be especially reliant on externally facilitated access to introduced materials because their own abilities to find, test, and adopt new trees will likely be inadequate relative to the pace of climate change. (See chapter III)

*Livestock.* As is the case for crops, forages, and trees, research to identify or develop livestock breeds that are better adapted to abiotic stresses will continue to be important. Germplasm movement in modern times has been facilitated largely through the private sector, and such movements will likely increase as climate change forces redistribution of breeds to match future conditions. (See chapter IV)

*Microbes.* Microbial genetic resources – which are discovered, identified, isolated, sometimes genetically modified, and reproduced rather than bred – will play an extremely important role in future climate-changed scenarios. On the one hand, crop diseases and disease vectors will likely redistribute and intensify as climate changes and as crops, crop cycles, and crop distributions also change. On the other hand, researchers will need to respond with microbial-based solutions to ongoing and new problems in the form of, for example, specific pathogens or parasites to counter insect pests and vectors of plant diseases. The success of such research efforts will depend upon continued global public access to microbial resources. (See chapter V)

*Aquatic resources.* Aquatic germplasm resources interdependence was discussed in a somewhat unique fashion because the transboundary nature of aquatic ecosystems has meant that aquatic resource management has necessarily been interdependent. Germplasm exchange of the few aquacultural species discussed will continue largely through commercial channels. The implications for climate change-related interdependence are unclear because it does not appear that breeding for new climate-related conditions will be a major part of future strategies. (See chapter VI)

The fact that the rate of climate change will likely exceed many organisms' adaptive capacity is a common denominator for all of the sectors studied. The case is most strongly made with respect to crops and forage varieties, animal breeds, and tree populations. The evidence is less conclusive for beneficial microbes and aquaculture species, but there are anecdotal accounts that point in this direction, and it is logical to expect that it should be so, although the greater mobility of organisms in these sectors could be a mitigating factor.

The gap between the rate of climate change and the organisms' adaptive capacities will require significant adjustments in national agricultural production systems and planning. As some countries' climates gradually become more like other countries' present climates, they will be able to turn to portfolios of crop and forage species, varieties, livestock breeds, trees, microbes, and fish that are currently used in the latter countries.

As most countries – particularly poor countries in areas already suffering drought, high temperatures, and devastating storms – move into having climates without precedent in the history of agriculture, they will be pushed together to seek common, internationally coordinated solutions. Such solutions will include reliance on “outside” sources of diversity, either of the same species currently in production or of new species entirely.

The impact of climate change *vis-à-vis* pathogenic microbes is, in some respects, the corollary of its impact on crops, forages, livestock, and trees. Climate change will provide opportunities for pathogenic microbes (and their insect vectors) to thrive in parts of the world where previously they have had no, or only limited, impact. The effect will be to augment countries’ dependence upon genetic resources from beyond their borders – in this case, as sources of genetic resistance to novel pests and diseases or as bio-control agents.

Internationally coordinated efforts involving international movements of germplasm and associated information will be critical for countries’ to be able to meet the challenges associated with climate change. It is critically important for policy makers to keep this increasing interdependence on GRFA in mind when developing policies concerning the conditions under which genetic resources can be accessed and used, and the ways in which benefits derived from their use should be shared.

## CHAPTER II: CROP AND FORAGE GENETIC RESOURCES: INTERNATIONAL INTERDEPENDENCE IN THE FACE OF CLIMATE CHANGE

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### 1. Introduction

Plant genetic resources for food and agriculture (PGRFA) are the biological cornerstones of global food security. Crops account for 84 percent of human caloric intake (Loladze 2002). An estimated 3.5 million hectares were under permanent pasture globally in 1997 (FAOSTAT 1997). About five million hectares of forage legumes and more than 42 million hectares of forage grasses are planted seasonally for livestock production in the tropics (Shelton et al. 2005). The efficient use of agricultural diversity and genetic resources will be needed both to maintain current levels of food production and to confront future challenges. Population is expected to grow to 9.1 billion by 2050 (United Nations 2005), with increasing consumption of dairy and meat products. This increased demand means increasing production without the option of increases of arable land. The expected impacts of climate change suggests that we face worsening multiple challenges and decreasing options to address these challenges. PGRFA will play a crucial role in providing the genes to help confront the challenges.

Improving yield – or even maintaining yields in the face of climate change – of major food crops will depend on combining genetic traits found in materials of a wide range of origins (Petit 2001), including crop wild relatives, landraces, breeding lines, and established varieties. The “Green Revolution” of the 1960s was unfortunately accompanied by losses of many crop landraces and, as such, by significant genetic erosion (Heal et al. 2004). Only some 150 plant species are now cultivated, and mankind depends largely on no more than 12 plant species (Esquinas-Alcázar 2005). Although only about 60 species are widely used as fodder, these have been moved around the globe. Most livestock systems depend on fodder species originating elsewhere. There are calls for diversifying agricultural production to adapt to climate change, to enhance nutritional security, and to service an increasingly complex global market for agricultural goods (Reidsma and Ewert 2008; Cavatassi et al. 2006; Cleveland et al. 1994). Neglected and underutilized species are expected to play an important role in such diversification (Genetic Resources Policy Committee 1999).

Perhaps more than any other group, PGRFA have been exchanged over the past 10,000 years through farmer exchange and, recently, by collection, ex situ conservation, and use by research organizations. The globalization of plant genetic resources is evident in the expansion of crops outside of their centres of origin (Vavilov 1926), with near global coverage of many crops whose origins were geographically restricted. Today, all countries rely on crop genetic diversity from all over the globe to provide potential adaptation to changes, to maintain production systems resilience, and to meet the needs of an expanding human population (Esquinas-Alcázar 2005).

Global interdependence in PGRFA has informed the development of international policies to facilitate access and exchange of plant genetic resources (Palacios 1998). These include the voluntary International Undertaking on Plant Genetic Resources (1983), the Convention for Biological Diversity, and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA, which entered into force 2004).

Studies using a variety of approaches have tried to quantify interdependence of plant genetic resources (e.g., Palacios 1998). It is important in the face of climate change to re-appraise interdependence and identify changes in demand for plant genetic resources to help create policies to address future

challenges. This chapter focuses on the effect climate change will have on the international interdependence of PGRFA. Rather than quantify current demand, we look for evidence of how climate change might enhance, reduce, or shift patterns of demand. Analysis is based on literature review and numerical analysis. We structure the chapter as follows:

1. review of current patterns of interdependence of PGRFA (to set the baseline);
2. review of the expected impacts of climate change on agriculture;
3. quantitative analysis of the changes in “climatic interdependence” for a number of crops;
4. discussion of likely changes in interdependence based on evidence from the other chapters; and
5. discussion of policy implications to address future interdependence patterns.

## 2. Current international interdependency on PGRFA: Setting the baseline

Virtually all countries depend on PGRFA that is received from others. Today’s improved varieties have resulted from innumerable crosses among materials from different countries (Zeven and De Wet 1982). The globally popular VEERY wheat is the product of 3,170 crosses involving 51 parents from 26 countries. Developing countries rely on non-indigenous crops and thus need to import germplasm: countries in south and central Africa rely on crops that originated outside the region for 50–100 percent of their food, with the majority of these countries exceeding 80 percent dependency (Palacios 1998). Such dependency is never below 80 percent in the Andean countries. Crops such as cassava, maize, groundnut, and beans originated in South America but became staples in sub-Saharan Africa. Cassava is a major food source for 200 million Africans in 31 countries with a farm-gate value of over US \$7 billion (Food and Agriculture Organization 1997). And Africa – with its indigenous millets and sorghums – makes a considerable contribution to other areas such as South Asia (13 percent) and Latin America (8 percent) (Kloppenburg and Kleinmann 1987). In the 1970s, *Helminthosporium maydis* destroyed more than half of the maize crop in the southern United States. The susceptible seeds had a narrow genetic base. In this case, as in many others, the problem could only be resolved by breeding resistant varieties using genetic diversity from other countries (National Research Council, Genetic 1972).

The case of forages is similar. Over 90 percent of the major cultivated forage grasses are indigenous to sub-Saharan Africa (Boonman 1993). These grasses have been used to improve the extensive cattle pastures in Latin America. By 1996, over 40 million hectares were sown to *Brachiaria* in Brazil (Miles et al. 1996). Ruzi grass (*Brachiaria ruziensis*) was introduced to Thailand and is increasing in demand (Phaikaew et al. 1993). *Cenchrus ciliaris* is now grown in 31 countries (Cox et al. 1988), with four million hectares planted in the United States, over six million hectares in Mexico, and 7.5 million hectares in Australia (Humphreys 1967). Other African grasses (e.g., *Panicum maximum*, *Chloris gayana*, and *Pennisetum purpureum*) are now also widely distributed throughout the tropics.

Forage legume interdependence is common for sub-tropical species. Alfalfa – extensively cultivated in the warm temperate, cool sub-tropical regions and tropical highlands – is native to southwest Asia. Today, it is the major forage legume crop covering 79 million hectares worldwide, including 13 million hectares in the United States where it is the third most important crop in value (Putnam et al. 2007). Vetch originated in the near East and is now grown on close to one million hectares worldwide (FAOSTAT 2009). Red and white clover originated in Europe and North Africa and are now widely cultivated in sub-tropical areas in North America, southern South America, Australia, and New Zealand. *Stylosanthes* from Latin America is now used in India (Ramesh et al. 2005) and Thailand (Phaikaew and Hare 2005) for improving pastures and leaf meal for monogastric feed.

Crop wild relatives, a key component of interdependence, provide researchers with genes useful for developing biotic and abiotic resistance (Maxted et al. 2008; Gurney et al. 2002; Lane and Jarvis 2007). The use of crop wild relatives has increased dramatically over the past decade and will continue to increase, thanks to biotechnology tools. A number of crops such as sugar cane, tomatoes, and

tobacco could not be grown on substantial commercial scales were it not for the contribution made by wild relatives of these crops to disease resistance (Food and Agriculture Organization 1997).

Developing countries have provided the biological basis for agriculture both in developed countries and for each other (Fowler et al. 2000). The dimension and direction of the flow of PGRFA (e.g., south to south and north to south) is difficult to track, monitor, and quantify. Information available on flows indicates a reverse flow in which material is no longer exported from their centres of origin. Rather, the opposite is occurring – farmers and research institutes in the developing world have become net recipients of both local varieties and of improved materials (Visser et al. 2003; Fowler and Smale 2000).

### **3. Climate change impacts on agriculture and PGRFA**

Climate change will likely bring increases in temperature of between 2–6 degrees Celsius, changes in rainfall regimes representing both an increase and decrease in precipitation, and an increased frequency of droughts and floods (Intergovernmental Panel on Climate Change 2007a). These changes will especially affect rain-fed agriculture, making adaptation necessary. Climate change will also have an impact on agricultural biodiversity by increasing the genetic erosion of landraces and threatening wild species including crop wild relatives (Jarvis et al. 2008). Severe pest outbreaks may increase with climate change, profoundly affecting agro-ecosystems and global food availability (Tubiello et al. 2008).

Modelling indicates that rain-fed agriculture yields in some regions of Africa could be reduced by up to 50 percent by 2020 (Intergovernmental Panel on Climate Change 2007b). Food production and access in many African countries will likely be severely compromised, exacerbating food security problems and malnutrition (Intergovernmental Panel on Climate Change 2007b). Most problematic are the regions of southern Africa where land suitable for maize, a major staple, will likely disappear by 2050, and south Asia where productivity of groundnut, millet and rapeseed will be heavily reduced (Lobell et al. 2008).

Even under the most conservative of baseline scenarios, climate change will cause shifts in suitable areas for cultivation of a wide range of crops. Shifts include a general trend of loss in suitable area in sub-Saharan Africa, the Caribbean, India, and northern Australia; and gains in the northern United States, Canada, and most of Europe for a number of staple crops (Lane and Jarvis 2007). Twenty-three crops are predicted to gain suitable area; while 20 are predicted to lose. Developed nations will see an expansion of suitable arable land to higher altitudes as well as the potential to increase production if those lands are brought under cultivation (Fisher et al. 2001). By the 2080s, rain-fed cereal production in the developing world will decrease by 3 percent in negatively impacted countries and increase by 6 percent in positively impacted countries. Production losses from climate change could worsen hunger in developing countries beyond the current one billion that are going hungry (Food and Agriculture Organization 2009).

Although farmers have always had to adjust and adapt their cropping systems to changing climatic and environmental conditions, the speed and complexity of current climate change poses a greater magnitude of problems (Adger et al. 2007). Rising temperatures and changed rainfall regimes will not decrease the global suitability for crops *per se* but, rather, will cause geographic shifts in suitable cropping areas. Varietal and/or crop substitution could be a key strategy to adapt smallholding agriculture to climate change (Lane and Jarvis 2007). For any given site, there is high likelihood that currently adapted crops will become mal-adapted. New crop diversity and/or different and better-adapted crops will be needed to respond to future conditions. The negative impacts of climate change can be mitigated if farmers can adapt by changing to more suitable varieties and, if necessary, crops (Lane and Jarvis 2007). Barriers to such adaptation, however, are discussed in subsequent sections.

The areas that are currently most food insecure will be most affected by climate change. These areas have the greatest need for new crop varieties that are tolerant to extreme conditions such as drought,

heat, flooding, submergence, and salinity. Adapting crop varieties to local conditions can reduce risk due to climate change. The need for adapted germplasm will require characterization, evaluation, and availability of materials now housed in gene banks. The amount or identity of currently conserved plant genetic resources that may be useful to adapt agriculture to climate change cannot be precisely known *a priori*. Needed are assessments of necessary traits and the conservation and characterization of the broadest of range of genetic resources available.

Conservation of genetic resources will become a key issue. Some of the more important traits to be found in varieties and genotypes for responding to climate change include: drought tolerance, extreme events tolerance, resistance to very hot and humid conditions, pest and disease resistance, and separation from certain climate sensitive pollinators or symbionts. Most of these traits may be present in traditional cultivars or wild species. Unfortunately, with modern crop intensification, many such traditional varieties were underutilized and lost. The US Department of Agriculture indicates that from 7,098 apple varieties in use between 1804 and 1904, 86 percent have been lost. Similarly, 95 percent of the cabbage, 91 percent of maize, 94 percent of the pea, and 81 percent of the tomato varieties no longer exist (Fowler 1994). Agricultural expansion also accounts for wild habitat loss and for the genetic erosion of many wild gene pools that could provide both biotic and abiotic resistances for traditional and modern crop varieties (Food and Agriculture Organization 1998).

Agricultural biodiversity needs to be collected, conserved, and characterized at the species and genetic levels (Jarvis et al. 2003). The Food and Agriculture Organization estimates that a large proportion of the gene pool of the major crops has been sampled and placed in *ex situ* collections. Much of the diversity found in farmer's fields today, and a great amount of diversity that no longer exists on farms, can now be accessed solely through gene banks (Fowler and Smale 2000). *Ex situ* conservation is a viable option, however, only for those sexually reproducing species that produce seeds that can germinate after being stored in cold, dry conditions, clonally reproduced crops whose tissue can be kept for long periods in slow-growth tissue culture, as adult plants in field gene banks, or those for which cryopreservation protocols and infrastructure have been developed. Most of these *ex situ* conservation methods are costly and require constant vigilance, maintenance, and periodic regeneration of the conserved materials, and, as such, are hardly a panacea for the conservation of plant genetic resources. Other disadvantages of *ex situ* conservation include the fact that:

- gene bank accessions are frequently, albeit inadvertently, duplicated;
- maintenance is expensive, and some gene banks cannot avoid germplasm losses due to budgetary constraints;
- only a small amount of genetic diversity present in a population is captured in a gene bank accession; and
- the most important natural and anthropocentric selection processes that take place *in situ* are halted (Fowler and Hodgkin 2004).

Although *in situ* conservation has the advantage of maintaining species interactions and therefore the major evolutionary dynamics of ecosystems that are produced by these dynamics, it can be difficult to implement as it typically involves traditional farming communities, indigenous communities and/or protected areas, and often these require major investments and political agreements to be established. One approach proposed is the preservation of a number of valuable crop species and varieties in selected areas of traditional agriculture (Brush 2000). One example of this approach is the "Globally Important Agricultural Heritage System Initiative" (Commission on Genetic Resources for Food and Agriculture 2000). Conservation of forests and pristine sites valued for their wildlife or ecological value is a means to achieve *in situ* conservation of wild species and wild crop relatives.

Forages in smallholder systems in the tropics are often intercropped, planted around fences, or used in crop fallow periods or for vegetation on degraded lands. This pattern leaves forages more vulnerable to land use change than other crop species since they are often a neglected part of the production system and not taken into account for conservation, especially where competition for land for

cropping, water, and soil fertility are high and resources are limiting. Climate change will require new management options and alternative forage species or increased use of existing forages in many areas. Use of specific forage species in smallholder livestock systems is limited by the length of the growing season and temperature (Cox et al. 1988; Thornton et al. 2006b). The predicted temperature increases of 2–6 degrees Celsius by the end of the century in Africa could allow for the spread of tropical species from countries in other agro-ecological regions into new environments where water is not the limiting factor (Hoffman and Vogel 2008; Collier et al. 2008). Many of the important forage grasses, including Napier, Rhodes, and *Brachiaria*, are not frost tolerant. As temperatures increase and the likelihood of frost decreases, these tropical species could be introduced into sub-tropical regions, including the tropical highlands.

Changes in climate in Africa are predicted to be more severe than in other regions (Collier et al. 2008). Impacts will be substantial on the use of cultivated forages and on indigenous forage diversity in grasslands and natural pastures. Some areas of east Africa are predicted to have 10–20 percent more rainfall (Collier et al. 2008). Current grazing or marginal lands may be used for growing crops, leading to a loss of forage diversity and to the opening up of now marginal lands to degradation. Climate change could also allow for the introduction of species from Latin America such as *Centrosema* and *Stylosanthes guianensis*, which are adapted to sub-humid areas. In areas predicted to get drier, continued cropping can result in more rapid degradation through the loss of land cover. Use of drought tolerant forages in these areas, such as buffel grass or *Stylosanthes scabra* could, on the other hand, increase soil cover and reduce soil degradation (Batjes and Sombroek 1997).

The effects of climate change will be greatest on the grasslands and rangelands that have the potential for land use change. Natural grasslands act as an important carbon sink (Morgan 2005). Increasing levels of carbon dioxide will increase overall biomass production but may result in reduced forage quality and digestibility due to lignification (Thornton et al. 2006a). Changes in carbon dioxide could result in changes in species richness in natural pastures because some legumes are more responsive to increased levels of carbon dioxide as a result of biological nitrogen fixation (Aguilar 2005).

#### **4. Numerical analysis of the changes in climatic similarity between countries for a number of crops**

We performed a numerical analysis of climate change predictions and crop distributions to identify the extent to which climate change will impact climatic compatibility of genetic resources among countries. We assume that climate itself is an important indicator of genetic resource compatibility between countries, hence, we analyzed the climatic similarities between countries under current and future conditions, using climatic similarity as a proxy for possible genetic resource interdependence. We selected 17 staple food crops that account for 75 percent of global harvested area (FAOSTAT 2009). There were a number of different climatic responses within these crops because they cover a range of different ecologies. Crops were cereals (i.e., wheat, maize, millets, rice, sorghum, and barley), legumes (i.e., beans, groundnut, and soybean), roots and tubers (potato, sugar beet, sweet potato, and cassava), fruit (banana and plantain), fiber (cotton), and high-value industrial and cash crops (sugarcane and coffee). “Climatic similarity” was described in terms of a four-dimensional matrix consisting of:

- climatic similarities between countries with the current climate (the baseline);
  - climatic similarity between countries in the future (this provides the likely changes in climatic similarity with respect to the baseline);
  - climatic similarity between each country’s current conditions and future conditions (this provides the extent to which the current climate upon which agriculture is built and for which genetic resources are adapted could be important for the future of other countries);
- and

- climatic similarity between each country's future conditions and current conditions (this provides the extent to which a country in the future could depend on other countries for genetic resources conserved presently).

The analysis looks at the similarity between countries for these four situations for each of the 17 crops under study. Current harvested areas of each crop were used to define the production environments for each crop within each country (FAOSTAT 2009). The absolute presence of each crop within each country of the world was determined using a spatial allocation model (You et al. 2006; You and Wood 2006). For each country and for cropped lands (per crop) within each country, the current distribution of climates was derived from WorldClim (Hijmans et al. 2005). Monthly minimum, maximum and mean temperatures, and monthly total rainfall were queried from this database and used to derive 19 bioclimatic indices (Busby 1991). The zonal average by country was taken as the country's current climate.

Changes in climate were derived from results of 18 global circulation models (GCMs) from the third and fourth Intergovernmental Panel on Climate Change's (IPCC) assessment reports for the decade around 2050 and for the A2 emission scenario (business as usual) of the Special Report of Emission Scenarios (SRES) (IPCC 2001; IPCC 2007b). GCM minimum, maximum, and mean monthly temperatures, and total monthly precipitation outputs were downscaled using a spline interpolation of anomalies and the current distribution of climates reported in WorldClim and used to derive the same 19 bioclimatic indices as for WorldClim (Ramirez and Jarvis 2008). The zonal average on a country basis was taken as an indicator of the country's future climate.

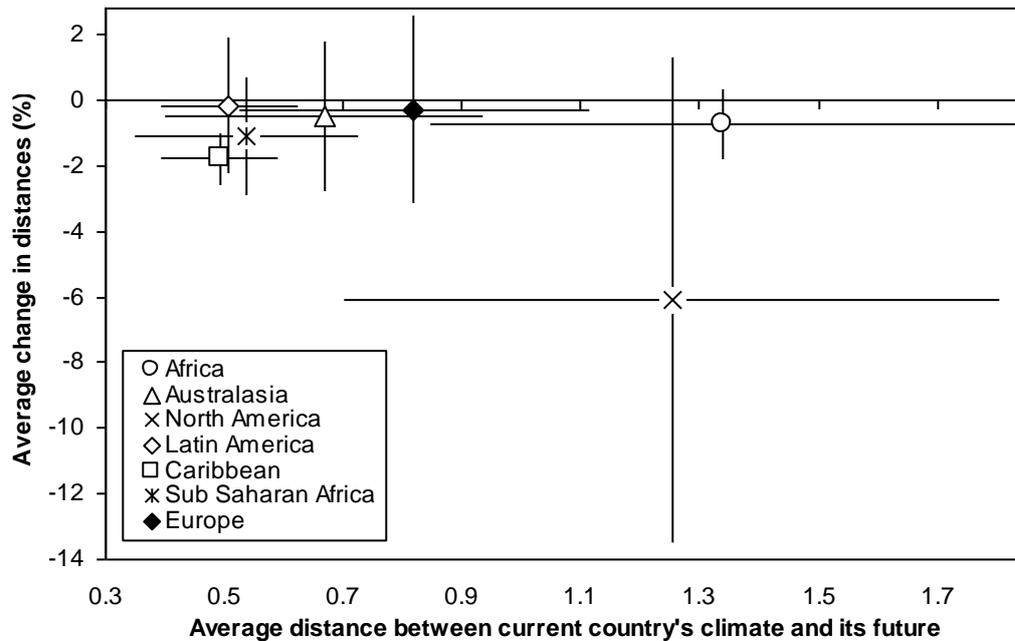
For each crop's distributional range, the 19 bioclimatic indices were standardized and three 19-dimensional Euclidean distance (ED) matrices of  $n$ -by- $n$  countries were computed:

- ED between current climates to measure the current status of climatic similarity between countries;
- ED between future climates to measure the likely change in climatic similarity between countries as well as to derive a consistent conclusion on the climatic similarities that may be gained and/or lost within the next 50 years; and
- ED between current and future climates to determine opportunities for sharing current genetic resources for countries that will reach similar conditions to what some other countries hold actually.

We then calculated the average changes in distances for each country and its future, the average changes in distances between each country and all of the others, the average distances from one country's current climates to future climates of all of the others and, *vice versa*, the country rates of gained and lost climatic similarities, and the key climatic similarities that may arrive within the context of each crop if a given climatic condition changes.

Current climatic similarity among countries for all crops was high. Regions not only provide genetic resources to other regions and import/export food crops to supply basic needs of their populations but also show high climatic similarity. The average rates at which country croplands hold significant similarities (relation between the number of "close" countries to the total number of countries) with others is above 80 percent for all crops. Globally, 116 out of the 188 countries (62 percent) will likely decrease their average climatic similarity in respect to all other countries (see Table 1 and Figure 1), indicating an increased similarity among global areas among these countries, and from the other 72 countries, 94 percent will likely decrease their average ED by only less than 5 percent. For all crops, the similarities are likely to strengthen for more than 40 percent of the countries (with sugar beet showing the maximum at 91 percent and cassava showing the minimum at 41 percent). Generally, moist environments are more likely to increase in climatic similarity, although no significant latitudinal trends were found (Figure 1a) as there were no separations among individual countries of different geographic areas (i.e., Europe, Sub-Saharan Africa, Latin America, Australia).

Considering the entire area of the country and the pooling results by region, climatic similarity is likely to increase with changing climates. On average, all regions showed reduced Euclidean distances in the 2050s, with North America presenting the greatest decrease and Latin America presenting the least decrease. These values, however, may hold a lot of within-country variations. Country self-distances (distance from a country's current status to its own future status) are the greatest for North Africa and North America, indicating a greater level of climatic similarity than in regions such as the Caribbean where countries are relatively climatically similar.



**Figure 1.** Average changes in ED pooled by continental zone (Y axis) plus a 95 percent confidence interval versus the average distance between current and future climates of each counter plus a 95 percent confidence interval, pooled by continental zone (X axis)

Although percentages of change range between minus 24 percent (Faroe Islands) and 54 percent (Grenada), 97 percent of the countries have changes between 10 and minus 10 percent. For 11 percent of the countries (i.e., Serbia and Montenegro, United Arab Emirates, Sweden, Romania, Macedonia, Lithuania, Iran, Iceland, Grenada, Georgia, France, Faroe Islands, Egypt, Canada, Bulgaria, Bosnia, Belgium, Azerbaijan), changing climate conditions will make at least one of the other country's current conditions closer to their future conditions than themselves.

**Table 1. Likely changes in countries interdependence for 17 crops for 2050**

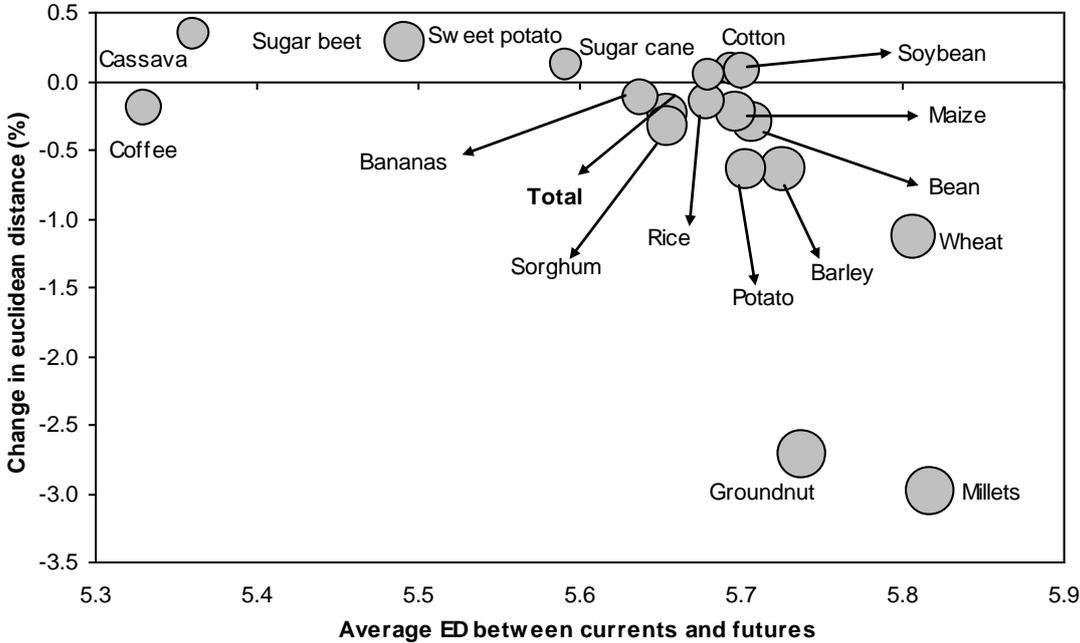
Area	Decreases in ED (percent)	Change in ED (percent)	Maximum loss of interdependence	Maximum gain of interdependence	Percentage of countries With key current actors to take PGR for future	Percentage of analogs that may be more important	Percent of analogs that may appear
Bananas*	52.4	-0.12	Solomon Islands	Pakistan	2.9	53.3	1.0
Barley	70.4	-0.65	Finland	Yemen	16.8	69.6	5.6
Bean	59.7	-0.31	Colombia	Saudi Arabia	14.2	67.2	3.0
Cassava	40.6	0.33	Solomon Islands	Guyana	0.0	40.6	0.0
Coffee	55.3	-0.21	Kazakhstan	Yemen	1.2	49.4	0.0
Cotton	45.4	0.08	Uganda	Saudi Arabia	8.3	65.7	2.8
Groundnut	90.2	-2.73	Iraq	Yemen	30.1	74.0	15.4
Maize	57.4	-0.23	Solomon Islands	Yemen	9.7	60.6	1.3
Millet	86.4	-2.99	Germany	Albania	42.1	73.9	22.7
Potato	68.8	-0.65	Finland	Oman	13.6	66.2	2.6
Rice	52.2	-0.16	Iraq	Somalia	8.8	59.6	0.0
Sorghum	63.3	-0.34	Peru	Oman	10.2	67.2	2.3
Soybean	46.8	0.07	Colombia	Turkmenistan	12.1	66.9	2.4
Sugar beet	61.1	0.27	Finland	Uzbekistan	31.5	90.7	27.8
Sugar cane	43.6	0.04	Colombia	Turkmenistan	6.4	52.7	4.5
Sweet potato	41.9	0.12	Bhutan	Saudi Arabia	1.7	51.3	0.0
Wheat	74.0	-1.15	Finland	Yemen	42.0	83.2	22.9
Total	61.7	-0.25	Faroe Islands	Grenada	11.7	69.1	3.7

*Notes:*\* banana and plantain

On the other hand, 98 percent of the countries strengthen at least one relationship if all of the other countries change their conditions (current versus future), and 69 percent of the countries will likely be climatically closer to at least one of the other country’s current conditions. For climatically “far” countries, 76 percent will become more similar to at least one country’s future climates, while 52 percent would be climatically more dissimilar to at least one other country's future. Areas in which each of the different crops are located, however, may hold a different picture than the general country’s overview.

There are different observed trends in crop-based climatic interdependency changes. The proportion of countries increasing their “closeness” is above 50 percent for 12 of the 17 crops considered (Figure 2, bubble size); and the average ED decreases for 11 out of the 17 crops (i.e., for bananas, barley, beans, coffee, groundnut, maize, millets, potato, rice, sorghum, and wheat). Cassava was the only crop for which no country showed a closer analogue than itself. Wheat, maize, and millets showed 42, 30, and 42 percent of their current cropping environments under analysis being nearer to at least one other future cropping environment. This outcome may indicate that environments included in these percentages may have at least one key actor with which they should consider reviewing existing and past flows of plant genetic resources.

Coffee had the least distance from current to future environments, probably due to the specialization of croplands. All crops’ current-future EDs, however, occur within a quite small range (from 5.3 to 5.9). Most of the changes in the different environments of crops are near to the total area, suggesting that all of those crops hold relatively similar patterns of interdependencies and that their environments may be relatively similar now and in the future. Cassava, coffee, sugar beet, and sweet potato from one side, and wheat, millet, and groundnut from the other are the only crops that showed significant differences in behaviour in comparison with the other ones.



**Figure 2** Changes in Euclidean distances pooled by crop for all countries having one or more hectares on each crop versus the average Euclidean distance between current climates and future climates of each country pooled by crop. Bubble size is the percentage of countries having one or more hectares on each crop and decreasing climatic distances (i.e., proxy of a higher interdependence).

Loss of similarity occurs when a cropping environment becomes further away from all climates of the other countries. Grain legumes environments (i.e., beans and soybeans) are predicted to reduce their climatic similarity in Latin American countries with croplands in the Andes. Cold environments such as those in Finland are also likely to lose climatic similarity in their croplands. Finland is actually the most frequent “loser” in the whole world for the selected crops. Asian countries tend to increase their climatic similarity at much higher rates than other countries (Table 1 and Figure 1a), which may be due to their sub-tropical conditions. There could be some additional opportunities for sub-Saharan African countries such as Somalia and others nearby, especially in rice cropping.

Novel climate conditions will appear for all crops except for cassava, coffee, rice, and sweet potato. This outcome may be due to either a very high similarity in current conditions (i.e., specialization of cropping environments) and thus a near-to-total coverage of the possible climatic similarities or to a differential effect on different countries that makes them further away in the future, or both. All cropping environments show a significant number of areas currently holding fundamental climatic conditions that may be near to their own current environment. Rates of lost dependencies, despite the fact that they are far less significant than rates of gained or strengthened dependencies should be also taken into account. For all crops, at least 30 percent of the cropping environments lose at least one climatic similarity with another country. Specific analyses within different cropping environments are required to further develop a collaborative and dynamic network that allows fluxes of relevant genetic materials from one country to another.

## 5. Expected changes in interdependency as a result of climate change

Two clear issues may lead to greater interdependency as a result of climate change:

1. Novel climatic conditions for countries will mean that currently adapted landraces and varieties may become maladapted, requiring the import of new materials with novel abiotic traits.
2. Climate change will bring about new types and increased demand for PGRFA globally, requiring greater volume and a variety of genetic materials.

As much as 35 percent of the global land area may experience “novel climates” – essentially climatic conditions currently not experienced anywhere – and the *geography* of the world’s climate may shift significantly (Williams et al. 2007). For agriculture, temperatures in the growing season in 2100 in the tropics and subtropics are likely to be hotter than experienced over the past century. Local planting material is unlikely to resist such conditions (Battisti and Naylor 2009).

Three crops (maize, millet, and sorghum) in Africa were examined in terms of genetic resource interdependency in the face of climate change. Shifts in crop climates to 2050 indicate that many countries will experience novel climates not currently found within their borders in 2050, and 75 percent of these will have analogs in at least five other countries. The international movement of germplasm is essential to enable adaptation (Burke et al. 2009). Overall, crops will become maladapted in the face of climate change. Given the speed of climate change, farmers will most likely be unable to adapt rapidly enough through traditional selection practices (*ibid.*). Needed will be the facilitated exchange of exotic varieties and landraces from analogous sites elsewhere.

Thus, climate change will bring new and enhanced demand for genetic resources in order to adapt. National and international breeding programs for a number of crops are already targeting new varieties with adaptations to future climatic stresses (e.g., Ortiz et al. 2008) including heat, drought, and water-logging tolerance. The effort to breed for traits valued both today and for the future is likely to increase the general demand for PGRFA.

Demand will also likely increase for crop wild relative genetic resources to address biotic and abiotic constraints (Lane and Jarvis 2007), many of which are being exacerbated by climate change. While demand for such genetic resources is global, their natural distribution is restricted to the centres of

origin of crops. For example, no wild relative of the cultivated peanut occurs outside of Brazil, Paraguay, Bolivia, Uruguay, and Argentina (Ferguson et al. 2005). The increased demand for these resources implies increased interdependence among countries, possibly driving greater South-to-North germplasm flows as many centres of origin occur in the south (Fowler and Smale 2000). Since crop wild relatives are poorly conserved in *ex situ* collections, policies must facilitate access to collect wild gene pools through targeted collection to fill gaps (Maxted et al. 2009).

Biotechnology will also affect the demand for PGRFA. On the one hand, new tools and methods mean that more accessions can be screened and potentially used. On the other hand, transgenics, marker assisted selection, and other biotechnology tools may reduce the amount of diversity required in breeding programs, as individual genes rather than collections of traits become the target. Although increased demand for new varieties to confront climate change will rely heavily on biotechnology, it is difficult to foresee the outcome of these developments on interdependency (Ortiz et al. 2008).

Climate change may also increase the importance of otherwise minor or underutilized crops and plant species. These include species suitable for bio-fuel production (bio-diesel, ethanol, and second and third generation bio-fuel technologies) and hardy crops and species that until now have had only local or regional significance, but which may in the future provide valuable alternatives to confront climate change especially in marginal environments.

## 6. Conclusions

This chapter reviewed the baseline of interdependence of PGRFA and discussed how climate change might *change* interdependence patterns and levels. The numerical analysis of climatic similarity is presented as a proxy for potential genetic resource interdependence. The analysis shows that similarity between countries will be greater for 75 percent of the global croplands. No matter how specialized the niche of a crop, there will be significant shifts in climates that may bring novel climates that often are nearer to the current climates of other countries. Exchange of PGRFA among countries will thus continue as a key issue in the face of climate change, although some changes in the mechanism may be required (i.e., clear definition of key providers and key receptors). Although some special cropping environments will decrease their climatic similarity, in all regions and crops gaining and strengthening rates will markedly overcome climatic interdependence loss rates. There will, therefore, be significant opportunities for setting collaborative networks to conserve, characterize, improve, and share PGRFA. There is a high likelihood of a change in the *types* of demands for PGRFA into the future and a likely *increase* in overall demand.

Changes in the *types* of demand are expected in the following ways:

- there will be an increased demand for PGRFA with characteristics that will help adapt agriculture to future climates (heat, drought, and water-logging tolerant materials among others);
- increasing demand for crop wild relatives to address biotic and abiotic constraints; and
- increased demand for “minor” crops (including neglected and underutilized crops) that might help communities adapt to climate change in marginal environments and/or contribute to climate change mitigation through bio-fuel or similar potential.

*Increases* in demand are expected for the following reasons:

- shifting geography of climate, leading to shifts in crop distribution among and within countries;
- appearance of globally and regionally novel climates making locally adapted genetic resources no longer suitable beyond the next 20–30 years; and

- increasing global population and expected negative impacts of climate change on agriculture leading to more and more need for new seed technologies to produce more food in less area with greater water productivity.

Facilitated access to PGRFA is and will be needed. While, at the level of international law, there is facilitated access and benefit sharing for Annex 1 crops from the ITPGRFA, there are important crops and forages that are not included in that Annex. These exclusions include major staples (including some of those studied in this paper in the climatic similarity analyses), numerous forage species, crop wild relatives, and many minor and/or neglected and underutilized crops. Facilitated access to these crops would enable *ex situ* conservation through new collecting (conservation status is incomplete for many of these crops and species) and would make the genetic resources themselves available for countries to adapt to the future challenges of climate change.

### CHAPTER III: TREE GENETIC RESOURCES: INTERNATIONAL INTERDEPENDENCE IN THE FACE OF CLIMATE CHANGE

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#### 1. Understanding the responses of tree species to climate change

Tree species have high levels of genetic diversity and often exhibit wide geographic and ecological ranges (Gutschick and BassiriRad 2003; Petit and Hampe 2006). Specific and inter-related characteristics such as fecundity, size, longevity, and persistence confer particular advantages and disadvantages in withstanding climatic change and other disturbances that are not found in other plants. For example, persistence associated with deep root systems allows trees to better withstand extreme weather events such as drought. Perennial growth means that although trees may be unable to reproduce in one season due to unfavourable weather conditions, they will still be able to do so in later years if and when circumstances are more amenable. For this reason, they can withstand seasonal stresses that annual plants cannot. On the other hand, longevity may have the effect of limiting opportunities for recruitment in natural stands, thereby slowing down the rate of possible adaptation to new conditions (Aitken et al. 2008). Trees are parts of complex ecosystems that are vulnerable to a series of other challenges apart from climate change, including ongoing forest loss, fragmentation and degradation, and agricultural intensification (Malcom et al. 2002; Kellomäki et al. 2001). In these circumstances, the additional pressure of climate change may provide the “tipping point” that causes a significant loss of tree species and forest ecosystem.

In common with other organisms, tree populations have three mechanisms to avoid extinction in a rapidly changing climate: (1) survival through migration to and/or from new environments; (2) genetic adaptation to new conditions in existing locations; and (3) persistence through the inherent flexibility (or “plasticity”) of species to a wide range of environments (Aitken et al. 2008).

#### 2. Migration

Paleobotanical data show that over the last 25,000 years, tree species’ ranges have moved in close correlation with global climatic cycles (Davis and Shaw 2001; Hamrick 2004) and that their ranges have expanded from refugia after extreme events (McLachlan and Clark 2004; Magri et al. 2006; Petit et al. 2002; Heuertz et al. 2004). This is evidenced by large current day genetic variation within tree populations across otherwise uniform distribution of many species (Karhu et al. 1996; Garcia-Gil et al. 2003). Migration rates are hard to quantify and model using paleobotanical data (Clark et al. 2003; Petit et al. 2004) and estimates of the rates differ considerably among species but are now considered to be less than 100 meters per year on average (Iverson and Prasad 1998; McLachlan et al. 2007). However, it has been calculated that migration rates of more than 1,000 meters per year are needed to respond to predictions of climate change models (Aitken et al. 2008). It therefore appears unlikely that natural migration will be adequate to cope with rapidly changing climate (Malcolm et al. 2002; Davis et al. 2005). Therefore, facilitated migration by humans is needed especially for species in fragmented landscapes and/or those that have small population sizes and lower than average fecundity (Aitken et al. 2008). Facilitated migration may not, however, be able to match with completely novel environments that will also develop as a result of climate change (Williams and Jackson 2007).

## 2.1. *Adaptation*

Few countries have developed national climate change adaptation policies that explicitly formulate ways to ensure that tree management and planting practices account for altering environments. The most frequent issues raised by decision makers include whether the use of local germplasm is best; whether local tree stands are likely to contain the necessary genetic variation to adapt to the predicted amount of change; and whether such response can be fast enough. The United Kingdom's Forestry Commission considers risk minimization as the best approach in view of current uncertainty. Their strategy for intervention involves maintaining existing genetic variation, promoting migration, and encouraging natural regeneration and provenance mixing in plantations (Hubert and Cottrell 2007). Similarly, the French Commission on Forest Genetic Resources has developed conservation measures needed to strengthen the adaptive capacity of forest ecosystems in the face of climate change (Commission Resources Génétiques Forestières 2008). The International Union of Forest Research Organizations (IUFRO), in a recently published report produced by the Global Forest Expert Panels of the Collaborative Partnership on Forests, presents the state of current knowledge about the impacts of climate change on forests and people and provides practical and policy options for adaptation (Seppälä et al. 2009). This comprehensive IUFRO report, however, does not explicitly highlight assisted migration through the transfer of germplasm as a strategic intervention. Other international bodies such as the Food and Agriculture Organization (FAO) and the International Tropical Timber Organization (ITTO) have recognized the importance of using tree germplasm sources adapted to the environmental condition of a given planting site (International Timber Organization 2002; Food and Agriculture Organization 2006b). Such recognition could stimulate the transfer of forest reproductive material adapted to new climatic conditions from other countries where similar climate already exists.

## 2.2. *Plasticity*

Tree species show a great deal of plasticity (i.e., different phenotypic responses to different environmental conditions) (e.g., Rehfeldt et al. 2001; Valladares et al. 2005; Piersma and Drent 2003), and observed changes in morphology and physiology also show variation among populations and species (Aitken et al. 2008; Skrøppa and Kohlmann 1997; Bouvarel 1960). Climate change is likely to favour high levels of phenotypic plasticity, whereas, conversely, low plasticity in important characters may lead to extinction (Rehfeldt et al. 2001; Parmesan 2006). Recent climate envelope modelling undertaken by Bioversity International and the Central America and Mexico Coniferous Resources Cooperative analyzes provenance variation and plasticity in two Central American pine species, *Pinus patula* and *P. tecunumanii*, which are both important globally for plantation forestry (van Zonneveld et al. 2009). Results from provenance trials in Colombia, Brazil, and South Africa indicate that both species performed well across a wide range of climates, including in conditions that models predicted to be unsuitable for growth. In other words, these pine species appear to be more resilient to climate change than climate envelope modelling would indicate. For the more vulnerable of the two species, *P. tecunumanii*, forest fragmentation and conversion of forest to agriculture land appear to be more threatening than climate change.

## 3. **Provenance research, adaptive variation, and zoning**

Evolutionary mechanisms that contribute to the adaptation of tree populations to local environmental conditions may result in shifts in gene frequencies and phenotypic traits. Genetic differences among populations can be observed as provenance variation. Field trials that bring together planting stock collected from different areas indicate that considerable variation in morphology and physiology is observed among tree stands (König 2005). Differentiation in phenotypic traits of adaptive significance such as flowering and fruiting phenology, hardiness, and drought tolerance can vary across longitudinal, latitudinal, altitudinal, and ecological gradients. This infra-specific variation may at times be as significant and practically important as the differences observed among tree species (Aitken et al. 2008). At the time of the establishment of many ongoing provenance trials, adapting to climate change was not considered to be a factor in design because it was an unknown issue. The main objective of trials was rather to identify the most productive material for foresters, farmers, and other

users to plant at a range of sites with a variety of ecologies. Local seed transfer zones were established for such trials on the assumption that locally sourced material often performs best, although this concept has been more recently challenged (e.g., Boshier and Stewart 2005). These zones are demarcated areas considered to be sufficiently ecologically uniform to support the assumption that the tree populations found within them will be the ones that will grow best throughout the zone (Graudal et al. 1997). Locally sourced material does not always perform best, however, and the principle that this should be the case (because natural selection has long acted to optimize the matching of population and native environment) has been challenged (Boshier and Stewart 2005). Clearly, such conventional wisdom can no longer hold in the context of shifts in environmental conditions brought about by climate change.

In proactive action to combat such changes, provenance zones for seed collection in British Columbia, Canada, were redefined to account for future climatic conditions. Whereas material planted within the province previously had to be of local origin, this will no longer be the case (Yanchuk and O'Neill 2006; Ying and Yanchuk 2006). This type of policy change will be necessary among and within countries if the challenge of climate change is to be met appropriately. Based on climate modelling to identify major conservation threats, Canada and the United States are now actively considering new measures to ensure the survival of *Picea breweriana*, a species that presently exists in scattered populations across a narrow range in the Klamath-Siskiyou mountains of northwestern California and southwestern Oregon. Models predict that by the year 2030 no suitable habitat will remain in the United States, but that an appropriate climate will remain in the Nass-Skeena region of British Columbia, where the species is not currently found but could be transferred.

In the context of new concerns of climate change, historical provenance trials have been revisited to reinterpret data in novel ways and to develop new transfer guidelines (Rehfeldt et al. 2002; Savolainen et al. 2004). Old provenance trials subjected to further measurement and/or re-analysis include those in dry areas of West Africa on *Parkia biglobosa* (Raebild 2009), *Vitellaria paradoxa* (Bayala et al. 2009), and *Prosopis africana* (Weber et al. 2008). In the last case, analysis of a trial established in 1994 and conducted on material collected from Burkina Faso and Niger indicated significant provenance differences in growth variables at a relatively dry site in the latter country. Populations collected from drier regions did better at the test site, and clines in growth and survival corresponded with regional rainfall patterns. Data are consistent with observations that climate change is resulting in a drier, warmer environment in the region, causing tree mortality in lower rainfall areas (Maranz 2009; Shanahan et al. 2009; Weber et al. 2008) recommended transfers of germplasm as a way to cope with climatic differences should only be made from north to south and from east to west in the area (i.e., unidirectionally from drier to wetter zones/countries). This strategy was adopted by an International Fund for Agricultural Development project involving the International Centre for Research in Agroforestry and other partners to rebuild and diversify parkland agroforestry systems in Niger, Burkina Faso, Mali and Senegal.

New provenance trial research is beginning to specifically consider the issue of climate change. Returning to the example of semi-arid West Africa, new studies have been established within the Sahelian Fruit Tree project. Early results from eco-physiological stress trials designed to study adaptation suggest that *Adansonia digitata* (baobab) collections from drier zones perform better in the nursery under a low-watering treatment than provenances collected from wetter zones (Sanou et al. 2007). The opposite is the case under high-watering conditions (Raebild 2009). In the same region, the Domestication and Development of Baobab and Tamarind initiative is also planning to characterize accessions from different ecological zones for physiological traits related to drought stress. The difficulty with this and other research will be to ensure that significant numbers of smallholders in different countries can actually access better adapted material in a timely way once it has been identified. The development of smallholder "germplasm delivery systems" for tree species has lagged behind that for agricultural crops, but it has generally followed the same trajectory. Centralized models of delivery, such as those based around national tree seed centres (NTSCs), were heavily supported by donors in the 1980s and 1990s, but it is estimated that, although they are appropriate for supplying the establishment of large-scale plantations, they have delivered less than 10 percent of the smallholder

demand for tree seedlings and seed. This is because small-scale farmers are widely dispersed and require only small volumes of particular species, making them expensive to reach (see further information presented later in this chapter; Graudal and Lillesø 2007). Low tree seed delivery from centralized suppliers to smallholders mirrors the situation observed in the crop sector in continents such as Africa, where the majority of small-scale farmers use their own saved seed for future planting (Jones and Rakotoarisaona 2007).

A trend in the 1990s to provide donor support to more decentralized models of tree germplasm supply, based around non-governmental organization (NGO) delivery, appears in general to have not fared much better in meeting smallholder demand than NTSCs have. This is due to the restricted timescale of projects, the lack of attention to the promotion of genetically superior material, and the insufficient technical knowledge in handling germplasm, which leads to poor physiological quality.

Research on how increasing tree genetic diversity in plantations can be used to manage risks imposed by climate change is limited (Thorsen and Kjær 2005). Work to date suggests that diversification of planting material is an important strategy. Modelling in Denmark has assessed the optimal amount of diversity needed in plantations (the number of clones) to ensure resilience (Bosselmann et al. 2008). In the absence of good information on the growth response of different genotypes to climate change, modelling data suggest considerable gains can be obtained by mixing a reasonable set of genotypes in planted stands and then later adjusting the relative representation of genotypes once performance in response to climatic conditions becomes evident. Similarly, using a mixture of provenances in plantation establishment, such as local seed sources and wider germplasm expected to be adapted to a range of climate change scenarios, has also been recommended (Ledig and Kitzmiller 1992).

#### **4. International movements of tree germplasm**

##### ***4.1. Current exchange and use***

Understanding past and current flows of tree planting materials is the basis for any discussion on the future role of international germplasm exchange in combating climate change. The different actors currently involved in carrying out transfers must also be understood, since engagement with these stakeholders will be an important element of any future response. In a recent survey undertaken by the FAO in collaboration with Bioversity and other expert institutions, spatial and temporal patterns in global tree germplasm transfer were assessed (Koskela et al., 2009). This study focused not only on a number of important commercial timber trees (e.g., eucalypts, acacias, and teak) but also included agroforestry species that are used for a range of purposes by small-scale farmers, such as for fruit, medicine, and fodder (Koskela et al., 2009).

The study showed that information on global transfers of tree germplasm is fragmented and that few organizations have kept systematic records on quantities. The available information, however, illustrates that the exchange has been considerable, with significant benefits realized in plantation forestry and agroforestry. Often, although not always, benefits have been gained reciprocally between donor and recipient countries. Sometimes benefits for donor countries have come through the development of new technologies in “exotic” locations, which have then been applied to increase efficiency in “local” production. The limited data that is available did not allow the authors to draw conclusions about the extent to which climate change was an influential variable (along with other variables such as land-use changes, major plantation efforts, and market developments) driving these exchanges. Indeed, in the absence of explicit references in the available literature to climate change as an influencing variable, it appears that most movements are based on long-standing challenges to production other than climate change.

Among the species that have undergone substantial international transfer are acacias and eucalypts that can be easily propagated and regenerated, that are fast growing, and that have numerous wood and non-wood uses (Koskela et al. 2009). River red gum (*Eucalyptus camaldulensis*) from Australia, for example, is extensively grown throughout the tropics to supply construction material and is one of the

world's most widely planted trees on which millions of people depend. Similarly, teak (*Tectona grandis*) from Asia has become one of the most important timber species for plantations in the tropics. Seeds of some pine species (e.g., *Pinus caribaea*, *P. maximinoi*, and *P. tecunumanii*) from Central America and Mexico also have great international demand.

More than one billion smallholders grow trees on farms, so it is crucial to consider the international exchange of the species they grow. Although information on transfers for most trees of interest to smallholders is even more limited than for commercial forestry species, insights are available from public databases such as the Agroforestry Database and the Tree Seed Suppliers Directory (TSSD) that are maintained online by the World Agroforestry Centre. A search of origin, distribution, and suppliers in these databases was carried out for 30 tree species in each of four important categories of use for smallholders: timber, fruit, medicinal, and fodder/soil fertility improvement functions. Database searches indicated very high levels of past international transfer of germplasm for all use categories. On average, each species was recorded to have been distributed to 21 countries beyond its native range, with 67 percent of the current range of each species (total indigenous and exotic distribution) being exotic.

On average across use categories, database searches recorded 11 suppliers of germplasm for each species, with a mean of four suppliers (36 percent) being located within the native range of a taxon and seven (64 percent) outside. The high proportion of suppliers recorded in exotic locations indicates interest in the further transfer of germplasm once a species has left its native range. These dealers may be handling landraces that contain genetic bottlenecks if the tree germplasm initially introduced into exotic locations is poorly evaluated and/or collected. Such limited material is more likely to have restricted adaptability to the new environmental conditions that result from climate change. In this case, new introductions of tree germplasm, possibly collected from wider regions than the material sampled during initial collection, will be required.

Kenya and India provide specific examples of past exchange (Table 1). These nations have been linked through maritime trade over at least the last millennium, leading to significant germplasm flows. Database searches reveal that in around a quarter of all cases where comparison was possible, trees indigenous to Kenya (and more widely in Africa) were found as exotics in India (14 cases), while the same applied reciprocally (16 cases). Database searches therefore indicate high past international interdependency and suggest that future transfers of improved types of the same species in the context of current and emerging constraints to smallholder production, which include climate change, will also be significant. For example, East Africa can take advantage of the greater capacity for tree species research in Asia, which has resulted in the development of improved varieties of various fruits that are currently unavailable in Kenya, Uganda, Tanzania, and other countries but which could be introduced to substitute for existing suboptimal landraces.

**Table 1.** Summary of Agroforestry database searches on tree distributions in Kenya and India, by category of smallholder tree use

Smallholder use	Number of comparisons <sup>a</sup>	Indigenous in both countries	Exotic in both countries	Indigenous in Kenya, exotic in India	Indigenous in India, exotic in Kenya
<b>Timber</b>	13	0	4	5	4
<b>Medicine</b>	17	9	1	4	3
<b>Fruit</b>	15	3	7	2	3
<b>Fodder/soil fertility</b>	14	2	3	3	6
<b>Total<sup>b</sup></b>	59	14	15	14	16

*Notes:*

To be included in the results, species must be present as indigenous or exotic trees in both countries (see text for further information).

<sup>a</sup> The subset of species present as indigenous or exotic trees in both Kenya and India, taken from database searches based on 30 taxa for each category of use.

<sup>b</sup> Sum for four categories of use.

#### 4.2. Understanding future exchange demands

General demand for tree germplasm will increase as plantation and agroforestry practices expand, as wood and non-wood forest products increasingly need to be sourced from planted rather than (diminishing) natural stands (Food and Agriculture Organization 2006b; 2009). In this setting, facilitated migration as a response to climate change is only one additional factor that will increase the need for germplasm transfers. An appropriate seed sourcing strategy that considers the speed of environmental change and the relatively long-time scale of production of trees compared to other plants (e.g., the decades between planting and harvesting of a hardwood or the centuries over which a tree can produce fruit) is required. It may not always be clear which source represents the best balance between adaptation to near current and to future conditions, especially in the face of very rapid change. However, as the conditions that seedlings face at the time of planting are crucial in determining overall survival, it may be that in many cases early establishment carries more weight than later performance (Hänninen 1996).

Moving from considerations about adaptation into mitigation strategies, it can be expected that movement of tree germplasm will further increase as the planting of trees for increasing carbon stocks and the production of new fuel crops will also accelerate. Tree planting is unique among plant cultivation in the role that it can take in building carbon stocks, and new, faster growing provenances and species may need to be imported to better accomplish mitigation efforts. Agroforestry also has an important role in mitigation, as it provides a public good in addition to the products that smallholders themselves obtain from trees. Key will be to source superior species and provenances that farmers want to plant and that provide maximum carbon benefits in the long term (Verchot et al. 2005). Species being assessed as bio-fuels include the small tree *Jatropha curcas*, which grows on marginal lands and may become an important smallholder crop in the tropics. Projections for Africa suggest production of at least 60,000 tonnes of oil each by 2017 in Ethiopia, Mozambique, and Tanzania (Food and Agriculture Organization 2008a). The species originated in Latin America and was apparently introduced to Africa and Asia through Cape Verde, where it was grown for oil extraction and soap making. Much of the material now being established for bio-fuel production in plantations and by smallholders in Africa, Asia, and Latin America is of little-researched performance and is believed to have a very narrow genetic base and to be suboptimal (Kjaer 2009). Much of the seed

planted is simply that which can be obtained. To increase benefits in the future, coordinated international exchange of higher-performing germplasm and further evaluation will be required (Food and Agriculture Organization 2008a).

Pest and disease resistance has been an essential part of crop breeding for many years, but it has only received limited attention in tree breeding. An increase in pest and disease attacks caused by climate change could become a crucial issue in plantation forestry. Such biotic stresses are likely to have much greater impact on stands in the short term than the consequences of environmental maladaptation (Aitken et al. 2008). Conventional tree selection and breeding for resistance requires complex and lengthy testing, especially since resistance patterns may change from young to adult trees. A worldwide survey of 260 breeding efforts for pest and disease resistance in forest trees indicated that past approaches may not be suitable to deal with rapid change and that new strategies focused on quickly producing generic forms of “resistance” are needed (Yanchuk and Allard 2009). Although successes so far have been limited to a few main commercial species, this area of work is facing a reduction of resources and research capacity. In addition, extreme weather events such as hurricanes and cyclones triggered by climate change may have a particular impact on tree stands, with significant destruction possible and large-scale replanting required. In the Pacific region, this threat has led to a greater emphasis on identifying cyclone-resistance species such as *Endospermum medullosum* (whitewood). In Vanuatu, the target is to establish 20,000 hectares of plantations of the species over the next 20 years, with a resultant high demand for germplasm. Tests conducted on a total of 97 families of whitewood with seed lots collected throughout the islands in Vanuatu and comparative studies on provenances clearly demonstrate that a large genetic variation is present for economic characters in this species.

In agroforestry systems, resistance and resilience are generally higher when more diversity is present because the risks presented by environmental (and market) fluctuations are spread among various crops and products (Atta-Krah et al. 2004). In such systems, the expectation about future trends in tree germplasm transfer in the face of climate change are less clear, because substitution of one species by another already found in the farming landscape may in some circumstances be a more appropriate response for smallholders than the introduction of better adapted germplasm of the initial species.

## **5. Elements of uncertainty**

Although the evidence presented above indicates that increased international exchange of tree germplasm as a response to climate change is likely to be important, accurate predictions are difficult as a result of a number of outstanding, unanswered questions, as set out below.

### ***5.1. What is the degree of plasticity of tree species?***

Our knowledge of genetic diversity, phenotypic plasticity, and the eco-physiological performance of different populations of trees in a changing climate, is limited and difficult to predict. Factors such as the coexistence of species with different plasticity levels add further complexity, and the role of phenomena such as epigenetics – in which environmentally induced carry-over effects are observed across generations – in acting as a buffer against change are unknown but of potentially high importance (Aitken et al. 2008; Skrøppa and Johnsen 2000).

### ***5.2. Are current modelling approaches appropriate?***

Although current models can serve as a first approximation, future management and conservation strategies require models that incorporate more detail and greater biological realism (Hampe 2004; Hampe and Petit 2005). Current models are unable to account for different life history characteristics effectively (e.g., age to maturity, fecundity, and seed dispersal) and do not consider range fragmentation adequately, nor the differential adaptation present among populations that is so evident in tree species (Mimura and Aitken 2007a). Models can also not account for differences between

“leading” and “trailing” edge populations (Hampe and Petit 2005) or the levels of gene flow received by populations in different positions relative to the overall species range (Mimura and Aitken 2007b).

### ***5.3. Are current practices adequate to foster adaptation?***

In recent decades, the promotion of local tree domestication has been an important part of agroforestry research. Participatory strategies have involved farmers, encouraged them to take advantage of the genetic diversity that they find within the landscapes around them, and allowed them to select and cultivate superior types (Leakey et al. 2007). However, with the rapid rate of environmental change proposed by many climate models and considering the nowadays well-accepted idea that local material is not always necessarily the best adapted to local conditions (e.g., Boshier and Stewart 2005), at issue is whether this approach remains adequate in providing sufficient adaptive variation. If adequate variation to respond (e.g., to increased drought) is not present locally, a more centralized approach to germplasm distribution, with infusions from outside, will be required (Jamnadass et al. 2009).

### ***5.4. What consideration needs to be given to pollination issues?***

For those tree species that depend on animal pollination, climate change will influence pollinators and plants in different ways. The timing of pollinator availability and the date of flowering of plants may become asynchronous, resulting in a decline in interactions and consequences for both classes of organism and for the ecosystems of which they are part (National Research Council 2007). The consequences of changes in pollinator abundance and behaviour may be particularly serious for tropical trees because not only are they generally preferentially out-breeding like most other trees, but they also rely heavily on animal vectors for pollen deposition (Dawson et al. 2008). Climate change effects on pollinators may particularly disadvantage fruit and nut production where the products themselves depend directly on pollination. For these species, there may be a greater need to introduce alternative varieties than for other trees (e.g., that are less dependent on animal vectors for pollination), but whether or not this is the case currently remains a matter for further research (Klein et al. 2007). Future interdependence may also extend to the exchange of pollinator populations as well as tree germplasm.

## **6. Conclusions**

Public acceptance of the problem of climate change has been accompanied by awareness of the global importance of trees and the environmental services that they provide. Particular emphasis is now being placed within international negotiations on reducing emissions from deforestation and forest degradation (REDD). While natural forests continue to decline globally, the area covered by plantations, smallholder forestry, and agroforestry has expanded and now represents an area of approximately 270 million hectares or around 7 percent of total global forest cover (2005 figures; Food and Agriculture Organization 2006a). Large-scale tree planting activities that would take place within the REDD framework (and in addition for producing alternatives to fossil fuels) could increase the demand for tree germplasm, although the question of which material has yet to be determined.

Adaptive responses to climate change are required for both wild and planted trees. For natural stands, emphasis must be placed on improved silvicultural management techniques, an area that has received significant attention in temperate regions although less so in tropical climes (Guariguata et al. 2008). Tropical foresters and end-user communities do not yet appear to appreciate the risks posed by climate change, and practical guidance on how to respond is limited. For planted trees, a greater range of options to respond to climate change exists. Particularly, movement of appropriate tree germplasm to new environments is a possibility, albeit one that has not yet received sufficient attention (Seppälä et al. 2009). A recent survey suggests that the international transfer of tree germplasm for research is becoming increasingly difficult and more costly as countries seek to conform to the Convention on Biological Diversity (Koskela et al. 2009). This access must be enhanced if the provenance trials that form the basis of informing possible adaptive responses to climate change are to be maintained.

In the case of smallholders practising agroforestry, the greater part of the movement of tree germplasm currently occurs informally among farmers, local seed dealers, and small-scale nursery operators, with limited links to national and international suppliers (Koskela et al. 2009). These farmers are therefore isolated from germplasm transfer interventions that occur at an international level. Better ways to link them into such developments are required, otherwise the bottleneck in delivery to a local level will result in a significantly delayed response (Graudal and Lillesø 2007). In other words, the international exchange of germplasm to combat climate change will mean little to smallholders unless improvements are made in the existing seed and seedling delivery systems that service them. Making such improvements represents both a significant challenge and an excellent development opportunity for the national tree seed programs and international non-governmental organizations that strive to support farmers and their agroforestry practices.

Several areas of research require greater attention in the future, including (1) understanding the role of epigenetics in adaptation, including the scale and duration of such effects; (2) field and nursery experiments that test the adaptive capacity of species in new ways and that take account of the scale of environmental change and include populations from the extremes of current distributions; (3) the development of more advanced simulation models that account for species-specific features and population variation; and (4) greater emphasis on the effects of climate change on animal pollinators of tropical trees (Aitken et al. 2008).

## CHAPTER IV: THE IMPACT OF CLIMATE CHANGE ON ANIMAL GENETIC RESOURCES AND COUNTRY INTERDEPENDENCE

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### 1. Introduction

Countries have long been highly interdependent with respect to animal genetic resources (AnGR). Most food and agricultural production systems worldwide depend on livestock originally domesticated elsewhere as well as breeds developed in other countries and regions. Nevertheless, relatively little baseline quantitative data on AnGR exchange is available, and the factors that will affect future gene flows and country interdependence also remain poorly understood. Such factors include climate change, together with other sources of dynamic change, such as globalization, biotechnology, disease, human population growth, urbanization, and growing demand as Southern affluence increases.

Regardless of the direction of climate change in any particular location, the above factors are likely to lead to changes in the gene pool and, consequently, in AnGR country interdependence. Two major scenarios are suggested: (1) that the portfolio of livestock species and breeds needed/demanded by society will change as a result of both increased demand and the environmental impacts of climate change (“livestock portfolio change”); and (2) that the livestock gene pool will be smaller than it is today because of a continuation of current trends, losses induced by the speed of climate change outpacing evolutionary adaptations, and the impact of globalization (“gene pool reduction”). These two scenarios suggest that the large-scale movement of livestock breeds may be increasingly necessary, further increasing AnGR country interdependence.

However, both the prediction of how climate change will affect the gene flows and interdependency of countries, as well as the development of appropriate policy responses, are constrained by the fact that relatively little baseline quantitative data on AnGR exchange is available. Quantitative information on gene flows through animal recording systems, national breed inventories with spatial distribution, monitoring of imports and exports, and scenario modelling are all urgently required.

This chapter draws on the work of several authors, including (1) M. Herrero et al. (2009), who describe the drivers of livestock system change operating at a variety of levels; (2) L. Iñiguez (2005a; 2005b), who shows the importance of transboundary breeds; (3) B. Rischkowsky et al. (2008), who note the increasing acknowledgement of the potential value of adaptive traits in the highly variable climates of the West Asia and North Africa (WANA) region, whose climatic conditions are increasingly representative of those predicted for other parts of the world; and (4) the climate-change related findings of a report commissioned by the Food and Agriculture Organization (FAO) and related papers (Hiemstra et al. 2006; Drucker et al. 2008), which drew on a scenario modelling approach.

### 2. Climate change, AnGR, and country interdependence

#### 2.1. AnGR and country interdependence

Countries have long been highly interdependent with respect to AnGR. The global exchange of AnGR has been vital for breed and livestock sector development across the world. Animal genes, genotypes, and populations have spread over the planet since ancient times through the diffusion of agriculture

and the prominent role of livestock in human migration. Over the last 500 years, AnGR have been systematically exchanged, deepening interdependence. In global terms, most food and agricultural production systems worldwide depend on livestock originally domesticated elsewhere as well as breeds developed in other countries and regions (Commission on Genetic Resources for Food and Agriculture 2006).

Historically, there have been several phases of gene flows and livestock breeding (Gibson and Pullin 2005; Food and Agriculture Organization 2007). Most recently, reproductive technologies have revolutionized the animal breeding sector and facilitated further and more rapid exchange of genetic material among countries and regions of the world. Such gene flow can both enhance and reduce diversity (Food and Agriculture Organization 2007). The type of impact depends on a number of factors, including environmental suitability in the receiving country and organizational structures on both the receiving and the providing side (Mathias and Mundy 2005). Importantly, the amount of material transferred is not indicative of its impact.

Although two recent studies have quantified and assessed the trends in the transfer of AnGR, the global flow of AnGR remains poorly understood and can only be grossly characterized (Valle Zárate et al. 2006; Mathias and Mundy 2005). There have been extensive North-to-North and South-to-South movements of livestock germplasm, although the latter is poorly documented. North-to-South flows have also been important. By contrast, South-to-North movements have been rare in the past century relative to movements in other directions, and, in most cases, the economic benefits to both North and South have been relatively small. Movements of germplasm, crossbreeding, and within-breed selection in the developing world are all likely to accelerate in the future (Gibson and Pullin 2005).

A range of factors will influence future interdependence of countries on AnGR: globalization,<sup>6</sup> biotechnology,<sup>7</sup> disease,<sup>8</sup> human population growth, urbanization, growing demand as Southern affluence increases, and climate change. The potential influence of climate change on AnGR exchange and interdependence are analyzed in this chapter through a review of the literature, a case study of recent transboundary movements in areas with high climatic variability (representative of predicted climatic changes elsewhere), and scenario modelling.

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<sup>6</sup> A “globalization” scenario, its impacts and potential policy implications, are described in detail in Hiemstra et al. (2005). The term “globalization” is understood to encompass the international integration of food markets that has generally been observable at the end of the twentieth century and that can be attributed to the liberalization of international commercial policy and the bundle of inter-related technological changes underlying the process (Hobbs and Kerr 1998). Globalization trends may be expected to result in a wider use of a limited number of breeds, standardization of consumer products, and a move towards large-scale production. Retailers and supermarkets will be leading actors in the globalization process. Vertical integration is expected to become the primary business model on a global scale. Furthermore, globalization may adversely affect smallholder competitiveness and threaten the sustainable use of local breeds (Delgado et al. 1999; 2001; Dirven 2001; Food and Agriculture Organization 1997; Hobbs and Kerr 1998; Popkin and Duy 2003; Sere et al. 1996; Tisdell 2003).

<sup>7</sup> According to S.J. Hiemstra et al. (2006), a series of developments in biotechnology may be expected to speed up ongoing developments in the livestock sector with major (potential) impact on exchange, use, and conservation of AnGR. These include: (1) continued progress in reproductive and cryopreservation technologies for all livestock species; (2) development of a new generation of quantitative genetic tools, linking genomics and quantitative genetics; (3) improved efficiency and safety of transgenic and cloning technologies; and (4) better control of animal diseases and increased availability of (marker) vaccines. Under a biotechnology development scenario, superior genotypes can be distributed and used across the globe even more easily than today, which may negatively affect the conservation of global farm animal genetic diversity. Furthermore, rapid developments in biotechnology are providing new opportunities to explore and possibly exploit genetic resources in ways that were not possible before. Exchange patterns may change and AnGR from developing countries may increasingly contribute to commercial breeding. Molecular biology is already having an increasing impact on the animal breeding sector, as well as playing a role in the introduction of patenting of processes and products used in animal breeding (Agriculture and Environment Biotechnology Commission 2002; Andersson and Georges 2004; European Commission 2003; Gibson and Pullin 2005; Hiemstra et al. 2005; Hoffman and Scherf 2005; Meuwissen 2005; Rothschild et al. 2003).

<sup>8</sup> S.J. Hiemstra et al. (2006) argue that international trade and human travel has already led to the rapid spread and, ultimately, the globalization of diseases, resulting in a deterioration of the global animal health situation during the period 1980–2000. This situation may be expected to worsen. Diseases, natural disasters, civil war, and other threats can have a serious impact on local AnGR and thus on the exchange, use, and conservation of global farm animal genetic diversity (Charron 2002; Food and Agriculture Organization 2004; Food and Agriculture Organization / World Organization for Animal Health 2005; Kadomura 1994; Kouba 2003; McDermott et al. 2001; Otte et al. 2004; Scoones et al. 1996).

## ***2.2. Climate change and livestock***

A review of the literature (Hiemstra et al. 2006) examined predicted impacts of climate change on livestock in six regions of the world (Anderson 2004; Australian Greenhouse Office 2004; Australian Bureau of Statistics 2004; Climate Change and Agriculture in Africa 2002; Charron 2002; Food and Agriculture Organization 2000; Frank et al., no date; Ministry of Agriculture, Food and Fisheries 2000; Intergovernmental Panel on Climate Change 2001; Kenny 2001; Kristjanson et al. 2001; Tisdell 2003; World Resources Institute 2000). The studies suggest that the main livestock-relevant impacts of climate change will relate to increases in the number and severity of diseases that animals will suffer, changes in fodder and water availability, land degradation, and the speed of climate change relative to livestock and forage evolutionary adaptation. Climate change can be expected to affect livestock productivity directly by influencing the balance between heat dissipation and heat production (making heat/cold tolerance in breeds attractive) and indirectly through its effect on the availability of feed and fodder and on the presence of disease agents.

The precise impact of climate change on livestock and AnGR country interdependence is difficult to predict as global climate change predictions hide complex spatial patterns of changes. For example, at mid- to high latitudes, crop productivity may increase slightly for local mean temperature increases of up to 1–3 degrees Celsius. At lower latitudes, crop productivity is projected to decrease for even relatively small local temperature increases (1–2 degrees Celsius) (Intergovernmental Panel on Climate Change 2007a). In the tropics and subtropics, crop yields may fall by 10 to 20 percent to 2050 because of warming and drying, although yield losses may be much more severe in particular areas (Jones and Thornton 2003). These changes will have a significant impact on feed resources such as stover and straw, which are key sources of feed in many systems (Herrero et al. 2009).

Changes in climate variability are also projected. Although there is considerable uncertainty about these changes, the total area affected by droughts is likely to increase, as is the frequency of heavy precipitation events. Increased frequencies of heat stress, drought, and flooding will have adverse effects on crop and livestock productivity over and above the impacts due to changes in mean variables alone (Intergovernmental Panel on Climate Change 2007a). Climate change is likely to have major impacts on poor croppers and livestock keepers and on the ecosystems goods and services on which they depend. These impacts will include changes in the productivity of rain-fed crops and forage, reduced water availability and more widespread water shortages, and changing severity and distribution of human, livestock, and crop diseases. Major changes can thus be anticipated in livestock breeds, livestock species mixes, crops grown, feed resources, and feeding strategies (Thornton et al. 2008; Thornton and Herrero, 2008). Table 1 shows diverse aspects of livestock systems that could be affected by climate change (Thornton et al. 2008).

## ***2.3. Non-climate change factors and livestock***

Climate change will not take place in isolation. Other sources of dynamic change are also likely to play an important role in AnGR exchange and country interdependence.<sup>9</sup> The world's population will reach seven billion by 2012 and 9.1 billion by 2050. In Africa alone, the human population is projected to double to nearly two billion by 2050 (UN Population Division 2008). Such population growth will be accompanied by rapid urbanization in many developing countries. The year 2008 was a watershed: for the first time more than half of the global human population (3.3 billion) lived in urban areas. By 2030, this number will have increased to almost five billion. The next few decades will see unprecedented urban growth, particularly in Africa and Asia (UN Population Fund 2008). Such demographic change will lead to significant livestock systems intensification in some places (Herrero et al. 2009). Table 2 presents population growth by areas and production systems in developing countries.

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<sup>9</sup> A distinction is made between climate scenarios, which describe the forcing factor of focal interest to the Intergovernmental Panel on Climate Change – and non-climatic scenarios, which provide socioeconomic and environmental “context” within which climate forcing operates (Intergovernmental Panel on Climate Change 2001, ch. 3).

Increasing affluence in the South as a result of development means that demand for livestock products will continue to increase as part of the “livestock revolution.”<sup>10</sup> The demand for livestock products is rising globally and will increase significantly in the coming decades because of income shifts, population growth, urbanization, and changes in dietary preferences. This increased demand will largely be based in developing countries (Delgado 2003). Figure 1 presents projected meat and milk demand changes in countries with different types of economy. Demand will be for both increased quantity, especially as incomes rise, and for increased quality, particularly among urban consumers who purchase from supermarkets. The consequences for both the volume of global food demand and its composition will be enormous. More cereals and meat will need to be produced from basically the same land and water resources as exist currently. While the increased demand will probably be met mostly by increases in chicken production, ruminant populations are also likely to increase substantially. Table 3 presents projected increases in livestock numbers to 2030 (Herrero et al. 2009).

Although the general trend in relative food prices has been downward since the early 1970s, the period from mid-2007 to late 2008 saw a sharp spike in grain prices, largely reflecting changes in demand – in turn due to population and income increases, and increases in the production of biofuels (Hazell and Wood 2008). Such increases may reoccur, with impacts on the poor and on farming in general being hard to gauge (as are interactions with high and/or fluctuating energy prices).

**Table 1: Summary of impacts of climate change on livestock and livestock systems**

Factor	Impacts
Water	<ul style="list-style-type: none"> <li>Water scarcity is an accelerating condition for 1–2 billion people. Coupled with population growth and economic development, climate change impacts will have a substantial effect on global water availability.</li> </ul>
Feeds	<p><i>Land use and systems change</i></p> <ul style="list-style-type: none"> <li>As climate becomes more variable, species niches change, leading in some cases to plant and crop substitution. Such necessary crop substitutions may compromise the ability of smallholders to manage animal feed deficits. For example, in parts of East Africa, maize is being substituted by crops that are more suited to drier environments (sorghum and millet) but that produce less stover. In marginal arid southern Africa, systems are being converted from mixed crop-livestock to those that are rangeland based.</li> </ul> <p><i>Changes in the primary productivity of crops, forages, and rangeland</i></p> <ul style="list-style-type: none"> <li>Effects depend significantly on location, system, and species. In tropical species with a C<sub>4</sub> photosynthetic pathway, temperature increases up to 30–35 degrees Celcius may increase the productivity of crops, fodders, and pastures (as long as water and nutrients do not significantly limit plant growth).</li> <li>In C<sub>3</sub> plants, temperature has a similar effect but increases in carbon dioxide levels will have a positive impact on the productivity of these crops.</li> <li>For food-feed crops, harvest indexes will change and so will the quantity of stover and the availability of metabolizable energy for dry-season feeding.</li> <li>In the semi-arid rangelands where contractions in the growing season are likely, rangeland productivity will decrease.</li> </ul>

<sup>10</sup> The Intergovernmental Panel on Climate Change (2001, ch. 3) notes significant uncertainties in developing scenarios of economic development. In the scenarios reviewed in J. Alcamo et al. (1995) and A. Grübler and N. Nakicenovic (1994), gross domestic product (GDP) per capita growth rates range between 0.8 and 2.8 percent per year over the period 1990–2100, leading to a per capita GDP of US \$10,000–US \$83,000 by 2100. While these figures do not differentiate between “North” and “South,” per capita GDP growth rates are expected to be higher for economies that currently have low per capita GDP levels.

	<p><i>Changes in species composition</i></p> <ul style="list-style-type: none"> <li>• As temperature and carbon dioxide levels change, optimal growth ranges for different species also change, species alter their competition dynamics, and the composition of mixed grasslands changes.</li> <li>• Proportion of rangelands used for browsing will increase as a result of increased growth and competition of browse species due to increased carbon dioxide levels.</li> <li>• Legume species will also benefit from increases in carbon dioxide, and, in tropical grasslands, the mix between legumes and grasses could be altered.</li> </ul> <p><i>Quality of plant material</i></p> <ul style="list-style-type: none"> <li>• Increased temperatures increase the lignification of plant tissues and thus reduce the digestibility and the rates of degradation of plant species. The resultant reduction in livestock production may have impacts on food security and the income of smallholders.</li> <li>• Interactions between primary productivity and quality of grasslands will demand modifications in grazing systems management to attain production objectives.</li> </ul>
Biodiversity	<ul style="list-style-type: none"> <li>• The loss of genetic and cultural diversity in agriculture – already occurring as a result of globalization, in crops as well as domestic animals – will accelerate in places.</li> <li>• A 2.5 degree Celcius increase in global temperature above pre-industrial levels will see major losses: 20–30 percent of all (includes wild) plant and animal species assessed could be at high risk of extinction.</li> <li>• Ecosystems and species show a wide range of vulnerabilities to climate change, depending on the imminence of exposure to ecosystem-specific, critical thresholds, but assessments are fraught with uncertainty related to carbon dioxide fertilization effects and so on.</li> </ul>
Livestock (and human) health	<ul style="list-style-type: none"> <li>• Major impacts on vector-borne diseases: expansion of vector populations into cooler areas (e.g., malaria and livestock tick-borne diseases in higher altitude areas) or into more temperate zones (e.g., bluetongue disease in northern Europe).</li> <li>• Changes in rainfall pattern may also influence expansion of vectors during wetter years, leading to large outbreaks of disease (e.g., Rift Valley Fever virus in East Africa).</li> <li>• Helminth infections are greatly influenced by changes in temperature and humidity.</li> <li>• Climate change may affect trypanotolerance in sub-humid zones of West Africa and could lead to loss of this adaptive trait that has developed over millennia and greater disease risk in the future.</li> <li>• Effects (via changes in crop, livestock practices) on distribution and impact of malaria in many systems and schistosomiasis and lymphatic filariasis in irrigated systems.</li> <li>• Increases in heat-related mortality and morbidity.</li> <li>• Climate variability impacts on food production and nutrition can affect susceptibility to HIV/AIDS as well as to other diseases.</li> </ul>

*Source:* As presented by Thornton and Herrero (2008) and adapted from broader reviews in Thornton et al. (2008).

**Table 2: Developing country farming systems: surface area and population 2000–30**

<b>Farming system</b>	<b>Area (10<sup>6</sup> km<sup>2</sup>)</b>	<b>Population 2000 (10<sup>6</sup> people)</b>	<b>Population 2030 (10<sup>6</sup> people)</b>
(Agro-)pastoral	35	295	497
Mixed extensive	14	1,099	1,670
Mixed intensive	10	2,674	3,640
Other	17	480	682

Source: Adapted from Herrero et al. 2009.

#### **2.4. Livestock and climate change scenarios**

These factors are likely to lead to changes in the gene pool and consequently AnGR country interdependence. Two major scenarios are suggested.

*Scenario 1: “livestock portfolio change.”* The portfolio of livestock species and breeds needed/demanded by society will change as a result of both increased demand and the environmental impacts of climate change. While globalization tends to lead to use of a limited number of “improved” breeds,<sup>11</sup> changes in consumer demand may, by contrast, lead to the expansion of extensive systems (Northern consumers prefer “outdoor” organic products; Southern countries expand extensive systems in order to meet increased demand). The overall direction of change in terms of species and breed preferences is therefore ambiguous but will be different from that which it is today.

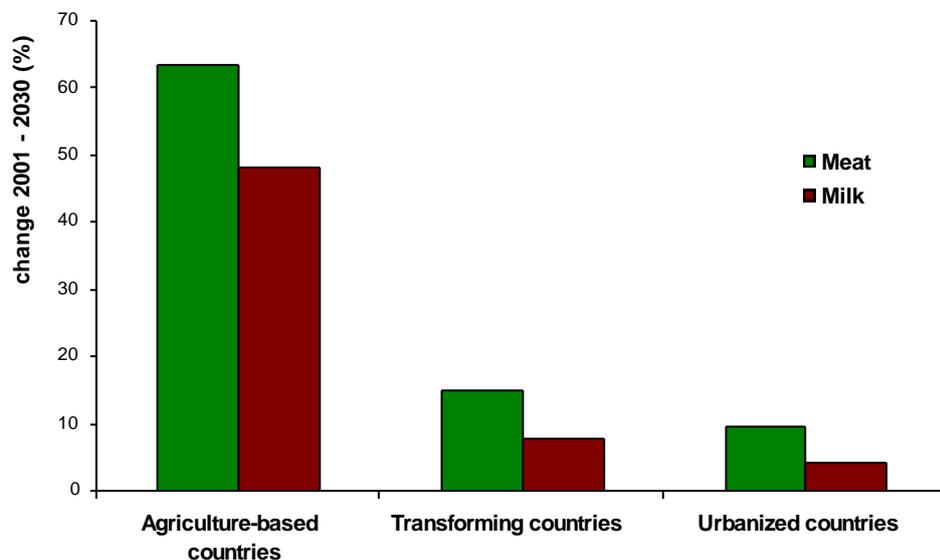
Areas where environmental effects of climate change are predicted to hit hardest will most likely have to rely on additional imported genetic resources that both thrive under changed conditions while meeting consumer demands and cultural preferences. Using the same indigenous livestock genetic resources is common in environments with specific climatic constraints, as is the case for ruminants that are more exposed to climatic conditions than monogastrics. Examples are indigenous transboundary regional breeds in humid West Africa (facing trypanosomiasis and hot, humid conditions); those breeds requiring drought tolerance and high mobility in the Sahel zone (Food and Agriculture Organization 2007); those with a tolerance to high variation (minus 5 to plus 47 degrees Celcius) in ambient temperature West Asia (see Box 1). Currently, these breeds have been mainly used in their home region as pure breeds or have contributed to better-adapted breeds through crossbreeding programs. There are indications of increasing interest in indigenous breeds with specific adaptive traits in other parts of the world, although export of local breeds has been poorly documented (for example, see Matthias and Mundy 2005).

*Scenario 2: “gene pool reduction.”* The livestock gene pool will be smaller than it is today because of the continuation of current trends, losses induced by the speed of climate change outpacing evolutionary adaptations, and the impact of globalization. The speed of climate change may make it difficult for countries to develop their own breeds rapidly enough to remain productive (Hoffmann 2008). Breed or species substitution (including with game species) will be required where the adaptive capacity of the currently used genetic portfolio is exceeded. Dromedaries replaced cattle, and goats replaced sheep, in the Sahel following droughts in the 1980s. Such substitution may also result in countries increasingly depending on exotic genetic resources, possibly leading to a reverse in the current flow of genetic resources. Advances in the characterization of tropical breeds would be

<sup>11</sup> Given that, worldwide, over 20 percent of indigenous livestock breeds are at some degree of risk, this scenario is also consistent with a continuation of existing trends (Food and Agriculture Organization 2007).

necessary before crossbreeding or gene transfer via biotechnology to increase adaptive traits of high output breeds would be likely to take place in practice.

**Figure 1. Changes in meat and milk demand to 2030 by economy type**



Source: As presented in McDermott et al. (in press) and adapted from IAASTD (2008).

**Table 3. Projected changes in livestock numbers to 2030 under a business as usual scenario**

	2000 (million TLU)	2030 (million TLU)	annual rate of change
Cattle	962	1216	0.88
Small ruminants	170	249	1.55
Chickens	203	315	1.85
Pigs	202	225	0.39

Notes: TLU = tropical livestock unit

Source: Adapted from Herrero et al. 2009.

The implications of both scenarios suggest, first, that there may be an increased need for the large-scale movement of livestock breeds in search of more appropriate climatic zones, as a direct result of increased livestock product demand and the change in the portfolio of breeds needed/demanded and, second, that relative demand for remaining breeds (for both productive and adaptive traits) will grow because of an absolute increase in livestock product demand, changes in the portfolios that are required, and the reduced gene pool.

It should also be appreciated that these scenarios take place within a context of changed disease challenge and biotechnology development. While stricter zoo-sanitary regulations may impede needed international germplasm flows, cheaper, more advanced biotechnology may itself permit compliance with stricter zoo-sanitary regulations (especially if costs become affordable to developing countries), thereby facilitating increased international germplasm flows. In this case, demand for both productive and adaptive traits may increase, and AnGR research could expand as biotechnology developments increase the returns to both public and private sector AnGR research. Furthermore, much of this germplasm may be increasingly accessible from *ex situ* and *in situ* conservation programs, assuming

that there is a decline in biotechnology costs and an increasing awareness and priority given to AnGR conservation and use.

The implications of increased conservation (*in vivo* and *in vitro*) and the improvement of indigenous AnGR, together with the associated support for this to occur, are that this would provide a level playing field with other breeds and would help create mechanisms to capture public good values of indigenous breed conservation. Such conservation and management support will be of increasing importance given the need to both slow the rate of AnGR loss from a shrinking gene pool and to facilitate conservation through sustainable use via access to well-characterized genetic materials.

The loss of animals through droughts, floods, and/or disease epidemics related to climate change may increase (Hoffman et al. 2008). Localized breeds are at risk of being lost in localized disasters. Precautionary cryo-conservation of genetic material or other measures may be required to ensure that such genetic material can be conserved.

Special provisions for indigenous AnGR in animal disease control acts may be needed. Climate change will increase the disease challenge and may result in wider-scale mass culling of animals than has already occurred independently of climate change (e.g., the UK response to the 2001 foot and mouth disease outbreak), potentially resulting in AnGR loss. Conservation programs are needed that will ensure that animals of the same genetic background would be available when restocking becomes necessary.

**Box 1: Country interdependence under conditions of high climatic variability: the case of small ruminant breeds in West Asia and North Africa**

The WANA region is a good example of how climatic variability shapes genetic diversity and the utilization of animal genetic resources (AnGR) across country boundaries. As a result of their high economic importance in the region, we use small ruminant breeds to illustrate distribution and utilization patterns (Iñiguez and Aw-Hassan 2004).

The WANA region has always been characterized by high climatic variability. An analysis of a normalized difference vegetation index (NDVI) across the region, for the period 1982–2000, showed clear evidence of “hotspots” of response and vulnerability to climatic fluctuations (Celis et al. 2007). This vulnerability was reflected in high coefficients of variation in maximum NDVI. The hotspots include North Africa, from Morocco into Tunisia; the Sahel, from Mauritania into Sudan, Eritrea, northern Ethiopia, and south into Somalia; and the Fertile Crescent, from Jordan, Syria, Iraq, turning southeast into Khuzistan province in southern Iran. These areas are characterized by severe droughts, degradation of land, water and vegetation resources, and sometimes famine. They are already facing the conditions that climate change is expected to cause in other countries in the region – extreme dryness and heat, erratic rainfall, and fragile water supply (Thomas et al. 2007; Intergovernmental Panel on Climate Change 2007b).

The Fertile Crescent is one of the main centres of domestication for sheep and goats. International Centre for Agricultural Research for Dry Areas, jointly with its National Agricultural Research System partners, documented the status and phenotypic characteristics of the sheep and goat breeds in the WANA region (Iñiguez 2005a; 2005b). The study described 75 sheep breeds and 32 goat breeds. Many of these breeds are adapted to semi-arid and arid conditions and are known for their tolerance to heat and cold stress and to low quality feeds supplied by degraded rangelands. Sheep breeds with fat tails dominate the region (53 out of 71 breeds), especially in West Asia. This adaptation allows them to cope with fluctuation in feed availability by depositing fat in the tail during periods of feed abundance and mobilizing the fat deposits during periods of scarcity.

Ten sheep breeds are shared by at least two countries. The Awassi is the most important breed in Mediterranean West Asia and is shared by Turkey, Syria, Lebanon, Jordan, and Iraq (Galal et al.

2008). It is the only sheep breed present in Lebanon and Syria, with a population of approximately 21.3 million sheep in these two countries alone (FAOSTAT 2009). Similarly, the fat-tailed Barberine sheep in North Africa is shared by Tunisia, Libya, and Algeria. A major difference is that the Barberine are only used for meat production, while the Awassi is a dairy breed.

Awassi are in high demand in countries with similar climatic conditions, with the Gulf countries generating demand for imports as Awassi meat is preferred and commands a price premium. Australia and countries in the Horn of Africa have already acquired Awassi populations and use them for straight- and crossbreeding programs (Hassen et al. 2002; Kingwell et al. 1995).

While Awassi sheep seem to be spreading even further, market trends in Tunisia indicate that the importance of the Barberine may be decreasing. The reason is that butchers tend to favour thin-tailed sheep because of the difficulty of selling the fat of the tail, which represents up to 15 percent of carcass weight. This has led to increased crossbreeding with thin-tailed breeds such as the Algerian Ouled Djellal and the Black Thibar (Bedhiaf-Romdhani et al. 2008).

Some breeds in the region are adapted to extremely hot, dry areas – for example, the fat-tailed Barki sheep found in the Egyptian desert and the very prolific thin-tailed D'man sheep. While the Barki is limited to the desert areas of Egypt, the D'man originated in Morocco and was later exported to Algeria, Tunisia, and probably to Libya (Galal et al. 2005). There is an interesting feature of the breed distribution in the WANA region: the diverse breeds indigenous to Egypt are still limited in their distribution to Egypt. This shows that breed distribution – and consequently country interdependence – not only depend on climatic conditions but also closely follow cultural preferences and the distribution of ethnic groups.

In recent years, the Shami (Damascus) goat, a breed with unique characteristics, has been exported to many North African countries. It is indigenous to Syria but is now reared in Syria, Jordan, Cyprus, and Egypt (Iñiguez 2005a). As a result of its superior dairy characteristics and its adaptation to high temperatures, the breed is also in demand for crossbreeding programs in North Africa – for example, in Libya. There is even an interest in India to import this breed (Nimbkar 2007). Shami goats also fetch high prices in countries of the Arabian Peninsula, where they are kept as pets because of their large size and peculiar head shape. Interest in the Shami from neighbouring Arabic countries has been so high that, despite a law prohibiting the export of females, exports in the last three decades have considerably reduced the size of the Syrian population and increased the risk of inbreeding (Kassem 2005).

*Source: Barbara Rischkowsky, International Centre for Agricultural Research in Dry Areas, Aleppo, Syria*

Livestock emissions could be included under “Son of Kyoto” trading mechanisms. Inclusion, given different productivity differentials and price elasticities among different livestock species, breeds, and other sectors may lead to dairying becoming the major focus of cattle production, with meat being produced from species with lower emissions (e.g., poultry and pigs). Consideration should be given to an exclusion for ruminants on marginal rangelands that have important livelihood functions or those used for landscape management (Hoffmann et al. 2008).

### **3. Limitations in assessment capacity**

Relatively little baseline quantitative data on AnGR exchange is available. Import and export figures of live animals from veterinary or commercial records do not usually distinguish breeding animals from slaughter animals/animal products. The origin of import and destination of export is often not clear. Multinational companies provide no data on the intra-company exchanges of genetic material between countries. In many parts of the world, animals cross borders without being recorded, as is the case of transhumance (Valle Zárate, Musavaya, and Schäfer 2006; Mathias and Mundy 2005). There is

a clear need for improving national inventories, including relevant spatial information and assessing future breed distribution (Hoffmann 2008).

The factors (both institutional and non-institutional) that will affect future gene flows also remain poorly understood. For example, it might be expected that the ongoing “livestock revolution” – which has already greatly reduced the genetic diversity in pigs and poultry and has resulted in a high dependence of the industry on a few sources of genetic resources – will have substantial effects. In the type of highly dynamic environment described earlier, it is difficult to predict how climate change will affect the gene flows and interdependency of countries. Doing so will require a considerable amount of work to provide the necessary inputs. These include quantitative information on gene flows through animal recording systems, national breed inventories with spatial distribution, monitoring of imports and exports, and scenario modelling. Only then can the impacts of future interventions be properly assessed and trade-offs between different groups of stakeholders evaluated.

#### **4. Conclusions: Interdependence of animal genetic resources in the face of climate change**

Countries are already highly interdependent with respect to AnGR, and such interdependence depends not only on climatic conditions but also closely follows cultural preferences and the distribution of ethnic groups. Regardless of the specific direction of future climate change in any particular location, the scenarios identified earlier (“livestock portfolio change” and “gene pool reduction”) suggest that large-scale movement of livestock breeds may become increasingly necessary, and, consequently, country interdependence on animal genetic resources may be expected to increase even further.

Maintaining/sustaining a diverse range of AnGR in the face of climate change will be particularly important for efforts to reduce global risks and strengthen global food security. Understanding the economics of AnGR conservation and sustainable use can support such endeavours and contribute to the identification of conservation priorities (Weitzman 1993; Simianer et al. 2003).

Both predicting how climate change will affect the gene flows and interdependency of countries, as well as developing appropriate policy responses, are constrained by the fact that relatively little baseline quantitative data on AnGR exchange is available. Quantitative information on gene flows through animal recording systems, national breed inventories with spatial distribution, monitoring of imports and exports, and scenario modelling are all urgently required.

## CHAPTER V: THE IMPACT OF CLIMATE CHANGE ON INTERDEPENDENCE FOR MICROBIAL GENETIC RESOURCES FOR AGRICULTURE

**By:** Fen Beed, *International Institute of Tropical Agriculture, Kampala, Uganda*

### 1. Introduction

Interactions among crops and microbes influence the quality, productivity, and sustainability of food production systems. Microbes, both beneficial and antagonistic, and the array of functions they perform are currently underestimated. Nutrient cycling microbes, endophytes, mycorrhizae, and natural enemies of pests and diseases contribute to durable farming systems, while other microbes are responsible for devastating diseases and toxin contamination of crops. Crops and microbes must therefore be considered together when considering why, and the extent to which, countries are interdependent upon them. In this context, microbial genetic resources (MGRs) are defined as functional units of heredity such as DNA or RNA and do not include biochemical extracts (Glowka 1995).

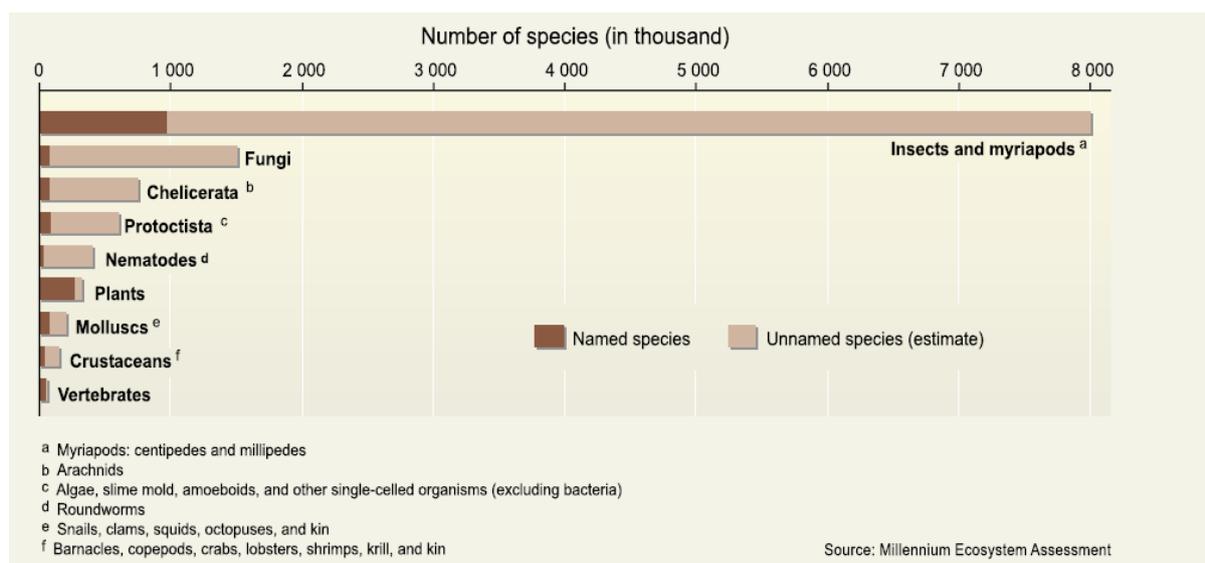
Agriculture intensification, land use management, globalization, and the wide distribution of crop germplasm will continue to create new selection pressures on microbes, which, in turn, will create a matrix of positive and negative pressures on food production systems. Climate change will provide an additional selection pressure on microbe species, strains, and populations by contributing to the geographic redistribution of crops and altering environmental parameters that limit their spread. To predict risk and develop appropriate adaptation strategies to such drivers, governments will become increasingly reliant on information and MGRs that originated, or are found, in other countries for the purpose of research, training, or direct use in agriculture.

### 2. Microbial diversity

Microbes have been largely ignored despite their key role in ecosystem function and service. Understanding the diversity of microbial genetic resources is necessary before describing the likely impacts of climate change. There are an estimated 5–30 million species globally – some two million have been formally described, while the remainder are unknown or unnamed. Of the one 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; and Figure 1). 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 an even more limited exploitation of MGRs.

### 3. The role of microbes in food production systems

Microbes are key to soil formation and quality. Fungi are the main agents of decomposition in many terrestrial and aquatic environments and are responsible for the degradation of 70 percent of cell wall material and lignocelluloses. In mutualistic associations, micro-organisms provide the biological interface with the physical and chemical environment that many higher organisms depend upon for survival. Micro-organisms control mineralization, organic matter production, geochemistry, and nitrogen availability (Stackebrandt 1994; Mooney et al. 1995).



**Figure 1.** Predicted number of species recorded and as yet unidentified

Microbes can play a role in climate change mitigation. Soil organic matter is the major global storage reservoir for carbon (and not forests as is commonly thought). Microbe (and invertebrate) diversity is responsible for breaking this material down and making it available to plants while, at the same time, contributing to the rate of production and consumption of carbon dioxide, methane, and nitrogen. Soil biota thus plays a role in climate stabilization and regulation. An estimated 140–70 million tons of nitrogen are fixed by microbes worldwide annually (worth an equivalent of US \$90 billion compared to nitrogen fertilizer use). Microbes provide the potential to rely on biological processes rather than on external inputs and climate change inducing inputs such as synthetic fertilizer for sustainable farming systems.

Genetic resources held by discrete projects and microbe collections across the world need to be understood in terms of functionality. For agriculture, such capacities will help screening programs to select appropriate crop germplasm for different agro-ecological zones or farming systems. The potential benefits or risks to farming systems posed by MGRs can be used in GIS models overlaid with other data (e.g., environmental factors, crop varieties, socio-economic, and demographic factors). In support of all of these efforts, it is already important, and it will be increasingly so with the impact of climate change, to be able to access, characterize, and pool, representative samples of the genetic diversity of microbial species and strains.

#### 4. The impact of climate change on microbes

Micro-organisms have survived major climate changes, such that the current projected scenarios of climate change are not likely to precipitate novel irreversible configurations of the microbial world. This hypothesis is predicated not only on the natural historical record of micro-organisms but also on their prolific and extremely effective adaptive strategies. For example, the elevated atmospheric concentration of carbon dioxide is likely to result in changes in plant growth characteristics, affecting root systems, exudates, and litter production. Changes in vegetation cover will in turn affect the growth and distribution of free-living fungi, mycorrhizal relationships, soil bacterial diversity, and the occurrence of plant diseases. These simple interactions may then cascade to modify the activities of fungivores, bacteriavores, and omnivores. All of these changes are likely to be accompanied by dramatic fluctuations in local nitrogen cycling and in the efficiency of other biogeochemical cycles (Wall et al. 2001).

Climate change is predicted to bring warmer temperatures, stronger storm systems, modified wind patterns, increased ozone and carbon dioxide, increased frequency of heavy precipitation events and extended dry periods, changes in humidity and cloudiness, and rising sea levels. The impacts of

climate change on microbes will be complex and highly variable and will be dependent on interactions with other organisms for each ecosystem. Some plausible direct effects are that due to warmer temperatures some microbes will exploit geographic locations to the North and South and in the tropics to higher altitudes. Unexpected impacts could be that, as a consequence of the increased diversity of microbes, adaptation or evolution through mutations may be more rapid than for other taxa. Several factors associated with climate change will affect microbes (nematodes and insects), including elevated temperature, extreme rain events, elevated carbon dioxide, and wind.

#### 4.1. *Elevated temperature*

As early as 1932, the importance of interaction between microbes and temperature was demonstrated. Wheat grown in sterilized soil and inoculated with the take-all fungal pathogen disease (*Gaeumannomyces graminis*) increased with temperature from 13 to 27 degrees Celcius. In natural, unsterile soil, however, the disease declined when the temperature exceeded 18 degrees Celcius because higher temperatures promote other micro-organisms such as *Pseudomonas* spp., which antagonize the take-all fungus (Henry 1932).

Although micro-organisms tend to be adapted to specific environmental conditions, many can tolerate one sub-optimal factor if all others are near optimal, while a combination of sub-optimal factors can prevent growth. Diel temperature oscillations (various time scales, including regular day and night fluctuations) affect organisms that respond quickly to temperature changes (Dang et al. 2009). These organisms include bacteria, fungi, and micro algae, which together drive a large portion of global biogeochemical cycles. The specific temperature-growth-response patterns of dominant species result in responses of ecosystem processes to temperature changes that are more complex than is generally acknowledged in large-scale models.

While microbial communities would by and large be expected to favour warmer conditions (if other growth parameters are non-limiting), the composition, biomass, respiration, and function as measured by enzyme activities decrease when exposed to increased soil temperatures (Waldrop and Firestone 2006). Furthermore, while warm temperatures speed up biochemical reactions (catabolism and anabolism) that expend energy – permitting increased activity, growth, development, and reproduction – this acceleration comes at a cost. Higher food consumption rates are required to maintain a positive energy balance. For instance, the survival of *Cryptosporidium parvum* cysts declines with prolonged exposure to warm temperatures because increased metabolism drains the energy reserves of cysts (Lafferty 2009).

The geographic range of *Phytophthora cinnamomi*, a soil-borne oomycete, has expanded due to global warming. This pathogen was previously restricted to tropical and sub-tropical regions but has been recently associated with oak declines in southern and Mediterranean Europe (Garrett et al. 2006). The southern root-knot nematode (*Meloidogyne incognita*) of coffee in Brazil has expanded its geographical distribution due to climate change. Elevated temperatures will make previously inclement environments conducive to microbes.

Losses to plant diseases caused by microbes are most severe in the sub-tropics and tropics because of warmer temperatures, longer growing seasons, and, in some regions, year-round production that creates favourable conditions for pathogen survival. It is possible that risk due to disease will be increased with increased temperatures because there will be a reduction in the number of frost days that normally reduce over wintering survival of pathogens. This is the case in the United States for late blight of potato caused by the fungal pathogen *Phytophthora infestans* and for soybean cysts caused by the nematode *Heterodera glycines* (Rosenzweig et al. 2005). 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). Aflatoxin (produced by fungi of the *Aspergillus* spp.) contamination of grains poses serious health threats. These microbes are native to warm arid, semi-arid, and tropical regions, and changes in climate result in large fluctuations in the quantity of producers. The most important species, *A. flavus*, competes poorly in cool areas

(temperatures below 20 degrees Celcius) and thus experiences reduced abundance compared to warmer regions (temperatures above 25 degrees Celcius) (Cotty and Jaime-Garcia 2007). Since 2003, frequent hot and dry summers in Italy have resulted in the increased occurrence of *A. flavus*, the most xerophilic of the *Aspergillus* genus, with consequent unexpected and serious outbreaks of aflatoxin contamination. Serious outbreaks of *A. flavus* in the United States have been reported for similar reasons (Leslie et al. 2008).

Potato and tomato late blight (caused by the fungus *Phytophthora infestans*) is most severe during periods of high moisture when temperatures are between 7.2 degrees Celcius and 26.8 degrees Celcius (Wallin et al. 1950). For each one degree Celcius 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 for control. Increased exposure to a fungicide of the pathogen 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 allowing for increased fungal inoculum to build up. Faster crop development would also result in reduced phyllochrons, which is the time between the emergence of one leaf and 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 the application of fungicides per year (Georghiou and Taylor 1986; Shelton et al. 2001). If host plant resistance rather than fungicides were used to manage diseases, the increased number of cropping cycles per year would confer a selection pressure on pathogen populations to overcome resistance mechanisms.

Increases in temperature can also have indirect affects on microbial pathogens by modifying host physiology and resistance (Coakley 1999). A rise in temperature above 20 degrees Celcius can inactivate temperature-sensitive resistance to stem rust in oat cultivars reliant on *Pg3* and *Pg4* genes. In contrast, lignification of cell walls increases in forages at higher temperatures to confer increased resistance. Resistance of tomato nematodes breaks down when soil temperature exceeds 28 degrees Celcius, and the expression of the banana streak virus increases with temperature (Dahal et al. 1998). A total breakdown of resistance of tomatoes to bacterial wilt (caused by *Ralstonia solanacearum*) has been reported with increased temperature (Tung et al. 1992; Kuun et al. 2001). For the Great Lakes banana-based cropping systems, pest and disease behaviour is subject to a balance of altitude and temperature with nematodes, weevils, and black Sigatoka having altitudinal limits of approximately 1,400 meters due to temperature thresholds (Speijer et al. 1994; Tushemereirwe 1996; Price 2006). Transmission of BXW (Banana Xanthomonas Wilt) by insect vectors varies with ecological conditions, being lower in cold, higher altitude regions (Mwangi et al. 2006). Male bud infection has not been observed in Ethiopia or the Democratic Republic of Congo above 1,700 meters above sea level (Ndungo et al. 2006; Addis et al. 2004).

Temperature will affect insect vectors of disease and disease distribution. Temperature is probably the single most important environmental factor influencing (cold-blooded) insect behaviour, distribution, development, survival, and reproduction (Bale et al. 2002). With a two-degree temperature increase, insects will experience an estimated one-to-five additional life cycles per season (Yamamura and Kiritani 1998). Stewart's wilt (*Erwinia stewartii*), a bacterial disease of sporadic importance in sweet corn in the northeast United States is vectored by the corn flea beetle (*Chaetocnema pulicaria*). Survival of the vector through winter is key to the severity of Stewart's wilt the following year (Castor et al. 1975). Climate change resulting in more winters that allow larger populations of flea beetles to survive would increase the frequency of growing seasons with severe Stewart's wilt. This would require additional insecticide sprays during the winter or deployment of resistant cultivars (Fournier 1999; Whitney et al. 2000; Baniecki and Dabaam 2000). On the other hand, hosts may pass through vulnerable life stages more quickly at higher temperatures, reducing the window of opportunity for parasitism.

Insect diversity decreases with higher latitude and altitude (Gaston and Williams 1996; Andrew and Hughes 2005). Rising temperatures could result in greater vector distribution (Bale et al. 2002). Barley

yellow dwarf potyvirus (BYDV) causes more severe disease following mild winters. Since BYDV is vectored by aphids, increased survival of pathogen reservoirs could greatly increase the economic losses caused by infection. Similar increases in viruses of potato and sugar beet are observed following warmer winters (Harrington and Stork 1995).

The same environmental factors that impact insects, acting directly as pests or indirectly as disease vectors, can also impact the predators, parasites, and disease organisms of insects (bio-control agents). At higher temperatures, aphids have been shown to be less responsive to the aphid alarm pheromone they release when under attack by insect predators and parasitoids – resulting in the potential for greater predation (Awmack et al. 1997). Fungal pathogens of insects are favoured by high humidity, and their incidence would be increased by climate changes that lengthen periods of high humidity and reduced by those that result in drier conditions. Overall, the (not easily predicted) geographic shifts of pests, pathogens, vectors, as well as predators, parasites, and disease-causing organisms of insects due to elevated temperatures will determine the extent to which countries are increasingly reliant on microbial genetic resources from sources beyond their own borders, as part of their responses to these threats.

#### **4.2. Extreme rain events**

Bacteria are better able to respond to moisture pulses regardless of temperature, while fungi only respond to moisture pulses during cooler periods. These organisms are involved in carbon and nitrogen cycling, and changes in their activity thus ultimately disrupts above-ground processes (Bell et al. 2008). Changes in the timing and magnitude of precipitation will be a key-limiting factor regulating primary productivity, soil microbial activity, and ecosystem dynamics in arid and semi-arid regions. Water availability is most closely associated with structural and functional changes in the microbial community, which has implications for seasonal effects of rainfall (Williams and Rice 2007). The composition and function of soil microbial communities is directly affected by water-related stress conditions (Schimel et al. 2007). Droughts may have significant implications for fungal community diversity and, therefore, the potential to interfere with ecosystem processes such as organic matter decomposition (Toberman et al. 2008).

Stress to crops due to intensified rainfall events and drought will increase susceptibility to diseases and pests. Dry periods tend to encourage insect and virus outbreaks, while wet periods encourage fungal and bacterial diseases. Some pathogens such as apple scab, late blight, and several vegetable root pathogens are more likely to infect plants under conditions of increased moisture. Other pathogens such as the powdery mildew species tend to thrive in conditions with lower (but not low) moisture. Some climate change models predict higher atmospheric water vapour concentrations with increased temperature, favouring pathogen infection and disease development. Hurricanes can facilitate transcontinental invasion of fungus – for example, Asian soybean rust (*Phakopsora pachyrhizi*) in the Americas. Excessive rains in Brazil in 2004 favoured the development of soybean rust and led to a massive epidemic (Rosenzweig et al. 2005).

Extended dry periods (and heat stress) can be associated with increased nematode damage in rain-fed and upland rice areas as well as in dryland cereal systems. Although aflatoxin-producing fungi are common throughout soils, air, and on crop surfaces, grain colonization is significantly increased when host crops are drought stressed (Cotty and Jaime-Garcia 2007). As climate warms and weather patterns become more erratic and drought events more intense, aflatoxin contamination could further restrict the area over which crops may be economically grown. Areas in Australia with both dry and hot climates have suffered an increased probability of higher aflatoxin risk compared with locations having either dry or hot conditions alone (Chauhan et al. 2008).

For altered moisture regimes due to climate change, as with temperature, the geographic shifts of pests, pathogens, vectors, as well as predators, parasites, and disease-causing organisms of insects – and interactions between them and with crops – will increase the need for knowledge of microbe function and access to living specimens to facilitate the adaptation of farming systems.

### 4.3. Elevated carbon dioxide

Microbial communities appear to be altered by elevated atmospheric carbon dioxide, and these changes may have implications for ecosystem function, especially via the effects on the cycling of essential elements (Lesaulnier et al. 2008). Increased carbon dioxide will increase plant growth with concomitant increase in soil microbial respiration and carbon turnover (Heath et al. 2005). Experimental data show that greater plant detritus production under elevated carbon dioxide significantly alters soil microbial community composition. Total bacterial and eukaryotic abundance remains unchanged, while heterotrophic decomposers and ectomycorrhizal fungi increases with reductions in bacteria implicated in nitrate reduction and ammonium oxidation (Lesaulnier et al. 2008).

Early season increased carbon dioxide levels have resulted in increased insect attack on soybeans (primarily Japanese beetle, potato leafhopper, western corn rootworm, and Mexican bean beetle) than in those grown in today's atmosphere, possibly due to increased concentrations of simple sugars in the leaves (Hamilton et al. 2005). Changes in the carbon-to-nitrogen ratio due to increases in carbon dioxide may influence the attractiveness of host plants to insect pests and impact on the rate of insect development (Beed et al. 1999; Hunter 2001). Reduced development rates due to increased carbon-to-nitrogen ratio due to elevated carbon dioxide levels could increase the duration of life stages vulnerable to attack by parasitoids (Coviella and Trumble 1999).

Enhanced plant growth under elevated carbon dioxide would increase carbon-to-nitrogen ratio of litter. Decomposition of high carbon dioxide litter occurs at a slower rate. Increased plant biomass, slower decomposition of litter, and higher winter temperatures could increase the survival of pathogen microbes and, hence, inoculum build up on over-wintering crop residues (Garrett et al. 2006). Elevated carbon dioxide would likely increase crop canopy size and density, resulting in greater biomass of high nutritional quality, which, if combined with increased canopy humidity, would promote foliar diseases such as rusts, powdery mildews, leaf spots, and blights (Coakley et al. 1999). However, it is impossible to generalize – *Colletotrichum gloeosporioides* has experienced delayed or reduced conidial germination, germ tube growth, and appressorium production when inoculated onto susceptible *Stylosanthes scabra* plants under increased carbon dioxide. Similar effects in other pathosystems include a reduction in the rate of primary penetration in *Erysiphe graminis* (barley powdery mildew). In this example, host resistance increased through the mobilization of assimilates into defence structures such as papillae and the accumulation of silicon at sites of appressorial penetration (Hibberd et al. 1996). To confuse matters further, following penetration, established colonies of *E. graminis* and *C. gloeosporioides* grew faster under elevated carbon dioxide. Sporulation per unit area of infected tissue increased several-fold under elevated carbon dioxide for *C. gloeosporioides*.

Increased carbon dioxide levels will alter microbial communities, insect pests, and crops in an interactive fashion. Again, changes in the global distribution of crop pests and diseases relative to predators, parasites, and disease organisms of insects would create conditions under which countries will be increasingly reliant on microbial genetic resources and related information from sources beyond their own borders.

### 4.4. Wind

Although wind patterns will be altered as climate changes, impacts on the dispersal of pathogens and their vectors is uncertain. Several pathogens rely on distribution via wind, particularly those with the smallest spores such as a new virulent strain of stem rust (Ug 99), which has moved from Uganda towards the Middle East courtesy of winds ([http://biogov.cpdr.ucl.ac.be/Biov\\_FAO\\_Workshops/Amri\\_percent20Ahmed.pdf](http://biogov.cpdr.ucl.ac.be/Biov_FAO_Workshops/Amri_percent20Ahmed.pdf)). Surveillance to pre-empt such invasions rely on Google Earth, a GIS system that can be employed by registered users to update pest distribution. RustMapper is being tested to map the distribution of wheat stem rust race UG99 across the world, coordinated by the International Maize and Wheat Improvement Center (<http://www.cimmyt.org/gis/rustmapper/>). In the United States,

the soybean rust caused by *Phakopsora pachyrhizi* is dispersed by wind and is being monitored using sentinel plots and GIS maps via the National Plant Diagnostic Network (Miller et al. 2009). Studies have shown that variation in the most toxigenic isolates of *A. flavus* is directly associated with climatic variations, as are the annual cycles in the composition of aerial and soil borne *A. flavus* communities (Bock et al. 2004). Severe winds and storms will also induce abiotic stress and physical damage to crop plants, making them more susceptible to disease. Climate change may blow new problems to cropped areas in yet unforeseen patterns (e.g., similar to the movement of the new variant of stem rust to the Middle East). The resulting geographic shifts in problems will undoubtedly increase interdependence.

## 5. Geographic redistribution of plant diseases and the need for surveillance systems

With agricultural globalization, many crops, often with a narrow genetic base, are grown far from their centres of origin and apart from the pathogens that have coevolved with them. Such crops lack resistance to new strains introduced via global trade. Crop varieties selected in centralized locations but distributed to wider geographies may be poorly equipped to resist or tolerate resident diseases. Plant diseases due to pathogenic micro-organisms represent a serious threat to global food security (Oerke 1994; Strange and Scott 2005). This scenario will be exacerbated by global redistribution of diseases due to changes in climate, making previously inclement environments conducive to pathogens. The risk to agriculture posed by this precarious situation can be limited by greater knowledge and access to microbes – for the selection of resistant/tolerant crop germplasm or for the introduction of microbes that are either antagonistic to those that cause plant disease or that enhance ecosystem resilience through the improvement of soil quality and, hence, sustainable crop growth. This need for interdependence between countries for microbe genetic resources would be linked to an assessment of risk that would be based upon sound quantitative and qualitative data routinely produced by robust surveillance systems.

Cassava mosaic disease (CMD) has adapted to selection pressure due to the mass deployment of cultivars with specific resistant mechanisms. Although CMD does not exist in the centre of origin of cassava (South America), a severe form of the disease (EACMV-Ug) had appeared in Uganda by 1999 and had then spread to the Democratic Republic of Congo, Kenya, Sudan, and Tanzania (Legg 1999) and thereafter to Burundi, Gabon, and Rwanda (Bigirmana et al. 2004, Legg et al. 2001; 2004). EACMV-Ug was accompanied by abundant populations of the whitefly vector that molecular studies identified as being distinct from the Ugandan indigenous biotype (Legg et al. 2002). Local cultivars succumbed to the disease, and breeding strategies were developed to select for resistance and to mass-produce resistant materials. Since then a more virulent variant of CMD has been discovered (Legg 2006). Another viral disease, cassava brown streak, has recently spread across East and Central Africa resulting in the need to again develop crop cultivars resistant to this disease and CMD. A recently introduced bacterial *Xanthomonas* wilt pathogen of banana (*Xanthomonas campestris* pv. *musacearum*) in the Great Lakes region of Africa has rapidly spread from Ethiopia to Uganda and then to Burundi, the Democratic Republic of Congo, Kenya, Rwanda, and Tanzania (Ndungo et al. 2006; Carter et al. 2009). The identification of this bacterial pathogen when it first arrived in Uganda was only possible because of comparisons with recovered cultures with those held in microbial collections that showed its similarity to cultures of *X. campestris* pv. *musacearum* originating from Ethiopia and collected in 1906 (Aritua et al. 2008). Despite the awareness of these diseases, virtually nothing is known of their epidemiology and invasion potential as controlled by shifts in temperature due to climate change. Furthermore, it is envisioned that as climate change impacts on agriculture through varied microbe survival and spread it will influence trade patterns that will further complicate distribution patterns of microbes. The new banana disease variant 4 of Panama Disease (*Fusarium oxysporum* f.sp. *cubense*) was first reported in Australia and has since spread across Asia and has been recently recorded in Madeira, the Canary Islands, and South Africa. Its arrival in the Great Lakes region is imminent (Ploetz and Pegg 2000; Bioversity International 2006). Research is needed to ascertain the distribution as well as the climatic and host ranges of the tropical (favouring higher temperatures) and non-tropical (favouring lower temperatures) types of race 4 in order to evaluate risk.

As a consequence of the current uncertainty as to which microbes are present in global farming systems and which are most likely to spread, the development of surveillance systems is urgently required. These systems would monitor current risks and, from the basis of predictive models, could evaluate the likely impact of climate change. While predictions have been made regarding climate change effects on pest development (Barker et al. 2006), including fungi (Smith et al. 2007) and nematodes (Pinochet et al. 1995), there is a lack of baseline data available on risk due to crop diseases for developing countries. Furthermore, surveillance systems are needed to evaluate the impact of management practices on the persistence and spread of microbes that cause plant disease. Climate-related changes causing increased 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). In a positive case, a bio-pesticide was developed to combat the desert locust in West Africa using the naturally occurring isolate *Metarhizium anisopliae* var. *acridum*. Compared to synthetic chemical insecticides, the bio-herbicide provided increased sustainable control efficacy without negative impacts on the environment or other natural enemies (Langewald et al. 2003).

Climate change will enhance pathogen and vector evolution (Anderson et al. 2004; Garret et al. 2006; Myerson and Reaser 2002; Smith et al. 2008; Waage and Mumford 2008). With damage caused by emerging, re-emerging (e.g., new races, pathotypes, and forms resistant to pesticides or antibiotics), and chronic/endemic pathogens, the potential for devastating impacts on food security and income generation are highly significant (Strange and Scott 2005).

## **6. The importance of awareness and access to MGRs through microbial collections**

The diversity of microbes and their function, both beneficial and antagonistic to sustainable agriculture, is poorly understood. In contrast, crop function is largely understood and cultivars with characteristics suited to changing climatic conditions are available, particularly through the Consultative Group on International Agricultural Research's (CGIAR) network of material held in trust under the framework of the International Treaty. However the deployment of crop germplasm to mitigate against potential impacts of climate change must be performed in unison with microbial germplasm. Beneficial microbes that confer ecological resilience include those that act to fix or cycle nutrients. The activity of these organisms, in turn, increases crop vigour and the sustainability of soils suitable for durable agricultural production. Antagonistic microbes include those that cause crop disease or produce toxins that render agricultural produce unsaleable to international markets and not safe for local consumption.

Agricultural systems are dependent on a range of ecological interactions both between microbes and microbes with other organisms. Many of these can be exploited to benefit agriculture such as the use of microbial bio-control agents of insect pests or deleterious microbes that cause crop disease. Climate change will modify the geographic distribution of microbes and increase the impact of particular microbes beyond current ranges. Microbes that cause disease specific to certain climatic conditions must be characterized, and any introduced crop germplasm must be screened to ensure that it will not succumb to existing or potentially introduced pathogens. An ecological perspective must be adopted to counteract the negative impact of plant disease. For example, any management techniques to curtail a crop disease caused by a virus must consider the potential spread of its insect vector, particularly as climatic conditions vary.

Climatic changes will increase the countries' interdependence on microbes as part of their responses to, for example, increased pathogen distribution across country borders or the loss of beneficial microbes in soil that suffers, for example, from drought levels not previously experienced. Countries' interdependence on microbial genetic resources will include both the knowledge of the presence and functionality of organisms and the prediction of risk as to the likelihood of movement into, or displacement from, neighbouring countries. Finally, access to live MGRs is required to introduce beneficial organisms to an environment and to select for resistant crop germplasm. Research is

required using live MGRs, for example, for pathogens to define their epidemiology and for beneficials to determine key parameters that support their activity and survival. To identify (taxonomically) a disease, or the new variants of a disease or a beneficial organism, expert knowledge is required combined with live reference samples (type strains). This knowledge requires the capacity to maintain microbe cultures and human skill that cannot be feasibly housed in every country, so a system of centres of excellence operated by highly trained staff linked to global information outlets needs to be established.

Increasingly, due to globalization, and most specifically due to climate change, countries will need to access information and MGRs from beyond their own borders in order to understand and enhance their agricultural sector. As countries deal with challenges associated with new pests and diseases, and to address environmental stresses that impact on the performance of beneficial microbes, countries are going to need to look beyond their borders for MGRs to assist in identifying the pests they are suffering from, to identify useful strains of pathogens for the bio-control of these pests, and so on. Therefore, there is a requirement to pool representative samples of microbial diversity (and, hence, function) for comparative taxonomy, research, and training for the deployment of specific species and strains. As a consequence of the increased movement of pathogens and changes to the persistence of beneficial microbes due to climate change, there needs to be greater internationalization of the coordination of knowledge networks and mechanisms to access MGRs.

The most obvious type of facility that can characterize the identity and function of microbes and place this information in the public domain are microbial collections. Awareness of the contents of each microbial collection combined with formal linkages between them would enable the formation of a knowledge network. Access to different types of microbes – for the introduction to farming systems to increase nutrient availability, for antagonism to pests and diseases, or for screening crop germplasm to ensure its suitability to a particular location – is fundamental. Once an awareness of the microbes that are available is known, an enabling policy environment is required to facilitate the safe exchange of microbial species and strains. Clearly, the knowledge and skills of microbial scientists based at microbial culture collections are critical to the global preservation of MGRs and knowledge of their function.

When considered alongside the richness of microbial diversity and its corresponding varied and crucial functionalities, our adaptive capacity to sustain agricultural production as climates change is extremely limited. This worrying situation is made worse by the fact that skilled systematic taxonomists for microbes are being lost and new staff are not being trained. There needs to be a global initiative to reverse this trend if collections of microbes are to be created with the capacity to serve the global good of sustained food production.

## **7. Conclusions: Interdependence for microbial genetic resources in the face of climate change**

MGRs are responsible for devastating diseases of crops and, positively, the bulk of decomposition, storage, and cycling of carbon, nitrogen, sulphur, and phosphate. Genetic resources for food and agriculture and biodiversity – namely, the diversity of genes, populations, species, communities, and ecosystems – underly all ecosystem processes and through appropriate management can provide resilience to change. Characterizing, conserving, and managing MGRs will help farming systems become more resilient to shifting global climate and changes in land management. Selection of suitable crop genetic resources for a given environment would be based upon testing for compatibility with beneficial MGRs for nutrient cycling and for resistance/tolerance to indigenous diseases. Climate change is unequivocal but must be considered as a selection force in addition to modern farming techniques, habitat destruction, and the adaptive capacity of different human populations.

The precise impact of climate change on MGRs 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 interactions between each micro-organism and their relationship with others in an ecosystem combined with shifts in relationships with plants that will dictate the impact of changes in climate. Climate change must be considered as a selection pressure in addition to existing pressures due to agricultural practices and changes in land use that adds a further level of complexity and uncertainty to the likely sustainability of farming systems. With this approach, climate change will not be studied in isolation of strategic research of ecosystems to identify interactions of key beneficial and antagonistic micro-organisms but, rather, as a routine part of the system of a hypothetical-based analysis.

Enhanced systems of disease surveillance will be needed to pre-empt the impact of existing, emerging, newly introduced diseases and, in terms of trade, of those classified as quarantine diseases. For many developing countries, knowledge of the presence and impact of disease is poor. A crucial first step is to provide a system of evaluation. Once this capacity is created, the uncertainty due to change resulting from climate and habitat disturbance can be overlaid.

Countries are interdependent on MGRs. Climate change will lead to situations where still more information and access to MGRs that originated, or are found, in other countries is needed for the purposes of research, training, or direct use in agriculture. Collections of MGRs will play a pivotal role in taxonomy, in facilitating preservation and characterization, and in the analysis of function. Collections and associated human and technical capacity need to be financed. Assessments of global risk due to MGRs that cause disease would facilitate priority setting and adaptation strategies to mitigate against pathogen spread and impacts on agriculture. Finally, the various impacts of climate change will alter microbial communities, insect pests, and crops in an interactive fashion. The global distribution and seriousness of crop pests and diseases relative to the needed distribution of predators, parasites, and disease organisms of insects will shift, perhaps in major ways. These factors must predict greater interdependence if new problems are to be successfully addressed.

## CHAPTER VI: INTERDEPENDENCE OF COUNTRIES IN THE MANAGEMENT OF GENETIC RESOURCES FOR AQUACULTURE AND FISHERIES IN THE FACE OF CLIMATE CHANGE

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### 1. Introduction: International borders and aquatic ecosystems

More than terrestrial ecosystems, aquatic ecosystems operate independent of national and international boundaries. Aquatic ecosystems are instead delimited by watersheds – the network of contiguous waterbodies and watercourses that drain the landscape from the top of some elevated landform downwards towards a lake or the sea. The interaction of geomorphology and aquatic ecology, which is essential to the understanding of how biodiversity depends upon ecosystem integrity, is the subject of this section.

Seldom are major watersheds or even single river courses contained within one political unit. In fact, major water bodies often serve as boundaries between political units, obliging aquatic resource managers to work with partners in one or sometimes several different countries to effectively regulate water use and fisheries. To manage both the biodiversity and fisheries of watersheds requires the cooperation of all or most of the countries in which lie the interconnected swamps, streams, marshes, estuaries, bogs, lakes, lagoons, and rivers that comprise the aquatic habitats within a watershed. One hundred and sixteen binding multilateral treaties have been signed since 1882 involving over 100 countries that have agreed to manage, conserve, and govern transboundary fisheries (<http://www.intfish.net/igifl/treaties/index.htm>).

Habitats within riverine ecosystems are diversified vertically along their length, beginning with bogs or small rivulets high in the watershed and gradually growing larger and more complex as they flow downstream towards the estuaries or lagoons that form the interface between rivers and the recipient water body (a lake or the sea). According to the availability of habitat, the same aquatic fauna occupies the entire watershed with diversity generally increasing downstream through the addition of species rather than through replacement. Many species of fish, particularly in the temperate zones, move up and down the river over their life cycles, spawning and nursing in shallower upstream areas protected from predators and then growing to adulthood in the more nutrient-rich lower reaches. For non-migratory species, water quality and physical structure can determine the degree to which the river can be fully inhabited. Waterfalls, in particular, can be major determinates of species distribution in rivers.

Lacustrine and oceanic habitats are diversified according to the depth of water and proximity to the shore: littoral (along the shore), benthic (near the bottom), and pelagic (open water) are the major habitats. In general, species can move from oceanic habitat to habitat relatively freely compared to movement in rivers. Typical of such oceanic systems are species that exploit different habitats during different parts of their life cycle with distinct breeding, nursery, and feeding areas to and from which species migrate according to the seasons. Mangrove forests and estuaries, for example, are major nurseries for many commercially important fish and shellfish species.

Tropical and floodplain rivers share this last feature in common with lakes. Rather than moving up or downstream to reproduce, most tropical species move laterally onto floodplains or into swamp forest during the rainy season to reproduce and/or nurse their young, moving back into the main river channel to feed and grow as the floodplain dries out and water recedes. Whatever the exact mechanism, in all rivers, lakes, and oceans, the integrity of the entire network of habitats is critical to the functioning of the ecosystem. Since aquatic genetic resources respect no international borders, so

too their wise use and conservation depend critically on the ability of nations to cooperate in their management, and this need is increasing in light of habitat alterations expected as a result of global climate change.

## 2. Aquatic genetic diversity

Most aquatic species have difficulty moving from watershed to watershed, and species dispersion is generally a long-term affair facilitated by flooding and geomorphic changes due to such events as landslides and volcanic activity. This chapter reviews the distribution of wild and captive aquatic genetic diversity. A number of euryhaline species move between salt and freshwater or spend different parts of their life cycle in either fresh or salt water. These species have at the genus level become nearly ubiquitous in their distribution. Salinity, however, generally serves as a major boundary and has acted as an isolating force through which individual river systems have biologically differentiated over geological time.

The importance of geographic isolating mechanisms in determining the extent of aquatic biodiversity can hardly be understated. Since oceanic systems are ultimately connected, there is far less biodiversity relative to quantities of water in the oceans than among more isolated freshwater ecosystems: there are 15,200 freshwater species (an underestimate from FishBase 2009) in 55,257 cubic kilometers of freshwater (0.3 species per cubic kilometer) (Gleick 2008), compared to 20,000 marine species (<http://www.coml.org/press-releases-2008>) in 1.4 billion cubic kilometers of salt water ( $1.4 \times 10^5$  species per cubic kilometer) (Garrison 2007). Even in the oceans, populations do diverge (especially, those that exhibit some type of homing behaviour) and, in some cases, (e.g., European seabass, *Dicentrarchus labrax*) may represent units of importance for conservation (Youngson et al. 2001).

Human activities have had a major impact on the distribution of aquatic resources. Such man-made structures as the Suez, Erie, Panama, and Rhine River canals have co-mingled faunas that had previously been isolated. Conversely, the world's 45,000 large dams have often cut riverine ecosystems into two or more parts and have reduced species diversity by eliminating or restricting the upstream – downstream movement of species (World Commission on Dams 2000). A relatively recent current mechanism facilitating the movement of species between watersheds and even continents is modern aquaculture and sport fisheries (Lever 1996).

## 3. Genetic resources for aquaculture

Some 250 species of fish, crustacean, and mollusk are used in aquaculture (Pillay and Kutty 2005). About 60 percent are indigenous to temperate regions, the balance coming from the tropics. Of the 67 million tonnes produced in 2006, by far the most important groups are the finfish families Salmonidae (2.1 million metric tonnes per annum, worth US \$9.9 million), Cyprinidae (20.5 million metric tonnes, US \$18.8 million) and Cichlidae (2.3 million metric tonnes, US \$2.8 million), marine crustaceans (3.2 million metric tonnes, US \$12.5 million) and the bivalve mollusks known commonly as mussels, clams, scallops, and oysters (12.3 million metric tonnes, US \$10.6 million) (FishStat 2008).

Domestication consists of the process of adaptation of organisms to an environment provided by humans. It involves both an evolutionary response via changes in gene frequencies between generations as well as environmentally induced shifts in developmental processes and behaviours that occur within each generation. Simply put, there are both genetic and non-genetic changes that result in domestication. Domestication can occur without loss in performance or fitness and in the presence of selection-enhancing performance. In other words, there may be instances in which the selective breeding program can be initiated while the population is being domesticated, with both processes taking place in parallel.

From the point of view of international cooperation in the conservation of genetic resources for food production, the common carp, *Cyprinus carpio*, which is found in cool freshwater; the Nile tilapia

(*Oreochromis niloticus*) from warm freshwater; the Atlantic salmon (*Salmo salar*), which is diadromous; the tiger shrimp (*Penaeus monodon*), which is a tropical marine species; and the Pacific cupped oyster (*Crassostrea gigas*) from temperate oceans, are representative of the main cultured species groups and thus provide useful case studies.

### 3.1. Common carp

The common carp is one of the oldest cultured species and is surely the most widely grown, being produced in at least 96 countries and on every continent except Antarctica (FishStat 2008). It is also one of the few domesticated fish species in the strict sense (Diamond 2002) – the principal distinguishing features of the domesticated carp compared to the wild progenitor being (1) a decrease in the relative size of the head; (2) a larger mouth; (3) scale pattern (which varies from fully scaled to an almost complete lack of scales); and (4) colour (Kirpichnikov 1981; Balon 2004), all of which are traits of importance in culture and/or marketing (Penman et al. 2005).

The common carp was probably first captured and held in ponds in the Danube Valley by the Romans some 2,000 years before present (Balon 2004). Sometime since the published studies in 1955, the wild form became extremely rare (FishBase 2009), if not extinct, at least partly as a result of the construction of the Gabčíkovo Dam, which altered the hydrology of the inland delta where they spawned (Balon 2004). According to E.K. Balon (2004), all modern wild (feral) carp populations are derivatives of escaped farmed carp. Whatever their origins, four subspecies in the wild have been recognized: *C.c. carpio* in Europe, *C.c. aralensis* in Central Asia, *C.c. viridiviolaceus* in southeast Asia, and *C.c. haematopterus* in the Far East (Kirpichnikov 1999; Kholmann et al. 2005). Of these, *C.c. carpio* and *C.c. haematopterus* are supported by DNA studies (Kholmann et al. 2005).

In addition to the typical variety (*C. carpio* var. *communis*), there are two other widely recognized varieties of common carp, the mirror (*C. carpio* var. *specularis*) and leather (*C. carpio* var. *nudus*) (Pillay and Kutty 2005), which are based on mutations called N (nudity) and s (scattered scales), which appeared early in the domestication of the species and are widespread among carp populations, both captive and feral, worldwide (Kirpichnikov 1981). In addition, dozens of captive strains have been reported (Kirpichnikov 1981; Jhingran and Pullin 1985; Main and Reynolds 1993; Penman et al. 2005; Pillay and Kutty 2005; FishBase 2009). Many of these strains were produced at national hatcheries in Eastern Europe and East Asia through inter-strain crossing followed by line breeding to improve culture performance (Main and Reynolds 1993; Bakos et al. 2006) and represent improvements in growth, food conversion efficiency, and market appeal over feral populations (Gjedrem 1993).

### 3.2. Nile tilapia

Native to the Senegal, Niger, Volta, and Nile River systems and Lake Chad, Nile tilapia have been widely introduced and are now grown in 61 countries on all continents, save Antarctica, in both commercial and subsistence aquaculture systems (Lévêque 1997). Inbreeding in *oreochromiine* *tilapias* is exacerbated by male dominance behaviour that limits the number of males contributing genes to the next generation to about one-third of the actual census number when stocked in communal spawning ponds (Fessehayé et al. 2006). It is possible that partly for this reason, early attempts at mass selection showed very limited success in improving aquaculture performance (Pullin and Capilli 1988).

The first successful tilapia genetic improvement program was carried out by the WorldFish Center, which was then known as the International Center for Living Aquatic Resources Management. The program was based on a combined family selection program that resulted in increased growth rate in a composite strain comprised of eight different wild and farmed populations by 64 percent over eight generations (Khaw et al. 2008). This genetically improved farmed tilapia (GIFT) has been widely disseminated in Asia where it substantially out-performs most local strains (Asian Development Bank 2005). At the time of writing, GIFT has not been legally re-introduced to Africa (although illegal

introductions are suspected). Since the development of GIFT, a number of improved strains based on GIFT have been produced, such as the GET Excel tilapia (Philippines).

Growth comparisons have shown significant differences among both wild and captive populations and relatively low genotype-x environment interaction, indicating that lines improved under one set of culture conditions will continue to perform well in other systems (Khater and Smitherman 1988; Eknath et al. 1993; Asian Development Bank 2005). Nile tilapia are territorial and thus tend to rapidly form distinct sub-populations, a characteristic that if reinforced by long-term geographical separation has led to a certain amount of genetic divergence (Nyingi 2007). E. Trewavas (1983) recognized seven subspecies of Nile tilapia in their natural ranges: *O. niloticus niloticus*, the largest group representing populations in West Africa and the Nile River valley; *O. n. eduardianus* in Lakes Edward, Kivu, Albert, and Tanganyika; *O. n. cancelatus* in Ethiopia; *O. n. barengoensis* in Lake Baringo; *O. n. vulcani* in Lake Turkana; *O. n. sugutae* in the Sugutu River of Kenya; and *O. n. filoa* in a hot spring in the Awash River basin of Ethiopia. An eighth subspecies was proposed by S. Seyoum and I. Kornfield (1992) from Lake Tana, and, based on micro-satellite and mitochondrial DNA analyses, D.W. Nyingi (2007) proposed a ninth subspecies found in a warm water spring in the Lobo Swamp near Lake Bogoria in Kenya. Overall, heterozygosity (less than 4.5 percent) and gene polymorphism (less than 3 percent) is relatively low in Nile tilapia compared to some other fish species (Gourène and Agnèsè 1995). Nile tilapia easily hybridize with other *oreochromiines* both in the wild and in captivity, although some of these crosses produce sterile offspring or skewed sex ratios (Wohlfarth and Hulata 1983; Agnèsè et al. 1998).

Many Nile tilapia introductions were of only a small number of individuals or of limited family representation (Pullin 1988; Agustin 1999). Characteristic of how Nile tilapia genetic diversity has been managed is the case of the Bouaké research station in Côte d'Ivoire. Captured in Burkina Faso in the 1950s and transferred to the Bouaké, what was originally a pure population of *O. n. niloticus* was hybridized with other strains and species and subsequently widely distributed in Africa and elsewhere (Thys van den Audenaerde 1988). C. Adou, in R.S.V. Pullin (1988), reported transfers from Bouaké to Paraguay (1968), Sierra Leone (1970), Venezuela (1971), Brazil (1971), Bénin (1979), Guinea (1978 and 1983), Mali (1982), and back to Burkina Faso (1982). The Bouaké case is by no means singular, with many such introductions and crosses having been made over the years. Today, most research stations and private tilapia hatcheries around the world maintain and disseminate strains derived from a number of sources.

### 3.3. Atlantic salmon

Atlantic salmon are native to rivers along the northern European and American coasts from the Douro in Portugal up through the North, Baltic, and Barents seas, around to Iceland, Canada, and as far south as Long Island Sound in New York. Atlantic salmon have been eradicated from much of this original range due largely to watershed deterioration, damming, over-fishing, and pollution (Watson 1999). According to the FAO, 19 countries produced Atlantic salmon in aquaculture in 2006 (FishStat 2008).

Atlantic salmon have a particularly strong tendency towards genetic differentiation due to their anadromous homing nature (Ayllon et al. 2006). Adaptation to the special hydrology of the particular stream where Atlantic salmon hatch and pass the first part of their life cycle confers large advantages in terms of fitness (McGinnity et al. 2003). The high environmental variability in salmon streams, however, elicits comparatively high levels of genotype x environment interaction, with more heterozygous individuals generally being more flexible and fit (McCarthy et al. 2003). There is generally more genetic variability among individuals in a population than among populations (Thodesen and Gjedrem 2006). Many scientists are concerned about the risk posed to the high levels of adaptation of natural stocks by hybridization with escaped farm salmon. The latter differ substantially in both genetic profile and behaviour from their wild conspecifics (Orlov et al. 2006; Roberge et al. 2006).

The Norwegian national salmon-breeding program (AKVAFORSK) was once the world leader in Atlantic salmon improvement but has since been privatized under the name NOFIMA. The original AKVAFORSK lines were at one time used in all Atlantic salmon-farming countries (McGinnity et al. 2003). Based originally on a composite stock constructed from individuals from 40 different rivers, the lines produced by AKVAFORSK and increasingly by breeders in Chile, the United States, Canada, and the United Kingdom grow twice as fast as wild salmon and are bred for disease resistance, food conversion efficiency, age at sexual maturity, fat content, flesh colour, and other commercially important traits (Roberge et al. 2006; Thodesen and Gjedrem 2006). In addition to the AKVAFORSK strain, other farmed strains include Bolaks, Mowi, Jakta, and Rauma.

### **3.4. Tiger shrimp**

The tiger shrimp is the largest and fastest growing of the penaeid shrimps used in aquaculture and is grown in some 23 countries, mostly in the Indo-Pacific from where it originates. The tiger shrimp prefers warm water (above 12 degrees Celsius), is euryhaline, and can tolerate a wide range of salinities down to nearly fresh water (Pillay and Kutty 2005). Tiger shrimp do not normally mature in captivity. Brood animals are difficult to obtain because adults live and reproduce far out to sea (Hadil and Gambang 1999). Consequently, many farms, particularly smaller-scale ventures in Asian coastal communities, continue to rely on wild-caught post larvae that drift in close to shore for stocking (Peterson 2002).

Tiger shrimp have high genetic diversity within populations (Kumar et al. 2007), but exhibit a relatively lower degree of genetic differentiation among populations across their range (Duda and Palumbi 1999; Klinbunga et al. 2006), although in some areas this may be greater than in others (Brooker et al. 2000). There appear to be three major geographic groups: the African (western Indian Ocean), southeastern Asian and Australian (Benzie 2000; Klinbunga et al. 2001; Benzie et al. 2002). The highest genetic diversity lies in southeastern Asia with evidence of further intra-population variability (Benzie 2000; You et al. 2008). S. Klinbunga et al. (1998) estimate gene flow among these groups at 2.6 female migrants per generation. Gene flow was much higher among just the southeastern Asian populations at 5.8 female migrants per generation.

Virtually all cultured *P. monodon* derive from wild-caught broodstock (Benzie, in press), but, with the growing importance of shrimp aquaculture, increasing emphasis is being put on captive breeding and domestication, which will drive an increase in the development of farmed strains and probably a reduction in genetic diversity associated with imperfect brood stock management (Dixon et al. 2008). Z. Xu et al. (2001) found that genetic differentiation among populations in the Philippines, for example, was associated with habitat loss and the development of shrimp aquaculture. If properly managed, however, the potential for selective breeding seems excellent. Variability within populations for growth is high, with moderate to high heritability of between 0.25 and 0.55 (Benzie et al. 1997; Kenway et al. 2006). Initiatives in Hawaii, the United States, Madagascar, Australia, and Thailand have established domestication programs for *P. monodon* (Benzie, in press).

### **3.5. Pacific oyster**

Native to Japan, the Pacific oyster has been widely introduced in both the Pacific and Atlantic oceans – first to the west coast of the United States in 1910, to Australia in 1950, and to Europe and New Zealand in 1970 (Lapègue and Boudry 2006). Pacific oysters are cultured in 31 countries (FishStat 2008). Oysters are generally produced in extensive production systems that depend for food on filtering naturally available plankton from the water. Oysters release their gametes into the water column. The larvae, known as spat, are free-living for about ten days. Since much of the spat settle in calm waters, which are not particularly conducive to high growth rates, the supply of oyster seed has generally evolved separately from the grow-out phase, with most growers at least initially purchasing spat from specialized producers (Pillay and Kutty 2005).

Environmental variables, especially temperature and salinity, play a large role in determining how much spat falls, when and where (Supan and Wilson 1993). This uncertainty, along with the desire to undertake selective breeding has created an interest in captive reproduction. The economics of controlled spawning and larval rearing remain problematic (Burnell et al. 1993) to the extent that most producers continue to rely on wild seed (Pillay and Kutty 2005).

Oysters have a relatively high load of deleterious recessive genes. S. Launey and D. Hedgecock (2001) estimate that individual oyster genotypes harbour a minimum of between 8 and 14 deleterious recessive genes compared to 2.8 in mammals, 4.3 in birds, 2.8 in *Drosophila*, and 8.1 in conifers (Lynch and Walsh 1998). This high number of deleterious genes and the associated high mortality rates in larvae is compensated by the oyster's high fecundity, which, in turn, creates opportunities for generating vigorous hybrids. Oysters are also protandrous: they first achieve sexual maturity as males, with some variable number later becoming females. Sex ratios in natural populations are proportionally variable with from 1 to 40 males per female, with a majority of females being fertilized by multiple males (Lapègue and Boudry 2006), creating conditions for inbreeding and complicating brood stock management (Gaffney et al. 1992; Launey and Hedgecock 2001).

As a result of the rather random mating system and the importance of water currents in determining where spat settle, population differentiation in oysters is largely a function of physical distance of one oyster bed to another (Lapègue and Boudry 2006). Although a number of Pacific oyster varieties associated with particular areas or farms are recognized by consumers (e.g., Hama Hama, Quilcene), the genetic underpinnings of differences among these "brands" is largely unknown.

The introduction of the Pacific oyster has been associated with reduction of indigenous shellfish such as the Olympia oyster, *Ostreola conchaphila*, in Puget Sound, Washington, and the blue mussel, *Mytilus edulis* in the Wadden Sea, primarily through competition but also through hybridization as in the case of *Crassostrea angulata* on the Iberian Peninsula.

#### **4. Climate change and aquatic biodiversity**

The importance of genetic diversity to both fisheries and aquaculture stocks is clear. Flexibility and the capacity to adapt to changing environments in the wild, and to respond to selection in farmed stocks, are directly linked to allelic variation and heterozygosity. Nile tilapia and the Pacific oyster have an intrinsic tendency to inbreed and, as a result, can be particularly vulnerable, as can species such as the Atlantic salmon that have life cycles strongly oriented around a particular river system. Species such as the common carp and tiger shrimp with large and widespread wild or feral populations are less vulnerable. How the anticipated effects of climate change could erode this diversity is the subject of this section.

Changes to the hydrological cycle are likely to be the major drivers of the most negative impacts of global climate change (Molden 2007; Bates et al. 2008). Increased variability and intensity of meteorological events are foreseen, with drier droughts and deeper floods (Bates et al. 2008). River and lake levels can be expected to decline, directly imperilling or fragmenting freshwater fish populations as freshwater becomes more intensively used for agriculture and industrial and domestic purposes (Dugan et al. 2007). Massive floods may erase boundaries between watersheds, mixing species and populations and leading to extinction and loss of locally adapted populations. Changes in plankton abundance and the availability of dissolved shell-forming minerals in the oceans as a result of acidification from increased carbon dioxide levels in a warmer climate is expected to have negative consequences for marine mollusks, such as clams and oysters (Guinotte and Fabry 2008).

The construction of dams and other water control structures is a common response to both drought and floods. Such structures are built and maintained by countries relative to political boundaries rather than watersheds, and conflict is likely to increase as individual nations prioritize their own needs over those living downstream. Extraction of water, damming, and canalization have major impacts on indigenous biodiversity. Changes in the faunal composition of rivers following damming can cause

extreme damage (Craig 2000). In the case of the Columbia River in the northwest United States, salmon runs that depended on the upper reaches were completely annihilated by the construction of the Grand Coulee Dam.

Even in systems where fish do not depend on long reproductive migrations, the impacts of dams (e.g., on the Volta, Niger, and Zambezi rivers) can be profound with rapid reduction in some species and explosive growth in others (Petr 1967; Balon 1974; Lewis 1974; Silvano and Begossi 1998; Songore 2002). The fish biodiversity of the Kafue River in Zambia was reduced from 56 to 24 species following the creation of Lake Iteshi-Tezhi (Kapasa 1994). A series of dams on the Senegal River built for irrigation, domestic water, and protection against saline intrusion during the dry season eradicated 12 fish species (Bosso 1994). Changing hydrological regimes, particularly reduction of seasonal flooding as a result of increasingly regulated water flows is expected to have major implications for the fish populations of many major and minor rivers around the world (Cowx et al. 2004; Smith and Jiffry 1986; Agnèsè and Brummett 2008).

Despite radical changes in biodiversity, in some cases significant increases in overall fish biomass resulting from the transformation of a river into a lake have been recorded (de Merona and de Morais 1997), although any gains in other cases have been less clear (Balon 1974; Petr 1968; Bosso 1994).

Most of the important species for aquaculture (e.g., Nile tilapia, common carp, and tiger shrimp) prefer warmer water and may not suffer from some elevation in average temperature but may be able to increase their ranges. In contrast, the cold-water salmonids are vulnerable to the loss of glacier and snow-fed riverine ecosystems, changes in ocean temperatures and currents, abundance of predators, and the availability and location of food. Associated with increasing temperature are rising sea levels, more violent storms, and increasing frequency of toxic algal blooms, all of which threaten oyster beds (Handisyde et al. 2005).

Changes in forest cover have also been anticipated as a result of climate change. Reduction of forest cover in general has a negative impact on aquatic biodiversity. In the temperate zones, warming of rivers resulting from the removal of tree cover has dramatically reduced salmonid populations (Nagata et al. 1998). Loss of mangroves and other types of deforestation directly or indirectly related to climate change particularly reduces nursery habitat for many tropical species, including the tiger prawn for which mangroves serve as a nursery.

## **5. Conclusion: Interdependence of aquatic genetic diversity in the face of climate change**

Aquatic organisms are more dependent upon international cooperation for their management and survival than most plant and animal genetic diversity because the ecosystems in which they occur do not respect national borders. The interdependence of nations in this respect will become more obvious as rivers dry and dams are constructed in response to climate change, further fragmenting aquatic ecosystems. In the short term (geologically speaking), the overall impact of global climate change on aquatic biodiversity may be expected to be generally negative. It should be remembered, however, that even in a time of cooler and more stable climate, the basic problems of hunger, poverty, disrespect, and abuse of the environment have had a major negative impact on aquatic biodiversity, and international accords have done little to help.

Unlike plants, fish genetic diversity is not easily conserved in seed banks (Main and Reynolds 1993; Khaw et al. 2008). Preservation of wild stocks through such *ex situ* techniques as cryopreserved sperm (used in research) is costly and complicated (Thrower et al. 2004). Lines maintained on well-managed farms and in hatcheries are probably less vulnerable than wild stocks but are subject to deterioration when not properly managed (Brummett and Ponzoni 2009). Small effective population size (with the consequent genetic drift) coupled with selection may lead to a reduction in genetic variability even under a careful brood stock management regime (Doyle 1983; Agnèsè et al. 1995; Glover et al. 2004).

The vast majority of fish genetic diversity remains in the wild. *In situ* conservation is probably the only effective long-term strategy (Fishelson and Yaron 1983; Pullin 1988), but one that will nevertheless require considerable effort, expense, and international cooperation (Cowx et al. 2004). Tribunals and international consortia aimed at the preservation of global biodiversity have produced thousands of pages of transactions but have so far failed to slow the rate of aquatic species loss worldwide. Needed are a clear set of efficacious activities and objectives (Center for Hydrology and Ecology 2004).

Realistic, effective, and affordable alternatives exist for maintaining food supplies. Captive breeding, domestication, and selective breeding of indigenous species have the potential to capture and hold on to much of the most important genetic diversity for aquaculture and stock-enhanced fisheries (Abellan and Basurco 1999; Brummett 2007a). Intensive aquaculture systems are relatively efficient in terms of water and nutrients, making fish farming more competitive and compatible with other water uses (Brummett 2007b). Aquaculture-agriculture integration is also a promising alternative—an example being the intensive management of reservoirs through stocking and/or cage culture (Petr 1998; Brummett 2006a, b).

As much of the most valuable aquatic biodiversity for fisheries and aquaculture is found in less developed countries in both hemispheres, the role of international cooperation in the effort to bring more genetic diversity under human control is probably critical to success. The first step should be investments in research to identify and document existing wild genetic diversity and characterize it in terms of aquaculture potential and other traits that may be important for survival in a changing climate such as temperature and salinity tolerance, stress, and disease resistance (Handisyde et al. 2005; Allison et al. 2008). To provide sound answers to the question of how climate change will impact aquatic biodiversity and what we can do about it, we need a profound understanding of the physiology and genetics of the organisms in question – the more we know the better able we will be to respond to new circumstances. This improved knowledge has to come from more and better research. To put this knowledge to work, extension to producers of sound brood stock management and best aquaculture practices should complement national and international hatchery management programs aimed at the development and maintenance of improved lines of major cultured organisms.

Increasing the number of species under cultivation and human protection is a matter of some urgency, but conservation has value *per se*, and we should not need to argue that it may be economically useful in the future. Our aim should be to conserve all species because the alternative (to exterminate some) cannot be defended – the web of life is extremely complex and the consequences of the disappearance of a particular species are difficult if not impossible to predict, but they are likely to be negative in some way. Hence, habitat and environmental protection should be a priority. Other action areas include:

- Improved guidelines for, and control over, the transfer of aquatic organisms for culture and conservation, with particular emphasis on better systems of avoiding the concurrent movement of parasites and diseases.
- Characterization and documentation systems to manage access to aquatic biodiversity conserved either *in* or *ex situ* in one place as well as used elsewhere and to assure the proper acknowledgment of property rights.
- Systems for management of the loss of genetic diversity associated with domestication and the facilitation of regular exchange of genetic material for use in maintaining variability in both wild and captive populations.
- Strengthen and enforce water-sharing agreements with a new emphasis on environmental flows.
- Although hundreds of millions of people worldwide depend upon fisheries and aquaculture for their food and livelihoods, freshwater biodiversity is among the most threatened (Brummett 2003). Compared to crops and domesticated livestock, fish domestication and

breeding is hundreds, if not thousands, of years behind. Rapid increases in our knowledge of how to manage aquatic biodiversity for the well-being of future generations should be considered an imperative for action.

## CHAPTER VII: CONCLUSIONS

In many parts of the world, climate change rates will likely exceed the adaptive capacity of a broad range of crop and forage varieties, animal breeds, and tree populations used in agricultural production systems. The evidence with respect to the relative adaptive capacity of beneficial microbes and aquaculture species is less conclusive but points in the same direction.

This mismatch between climate change rates and adaptive capacities will require adaptations of production systems. As part of their strategies to adapt, countries will need still more “outside” sources of diversity of the same species, or new species entirely. This finding is based on the assumption that countries will seek to maintain agricultural production in areas currently being farmed. It is possible, of course, that in some areas environmental and related biotic stresses will be such that agriculture will have to be abandoned altogether. Interdependence on germplasm of crops will perhaps continue to be at higher levels than other GRFA, with existing, well documented levels of countries’ dependence on each others’ germplasm being still further augmented.

The impact of climate change *vis-à-vis* pathogenic microbes is, in some respects, the corollary of its impact on crops, forage, animals, and trees. Climate change will provide opportunities for pathogenic microbes (and their insect vectors) to thrive in parts of the world where, previously, they have had no, or only limited, impact. The effect will be to augment the dependence of countries on genetic resources from beyond their borders – in this case, as sources of genetic resistance to novel pests and diseases or to bio-control agents.

Climate change is increasing countries’ interdependence on GRFA. This increased interdependence means there will be an increased need for international movements of GRFA to meet agricultural production challenges associated with climate change. It is important for policy makers to consider the importance of these international movements of GRFA when considering options for access and benefit sharing norms.

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