



Chapter 1

The state of diversity

1.1 Introduction

Chapter 1 of the first SoW report described the nature, extent and origin of genetic diversity between and within plant species, the interdependence among countries with respect to their need for access to resources from others and the value of this diversity, especially to small-scale farmers. This chapter updates the information provided in the first SoW report and introduces a number of new elements. It seeks to place PGRFA in the wider context of changing food production and consumption patterns and it summarizes what is known with regards to changes in the state of diversity in farmers' fields, *ex situ* collections and protected and unprotected natural areas across the globe. It provides an updated review of the status of genetic vulnerability and of the interdependence among countries and regions in the conservation and use of PGRFA. Furthermore, new information is provided on indicators of genetic diversity and on assessment techniques. The chapter ends with a summary of major changes that have taken place since 1996, and a list of gaps and needs for the future.

Since the first SoW report was published, certain trends have become more visible and new trends have emerged. Globalization has had a growing impact, food and energy prices have risen, organic foods have become increasingly popular as well as economically attractive and the cultivation of genetically modified (GM) crops has spread widely, although not without opposition. Investment in agricultural research, both in developed and developing countries has continued to show high economic rates of return, not least through the development and deployment of new crop varieties. Food security continues to be a worldwide concern and is likely to remain so for the foreseeable future as the world population continues to expand, resources become scarcer and pressure mounts to develop productive land for alternative uses. Climate change is now widely considered to be unavoidable. All these factors can be expected to have had an effect on the state of diversity in farmers' fields.

The development of new varieties and cropping systems adapted to the new environmental and socio-economic conditions will be crucial in order to limit

yield losses in some regions and to take advantage of new opportunities in others (see Section 4.9.5).^{1,2,3} In many areas of the world, crop yields have started to plateau or even decline as a result of environmental degradation, increasing water and energy shortages and a lack of targeted investment in research and infrastructure (see Chapter 8).⁴ Facing these challenges will require an increased use of genetic diversity, resulting in an increasing demand for novel material from the world's genebanks.

1.2 Diversity within and between plant species

Only a few of the country reports contain data that allow a direct and quantitative comparison of changes in the status of diversity within and between crops in the period since 1996. Furthermore, where quantitative comparisons have been included, these mainly concern the number of released varieties or changes in crop acreages, both of which are only very indirect indicators of change in genetic diversity in farmers' fields. However, it seems clear that on-farm management initiatives have expanded in the past decade as the scientific basis of such work has become better understood and appropriate methodologies developed and implemented. The linkages between those primarily concerned with on-farm management of PGRFA and those involved in *ex situ* conservation and use have also become stronger, although in many ways the two sectors remain compartmentalized. The continued growth of *ex situ* collections and the increased inclusion of threatened genetic diversity within them is a positive trend, although backlog in regeneration and over-duplication continue to be areas of concern. No quantitative data were provided in the country reports on the changing status of CWR, but several countries reported on specific measures that had been undertaken to promote their conservation. Finally, there is evidence that public awareness of the importance of crop diversity, especially of formerly neglected and underutilized species such as traditional vegetables and fruits, is growing both in developing and developed countries.

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1.2.1 Changes in the status of on-farm managed diversity

Throughout most of the developed world, industrialized production now supplies the majority of food. Modern breeding has resulted in crop varieties that meet the requirements of high-input systems and strict market standards (although there is also limited breeding work aimed at low-input and organic agriculture). Strong consumer demand for cheap food of uniform and predictable quality has resulted in a focus on cost-efficient production methods. As a result, over the last decade multinational food companies have gained further influence and much of the food consumed in industrialized countries is now produced beyond their national borders.⁵ This pattern of food production and consumption is also spreading to many developing countries, especially in South America and parts of Asia,⁶ as incomes rise in those regions.

However, in spite of this trend, a substantial portion of the food consumed in the developing world is still produced with few, if any, external chemical inputs and is sold locally. Such farming systems generally rely heavily on diverse crops and varieties and in many cases on a high level of genetic diversity within local varieties. This represents a traditional and widespread strategy to increase food security and reduce the risks that result from the vagaries of markets, weather, pests or diseases. Through the continuing shift from subsistence to commercial agriculture, much of the diversity that still exists within these traditional systems remains under threat. The maintenance of genetic diversity within local production systems also helps to conserve local knowledge and vice versa. With the disappearance of traditional lifestyles and languages across the globe, a large amount of knowledge about traditional crops and varieties is probably being lost and with it much of the value of the genetic resources themselves, justifying the need for greater attention to be paid to the on-farm management of PGRFA. The concept of agrobiodiversity reserves has gained currency in this context. These are protected areas whose objective is the conservation of cultivated diversity and its associated agricultural practices and knowledge systems.

Over the last decade, promoting and supporting the on-farm management of genetic resources, whether in farmers' fields, home gardens, orchards or other cultivated areas of high diversity, has become firmly established as a key component of crop conservation strategies, as methodologies and approaches have been scientifically documented and their effects monitored (see Chapter 2). Having said this, it is not possible from the information provided in the country reports to make definitive statements about overall trends in on-farm diversity since 1996. It seems clear that diversity in farmers' fields has decreased for some crops in certain areas and countries and the threats are certainly getting stronger; but, on the other hand, other attempts to rigorously measure changes in crop genetic diversity in published literature have not yielded the expected evidence of erosion. This issue will be dealt with in more detail in Section 1.3.

Participatory plant breeding (PPB) has become more widely adopted as an approach to the management of diversity on farm, with the objective of both developing improved cultivars and conserving adaptive and other traits of local importance. It provides a particularly effective linkage to both *ex situ* conservation and use. More information on the status of PPB is given in Section 4.6.2.

1.2.2 Changes in the status of diversity in *ex situ* collections

As reported in Chapter 3, the total number of accessions conserved *ex situ* worldwide has increased by approximately 20 percent (1.4 million) since 1996, reaching 7.4 million. It is estimated, however, that less than 30 percent of this total are distinct accessions (1.9-2.2 million). During the same period, new collecting accounted for at least 240 000 accessions and possibly considerably more (see Chapter 3). Major trends can be inferred by comparing the current state of diversity of a set of well-documented *ex situ* collections with that pertaining to the time when the first SoW report was produced. To that end, data on 12 collections held by the centres of the CGIAR and the Asian Vegetable Research and Development Centre (AVRDC) as well as 16 selected collections held

TABLE 1.1
Comparison between the collections maintained by AVRDC and the CGIAR centres in 1995 and 2008

Centre ^a	1995 (no.)			2008 (no.)			Change (%)		
	Genera	Species	Accessions	Genera	Species	Accessions	Genera	Species	Accessions
AVRDC	63	209	43 205	160	403	56 522	154	93	31
CIAT	161	906	58 667	129	872	64 446	-20	-4	10
CIMMYT	12	47	136 259	12	48	173 571	0	2	27
CIP	9	175	13 418	11	250	15 046	22	43	12
ICARDA	34	444	109 223	86	570	132 793	153	28	22
ICRAF	3	4	1 005	3	6	1 785	0	50	78
ICRISAT	16	164	113 143	16	180	118 882	0	10	5
IITA	72	155	36 947	72	158	27 596	0	2	-25
ILRI	358	1 359	13 470	388	6	18 763	0	28	39
INIBAP/Bioversity	2	21	1 050	2	1 746	1 207	0	10	15
IRRI	11	37	83 485	11	23	109 161	0	5	31
WARDA	1	5	17 440	1	39	21 527	0	20	23
Total	494	2 813	627 312	612	3 446	741 319	24	23	18

Sources: Individual genebanks; System-wide Information Network for Genetic Resources (SINGER) Web site 2008; WIEWS 1996, 1995 data for IITA and ICRAF are from SINGER CD 1997. Undetermined genera were not counted.

^a Asian Vegetable Research and Development Centre (AVRDC); Centro Internacional de Agricultura Tropical (CIAT); Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT); Centro Internacional de la Papa (CIP); International Centre for Agricultural Research in the Dry Areas (ICARDA); International Centre for Research in Agroforestry [now the World Agroforestry Centre] (ICRAF); International Crops Research Institute for the Semi-Arid Tropics (ICRISAT); International Institute of Tropical Agriculture (IITA); International Livestock Research Institute (ILRI); International Network for the Improvement of Banana and Plantain, (INIBAP); International Rice Research Institute (IRRI); West African Rice Development Association [now the Africa Rice Centre - AfricaRice] (WARDA).

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TABLE 1.2
Comparison between the collections maintained by selected national genebanks in 1995 and 2008^a

Country	Genebank	1995 (no.)			2008 (no.)			Change (%)		
		Genera ^b	Species	Accessions	Genera	Species	Accessions	Genera	Species	Accessions
Brazil	CENARGEN	136	312	40 514	212	670	107 246	56	115	165
Canada	PGRC	237	1 028	100 522	257	1 166	106 280	8	13	6
China	ICGR-CAAS	-	-	358 963	-	-	391 919	-	-	9
Czech Republic	RICP	34	96	14 495	30	175	15 421	-12	82	6
Ecuador	INIAP/DENAREF	207	499	10 835	272	662	17 830	31	33	65
Ethiopia	IBC	71	74	46 322	151	324	67 554	113	338	46
Germany	IPK Gatersleben ^c	633	2 513	147 436	801	3 049	148 128	27	21	0
Hungary	ABI	238	742	37 969	294	915	45 321	24	23	19
India	NBPGR	73	177	154 533	723	1 495	366 333	890	745	137
Japan	NIAS	-	-	202 581	341	1 409	243 463	-	-	20
Kenya	KARI-NGBK	140	291	35 017	855	2 350	48 777	511	708	39
Nordic Countries	NGB ^d	88	188	24 241	129	319	28 007	47	70	16
Russian Federation	VIR	262	1 840	328 727	256	2 025	322 238	-2	10	-2
Netherlands	CGN	30	147	17 349	36	311	24 076	20	112	39
Turkey	AARI	317	1 941	32 122	545	2 692	54 523	72	39	70
United States of America	NPGS ^e	1 582	8 474	411 246	2 128	11 815	508 994	35	39	24
Average		289	1 309	140 205	502	2 098	178 294	74	60	27

TABLE 1.2 (continued)
Comparison between the collections maintained by selected national genebanks in 1995 and 2008^a

- ^a Genebanks selected according to the size of the collections and availability of data. Figures represent accession numbers. Data sources are as follows: Brazil genebank manager; Canada genebank manager; Country reports China, 1995 and 2008; Czech Republic, WIEWS 1996 and EURISCO 2008; Ethiopia, WIEWS 1996 and NISM (2007); Ecuador, genebank dataset, WIEWS 1996 and NISM (2008); Germany, WIEWS 1996, EURISCO 2008. Country reports 1995 and 2007; Hungary, genebank manager; India, genebank manager; Kenya WIEWS 1996 and NISM (2008); Nordic Countries, genebank dataset; the Russian Federation, genebank manager; the Netherlands, genebank manager; Turkey, genebank manager; United States of America, USDA Germplasm Resources Information Network (GRIN) dataset.
- ^b Taxonomic systems vary among genebanks, and may have changed over time. Hybrids and unidentified species are included.
- ^c 1995 data refer to germplasm holdings from IPK and its two external branches in Gross-luesewitz and Malchow, plus those from PGRC in Braunschweig, as this was shut down and the biggest part of its collections was transferred to IPK by 2004.
- ^d Excluding accessions held in field genebanks, but including special seed collections and genetic stocks. Additional data from Sweden's Country report, 1995.
- ^e The National Plant Germplasm System (NPGS) includes the following repository centres: C.M. Rick Tomato Genetic Resources Centre (GSIY), Davis, California; Clover Collection, Department of Agronomy, University of Kentucky (CLO), Lexington, Kentucky; Crop Germplasm Research Unit (COT), College Station, Texas; Dale Bumpers National Rice Research Centre (DB NRR), Stuttgart, Arkansas; Desert Legume Programme (DLEG), Tucson, Arizona; Fruit Laboratory, ARS Plant Germplasm Quarantine Office (FGOO), Beltsville, Maryland; G.A. Marx Pea Genetic Stock Centre, Western Regional Plant Introduction Station (GSP), Pullman, Washington; Maize Genetics Cooperation, Stock Centre (MGCS-C; GSZE), Urbana, Illinois; National Arctic Plant Genetic Resources Unit, Alaska Plant Materials Centre (PAM), Palmer, Alaska; National Arid Land Plant Genetic Resources Unit (PAR), Parlier, California; National Centre for Genetic Resources Preservation (NCGRP), Fort Collins, Colorado; National Clonal Germplasm Repository (COR), Corvallis, Oregon; National Clonal Germplasm Repository for Citrus and Dates (NCGRCD), Riverside, California; National Germplasm Repository (NAV), Davis, California; National Germplasm Repository (HLO), Hilo, Hawaii; National Germplasm Resources Laboratory (NGRI), Beltsville, Maryland; National Small Grains Germplasm Research Facility (NSGC), Aberdeen, Idaho; National Tree Seed Laboratory, Dry Branch, Georgia; North Central Regional Plant Introduction Station (NC7), Ames, Iowa; Northeast Regional Plant Introduction Station, Plant Genetic Resources Unit (NE9), Geneva, New York; Ornamental Plant Germplasm Centre (OPGC), Columbus, Ohio; Oxford Tobacco Research Station (TOB), Oxford, North Carolina; Pecan Breeding and Genetics, National Germplasm Repository (BRW), Somerville, Texas; Plant Genetic Resources Conservation Unit, Southern Regional Plant Introduction Station (S9), Griffin, Georgia; Plant Genetic Resources Unit, New York State Agricultural Experiment Station (GEN), Geneva, New York; Potato Germplasm Introduction Station (NR6), Sturgeon Bay, Wisconsin.

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in national agricultural research systems (NARS) have been analysed (see Tables 1.1 and 1.2, respectively). These collections account for a substantial proportion of total global *ex situ* resources. They are not meant to provide a comprehensive or regionally-balanced view of the global situation: they are simply the genebanks for which sufficiently high-quality data is available for both 1996 and today, allowing a reasonable estimate to be made of trends.

Overall, these *ex situ* collections have grown considerably in size. Between 1995 and 2008, the combined international collections maintained by the CGIAR and AVRDC increased by 18 percent and national collections by 27 percent. However, how much of this is completely new and distinct material and how much represents the acquisition of materials already present in other genebanks is unknown.

Although the prevailing opinion in 1995 was that the coverage of the diversity of the major staple crops⁷ within the CGIAR collections was fairly comprehensive,⁸ many collections have grown since then as gaps in the geographic coverage of the collections have been identified and filled and additional samples of CWR added. Adjustments to the numbers have also been made as a result of improved documentation and management. In addition, several of the CGIAR genebanks have taken on responsibility for collections of materials with special genetic characteristics and orphan collections provided by others.

Although the major growth in the CGIAR collections regards species that were already present before 1995, a considerable number of new species has also been added.

In the case of the national collections analysed, there has been a particularly large increase in the number of species and accessions of non-staple crops and CWR conserved – although these are still generally under-represented in collections.⁹ The increase in species coverage has been dramatic: an average of 60 percent since 1995. However, there are large differences among countries: some collections are still being put together and have shown large increases (e.g. Brazil, Ecuador and India), others are stable or in a consolidation phase (e.g. Germany and the Russian Federation). Even greater variability is to

be expected across the full range of genebanks in all regions.

The standard of conservation of the CGIAR collections has advanced over the past decade, largely as a result of additional financial support from the World Bank. Regeneration backlogs have decreased substantially and no significant genetic erosion is reported. However, in the case of national genebanks, a more complex picture emerges. A recent series of studies supported by the GCDT covering 20 major crops¹⁰ reports large regeneration backlogs in a considerable number of national collections. Other concerns include:

- neglected and underutilized species remain generally under-represented in collections;
- the situation may become even more serious if there is a greater shift in the focus of attention to crops that are included within the multilateral system (MLS) of access and benefit-sharing (ABS) under the ITPGRFA;
- the number of individuals (seeds, tissues, tubers, plants, etc.) conserved per accession is frequently below the optimum for maintaining heterogeneous populations;
- CWR are generally expensive to maintain and remain under-represented in *ex situ* collections, a situation that is unlikely to change unless considerably more resources are provided for the task.

While it appears that substantially more diversity is now conserved *ex situ* than a decade ago, a word of caution is warranted, as suggested above. Some, and perhaps most of the increases, result from the exchange of existing accessions among collections, leading to an overall increase in the amount of duplication.¹¹ This may at least in part, reflect a tendency for increased “repatriation” of collections. In addition, at least part of the change may be attributed to better management of the collections and more complete knowledge about the numbers involved. However, it should also be noted that numbers of accessions are not necessarily synonymous with diversity. Sometimes a smaller collection can be more diverse than a larger one.

Efforts to rationalize collections have been reported by several genebanks and networks. One example is an initiative of the European Cooperative Programme for Plant Genetic Resources (ECPGR) to rationalize European

plant genetic resources collections that are dispersed over approximately 500 holders and 45 countries. The identification of undesirable duplicates is an important component of the initiative, named AEGIS (A European Genebank Integrated System for PGRFA). The so-called ‘most appropriate accessions’ are being identified among duplicate accessions, based on criteria such as genetic uniqueness, economic importance and ease of access, conservation status and information status. The adoption of common data standards greatly facilitates the comparison of data and hence the identification of duplicates and unique accessions.¹²

1.2.3 Changes in the status of crop wild relatives

The *in situ* management of CWR is discussed in Chapter 2 and figures on the *ex situ* conservation of CWR are provided in Chapter 3. While *ex situ* conservation and on-farm management methods are most appropriate for the conservation of domesticated crop germplasm, CWR and species harvested from the wild, *in situ* conservation is generally the strategy of choice, backed up by *ex situ*, which can greatly facilitate their use. In spite of a growing appreciation of the importance of CWR, as evidenced by many country reports, the diversity within many species, and in some cases even their continued existence, remains under threat as a result of changes in land-use practices, climate change and the loss or degradation of natural habitats.

Many new priority sites for conserving CWR *in situ* have been identified around the world over the last decade, generally following some form of ecogeographic survey.¹³ In some cases, new protected areas have been proposed for conserving a particular genus or even species. The diversity of CWR in some existing protected areas has decreased over this period, while others still harbour significant diversity.

Across regions, the distribution of reserves that include CWR populations within their boundaries, remains uneven and several major regions, such as Sub-Saharan Africa, are still under-represented. However, *in situ* conservation of CWR has gained increasing attention in many countries, for example, in those countries that are participating in a project managed by Bioversity International entitled ‘*In situ*

conservation of CWR through enhanced information management and field application’ (see Box 2.1). Preparatory activities, such as research and site selection, were mentioned in several country reports, however, there is still a need for formal recognition and/or the adoption of appropriate management regimes. The CGRFA recently commissioned a report on the “Establishment of a global network for the *in situ* conservation of CWR: status and needs”.¹⁴ This report identifies global conservation priorities and suggests locations for CWR reserves of 12 selected crops (see Figure 1.1 and Table 2.1). These, together with additional priority locations to be identified in the future when further crop gene pools are studied, will form a global CWR *in situ* conservation network.

The threat of climate change to CWR has been highlighted by a recent study¹⁵ that focused on three important crop genera: *Arachis*, *Solanum* and *Vigna*. The study predicts that 16–22 percent of species in these genera will become extinct before 2055 and calls for immediate action in order to preserve CWR *ex situ* as well as *in situ*. Back-up samples conserved *ex situ* will become increasingly important, especially when environmental change is too rapid for evolutionary change and adaptation, or migration (even assisted migration), to be effective. Samples stored *ex situ* also have the advantage of being more readily accessible. However, significant gaps exist in the taxonomic and geographic coverage of CWR in *ex situ* collections. A recent study by CIAT and Bioversity International has highlighted these gaps for a number of gene pools.

Figure 1.2 summarizes the findings for the 12 crops in question.¹⁶ It highlights areas of the world where CWR species are expected to exist for these crops, based on herbarium specimens, but are missing from *ex situ* collections.

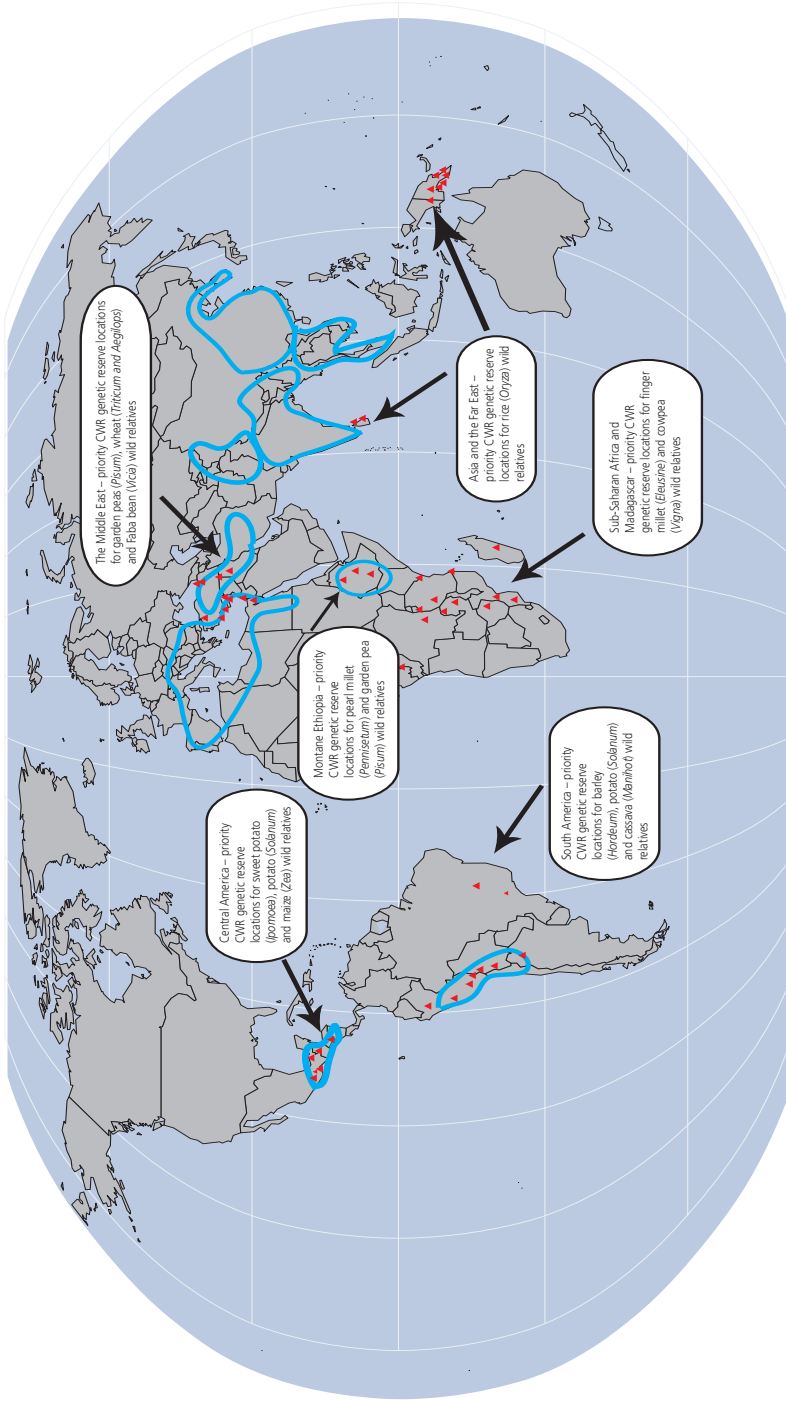
Advances in research techniques and their greater availability during the past decade have resulted in some significant new insights into the extent and distribution of genetic diversity, both in space and time, as outlined in the following sections.

1.2.3.1 Molecular technologies

Since the first SoW report was published, there has been a proliferation of new molecular techniques,

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FIGURE 1.1
Global priority genetic reserve locations for wild relatives of 12 food crops



Source: Maxted, N. & Kell, S.P. 2009. The eight Vavilov centres of origin/diversity of cultivated plants, indicated by the enclosed lines, are likely to contain further priority sites for other crop gene pools.

many of which, are simpler to use and less expensive than earlier techniques. This has led to the generation of a vast and rapidly increasing amount of data on genetic diversity, much of which is publicly available. The huge increase in Deoxyribonucleic acid (DNA) sequence capacity has, for example, enabled the rice genome to be sequenced, as well as comparisons to be made between the *japonica* and *indica* rice genomes and between rice and wheat genomes.¹⁷ The application of molecular techniques is increasing rapidly both in crop improvement (see Section 4.4) and in the conservation of plant genetic resources. However, the process has generally been slower than was foreseen a decade ago and few country reports, especially from the less developed countries, mention these techniques. Box 1.1 lists a few selected examples to illustrate some of the uses being made of these new techniques.

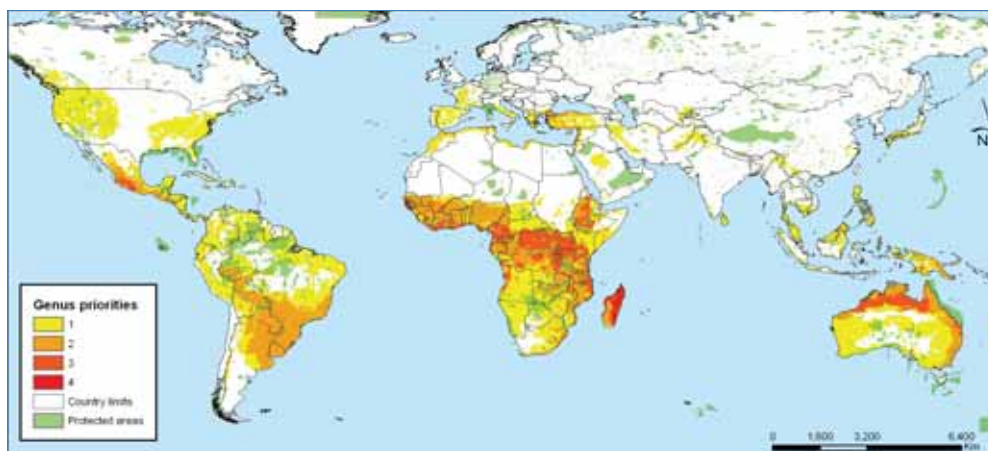
While many molecular techniques, from allele identification and marker assisted selection (MAS) to gene transformation, have been developed specifically

to enhance crop improvement, many are also proving invaluable in conservation. These include, for example: techniques for estimating the spatial and temporal distribution of genetic diversity and relationships between and within populations;¹⁸ gaining insights into crop domestication and evolution;¹⁹ monitoring gene flows between domesticated and wild populations;²⁰ and increasing the efficiency and effectiveness of genebank operations²¹ (e.g. deciding what material to include within a collection;²² identifying duplicates;²³ increasing the efficiency of regeneration;²⁴ and establishing core collections). As a result, much more is known about the history and structure of genetic diversity in key crop gene pools than was the case a decade ago.

1.2.3.2 Geographic Information Systems

New geographic methods are also proving to be of significant value in the management of plant genetic resources. Global Positioning Systems (GPS) are highly

FIGURE 1.2
Gaps in *ex situ* collections of selected crop gene pools^a



^a The coloured areas are those that have the greatest number of CWR gene pool gaps. The darker the shading (orange and red) the larger the number of CWR gene pool gaps present.

Source: Ramirez, J., Jarvis, A., Castaneda, N. & Guarino, L. 2009, Gap Analysis for crop wild relatives, International Centre for Tropical Agriculture (CIAT), available at <http://gisweb.ciat.cgiar.org/gapanalysis/>

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Box 1.1 Examples of the use of molecular tools in conservation and characterization, as reported in selected country reports

AFRICA

- **Benin** Molecular characterization of yam germplasm has been initiated.
- **Burkina Faso** Molecular characterization of millet, sorghum, taro, bean, *Abelmoschus esculentus*, *Macrotyloma geocarpum*, *Pennisetum glaucum*, *Solenostemon rotundifolius*, *Sorghum bicolor*, *Colocasia esculenta*, *Vigna unguiculata* and *Ximenia americana*.
- **Ethiopia** Molecular techniques used in characterization and genetic diversity studies for several field crop species.
- **Kenya** Application of Restriction Fragment Length Polymorphisms (RFLPs), DNA finger printing and Polymerase Chain Reaction (PCR) techniques.
- **Malawi** Molecular characterization of sorghum accessions has been initiated.
- **Namibia** Genetic diversity studies in sorghum and *Citrullus*.
- **Niger** Molecular characterization of millet has been initiated.
- **United Republic of Tanzania** Molecular markers have been used for 50 percent of coconut collection, 46 percent of cotton *Gossypium* spp. collection and 30 percent of cashew nut *Anacardium occidentale* collection.
- **Zimbabwe** Molecular characterization has been done on landraces collected in the Nyanga and Tsholotsho areas and for accessions held in the Genetic Resources and Biotechnology Institute.

AMERICAS

- **Bolivia (Plurinational State of)** Molecular characterization has been applied to a limited number of collections, primarily Andean root and tuber crops.
- **Brazil** Geographic Information System (GIS) studies on the distribution of wild relatives of groundnut.
- **Costa Rica** Molecular characterization has been carried out for clones of chayote, banana germplasm, cocoa and in the establishment of the world's first cryoseed bank for coffee.
- **Ecuador** Molecular characterization and evaluation has been completed for several crop species.
- **Jamaica** MAS breeding was adopted in the improvement of scotch bonnet peppers and a state-of-the-art molecular biology laboratory is in use for coconut variety improvement.
- **Mexico** Sequencing and transcript analysis has been carried out with accessions of *Agave tequilana* at the Campeche Campus of the Colegio de Postgraduados.
- **Peru** Molecular characterization has been carried out with accessions of yuca, yacon, mani, aji (Chile) and 75 varieties of native potato.
- **Venezuela (Bolivarian Republic of)** Molecular characterization of sugar cane, cacao, potato and cotton genebank accessions, among other taxa, has been carried out.

Box 1.1 (continued)**Examples of the use of molecular tools in conservation and characterization, as reported in selected country reports**

ASIA AND THE PACIFIC	
• Bangladesh	Molecular characterization of lentil and barley has been carried out through collaboration between the Bangladesh Agricultural Research Institute and ICARDA.
• China	On the basis of modern molecular marker technology, core collections and mini-core collections have been assembled for many crops and used to associate molecular markers with targeted genes.
• Fiji	With collaboration from regional and international institutions, molecular approaches have been used in germplasm characterization.
• India	Molecular markers for disease and insect-pest resistance have been deployed for wheat and triticale improvement.
• Indonesia	Analysis of molecular genetic diversity was used to confirm Papua as a secondary centre of diversity for sweet potato. Molecular markers have been in use for several years for characterization of accessions of several food crops (rice, soybean and sweet potato) and for crop improvement programmes.
• Japan	Molecular markers have been integrated into the characterization activity of the national genebank and MAS is routine for improvement of crops such as rice, wheat and soybeans
• Lao People's Democratic Republic	Molecular markers for quantitative trait loci (QTL) traits have been incorporated into rice breeding programmes.
• Thailand	Genetic diversity of <i>Curcuma</i> , mangrove tree species (<i>Rhizophora mucronata</i>) and <i>Tectona grandis</i> . The country has also used agroclimatic data together with molecular marker data in GIS studies to predict the location of diverse populations in order to identify areas for <i>in situ</i> conservation and for future collecting missions.
EUROPE	
• Belgium	The majority of the 1 600 apple accessions in the Centre for Fruit Culture have been described by use of molecular markers.
• Estonia	Molecular markers were used to map some wheat accessions.
• Finland	Molecular marker analysis has been used in estimations of genetic diversity in CWR.
• Greece	Molecular characterization and evaluation of cereal and vegetable crops have been initiated.
• Ireland	Analysis of the diversity of collected samples of wild oats (<i>Avena fatua</i>), wild rape (<i>Brassica rapa</i> subsp. <i>campestris</i>) and Irish populations of wild asparagus (<i>Asparagus officinalis</i> ssp. <i>prostratus</i>) was carried out.
• Italy	Molecular analysis has played a key role in evaluating the genetic variation expressed in clones of the same variety for some fruit species.
• Portugal	Molecular characterization of plum, apricot, cherry and almond accessions in Portuguese collections has been partially carried out.
• Netherlands	The Centre of Genetic Resources' collections of lettuce (2 700 acc.) and (partly) <i>Brassica</i> (300 acc.) and potato (300 acc.) and a selection of eight Dutch apple collections (800 acc.) have been screened in order to improve insight into the collection structure, whereas part of the potato collection (800 acc.) has been analysed by molecular means for the presence of certain potential resistance genes.

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Box 1.1 (continued)**Examples of the use of molecular tools in conservation and characterization, as reported in selected country reports****NEAR EAST**

• Cyprus	Molecular tools for the assessment of genetic material have been introduced and molecular assessment for tomato accessions is in process.
• Egypt	Molecular genetic data employed in PGR evaluation of accessions in national genebank.
• Iran (Islamic Republic of)	Molecular markers have been integrated into characterization programmes of national plant genebank and MAS and genetic transformation technologies are being used for breeding new cultivars.
• Jordan	Molecular biology laboratories are in place at the national research centre as well as at several universities and GIS and remote sensing are being used in three institutions.
• Kazakhstan	The assessment of genetic diversity and study of pedigree using molecular markers was made for wheat and barley.
• Lebanon	Molecular genetic characterization has been conducted for olive and almond varieties.
• Morocco	Molecular markers and GIS have been used in evaluation of germplasm of cereals to target regions for collection.
• Oman	Molecular markers used for characterizing alfalfa accessions (Random Amplification of Polymorphic DNA - RAPDs) and evaluating progeny in date palm breeding populations.
• Yemen	The national genetic resources centre has the capacity to undertake molecular characterization of germplasm.

effective at pinpointing the exact location where a plant was collected in the field. Such data is invaluable, especially when combined with other georeferenced data, e.g. on topography, climate or soils, and analysed using GIS software. This information can greatly facilitate decisions on what to collect and where, and can help elucidate relationships between crop production, genetic diversity and various agro-ecological parameters. Such techniques can also be used to draw up agro-ecological models that can predict, for example, the impact of climate change on different crops and in different locations. These methods have demonstrated through the Focused Identification of Germplasm Strategy (FIGS) that they have a significant impact on the effectiveness and efficiency in 'mining' germplasm for specific adaptive traits for crop improvement.²⁵

No country report indicates the extent to which geographic information tools are available and used within the country concerned and most of the reports

that do mention studies involving GIS do not describe the outcomes of the work. Rather, such studies appear to have been largely subsumed within crop distribution, ecogeographic and other similar studies. Their relevance to PGRFA management is not generally as well recognized as it perhaps should be.

1.2.3.3 Information and communication technologies

The ability to measure and monitor the state of diversity has benefited from huge advances in information and communication technologies during the past decade, in the form of faster and cheaper computer processors with larger memory and storage capacities, incorporated into a wide range of instruments and devices equipped with more advanced software and better user interfaces. The speed and effectiveness of communication and of gathering, managing and sharing data have improved dramatically since 1996

as a result of the incorporation of computers into data capture devices, improvements in data and database management software and the expansion of local computer networks and the Internet. These improvements have also resulted in rapid advances in the ability to undertake sophisticated processing and analysis of large complex datasets as, for example, in the emergence and application of the science of bioinformatics for molecular data.

1.3 Genetic vulnerability and erosion

As defined in the first SoW report, genetic vulnerability is the “condition that results when a widely planted crop is uniformly susceptible to a pest, pathogen or environmental hazard as a result of its genetic constitution, thereby creating a potential for widespread crop losses”. Genetic erosion, on the other hand, was defined as “the loss of individual genes and the loss of particular combinations of genes (i.e. of gene complexes) such as those maintained in locally adapted landraces. The term ‘genetic erosion’ is sometimes used in a narrow sense, i.e. the loss of genes or alleles, as well as more broadly, referring to the loss of varieties”. Thus, while genetic erosion does not necessarily entail the extinction of a species or subpopulation, it does signify a loss of variability and thus a loss of flexibility.²⁶ These definitions take into account both sides of the diversity coin, that is richness and evenness, the first relating to the total number of alleles present and the second to the relative frequency of different alleles. While there has been much discussion of these concepts since the first SoW report, these definitions have not changed.

1.3.1 Trends in genetic vulnerability and erosion

While few country reports give concrete examples, about 60 report that genetic vulnerability is significant and many mention the need for a greater deployment of genetic diversity in order to counter the potential threat to agricultural production. In Benin, for example, there was concern that the current agricultural system

is dominated by monocultures, in particular of yam and commercial crops. China reported cases in which rice and maize varieties have become more uniform and thus more genetically vulnerable. Ecuador reports that endemic plants are particularly vulnerable due to their restricted distribution. In the Galapagos Islands, at least 144 species of native vascular plants are considered rare; 69 of these are endemic to the Archipelago, including 38 species which are restricted to a single island. In Lebanon, the decrease in national production of almonds has been attributed to the genetic vulnerability of the few varieties grown. The largest global example of the impact of genetic vulnerability that has occurred since the first SoW report was published is the outbreak and continued spread of the Ug99 race of stem rust, to which the large majority of existing wheat varieties is susceptible. On the other hand, some countries reported on successful measures that had been put in place to counter genetic vulnerability. Cuba, for example, reported that the introduction of a wide range of varieties and the increased use of diversified production systems has reduced genetic vulnerability. Thailand promotes the use of greater diversity in breeding programmes and released varieties.

In the case of genetic erosion, while the country reports mention a substantial number of causes, in general these were the same as those identified in 1996. Major causes included: replacement of local varieties, land clearing, overexploitation, population pressures, environmental degradation, changing agricultural systems, overgrazing, inappropriate legislation and policy, as well as pests, diseases and weeds. From an analysis of country reports, it also appears that genetic erosion may be greatest in the case of cereals, followed by vegetables, fruits and nuts and food legumes (see Table 1.3). This may, however, be an artifact of the greater attention that is generally paid to field crops.

The following examples of genetic erosion cited in five of the country reports give a flavour of the diversity of situations and may serve to illustrate the overall situation. It should be noted, however, that the list is not intended to be complete and as the information contained in the country reports was not standardized, it is not possible to make cross-country or cross-crop

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comparisons, or use the information as a baseline for future monitoring. Madagascar reported that the rice variety Rojomena, appreciated for its taste, is now rare whereas the Botojingo and Java varieties of the northeastern coastal area have disappeared. The cassava variety Pelamainty de Taolagnaro and certain varieties of bean have disappeared from most producing areas and in the case of coffee, 100 clones out of 256, as well as five species (*Coffea campaniensis*, *C. arnoldiana*, *C. rostandii*, *C. tricalysioides* and *C. humbertii*) have disappeared from collections in the last 20 years. Wild yam species are also considered likely to disappear soon. Costa Rica reports that *Phaseolus* spp., including *P. vulgaris*, are threatened by serious genetic erosion; the same occurs to the indigenous crop *Sechium tacaco* and four related species: *S. pittieri*, *S. talamancense*, *S. venosum* and *S. vellosum*. In India, a large number of rice varieties in Orissa, some rice varieties with medicinal properties in Kerala and a range of millet species in Tamil Nadu, are no longer cultivated in their native habitats.²⁷ Yemen reports that varieties of finger millet (*Eleusine coracana*) and *Eragrostis tef* as well as oil rape (*Brassica napus*), which used to be among the most important traditional crop varieties grown in the country, are no longer grown or only grown in very specific areas and that the cultivation of wheat, including *Triticum dicoccum*, has drastically decreased. In Albania, all primitive wheat cultivars and many maize cultivars, have reportedly been lost.

Notwithstanding such reports on the loss of local varieties, landraces and CWR, the situation regarding the true extent of genetic erosion is clearly very complex. While some recent studies have confirmed that diversity in farmers' fields and in protected areas has indeed decreased, it is not possible to generalize and in some cases there is no evidence that it has occurred at all. For example, a large on-farm conservation project that studied genetic diversity in farmers' fields in nine developing countries found that, overall, crop genetic diversity continued to be maintained.²⁸ Other studies, however, have reported genetic shifts in farmers' varieties, for example in pearl millet in the Niger²⁹ and sorghum in Cameroon,³⁰ and in studies on the adoption by farmers of improved varieties of rice in India³¹ and Nepal,³² it was found that

TABLE 1.3
Crop groups and number of countries that provide examples of genetic erosion in a crop group

Crop group	Number of countries reporting genetic erosion
Cereals and grasses	30
Forestry species	7
Fruits and nuts	17
Food legumes	17
Medicinal and aromatic plants	7
Roots and tuber	10
Stimulants and spices	5
Vegetables	18
Miscellaneous	6

adoption can result in the substantial disappearance of farmers' varieties. On the other hand, it has also been noted that many farmers who plant modern varieties (especially large and medium landholders) also tend to maintain their landraces and that in such circumstances adoption of modern varieties might increase diversity in farmers' fields rather than reduce it.³³ In summary, it seems that general statements purporting to quantify the overall amount of genetic erosion that has occurred over the past decade are not warranted.

As with the situation of traditional farmer varieties and CWR, studies on diversity trends within released varieties also do not give a consistent picture over time. Some report no reduction nor even an increase in genetic diversity and allelic richness in released varieties, for example in the CIMMYT spring bread wheat varieties,³⁴ maize and pea varieties in France,³⁵ fruit varieties in Yemen³⁶ and barley in Austria and India³⁷. In cases such as these, the new varieties may be less vulnerable than was originally thought. Other studies report either an initial decrease followed by an increase of genetic diversity, e.g. in *indica* and *japonica* rice varieties in China,³⁸ or a continuous decline such as for wheat in China,³⁹ oats in Canada,⁴⁰ and maize in Central Europe.⁴¹ A meta analysis based on these

and other published reports on diversity trends has shown that, overall, there appears to have been no substantial reduction in genetic diversity as a result of crop breeding in the twentieth century and no overall gradual narrowing of the genetic base of the varieties released.⁴² However, the context of the meta analysis needs to be carefully considered to understand whether the results might be extrapolated, in particular to developing country conditions and a wide range of different crops.

Whereas convincing evidence may be lacking for genetic erosion in farmer varieties on the one hand and released varieties on the other hand, much more consensus exists on the occurrence of genetic erosion as a result of the total shift from traditional production systems depending on farmer varieties to modern production systems depending on released varieties.

1.3.2 Indicators of genetic erosion and vulnerability

Over the last decade, interest in direct and indirect indicators of genetic vulnerability and erosion has increased, at least in part, due to the paucity of concrete evidence for either process. The CGRFA called for the development of 'higher level indicators' for genetic erosion and genetic vulnerability in relation to monitoring the implementation of the GPA.

The 2010 Biodiversity Indicators Programme under the auspices of the CBD brings together a large number of international organizations to develop indicators relevant to the CBD, including those for the monitoring of trends in genetic diversity. However, to date, no really practical, informative and generally accepted indicators of genetic erosion are available and therefore their development should be a priority. Several qualities are important for such indicators to be effective:

- they should be sensitive to changes in the frequency of important alleles and give these more weight than less important alleles: the loss of an allele at a highly polymorphic microsatellite locus, for example, is likely to be of only minor importance compared with the loss of a disease resistance allele;
- they should provide a measure of the extent of the potential loss, e.g. by estimating the fraction

of genetic information at risk compared with the total diversity;

- they should enable an assessment to be made of the likelihood of loss over a specific time period, in the absence of human intervention.

Indicators for estimating genetic vulnerability should consider not only the extent of genetic uniformity *per se*, but also take into consideration possible genotype x environment interactions. A given genotype (population or variety) might succumb to a particular biotic or abiotic stress differently in diverse environments. Useful indicators of genetic vulnerability might include:

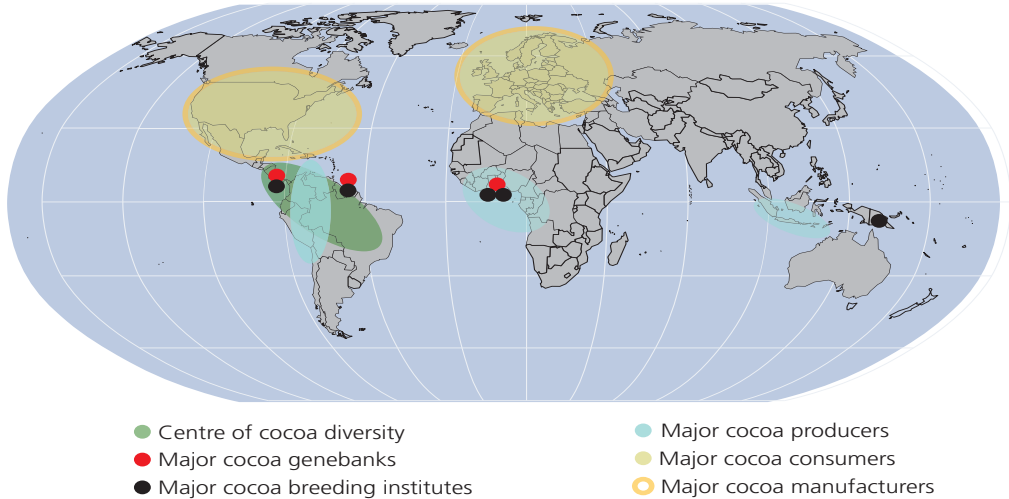
- the extent of genetic diversity of genes conferring resistance to, or tolerance of, actual and potential major pests and diseases or abiotic stresses;
- the extent of diversity in host-pathogen interactions and the occurrence of differential responses to different biotypes of pests and diseases. This indicator would provide information on the variety of coping mechanisms available and hence the likelihood of a shift in pathogen population resulting in widespread virulence;
- the occurrence of severe bottlenecks during domestication, migration or breeding: indicators of a genetic bottleneck could be derived from molecular data, historic information or pedigree analyses;
- the extent to which single varieties dominate over large areas could be a useful first indicator for estimating genetic vulnerability, based on the assumption that genetic vulnerability is higher when large areas are cropped with one variety;
- the genetic distances between the parental lines of a variety could be a proxy indicator, in certain circumstances, for the degree of heterogeneity and hence genetic vulnerability of the variety.

1.4 Interdependence

Interdependence regarding PGRFA can take many forms and may involve a wide range of stakeholders over space and/or time. Most crops, CWR and other useful wild plant species, are not confined within national boundaries. Their distribution reflects the

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FIGURE 1.3
Interdependency illustrated by the example of cocoa genetic resources



geography of ecosystems and global dispersal by humans or nature. As a result, people interested in using PGRFA often have to access material and the knowledge that goes with it, from beyond the borders of the country where they happen to be working. Whereas all countries are both providers and recipients of PGRFA, not all countries have been equally endowed with them, or with the capacity to use them. This has led to a mutual but unequal interdependence and can be seen as either a potential threat to national sovereignty or as an opportunity for constructive collaboration⁴³ (see Figure 1.3 and Table 1.4).

The concept of interdependence applies not only to the international level, but also in the respective roles of farmers, breeders and genetic resource managers. Farmers are the managers of the genetic resources they grow, genebank managers have been entrusted with safeguarding collections of this diversity, and breeders, to a large extent, depend on both for the raw materials they need to produce new varieties for farmers' use. All are interdependent.

Considerable interdependence also occurs at the local level among farmers who frequently trade or barter seed and other planting materials with each other. Local systems of germplasm exchange are often

deeply ingrained in rural societies and may be an important element in relationships among families and local communities. Such systems are generally 'robust' and able to cope well under stress⁴⁴ as their high level of interdependence contributes to their resilience.

At the regional and global levels, a major consequence of interdependence among nations is the need for international exchange of germplasm. Studies have suggested that in many cases, such exchange has become more complex and difficult over recent years. There is a danger that reduced international flows of PGRFA may pose a threat not only to its use, but also to its conservation and ultimately to food security. These were among the key factors that led to the adoption of the ITPGRFA.

With the growing impact of climate change, there will undoubtedly be an increase in demand for varieties that are adapted to the new environmental conditions and pest and disease spectra. The ability to access a wide range of genetic diversity is central to meeting this demand, implying that in future there will be even greater interdependence between countries and regions than today.

Uncertainty about legal issues is widely considered to be a significant factor hindering international and

TABLE 1.4
Indicators of global interdependency of selected crops

Crop	Region(s) of significant genetic diversity ¹	Major <i>ex situ</i> collections ²	Major producing countries ³	Major breeding and research activities	Countries for which major consumption has been recorded ⁴	Products/importing countries ⁵
Cacao (<i>Theobroma cacao</i>)	Amazon Basin, Central America	Brazil, Costa Rica, Trinidad and Tobago, Venezuela (Bolivarian Republic of)	Brazil, Côte d'Ivoire, Ghana, Indonesia, Nigeria	Brazil, Costa Rica, Côte d'Ivoire, Ghana, Papua New Guinea, Trinidad and Tobago	France, Germany, Japan, Russian Federation, United States of America	Cocoa beans Belgium, Germany, Malaysia, Netherlands, United States of America
Eggplant (<i>Solanum melongena</i>)	Indo-Myanmar region	AVRDC, India	China, India, Egypt, Turkey, Indonesia	AVRDC, India	African countries, China, India, Indonesia, Malaysia, Nepal, Pakistan, Sri Lanka	France, Germany, Iraq, United Kingdom, United States of America
Groundnut (<i>Arachis hypogaea</i>)	South America	CGIAR, USDA, India, China, Senegal/Brazil	China, India, Indonesia, Nigeria, United States of America	Australia, Brazil, China, India, United States of America	Confectionary China, India, Indonesia, Nigeria, United States of America	Groundnut shelled Canada, Mexico, Netherlands, Russian Federation, United Kingdom
Maize (<i>Zea mays</i>)	Asia, Central America and Mexico, North America, South America	CGIAR, India, Mexico, Russian Federation, United States of America	Argentina, Brazil, China, Mexico, United States of America	CGIAR, Africa, Brazil, China, Europe, India, United States of America	China, India, Indonesia, Mexico, South Africa	China, Japan, Mexico, Republic of Korea, Spain
Noug (<i>Guizotia abyssinica</i>)	Horn of Africa	Ethiopia, India	Ethiopia, India, Nepal	Ethiopia, India	Ethiopia, India, Nepal, United Kingdom, United States of America	United Kingdom, United States of America
Oil Palm (<i>Elais spp.</i>)	Amazon Basin, West Africa	Brazil, Ghana, Malaysia	Colombia, Indonesia, Malaysia, Nigeria, Thailand	Malaysia, MPOB	China, India, Indonesia, Nigeria, Pakistan	China, Germany, India, Netherlands, Pakistan

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TABLE 1.4 (continued)
Indicators of global interdependency of selected crops

Crop	Region(s) of significant genetic diversity ¹	Major <i>ex situ</i> collections ²	Major producing countries ³	Major breeding and research activities	Countries for which major consumption has been recorded ⁴	Products/ importing countries
Potato (<i>Solanum tuberosum</i>)	South America	CGIAR, Colombia, Czech Republic, Japan, Netherlands	China, India, Russian Federation, Ukraine, United States of America	CGIAR, Argentina, Australia, Canada, Chile, China, Colombia, Ecuador, France, Germany, India, Netherlands, Poland, Republic of Korea, South Africa, United Kingdom, United States of America	China, India, Russian Federation, United Kingdom, United States of America	Belgium, Germany, Italy, Netherlands, Spain
Quinoa (<i>Chenopodium quinoa</i>)	Andean Cordillera	CGIAR, United States of America	Bolivia (Plurinational State of), Ecuador, Peru	Bolivia (Plurinational State of), Peru	Bolivia (Plurinational State of), Canada, Europe, Peru, United States of America	N/A
Rice (<i>Oryza</i> spp.)	South, East, and Southeast Asia, Africa	CGIAR, Benin, China, India, Philippines, Thailand, United States of America	China, Bangladesh, India, Indonesia, Viet Nam	CGIAR, China, India, Philippines United States of America	Bangladesh, China, India, Indonesia, Viet Nam	Rice, milled Iran (Islamic Republic of), Iraq, Nigeria, Philippines, Saudi Arabia
Safflower (<i>Carthamus tinctorius</i>)	Egypt, Ethiopia, Far East, India, Middle East, Pakistan, Southern Europe, Sudan	China, Ethiopia India, Mexico, United States of America	Australia, China, India, Kazakhstan, United States of America	Australia, Canada, China, India, Mexico, Spain, United States of America	Seed Belgium, China, Netherlands, Philippines, United Kingdom Oil Germany, Japan, Netherlands, United States of America, Yemen	Safflower seed Belgium, China, Netherlands, Philippines, United Kingdom
Sesame (<i>Sesamum indicum</i>)	Central Asia, China, Horn of Africa, India, Near East	China, India, Israel, Mexico, Venezuela (Bolivarian Republic of)	China, India, Myanmar, Sudan, Uganda	India, Turkey, United States of America	Seed China, Egypt, India, Japan, Uganda Oil China, India, Myanmar, Republic of Korea, Sudan	Sesame seed China, Japan, Republic of Korea, Syrian Arab Republic, Turkey

TABLE 1.4 (continued)
Indicators of global interdependency of selected crops

Crop	Region(s) of significant genetic diversity ¹	Major <i>ex situ</i> collections ²	Major producing countries ³	Major breeding and research activities	Countries for which major consumption has been recorded ⁴	Products/ importing countries
Soybean (<i>Glycine max</i>)	East Asia	AVRDC (Regional), China, Russian Federation, Ukraine, United States of America	Argentina, Brazil, China, India, United States of America		Seed Brazil, China, Indonesia, Japan, Republic of Korea	China, Germany Japan, Mexico, Netherlands
Sunflower (<i>Helianthus annuus</i>)	North America	France, Romania, Russian Federation, Serbia, United States of America	Argentina, China, France, Hungary, India, Russian Federation, Turkey, Ukraine, United States of America	Russian Federation, United States of America	Oil China, India, Russian Federation, Spain, Ukraine	Sunflower seed France, Italy, Netherlands, Spain, Turkey
Wheat (<i>Triticum aestivum</i>)	Central Asia, East Africa, East Asia, Europe, South and East Mediterranean, South Asia, West Asia	CGIAR, Australia, Italy, Russian Federation, United States of America	China, France, India, Russian Federation, United States of America	CGIAR, Australia, Brazil, Canada, China, France, India, United Kingdom, United States of America	China, India, Pakistan, Russian Federation, United States of America	Brazil, Egypt, India, Italy, Japan

¹ Source: first SoW report.

² Source: first SoW report and Country reports for the SoWPGR-2.

³ Source: FAOSTAT, 2007.

⁴ Source: FAOSTAT, 2003; for safflower import data for 2006; for quinoa and eggplant anecdotal evidence.

⁵ Source: FAOSTAT, 2006.

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even national, germplasm exchange. While the CBD has been in force for many years, a lack of clear and efficient procedures for accessing PGRFA still hampers the collection and/or cross-boundary movement of genetic resources in many countries (see Chapter 7). Likewise, a number of national governments have yet to join the ITPGRFA even though it is essential for ensuring the facilitated flow of PGRFA, that as many countries as possible ratify the ITPGRFA and put in place the necessary procedures to ensure its effective implementation.

Just as the world's plant genetic resources are unevenly distributed, so is the capacity to use them. Many countries lack adequate institutions, facilities or breeders to effectively undertake modern, or even conventional, crop improvement work, especially on minor crops. Thus, there is still a heavy reliance by many countries on outside support for plant breeding, whether directly for improved varieties or indirectly through training and research collaboration. There have been a number of positive developments in this area recently, including the GIPB⁴⁵ and the development of regional centres of excellence for biotechnology, such as Biosciences Eastern and Central Africa (BECA).⁴⁶ Such centres enable scientists from developing countries to apply their knowledge and skills to specific national crop improvement challenges. These and other similar initiatives are an important aspect of interdependence and are an integral part of systems for benefit-sharing. More detail on the status of crop improvement and other uses of PGRFA is provided in Chapter 4.

1.5 Changes since the first State of the World report was published

Key changes that have occurred in relation to the state of diversity since the publication of the first SoW report include:

- *ex situ* collections have grown substantially, both through new collecting and through exchange among genebanks. The latter has contributed to the continuing problem of unplanned duplication;
- scientific understanding of the on-farm management of genetic diversity has increased, and this

approach to the conservation and use of PGRFA has become increasingly mainstreamed within national programmes;

- interest in and awareness of the importance of conserving CWR, both *ex situ* and *in situ* and their use in crop improvement have increased substantially;
- there is growing interest in hitherto 'neglected' and underutilized species such as traditional vegetables and fruits;
- with modern molecular genetic techniques, it has been possible to generate a large amount of data on the extent and nature of genetic erosion and vulnerability in specific crops in particular areas. The picture that is emerging is complex and it is not possible to draw clear conclusions about the magnitude and extent of these effects;
- the extent of interdependence among countries with respect to their need to have access to materials held by others is arguably more important than ever. This is especially true in the face of the need to develop varieties that are adapted to the new environmental conditions and pest and disease spectra that will result from climate change. The ITPGRFA has provided a sound basis for improving and facilitating such access.

1.6 Gaps and needs

Based on the information provided in this chapter, the following points describe some of the major gaps and needs that have been identified with regards to genetic diversity:

- there is still an ongoing need to improve the coverage of diversity in *ex situ* collections, including CWR and farmers' varieties, coupled with better characterization, evaluation and documentation of the collections;
- a better understanding of, and support for, farmers' management of diversity is still needed, in spite of significant advances in this area. Opportunities exist to improve the livelihoods of rural communities through an improved management of diversity;
- there is still a need for greater rationalization of the global system of *ex situ* collections, as called

for in the GPA and the ITPGRFA and as reflected in initiatives such as those of the GCDT and AEGIS;

- greater attention is needed regarding the conservation and use of PGRFA of neglected and underutilized crops and non-food crops. Many such species can make a valuable contribution to improving diets and incomes;
- there is a need to promote standard definitions and means of assessing genetic vulnerability and genetic erosion, as well as to agree on more and better indicators, in order to be able to establish national, regional and global baselines for monitoring diversity and changes in it and for establishing effective early warning systems;
- many countries still lack national strategies and/or action plans for the management of diversity, or if they have them, they do not fully implement them. Areas that require particular attention include setting priorities, enhancing national and international cooperation, the further development of information systems and identifying gaps in the conservation of PGRFA, including CWR;
- in spite of the growing awareness of the importance of CWR, there is still a need in many countries for appropriate policies, legislation and procedures for collecting CWR, for establishing protected areas for CWR and for better national coordination of these efforts.

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- ⁷ In the context of this chapter staple crops include the large cereals (wheat, maize, rice, sorghum and barley), beans, cowpeas, groundnuts, potatoes, bananas and cassava.
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