



Crop Genetic Resources as a Global Commons

CHALLENGES IN INTERNATIONAL LAW
AND GOVERNANCE

EDITED BY

Michael Halewood, Isabel López Noriega,
and Selim Louafi



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For my parents, the first farmers in my life, Deane and Bill
Michael Halewood

For my inspiring educators and colleagues: Enrique, Alejandro,
Michael, Gerald, Devra, Toby, Pablo
Isabel López Noriega

For all my former colleagues at the International Treaty Secretariat
Selim Louafi

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DEMONSTRATING INTERDEPENDENCE ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

Marleni Ramirez, Rodomiro Ortiz, Suketoshi Taba, Leocadio Sebastián, Eduardo Peralta, David E. Williams, Andreas W. Ebert and Anne Vézina

Introduction

Plant genetic resources for food and agriculture (PGRFA) are strategic goods for crop breeding through farmer selection, conventional plant breeding and modern biotechnological techniques. Crop improvement enables their adaptation to biotic and environmental changes as well as the development of new foods and new uses. Currently, all countries depend in great measure on the PGRFA resources of plants domesticated, and subsequently developed, in other countries or regions for their food and sustainable agricultural development (Kloppenborg and Kleinman, 1987; Gepts, 2004). Even the world centres of crop diversity (Vavilov, 1926; Zeven and de Wet, 1982), which coincide with the centres of domestication, mostly rely on non-indigenous crop genetic resources to meet their food needs (Gepts, 2004). In her study of the regions, Ximena Flores Palacios (1998) showed that the southwest Asian centre of agricultural origin uses non-indigenous crops for 30 per cent of its production, while the Latin American and Chinese centres employ 60 per cent of their non-indigenous crops for their production. Furthermore, the new conditions that will be imposed by a changing climate will require that plant breeders and farmers have access to an even greater genetic diversity to attempt to adapt to the novel situations (Fujisaka et al., 2009).

The interdependence on plant genetic resources has been documented by looking at the pedigrees of crop varieties of worldwide importance for food security and by studying the flows of plant genetic resources. For an annotated bibliography on the subject of international pedigrees and flows of PGRFA, see the text by Christine Frison and Michael Halewood (2006). Crop varieties that are often cited to illustrate pedigree complexity include Sonalika, the most widely cultivated bread wheat variety in the world. Released in India in 1966, it has 17 generations in its pedigree, 420 parental combinations and 39 landraces, and breeders in 14 countries have contributed lines to

its pedigree (Smale et al., 1996). The Veery cultivar, which was released in Mexico in 1977, includes an even larger pedigree with 23 generations, 3,169 parental combinations and 49 different landraces.

Between 1976 and 2000, the International Center for Tropical Agriculture (CIAT) bred and distributed, upon request, 205 bean varieties to 18 countries in Latin America. In most countries, local materials contributed to these released varieties with less than 50 per cent of the ancestors. In only two countries did more than half of the ancestors come from the same countries, while in five countries more than 90 per cent of the genetic material included in the released varieties was contributed from other countries (Johnson et al., 2003).

More than 60,000 samples of germplasm were reported to be distributed annually by the gene banks of the Consultative Group on International Agricultural Research (CGIAR) (S. Gaiji, International Plant Genetic Research Institute, unpublished information cited by Fowler and Hodgkin, 2004). Such data indicate that almost all countries are net recipients of such transfers (Fowler et al., 2001). More recent data for 2007–8 indicate that most (81 per cent) of the recipients of germplasm distributed by the International Agricultural Research Centres (IARCs) are developing countries, and the rest (19 per cent) are developed countries. Within these countries, 40 per cent of the germplasm goes to the national researchers of developing countries, 13 per cent to universities, 4 per cent to private breeders and 24 per cent to other individuals and organizations (SGRP, 2009). It is notable that in the first 19 months of operating under the International Treaty on Plant Genetic Resources for Food and Agriculture's (ITPGRFA) framework, the centres distributed approximately 550,000 samples of PGRFA all over the world using the Standard Material Transfer Agreement (SGRP, 2010).¹ A quarter of the materials were PGRFA as they were originally acquired, and the other three-quarters were materials that the centres had been involved in improving.

The flow of genetic resources from the IARCs to the National Agricultural Research Systems (NARS) breeding programmes are analysed in detail in the volume edited by Robert Eugene Evenson and Douglas Gollin (2003a). The authors note that in essentially all crops and throughout all regions the continuing diffusion of modern varieties to developing countries has depended to a large degree on germplasm coming from international research centres. Crop varieties being grown by farmers as well as those used in national breeding programmes appear to be based – in part or in whole – on genetic material supplied by these international centres (Evenson and Gollin, 2003b). The flows from the IARCs, which by design rely on access to an international genetic pool for the most important crops, therefore attest to the public benefits of having access to a wide array of genetic diversity.

In addition, the advantages of cooperation for germplasm improvement and exchange were recently demonstrated in response to the spread of wheat stem rust. The race Ug99 (*Puccinia graminis* Pers. f. sp. *tritici*), which is gradually moving out of Africa towards Yemen and West Asia, is highly virulent against the stem rust resistance genes that are commonly present in wheat germplasm and that have been effective in the control of the disease for over 30 years (Njau et al., 2010). Ug99 thus posed a serious threat to wheat production worldwide. In an effort to identify the sources of

resistance, about 2,000 advanced and elite bread wheat lines from the International Centre for Maize and Wheat Improvement (CIMMYT) were evaluated in the field in Kenya from 2005 to 2007, while the seedlings were tested in St. Paul, Minnesota. This effort resulted in the identification of two race-specific resistance genes and three possibly new sources of resistance from synthetic, Chinese and other unknown origins, which represent very valuable genetic resources for breeding Ug99 resistance.

In the following pages, we present six cases that document broad interdependence on PGRFA between countries to supply their food needs and secure their access to materials for breeding and for other research. Rodomiro Ortiz and Suketoshi Taba outline maize's journey from its domestication in Meso-America to its current position as one of the primary foods of the world and how access to genetic diversity from multiple sources, including wild relatives, has allowed the crop to respond to the needs for increased grain yield, resistance to diseases and pests, and improved nutritional content. Leocadio Sebastián reminds us that rice would not have become the most important food crop in the world if it were not for germplasm exchange. Eduardo Peralta narrates the ascendance of chocho, an Andean legume, in the poorest provinces of Ecuador thanks to the availability of early materials from other countries, resulting in improved diets and sources of income for populations living in marginal conditions. David E. Williams underscores the high degree of countries' interdependence on peanut genetic resources, while Andreas W. Ebert demonstrates how access to genetic diversity is critical for developing resistance to diseases that have caused enormous losses for small-scale cacao farmers. Anne Vézina recounts the international collaboration on banana breeding that served the needs of small farmers and commercial producers and makes a call to take advantage of the multilateral system of access and benefit sharing (multilateral system) under the ITPGRFA for the benefit of banana growers, breeders and consumers.

Case 1: International dependence on maize germplasm to enhance global diets

In terms of total production, maize is the most important grain crop worldwide, at more than 800 million metric tonnes (FAO, 2010). Cultivated maize (*Zea mays* L. subsp. *mays* Iltis) was domesticated by early farmers in a region that is now occupied by southern Mexico from its wild relative teosinte (*Z. mays* ssp. *parviglumis* Iltis and Doebley) (Matsuoka et al., 2002). The direct maize ancestor was initially domesticated not for its grain but, rather, for its sugary pith (Smalley and Blake, 2003). Maize was subsequently selected for large cobs with many rows of kernels, thereby becoming an important food staple across Meso-America.

Maize was introduced to Europe with the shipments from the second voyage of Columbus and spread rapidly worldwide. Maize cultivation started in southern Spain at the end of the fifteenth century and spread to Africa in order to feed the growing numbers of slaves awaiting their transport to southwest Asia and the Americas. The multiple diversity flows from the American continent to the rest of the world served to widen the maize genetic base, which allowed additional selections to spread to all

of the other continents (Ortiz et al., 2007). Today, maize is the most widely grown crop in the world based on number of countries and agro-economic zones, and it demonstrates a great culinary adaptation to diverse cultures worldwide.

In the early decades of the twentieth century, hybrid maize was developed using inbred lines from open-pollinated cultivars of North American origin, thus initiating one of the world's most profound changes in modern agriculture (Taba et al., 2005). Likewise, many tropical maize-breeding populations, largely based on dents from Mexico and flints from the Caribbean, further led to national cultivar releases – for example, the cultivar 'Eto' in Colombia (Chavarriaga, 1966), which, in turn, was used to breed exotic germplasm to broaden the genetic base of the US corn belt (Hallauer and Smith, 1979).

In the developing world, 82–92 per cent of crop yield is lost primarily due to abiotic and biotic stresses, with 17 per cent of loss due to drought, 20 per cent to infertile soils, 5 per cent each to leaf diseases and ear rots, 10 per cent or more to stem-boring insects, 10–20 per cent to insects that attack stored grain, and 15 per cent to the parasitic weed *Striga* (CIMMYT, 2004). The next four examples illustrate where it has been absolutely essential to get access to, and to use, maize genetic resources from a variety of countries and continents to address threats to maize crops and promote food security.

Tuxpeño maize: a truly global public good

The Tuxpeño landrace, a subset of the 250 maize landraces found in the New World, combines desirable traits such as resistance to important diseases and the ability to respond to high fertility conditions with some undesirable traits such as excessive plant height and a low harvest index. In the 1970s, CIMMYT researchers reduced the height of some of the Mexican Tuxpeño landraces with the aim of achieving greater per-plant grain yield (Taba, 1997). Bred populations were shared with partners across 43 countries in Asia, Africa and Latin America (CIMMYT, 1986). Furthermore, in the early 1980s, the CIMMYT and the International Institute of Tropical Agriculture (IITA) bred maize populations derived from La Posta (a Tuxpeño landrace), which showed host plant resistance to the maize streak virus (MSV), a significant disease in sub-Saharan Africa. With a reliable screening method and appropriate sources of resistance, IB32 – a streak-resistant line that was developed from this maize-breeding population – and La Revolution, a line from Reunion Island, gave rise to more than 100 cultivars and hybrids to encompass all of the relevant farming systems and agro-ecologies in sub-Saharan Africa.

Likewise, leading up to the 1990s, cooperating national programmes released 147 cultivars and hybrids that were bred from Tuxpeño populations, which went on to be grown in approximately 3.8 million hectares worldwide. Furthermore, Tuxpeño accessions are still in the pedigrees of many CIMMYT gene pools, populations and elite lines – for example, Thai Composite 1 (later called Suwan 1), which is a downy mildew resistant cultivar bred by Thai researchers and subsequently used in global maize breeding (Sriwatanapongse et al., 1993). The US-bred germplasm BS28

and BS29 were also derived from Tuxpeño Composite and Suwan 1, respectively (Hallauer, 1994).

Use of Teosinte for host plant resistance to Striga hermonthica in sub-Saharan Africa

Striga hermonthica infests millions of hectares of arable land in Africa and limits maize, pearl millet and sorghum production throughout the continent. IITA researchers bred maize lines with host plant resistance to this parasitic weed using genetically broad-based populations (including BC4, which is derived from *Zea diploperennis* Iltis, Doebley and Guzman, from Mexico) as well as synthetics that also possess resistance to MSV (Menkir et al., 2006). The BC4 population supported little or no *Striga hermonthica* emergence as a donor parent (Kling et al., 2000). The wild accession was crossed to an adapted maize germplasm, and the resulting F1 was backcrossed four times to four adapted maize genotypes (including Suwan 1-SR, which is resistant to downy mildew and bred by Thai researchers) under artificial infestation with *Striga hermonthica* in the screen house at Ibadan, Nigeria, to form a *Zea diploperennis* BC4 population. These *Striga*-resistant maize inbred lines have been useful sources of genes for developing germplasm with host plant resistance to *Striga hermonthica* and have been adapted to the lowland and mid-altitude areas of sub-Saharan Africa, where this weed is endemic.

Insect resistance from Central America to Eastern Africa

The larger grain borer, a native insect pest of Central America, was first observed in Tanzania in the late 1970s and early 1980s. CIMMYT researchers found host plant resistance to the borer in Caribbean accessions held in trust at the centre's gene bank. Conventional plant breeding techniques such as crossing those accessions with maize adapted to Eastern Africa led to combining the resistance of the Caribbean maize with key traits valued by Kenyan maize farmers. This newly bred maize was tested for resistance at the national programme research station in Kiboko, Kenya. New maize cultivars resulting from this research will clearly benefit farmers throughout Kenya (CIMMYT, 2007).

Opaque-2 and quality protein maize: the long journey of a Peruvian gene

A naturally occurring recessive mutant gene known as *Opaque-2*, which was first observed in a Peruvian maize landrace, gives a chalky appearance to the kernels and improves the protein quality of this crop by increasing levels of lysine and tryptophan (Crow and Kermicle, 2002). Since its discovery in 1963 (Mertz et al., 1964), the trait has been transferred through careful selection and meticulous breeding to quality protein maize breeding lines and cultivars (Vasal, 2000). Today, these lines grow from Latin America eastwards and westwards, reaching farmers' fields and users throughout

sub-Saharan Africa (Krivaneck et al., 2007) and Asia (Gupta et al., 2009), respectively. This quality protein maize improves the diets of people who depend on maize as a staple and also shows promise in animal feed.

Case 2: Interdependence on germplasm exchange for rice improvement

Rice is the most important staple food crop in the world. More than half of the world's population eats rice. Rice is also the one crop whose rapid development has been very dependent on the exchange of germplasm. The Green Revolution in rice-growing countries began with the introduction of IR8, a cultivar derived from a cross between the semi-dwarf variety Degeowoogen from Taiwan with the tall variety Peta. Peta was derived from a cross between Cina from China and Latisail from Pakistan. Subsequently, many other landraces have been used by the International Rice Research Institute (IRRI), the CIAT and national breeding programmes to increase yield, improve pest and disease resistance, confer tolerance to abiotic stresses and improve grain quality and other characteristics. The wide use of landraces from different countries as a source of desired traits has contributed to the increase in rice production in most rice-growing countries.

The availability of rice germplasm from the more than 125,000 accessions held at the IRRI has enabled a great deal of screening to uncover rice lines that carry the desired traits. It is important to note that the selected landraces were only discovered after screening thousands of accessions for different traits. Such tremendous effort is exemplified by the case of rice tungro virus resistance, which was identified in only a few accessions after more than 20 per cent of the IRRI rice germplasm collection was evaluated (Jackson, 1997; Angeles et al., 2008).

The pedigrees of lines developed by the IRRI and the national programmes evidence the use of several landraces coming from within the same country as well as from other countries. Major rice growing countries such as Bangladesh, Indonesia, India, Vietnam, Philippines and Thailand are using landraces that have been developed in their own breeding programmes as well as those obtained from other breeding programmes such as the IRRI. The use of IRRI breeding lines as the sources of desired traits has served to enrich local varieties with traits that help them cope with such diseases as bacterial leaf blight and grassy stunt virus as well as pests such as brown plant hopper and green leaf hopper (Hossain et al., 2003).

In the case of 78 Philippine cultivars released from 1968 (IR8) to 1995 by three rice breeding programmes, the cultivars can be traced to a total of 57 landraces coming from the Philippines and 15 other countries: Brazil, Burma, China, India, Japan, Korea, Malaysia, Nigeria, Pakistan, Senegal, Sri Lanka, Taiwan, Thailand, United States and Vietnam (Hossain et al., 2003). The combined traits from these landraces conferred the necessary characteristics that allowed the different cultivars to cope with changing pest and disease pressures, various soil and nutrient conditions and particular regional climatic conditions (Sebastian et al., 1998). None of the landraces, however, can be considered to have had a predominating influence in the

genotype of the modern Philippine cultivars. Furthermore, molecular studies of these landraces reveal that they have come from very diverse genetic backgrounds.

Many of the improved lines that have been developed using these landraces have also spread back to many countries and have benefited thousands of farmers, including numerous rice lines developed by the IRRI that have been released as cultivars in several countries. The most widely planted rice variety in the world is IR64, which was first released in the Philippines but was subsequently released in 11 other countries. At its peak, it was estimated to have been planted over approximately 13 million hectares of land in Asia. It was most popular in Indonesia and the Philippines and was well liked by farmers for its high yield, by traders for its high milling recovery, and by consumers for its good quality as food. The pedigree of this variety comprises 20 landraces originating from nine countries: China, India, Indonesia, Japan, Korea, Philippines, Thailand, Vietnam and the United States. Another very widely planted IRRI variety is IR36, which is known as the first IR variety to be bred with multiple resistances to pests and diseases. Its pedigree includes 15 landraces coming from six countries and was released as a variety in 13 countries (Khush and Virk, 2005).

Most of the exchanged materials under the International Genetic Exchange in Rice (INGER) programme were in the form of advanced lines carrying desired traits derived from different countries. More than 48,000 nursery entries have been shipped to rice breeding programmes in 80 countries for adoptability tests or for use as possible parental material. The materials distributed include those from the IRRI breeding programmes as well as national breeding programmes nominated for inclusion in the breeding nurseries distributed by INGER. The exchange programme also facilitated the exchange of data and information on the performance of genetic materials, which has further enhanced the national and international breeding programmes.

This exchange of advanced lines has resulted in the release of more than 328 IRRI lines as varieties in 75 countries as well as many others that were used as parental lines in national breeding programmes (Khush and Virk, 2005). Many national programme entries in INGER have also been released as varieties in other countries or used as parental materials. Similar exchange and use of genetic materials has also been observed in Latin America. About 40 per cent of the approximately 300 varieties released in Latin America came from the CIAT breeding programme, and another 36 per cent came from international networks – mostly from INGER (Hossain et al., 2003). Many lines from other countries and sources (for example, materials from the Centre for Agricultural Research for Development (CIRAD)) were also released as varieties or used in national rice breeding programmes in the region (Chatel and Guimaraes, 2002).

The case of rice illustrates the great benefits of making available a wide range of genetic diversity for the benefit of humankind. The accessibility and availability of diverse sets of germplasm to rice breeders has enabled them to develop rice lines that can cope with various challenges in rice production. The reciprocal accessibility and availability of thousands of improved breeding lines has also allowed national breeding programmes to test for possible local releases or to use them as parental materials in developing locally adapted cultivars. Such activities have enabled a more rapid release of varieties as well as the development of locally adapted and improved cultivars.

Although it is difficult to attribute the reasons for the sharp increase in production, the world's production of rice has increased from about 215 million metric tonnes in 1961 to about 634 million metric tonnes in 2006 (a 296 per cent increase), while the area of land that is being harvested has increased from 115 million hectares to 154 million hectares (a 134 per cent increase) during the same period. Estimates indicate that the adoption of modern rice varieties in Bangladesh, West Bengal in India, Java in Indonesia, and Philippines and Vietnam has resulted in an average net gain of 943 kilograms of rice per hectare or about \$150 per hectare over what would have been harvested without these varieties (Hossain et al., 2003)

Future challenges will no longer be focused on meeting the increasing demand for rice but, rather, on developing ecologically sound, sustainable production systems as well as improved value chains under conditions involving less land, less water, fewer resources and the increasing effects of climate change. The need to develop varieties that can meet these challenges will require harnessing the available rice genetic resources. New traits will have to be discovered from cultivated and wild relatives, or existing traits will need to be combined in new ways to not only meet the need for increased production but also to cope with biotic (new pests and diseases or complex diseases) and abiotic (drought, flood and temperature changes) stresses, to use resources more efficiently (water and nutrients) and to meet the demand for high value rice (based on quality and speciality preferences). The new varieties will have to fit into the farming systems of the future.

Case 3: Harnessing introduced germplasm of chocho or lupin (*Lupinus mutabilis* Sweet) for Ecuador's benefit

In 1983, the first gene banks of Andean crops were established in Ecuador under the leadership of the Santa Catalina Experimental Station in Quito (INIAP, 2009). As a result of this initiative, a high percentage of the genetic variability of grains, tubers, roots and some native Andean fruits was collected. Among the first accessions to be collected were 257 accessions of Andean grain, chocho (*Lupinus mutabilis* Sweet).

Chocho or lupin is a legume that is native to the Andes of Bolivia, Ecuador and Peru. Its high protein content, which is even higher than soybeans, makes it a crop of great interest for human and animal nutrition. The National Department of Plant Genetic Resources and Biotechnology subjected the chocho collection of the Instituto Nacional Autónomo de Investigaciones Agropecuarias (INIAP) to an exhaustive morphological characterization and agronomic assessment. Many interesting traits were reported from this collection, but no early materials have been identified.

At the time, the research institutions in the Andean countries freely exchanged promising germplasm, and joint collecting trips were common practice. In 1992, as part of this cooperative framework and with the support of projects and regional and international institutions, a few sets of chocho populations from Peru and Bolivia were introduced to the INIAP and were evaluated at production locations in the Ecuadorian highlands. The best lines from this collection were stored at the INIAP gene bank. Subsequently, the gene bank material was assessed according to its

adaptability and stability in different environments, and, based on this information, the accession ECU 2659, which is native to Peru, stood out as the most promising line for its adaptability, stability, high yield, grain quality and, especially, its earliness. Whereas local genotypes are usually harvested from 11 to 14 months after sowing, these varieties are harvested six to eight months after sowing. The lengthy growing period of the local genotypes results in many more risks, including frost, hailstorms, excess rain or drought. Obviously, by reducing this period of growth, farmers could substantially reduce their risks. In 1997, the responsibility for continuing this research was transferred from the Andean Crop Programme to the National Programme for Andean Legumes and Grains, which later distributed this material of chocho in Ecuador under the name INIAP-450 Andino (Caicedo and Peralta, 1999).

By growing the INIAP-450 Andino variety, farmers were able to improve their yield substantially – from 400 kilograms per hectare for the native local varieties to 1,350 kilograms per hectare with Andino. The earliness and pleasing appearance of the new variety were also beneficial and, combined with favourable agronomic characteristics and more efficient processing, encouraged a revival of chocho cultivation and consumption, which prior to 1997 had been very marginal in the rural areas and negatively affected by social prejudice in the cities (Peralta et al., 2009a).

Thanks to various efforts in public awareness, including the involvement of local agricultural research committees and individual training, the cultivation of the variety has spread successfully throughout the highlands. At the same time, its consumption has been promoted across all economic sectors by emphasizing its nutritional values, while the development of artisanal processing at the grassroots level has been encouraged and financially supported (Villacrez and Peralta, 2006). In recent years, small family enterprises have begun to offer high-quality chocho, packaged under proper sanitary conditions. The crop has gone from a product that was marginally consumed to a quality product that has a potential market abroad.

In poor communities throughout the state of Cotopaxi, which is located in the central high-Andean zone of the country, it is estimated that over 70 per cent of farmers are growing this variety, and, as a result, the amount of cultivated land has increased significantly each year (Peralta et al., 2009b). In 1999, in the communities of Ninin Cachipata and Chaluapamba, two families began to grow INIAP-450, and, today, this number has grown to 96, out of a total of 120 families. In the provinces of Chimborazo and Bolivar, the cultivation of this variety was re-started, and in three southern states of the country its consumption and cultivation was also introduced. In addition, four agro-industrial enterprises are producing high-quality chocho both in the form of processed branded products as well as the raw material that is of a very uniform quality (one of them uses only INIAP technology). Such production capabilities have enabled them to offer the product in different presentations and in places ranging from small bars to large food chains.

The chocho INIAP-450 Andino variety took Ecuador by storm. This case highlights the importance of having access to pooled materials from several countries to help in the search for varieties that may respond to local needs. Without access to precious chocho materials from neighbouring countries, this project would not have

been possible. Today, INIAP-450 Andino and chocho cultivation and consumption have become emblematic of what is possible in the agricultural sector in the poorest and most marginal provinces of Ecuador.

Case 4: Worldwide interdependence on peanut genetic resources (*Arachis* spp.)

The peanut or groundnut (*Arachis hypogaea* L.) is the most widely cultivated grain legume in the world, with current annual production in excess of 35 million metric tonnes (FAO, 2010). The peanut's high protein (approximately 25 per cent) and oil (approximately 40 per cent) content make it a highly nutritious, easily processed and widely accepted food for millions of small-hold and subsistence farmers throughout the tropics.

It is postulated that the cultivated peanut originated about 7–8,000 years ago in the semi-arid region that is now southeastern Bolivia and northwestern Argentina. The cultigen is probably the result of a fortuitous naturally occurring hybridization event between two wild species of *Arachis*, giving rise to a larger, more vigorous species (*A. hypogaea* L.) that was subsequently propagated and ultimately domesticated by incipient Amerindian agriculturalists (Smartt, 1985). Over the next several millennia, an impressive amount of cultivated peanut diversity was generated as the crop was widely disseminated throughout the neotropics where it adapted to the different geographic, climatic and agricultural contexts in which it was grown by countless different ethnic groups.

The breadth of diversity within the cultivated peanut species is reflected in its infra-specific taxonomic classification (Krapovickas and Gregory, 2007). *Arachis hypogaea* is divided into two clearly distinguishable subspecies. The first (ssp. *hypogaea*) has a somewhat prostrate growth habit, with its branches often trailing along the ground, a long growth cycle and is often higher yielding; while the second (ssp. *fastigiata*) has a distinctly upright growth habit, a shorter growth cycle and tends to be more drought tolerant. The first subspecies is made up of two distinct botanical varieties, and the second subspecies is comprised of four botanical varieties. Furthermore, within each of these six botanical varieties, there are dozens of different local varieties, or 'landraces', each with unique traits and qualities. The result when viewed together is a colourful riot of different peanut shapes, sizes, seed colours, plant types and agronomic characteristics that few people other than peanut researchers have ever seen or imagined.

The great Columbian exchange that began in 1492 initiated the peanut's rapid diffusion to and widespread adoption in Africa, Asia and the Pacific and eventually to North America (Williams, 2004). Today, peanut production on other continents has far surpassed that of its South American home, and it now plays a more important role in the traditional diets of Asia, Africa and North America than it ever did in its region of origin. China, India and the United States are currently the three largest peanut-producing countries in the world. During the last three decades, improved peanut varieties developed in the United States and India have become widely adopted in Asia, Africa and Latin America, underscoring the pronounced global interdependence on *Arachis* genetic resources.

Nevertheless, the greatest concentration of peanut genetic diversity – including its related wild species – continues to survive in the fields of small-scale farmers and in unprotected natural areas in South America. The genetic diversity present within the cultivated peanut represents a wealth of options to better respond to the changing needs and preferences of peanut farmers, breeders and consumers. The important diversity of cultivated peanuts is complemented and greatly enriched by the even broader range of genetic diversity contained in the crop's wild relatives. Experts estimate that the genus *Arachis* comprises around 100 wild species, 80 of which are described, several more are in the process of being described and another dozen or so are believed to exist but remain undiscovered (Krapovickas and Gregory, 1994, 2007; Valls and Simpson, 2005). The wild species of *Arachis* are endemic to the grasslands and open-forested areas of lowland Bolivia, northwestern Argentina, Paraguay, Brazil and Uruguay. Of these wild species, around 30 are considered to be closely related to the cultivated peanut and therefore can serve as important sources of resistance to drought, pests and diseases for breeders, using conventional cross-breeding techniques without having to resort to genetic transformation.

Modern peanut-breeding efforts rely heavily on the large international peanut germplasm collections maintained by the International Crop Research Institute for the Semi-Arid Tropics (ICRISAT) and the National Plant Germplasm System in India, the US Department of Agriculture in the United States, the Agricultural Research Corporation in Brazil, the Instituto Nacional de Tecnología Agropecuaria in Argentina, and the Chinese Academy of Agricultural Sciences. These important collections contain thousands of accessions of landrace materials, high-yielding improved varieties, experimental breeding lines and wild relatives, and they each have some unique accessions of peanuts collected from a different region of the world that are not duplicated anywhere else. However, these great collections do not hold all of the answers to our breeding needs because, even when considered together, the current gene bank collections do not yet have a representative sampling of the full scope of existing peanut diversity. Significant gaps remain to be filled by collecting missions before the full spectrum of peanut diversity can be known, studied and protected and before peanut breeders can have access to a safe and comprehensive source of the genetic resources they need to develop improved peanut varieties for the future.

Peanut breeders have already made use of peanut diversity obtained from many countries to produce agronomically and commercially successful improved varieties (Isleib and Wynne, 1992). Inter-subspecific hybrids are routinely employed to take advantage of the earliness of one subspecies combined with the higher-yielding qualities of the other. Through a complicated and painstaking process involving thousands of hand pollinations over a period of many years, conventional breeding techniques have been successfully employed to introduce nematode resistance from a wild *Arachis* species from Bolivia into a commercially acceptable peanut variety known as COAN, which has effectively solved a serious pest problem that had been plaguing peanut growers across a large area of southwestern United States (Simpson, 2001). Subsequently, other improved varieties have been released, building upon the nematode-resistance of

COAN, which are suited to the particular growing conditions of southeastern United States and elsewhere (Holbrook et al., 2008). Work at ICRISAT, where the world peanut collection of over 12,000 accessions is held, includes a peanut breeding programme that actively seeks out traits from South American landraces and wild species for breeding improved varieties that are better suited to the needs of peanut farmers in Africa and Asia. As part of a collaborative research programme between Bolivia and the United States, Bolivian peanut landraces of interest were made available to US researchers, while advanced breeding lines of improved US varieties with traits suitable for the Bolivian market and growing conditions are being evaluated in Bolivia for their potential for large-scale production (Peanut Collaborative Research Support Program, 2007).

Another important use of wild *Arachis* species is as forage, pasture, soil conservation and ornamental groundcover crops. Two species, *A. pintoii* and *A. glabrata*, which are both native to Brazil, have already been improved through selection, and commercial varieties of these species are now cultivated extensively in Australia, Central America, the United States and Africa. Sometimes referred to as ‘tropical alfalfa’, these ‘forage peanuts’ are valued for their vigorous growth, palatability for livestock, high protein content and tolerance to high temperatures – all traits that suggest their enormous potential for improving pastures and increasing livestock productivity in the tropics.

Drought tolerance is a general characteristic of the peanut, and valuable sources of resistance can be found in unimproved peanut landraces and closely related wild species, many of which have evolved in areas that are extremely arid during much of the year. This particular trait will be especially important as different crops and new varieties are sought that will provide viable alternatives to farmers and farming nations worldwide as they are faced with production constraints associated with climate change.

The global interdependence on peanut genetic resources is abundantly evident, perhaps even more than in most other crops. There are, however, two main obstacles that hinder the present and future exchange and use of peanut genetic resources. The first is that the peanut is not currently on the Annex 1 list of crops covered by the multilateral system of the ITPGRFA. This omission needs to be corrected as soon as possible to ensure that these globally important genetic resources can benefit from the same legal protection and facilitated access afforded by the multilateral system to the world’s most important crops. Although the *Arachis* collection held by ICRISAT is subject to the terms and conditions of the multilateral system, thanks to the agreements between ICRISAT and the Governing Body of the ITPGRFA under Article 15 of the Treaty, this collection still lacks good representative coverage in some regions of known peanut diversity, particularly in regard to landrace materials and wild peanut species from South America. This situation is due in part to strict quarantine regulations in India (where ICRISAT’s *Arachis* collection is located) that make it difficult to import germplasm from South America. Consequently, many unique accessions of both wild and cultivated *Arachis* are conserved *ex situ* only by national programmes in the Americas. The other main obstacle involves the extremely precarious state of conservation of wild *Arachis* species in their natural habitat where they are seriously threatened with extinction due to habitat destruction caused by the

massive expansion of soybean cultivation, cattle ranching, urbanization and climate change (Jarvis et al., 2003). Many wild *Arachis* species are notoriously difficult to maintain in *ex situ* gene banks, and, as mentioned earlier, some wild species have yet to be discovered while many others have been scarcely collected.

Case 5: Searching for disease resistance in cacao (*Theobroma cacao* L.) in the gene bank of the Tropical Agricultural Research and Higher Education Centre (CATIE)

Latin America is the centre of origin and domestication of cacao (*Theobroma cacao* L.), which was introduced to Meso-America from South America in prehistoric times (Motomayor et al., 2002) and has been traded as far as North America since pre-Columbian times (Crown and Hurst, 2009). Cacao cultivation started in the lowlands of Mexico 2,000 years ago (Cope, 1976). It is a perennial crop cultivated in agroforestry systems under the shade of timber or fruit trees and, hence, is beneficial for the protection of tropical environments. Moreover, cacao has enormous socio-economic value as it is primarily cultivated by small-hold farmers worldwide and more than 20 million people depend directly on it for their livelihood.

Unfortunately, cacao is not included in the list of Annex I crops covered by the multilateral system of the ITPGRFA. By signing an agreement with the Governing Body of the Treaty, however, CATIE and the Cocoa Research Unit (hosted by the University of West Indies in Trinidad) have placed the international collections of cocoa germplasm that they maintain under the auspices of the ITPGRFA under the mandate of the multilateral system and have committed to make them available according to the Treaty. However, these two international gene banks conserve only a portion of the existing diversity of cacao, much of which is in national gene banks and in farmers' fields. To facilitate scientific cooperation and knowledge sharing aimed to optimize the conservation and use of cacao genetic resources, a global network entitled CacaoNet was established in 2006 (Engels, 2006).

About 30 per cent (810,000 metric tonnes) of the world's cacao production is lost every year due to three major diseases: (1) 'witches broom' caused by *Moniliophthora* (= *Crinipellis*) *perniciosa*; (2) frosty pod rot caused by *Moniliophthora roveri*; and (3) black pod disease caused by *Phytophthora palmivora* and/or *P. capsici* (Guiltinan, 2007). Among these three pathogens, frosty pod rot is the most devastating since it can lead to the abandonment of cacao cultivation. Frosty pod, which is believed to have originated in northeastern Colombia, has spread to ten countries over a period of 200 years. Starting in Colombia in 1817, damage was reported in Ecuador in 1917 and in Venezuela in 1941 (Phillips-Mora, 2003). In 1956, frosty pod rot was reported in Panama and subsequently spread to Costa Rica in 1978, Nicaragua in 1979, Honduras in 1997 and Guatemala in 2002. In 2004, the disease was detected in Belize and in 2005 it was detected in Mexico (Phillips-Mora et al., 2006a) where it destroyed up to 80 per cent of cacao production in infected areas.

Cultural practices and plant protection measures to combat the pathogen are inefficient and costly, and, hence, small-scale farmers generally abandon their cacao fields once the

disease has spread, leading to huge harvest losses. The most economic and long-lasting solutions are resistant cacao cultivars that reduce the need for chemical treatments, thus rendering cacao production once again attractive for farmers and beneficial for the environment.

The cacao breeding programme undertaken by CATIE extensively evaluated the international cacao collection comprising in 2006 of a total of 942 accessions of different origins (Phillips-Mora et al., 2006b). This programme aimed at identifying genotypes with high productivity, resistance to frosty pod rot and black pod disease and outstanding industrial quality. Tolerance to frosty pod rot is a rare trait, as only five genotypes out of over 600 accessions evaluated showed resistance. These five genotypes were acquired from diverse sources: UF-273 and UF-712 from Costa Rica in 1960; EET-75 from Ecuador between 1965 and 1966; ICS-95 from Trinidad in 1959; and PA-169 from Peru in 1961.

Recent breeding results are very promising as numerous superior genotypes have been developed, whose industrial quality is being evaluated in collaboration with international chocolate manufacturers. The best genotypes of the CATIE breeding programme were established in clonal gardens for multiplication and subsequent validation in multilocational trials under a wide range of agro-ecological conditions in different regions of Latin America.

Testing started in Costa Rica in 2005 with the transfer of elite material to cacao farmers in different strategic locations. With the introduction of a regional cacao project for Central America in 2007, a massive multiplication and dissemination process began, which was aimed at assisting at least 2,500 indigenous families and small-scale farmers in six countries (Panama, Costa Rica, Nicaragua, Honduras, Belize and Guatemala). Five clonal gardens of one hectare each were established in these countries for local multiplication of the planting material, thus avoiding the cost of long distance transportation of the grafted plants. Five superior frosty pod rot resistant breeding materials were selected for multiplication, together with three outstanding local and/or international cacao lines and four lines that will serve as rootstock. In addition, 22 superior lines, the majority of which are frosty pod rot resistant, will be validated alongside ten locally selected and/or international varieties in multilocational trials in these countries.

The CATIE breeding programme is also sending frosty pod rot resistant lines to national breeding programmes in Nicaragua, Honduras, Mexico, Trinidad, Ecuador, Peru and Brazil as well as to the Intermediate Cocoa Quarantine Facility at the University of Reading in the United Kingdom for disease testing and subsequent worldwide distribution if found safe.

The accelerated dissemination of frosty pod rot in Central America in recent years suggests active human participation. If the disease was to spread to Africa and Asia, which are the main production areas of cacao, the livelihood of tens of thousands of poor farmers would be at risk and the entire chocolate industry worldwide would be threatened. The deployment of frosty pod resistant genotypes to Africa and Asia, through the Intermediate Cocoa Quarantine Facility at the University of Reading, could ensure that these countries could cope with the possible arrival of the

devastating disease, without suffering the enormous production losses experienced in Central America.

The successful completion of the breeding programme at CATIE would not have been possible without easy access to its international germplasm collection, composed of numerous valuable genotypes from different Latin American countries. The dissemination of superior genotypes developed by this and other breeding programmes has enabled cacao producers worldwide to cope with major disease threats, providing substantial benefits to small-hold farmers, the chocolate industry, consumers and the environment.

Case 6: The importance of accessing *Musa* genetic resources for Latin America and the Caribbean

Bananas originate from the tropical and sub-tropical humid forests that extend from India to Papua New Guinea. Domestication of its seedy fruits is believed to have started more than 7,000 years ago with the selection by farmers of fruits with more pulp than seeds (Denham et al., 2003). Dispersal from the centre of origin resulted in the development of additional groups of bananas arriving in Polynesia between 3,500 and 4,500 years ago (De Langhe and De Maret, 1999) and to East Africa 4,500 years ago where they diversified into East African highland bananas and plantains in west and central Africa (Lejju et al., 2006). Introduction to the Americas happened much later and has not resulted in the evolution of significant diversity since most domesticated varieties are, for all practical purposes, sterile, and genetic diversity is generated by occasional, naturally occurring mutations. The Portuguese brought the banana from West Africa to the Canary Islands some time after 1402, and they were later transported on the ships sailing to the New World during the Spanish conquest (Simmonds, 1966). Plantains were introduced to the Americas via the Caribbean in the seventeenth century and are now widely grown for local consumption.

Bananas are a staple in many developing countries.² The major banana-growing regions of the world – Latin America and the Caribbean, Asia-Pacific and Africa – each produce about one-third of the annual production, which was estimated at 95 million metric tonnes in 2009 (FAO, 2010). The majority of producers are small-hold farmers who grow the crop for either home consumption or for local markets. Only about 15 per cent of the global production is exported. Even in Latin America and the Caribbean, which produce most of the bananas for the export market, only 30 per cent are exported.

Bananas are unusual among major crops in that most of the types grown, either for export or local consumption, are farmer-selected varieties rather than improved hybrids produced by breeding programmes. Current banana-breeding efforts are inadequate to address the scale of the problems faced by small-hold producers. Meanwhile, the genetic base on which solutions to these problems depend – either through genetic improvement or a better use of diversity in production systems – is being eroded (Karamura and Mgenzi, 2004; Sharrock and Frison, 2004). Market forces, in particular, have encouraged small-hold farmers to focus on the commercial

varieties, leading to the loss of traditional cultivars and, thus, making the crop even more vulnerable to pests and diseases.

Although a significant share of the crop's gene pool is conserved in gene banks, the coming into force in 1993 of the Convention on Biological Diversity and the concurrent uncertainty and politicization of issues surrounding genetic resources has severely limited the acquisition of new materials, especially of wild *Musa*.³ The situation is especially challenging for Latin American and Caribbean countries, which are dependent on banana genetic resources from beyond their borders.

The commercial potential of bananas was first exploited in Central America and the Caribbean. By the 1900s, the market was increasingly reliant on the dessert variety Gros Michel, and this variety was planted over a widespread area, thereby creating a favourable environment for the spread of diseases. Indeed, a disease caused by a fungus thought to have originated in Southeast Asia was reported in Panama in 1890 (Simmonds, 1966). By 1930, Fusarium wilt, or Panama disease, had spread to Costa Rica, Surinam, Honduras, Guatemala and Jamaica. Since the soil-dwelling fungus cannot be controlled with chemical pesticides, the only way to grow susceptible cultivars such as Gros Michel on a large scale was to clear forests to set up new plantations and move on as soon as the disease arrived.

Panama disease triggered the first breeding efforts to produce a disease-resistant Gros Michel-like export banana. In the 1920s, breeding programmes were started in Trinidad and Jamaica by the British government and in Panama by the United Fruit Company, which was later moved to Honduras (Rowe and Richardson, 1975). Progress to produce a disease-resistant Gros Michel variety using pollen from wild bananas resulted in inferior progenies. Breeders then decided to concentrate on breeding 'improved' male parents that possessed both disease resistance and good agronomic characteristics (Rowe and Richardson, 1975). Meanwhile, the banana companies had solved their Panama disease problem by switching to Cavendish varieties that were resistant to the disease, although they are susceptible to other pests and diseases that could be controlled using chemical pesticides. By the beginning of the 1980s, with no new commercial cultivars in sight, the main breeding programmes were facing closure. At the same time, donors were considering creating an independent networking organization to encourage cooperation at the international level regarding, among other things, the safe exchange of *Musa* germplasm for the development of disease-resistant varieties (Nestel, 1984).

Progress towards international cooperation was made when the International Network for the Improvement of Bananas and Plantains (INIBAP) was created in 1985. One of its first actions was to establish a collection of *Musa* germplasm at the International Transit Centre (ITC) in Leuven, Belgium. It addressed quarantine issues by setting up virus indexing centres to screen germplasm and started channelling financial support to the Fundación Hondureña de Investigación Agrícola (FHIA). The FHIA soon delivered disease-resistant hybrids, many of which, along with improved male parents, are available for international distribution through the ITC. In 1994, the International *Musa* Germplasm Collection at the ITC became part of the international network of *ex situ* gene banks following the signature of an agreement

between Bioversity International, which INIBAP had joined, and the Food and Agriculture Organization (FAO).

However, the legal and policy uncertainties surrounding the access to genetic resources has led several countries to withhold the export of PGRFA, inaugurating a period of drastically reduced access to *new* germplasm for subsequent global distribution, even after the adoption of the ITPGRFA in 2001. The ITC was not exempted. The number of accessions acquired in the last few years has been reduced to nearly zero except for African cultivars (Vézina, 2008). Meanwhile, over the same period of time, the number of samples from the ITC's existing collection that have been distributed around the world for research, field evaluation and breeding purposes has risen dramatically.

The genetic pedigree of the FHIA hybrids (the most important improved varieties currently being distributed internationally) demonstrates the importance of being able to draw upon a wide range of genetic resources and the value of sharing resources across regions. For example, Jonathan Robinson (2000) traced the genetic resource history that led to the making of FHIA-03, a cooking banana bred by Phillip Rowe and Franklin Rosales, as part of an exercise to examine the impact of genetic resources. In total, some 14 crosses involving 11 wild types and two triploid landraces took place to bring about FHIA-03. Crosses between four wild types from Papua New Guinea, Java, Malaysia and the Philippines gave birth to a vigorous diploid (SH-2095), which produces large bunches weighing up to 30 kilograms. SH-2095 is a parent of many of the FHIA varieties.

Although the FHIA hybrids are highly productive and disease-resistant, and tens of thousands of plantlets of these varieties have been distributed to farmers through various projects in Latin America, Africa and Asia, the factors that favour adoption are still not fully understood. In Tanzania, growing FHIA banana hybrids substantially and significantly reduced expected yield losses from pests and diseases (Nkuba et al., 2006). Furthermore, since hybrid cultivars yield larger bunches, fewer plants are required to meet the consumption needs of the household, leaving more land available for the production of other crops or pasture. In Uganda, however, adoption rates have been lower, perhaps because of the differences in the severity of pest and disease pressures, the cooking qualities of the hybrids and the dissemination strategies that are being used (Nkuba et al., 2006).

The most enthusiastic adoption of the FHIA's hybrids has been in Cuba, with more than 14,000 hectares planted since 1991. This enthusiastic adoption came about at a time when the cost of controlling black leaf streak disease on the Cavendish varieties had quadrupled, shortly after the arrival of the disease on the island (Perez Vicente et al., 2003).

In the meantime, public sector support for the FHIA ended in 2004, and the banana breeding programme is back to being funded by commercial interests, with its objectives more aligned with the needs of the export industry and its products no longer readily available for distribution to small-hold farmers and public sector research programmes. Other programmes that have been established by other organizations, such as the Agricultural Research Corporation in Brazil, are continuing to produce hybrids for small-hold farmers, but despite the fact that these efforts are

being made by the public sector their efforts are essentially targeted towards serving national producers. Still, the main factor limiting the anticipated benefits of future breeding efforts is access to PGRFA. For example, the demand for varieties that are tolerant to cold, excessive moisture or drought in order to help banana growers cope with climate change or increase the amount of arable land is unlikely to be met unless more wild species are collected and conserved in gene banks. One of the priorities of the ITC is to boost its holding of wild species so that the benefits that could be derived from them are spread more widely.

Concluding remarks

The cases reviewed in this chapter amply demonstrate the importance of access to as broad a range of diversity of PGRFA as possible to respond to the needs of farmers. They constitute a compelling argument in favour of a system that guarantees access to a wide range of germplasm to overcome the food, nutrition and livelihood constraints faced by tens of thousands of small-scale farmers and their families. It is expected that the increased use of molecular tools will lead researchers to make even greater use of the diversity available in wild and cultivated crops in improving crop varieties, thus strengthening the case for the need to improve the availability and accessibility of genetic resources (Hajjar and Hodgkin, 2007).

The multilateral system of the ITPGRFA provides the legal framework within which genetic resources of the most relevant crops and forages (many of which are already included in vast *ex situ* collections) can be virtually ‘pooled’ and accessed and used for the purposes of training, research and breeding for food and agriculture. The multilateral system also includes mechanisms for sharing benefits associated with the use of genetic resources accessed from the system. The criteria for crops or forages to be included in the Treaty’s multilateral system include their importance to ‘food security and interdependence’ (Article 11.1).

All six of the crops examined in this chapter are important for food security, and each of them is greatly depended upon by their countries. (The number of countries interdependent on lupin are clearly fewer, and all are located within the same region.) Yet three of these crops – peanuts, lupin and cacao – are not included in the ITPGRFA’s multilateral system. The case of lupin (chocho), which is a locally important crop in the Andean subregion, shows how a national programme can make use of materials obtained through collaborative collecting beyond its frontiers in order to undertake important research on its own. The authors of the sections on cacao and peanuts, which are both crops of worldwide importance, warn us that much-needed research on these crops can be hindered by the lack of facilitated access to their genetic diversity. Subsequent chapters in this book illustrate how it came to be that some of these important crops were not included in the Treaty’s multilateral system. Politics, rather than the significance of these crops for food security and interdependence, has led to this outcome. There are clearly scientifically sound arguments to make – regardless of whether or not there is political will to make them – that these crops, and others like them, should be included in the multilateral system.

The ITPGRFA and its multilateral system are components of the global system of conservation and use of PGRFA as envisaged by the FAO. The multilateral system is under implementation, and although there is still quite a way to go it remains the best hope to deal with the challenges of increasing productivity in a sustainable manner by expanding the use of agricultural biodiversity. At its heart lies the principle of access to the broadest range of crop diversity.

Notes

- 1 International Treaty on Plant Genetic Resources for Food and Agriculture, 29 June 2004, www.planttreaty.org/texts_en.htm (last accessed 30 March 2011). Standard Material Transfer Agreement, 16 June 2006, <ftp://ftp.fao.org/ag/agg/planttreaty/agreements/smta/SMTAe.pdf> (last accessed 30 March 2011).
- 2 Here we are using the term banana broadly to encompass both dessert and cooking varieties that belong to the genus *Musa*.
- 3 Convention on Biological Diversity, 31 I.L.M. 818 (1992).

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